Genome Wide Association Mapping for Stem Water Soluble Carbohydrates in Bread Wheat (*Triticum aestivum* L.) Under Terminal Water Stress

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CERTIFICATE–I

This is to certify that thesis entitled, **"Genome wide association mapping for stem water soluble carbohydrates in bread wheat (*Triticum aestivum* L.) under terminal water stress"** submitted for the degree of Doctor of Philosophy in the subject of **Genetics and Plant Breeding** to the **CCS Haryana Agricultural University**, **Hisar** is a bonafide research work carried out by **Mr. Arpit Gaur**, **Admn. No. 2016A27D** under my supervision and guidance and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation have been duly acknowledged.

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CERTIFICATE –II

This is to certify that thesis entitled, **"Genome wide association mapping for stem water soluble carbohydrates in bread wheat (*Triticum aestivum* L.) under terminal water stress"** submitted by **Mr. Arpit Gaur**, **Admn. No. 2016A27D** to the **CCS Haryana Agricultural University**, **Hisar** in partial fulfilment of the requirements for the degree of **Doctor of Philosophy** in the subject of **Genetics and Plant Breeding** has been approved by the student's advisory committee after an oral examination on the same in collaboration with an external examiner.

MAJOR ADVISOR **EXTERNAL EXAMINER**

HEAD OF THE DEPARTMENT

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CHAPTER-I

INTRODUCTION

Wheat (*Triticum aestivum* L.) has proved to be a sustainable source of global and national food and nutritional security and is cultivated as a primary staple food on an approximately 220 million hectares of land across 89 countries and consumed by nearly 2.5 billion people (FAOSTAT, 2018). However, it was cultivated on 30.54 million hectares land during *Rabi* 2017-18 in India which is almost 14% of total cultivated area across the world (Ramadas *et al.*, 2019). *Rabi* 2017-18 recorded a production of 99.70 million tonnes of bread wheat in India contributing nearly 14% of the total global wheat production of 759.60 million tonnes (Ramadas *et al.*, 2019). With increase in population pressure, depleting natural resources and climate change, a big question that raises is "Could present wheat production meets the needs of future?" at both global as well as national levels. Policy makers have predicted that global population might touch the figure of nine billion by 2050 (Santra *et al.*, 2017). To meet the needs of this big human population, sixty percent increase in wheat production will be needed (Daryanto *et al.*, 2016). In fact, the demand of wheat for India is predicted to reach 140 million tonnes by 2050 (Ramadas *et al.*, 2019). But, with the present scenario of climate change, constraining natural resources, change in urbanization patterns and exponentially growing human population, aimed wheat production seems to be quite daunting. In recent years, advancements in human life style towards a better future have triggered climate change in negative direction. Climate change has seriously affected the world's hydrological cycle which in turn has affected water availability in many parts of the world, including India (Gunathilaka *et al.*, 2018).

An event of prolonged water scarcity in atmosphere, surface and/or in ground is called as drought. Drought is a slowly growing costly natural disaster which severely affects human societies, agriculture and ecosystem. Frequent droughts have been observed by geologists in past few years in those areas which were never exposed to it. Crop production extensively depends on environmental factors among which water availability and/or temperature are critical (Awika, 2011). Water availability becomes a major limiting factor for crop production under marginal environments like semi-arid and arid regions where drought conditions occur very frequently and rainfed agriculture system is practiced (Daryanto *et al.*, 2017). Since crop yield shows low heritability and high fluctuations under water stressed conditions, drought could drastically affect food security and livelihood in coming years (Cattivelli *et al.*, 2008). Wheat plays key role in future food security. Fifty percent of wheat produced by developing countries is cultivated under rainfed conditions where annual rainfall is less than 600mm and are characterized by frequent droughts and inadequate irrigation water due to declined water table during cropping season(s) (Gupta *et al.*, 2017). Eighty percent of wheat in India is cultivated under irrigated conditions. Only 66% of this area receives partial irrigation which in turn leads to water-stress in crop and eventually decline overall production (Kang *et al.*, 2009). Inadequacy of water at any point of plant life cycle may drastically affect growth and development. Water stress affects overall growth and development of plant by disturbing water-plant relationship. It severely affects final grain yield by reducing plant population by means of reduced seed vigour and germination percentage. In later stages, it affects cell integrity, osmolyte balance, photosynthetic rate and assimilation rate. This reduces biomass of plant, spikelet fertility, grain growth rate and kernel weight and density which ultimately hampers total grain yield of plant. Though some plant species, like succulent plant species, have mechanisms to withstand high water stress, most of the important food crops such as maize, rice, wheat, pearl millet, *etc.* are, to varying level, susceptible to water stress. Therefore, when these crops receive inadequate water either by no or low rainfall and/or irrigation, their productivity limits substantially. Wheat is the most water consuming *Rabi* crop with 7551 to 8275 $m^3 ha^{-1}$ water consumption (Kumari *et al.*, 2017). In wheat, depending upon the growth stage and duration of water deficit, water stress may reduce yield up to 90% (Olivares-Villegas *et al.*, 2007). Therefore, to achieve target of food security with limited water resources, it is necessary to target drought resistance in wheat crop for its stable performance.

Plant responses to water stress are highly variable and complex ranging from cellular to organ level. This complexity often leads to wrong evaluation of degree of water stress in plant(s). Therefore, it is suggested to take yield as an important index of crop susceptibility or resistance to water stress (Pandey and Shukla, 2015). However, yield under stressed conditions shows low heritability and wide range of fluctuation as a result of genotypic x environment (GXE) interactions (Ceccarelli, 1989). Yield is a complex trait associated with many morphological (leaf length, leaf angle, cuticle, *etc.*), phenological (time of heading, flowering and maturity), agronomical (plant height, number of tillers, spike length, *etc.*), physiological (chlorophyll content, chlorophyll florescence, canopy temperature, *etc.*) and biochemical (proline, reactive oxygen species, soluble sugars, heat shock proteins, *etc.*) traits (Mwadzingeni *et al.*, 2017). These traits have high heritability, high genetic advance and varying degree of correlation with yield under stressed and non-stressed environments. Therefore, these trait(s) are useful in indirect selection for adaptiveness to water stressed conditions and achieving maximum yield (Crain *et al.*, 2017).

In wheat, grain yield and associated trait(s) extensively depend on photosynthetic assimilates transferred to grain(s) during grain filling stage (Li *et al.*, 2015). These assimilates are transferred through two major carbon sources *viz.* current photosynthetic assimilates and reserved water-soluble carbohydrates (WSCs) (Ehdaie *et al.*, 2008). WSCs work as food reservoirs and have positive correlation with grain yield and thus play an important role in grain yield under normal as well as water-stressed environments (Wardlaw and Willenbrink, 2000). WSCs are non-structural sugars (mainly sucrose, fructose, glucose and fructans) and accumulate temporarily as a major carbon source in stem and leaf sheaths during stem elongation and early grain filling period (*i.e.* up to 15 days after anthesis) (Ruuska *et al.*, 2006). In water stress environment, rate of photosynthesis substantially reduces down which further limits the transfer of photosynthetic assimilates from leaves to grains. In stress conditions, remobilization of WSCs accumulated in stem (mainly of peduncle and penultimate) plays a very crucial role in buffering grain yield in wheat (Hou *et al.*, 2018). Previous studies support that under optimal and water stressed conditions, WSCs may contribute up to 20% and 50%, respectively, in grain yield (Dreccer *et al.*, 2009). Moreover, not only amount of total WSCs (especially fructans) but expression of related gene(s) has been found significantly higher in drought tolerant genotypes as compared to susceptible ones under water stress (Yáñez *et al.*, 2017). Therefore, ability of storing large amount of WSCs and efficient remobilization to grains must be considered important for selection in drought tolerant wheat breeding programs.

Conventional plant breeding has been very successful in crop improvement since time immemorial but, it takes too much time and labour to bring desirable improvement(s). Looking towards the present and future needs of world, slow progress rate of conventional plant breeding is not desirable. In recent years, new genomic tools and methodologies have empowered conventional plant breeders and accelerated the rate of crop improvement. These tools eliminate the limitation of GXE interaction of conventional plant breeding thus allow screening of huge number of genotypes in short span of time. Genome sequencing technologies have allowed scientists to deep dive inside wheat genome and improve their understanding for complex traits (Abdurakhmonov, 2016). Such a technique, namely quantitative trait loci (QTL) mapping allows identification of genomic regions associated with targeted trait(s) and enables plant breeders to improve their abilities. A recently developed technique, namely genome wide association studies (GWAS) which was initially developed for humans, is receiving more success in plants (Brachi *et al.*, 2011). GWAS break the restrictions of limited allelic and phenotypic variations which are major constrains of bi-parental QTL mapping (Abdurakhmonov and Abdukarimov, 2008). GWAS provide higher resolution than bi-parental QTL mapping. Additionally, GWAS coupled with high density single nucleotide polymorphism (SNP) genotyping allows identification of small haplotype blocks significantly associated with phenotypic variations (Brachi *et al.*, 2011). However, many QTLs associated with water-soluble carbohydrates (WSCs) and yield related traits have been identified using conventional bi-parental mapping population, little progress has been achieved through high density SNP based GWAS for WSCs and its components under water stressed environment in wheat (Khalid *et al.*, 2019 and Yuan *et al.*, 2019).

Present study entitled ‘Genome wide association mapping for stem water-soluble carbohydrates in bread wheat (*Triticum aestivum* L.) under terminal water stress’ has been designed to aim the following objectives:

1. To evaluate the germplasm for total stem water-soluble sugars (WSCs)
2. To identify the genomic regions associated with stem WSCs under terminal water stress
3. *In silico* genome wide identification of genes involved in fructans metabolism

CHAPTER-II

REVIEW OF LITERATURE

Wheat is one of the most widely cultivated crops with nearly 220 million hectares cultivation area and about 670 million tons of annual production. In prospective of global food security, it is the second most important food crop of developing world after rice because an estimated 80 million farmers rely on wheat for their livelihood and it contributes to 41% of total calories and 50% of total proteins consumed from cereals, globally (Shiferaw *et al.*, 2013). India is the second highest wheat producer with 99.7 million tons of production (13.6% of global wheat production), cultivated on over 30 million hectares (14% of global wheat area), with an average productivity of 3371 Kg/ha (Ramadas *et al.*, 2019). It accounts to 35% of total food grain production and 21% of total cultivable area thus by providing 20% of daily protein intake and 20% calorie intake of daily consumption, it plays an important role in nutritional security of country (Vaid, 2020). Therefore, wheat is a crop of national importance from both production and consumption perspectives and plays an important role in the socio-economic growth of country (Tripathi and Mishra, 2016). In India, wheat is cultivated in *Rabi* season which receives very less rainfall. Therefore, success or failure of aimed wheat production depends on availability of irrigation which has direct link with rainfall received from South-West monsoon (Kumar *et al.*, 2004). Summer droughts are recurring phenomenon in India due to its geographical distribution. In recent years, frequency of agricultural droughts has substantially increased due to shift in rainfall patterns, especially in Eastern and Western plains which are major wheat producing areas (Verma *et al.*, 2019). Drought is a serious limiting factor for sustainable wheat production and a huge barrier in achieving national and global food security in near future. Therefore, improving tolerance to drought in wheat through adaptive strategies may ensure sustainable food security with available natural resources (Khan *et al.*, 2019). An underexploited trait, water-soluble carbohydrates (WSCs), may plays an imperative role in achieving sustainable wheat production under drought stress as recent studies have suggested their significant role in maintaining grain yield under various water stress conditions. The brief resume of relevant research works is being reviewed here under the following headings:

2.1. Effect of water stress on agro-phenological traits
2.2. Water-soluble carbohydrates
2.3. Genetic variability and correlation studies
2.4. Multivariate analysis of genetic divergence
2.5. Genome wide association mapping in wheat
2.6. *In-silico* gene identification

2.1. Effect of water stress on agro-phenological traits

Drought is a multifaceted climatic hazard which negatively affects grain yield. Depending upon intensity and duration of drought, crop growth stage and genetic architecture of plant, yield may reduce up to 92% in wheat crop (Senapati *et al.*, 2019). In a meta-analysis on effect of drought stress on wheat yield, Zhang *et al.* (2018) revealed that yield reduction may vary between 9 and 52% depending upon the intensity of soil moisture and temperature. Reduction in grain yield is a result of correlated responses of morphological, physiological and biochemical changes occurred under water stress conditions.

Number of tillers per plant is a major yield contributing trait in wheat. Higher number of tillers per plant assures higher canopy, a greater number of spikes and higher above ground biomass which contributes in increase in grain yield (Acevedo *et al.*, 2009). In a screening study of 88 bread wheat genotypes from international drought and heat nursery of CIMMYT, Mwadzingeni *et al.* (2016b) recorded 19.1% reduction in number of tillers per plant which resulted in 40.6% yield loss per plot. Chaturvedi *et al.* (1981) demonstrated substantially lower tillering in wheat under limited water conditions as compared to controlled one; however, it was also found that tiller mortality in control was higher than that of unirrigated field due to lesser competition.

Optimal plant height is a desirable trait for higher grain production in wheat. In water limiting conditions, plant height reduces by means of reduction in internodes, peduncle length and spike length. However, overall plant height has not shown any direct effect on grain yield under water stress, but significant role of peduncle and spike length in assimilation of photosynthates and their remobilization had been advocated in previous studies (Dodig *et al.*, 2017). In a study on 80 wheat genotypes up to 1.23%, 2.17%, and 2.58% reduction in plant height, peduncle length and spike length, respectively was observed by Amiri *et al.* (2013) under terminal drought stress. Similar results for reduction in plant height, peduncle length and spike length were also reported by Boussakouran *et al.* (2019) and Bogale *et al.* (2011). Reduced cell elongation and early senescence are attributed to reduction in these traits (Fahad *et al.*, 2017).

Number of spikelets per spike (SPS) affects grain yield by means of number of grains per spike. Eskandari and Kazemi (2010) studied effect of post anthesis drought on four bread wheat genotypes and recorded a reduction of 1-2 SPS under water limiting conditions. In another study on modern cultivars and landraces, Denčić *et al.* (2000) reported a mean difference of one SPS between irrigated and drought stress in modern cultivars whereas, there was no reduction for this trait in landraces.

Thousand kernel weight (TKW) and total number of grains per plant (TNG) are highly sensitive traits to water stress. Both traits directly affect grain yield. Reduction in TKW is mainly affected by grain filling duration rather than grain filling rate. Drought stress at the time of anthesis affects grain size which produces shriveled grain (Ji *et al.*, 2010). Besides, TKW may be an indicator for pre-anthesis anther sink strength efficiency of accumulation of assimilates and their allocation in developing grains (Li *et al.*, 2019). Del Pozo *et al.* (2016) studied performance of various traits associated with grain yield under drought stress and reported up to 21% reduction in TKW. Johnson and Moss (1976) reported 14% reduction in TKW in water stressed wheat plants. Drought stress during reproductive stage largely influences TNG by means of anther indehiscence, under-developed pollen tube and pollen abortion (Qaseem *et al.*, 2019). In a meta-analysis of effect of drought stress in 336 wheat genotypes, Wang *et al.* (2017) demonstrated up to 16% reduction in TNG under different water levels. Khakwani *et al.* (2012) demonstrated a significant reduction of 26 to 59% in grain numbers per main spike in six different bread wheat genotypes exposed to water stress at booting and anthesis stages.

Harvest index (HI) is a critical trait to be influenced under limited water conditions (Kobata *et al.*, 2018). HI describes conversion of biomass into yield. Water deficit conditions hamper the assimilation and allocation of photosynthates which reduces dry matter of plant (Shareef *et al.*, 2018). High HI under water deficit environment indicates potential of plant to transform assimilates into grain yield (Tardieu, 2013). Additionally, high HI is an indication of better water use efficiency of plant which is an important key to complete life cycle in limited water conditions (Rattey *et al.*, 2011). Various studies have advocated significant reduction in HI of wheat plants under drought stress. Qaseem *et al.* (2019) reported 41% reduction in HI of different bread wheat genotypes due to pre- and post- anthesis drought stresses. In a two years field experiment on different genotypes of bread and durum wheat, Nakhforoosh *et al.* (2015) reported up to 14% reduction in HI.

Growth period significantly reduces as an adaptive mechanism against drought stress. Shorter growth period significantly affects the accumulation and allocation of photosynthates which in turn affects grain yield by reducing kernel numbers and weight (Tarawneh *et al.*, 2019 and Oladi *et al.*, 2014). Shorter growth period reduces harvest index and overall growth of plant also. Therefore, long grain filling duration (GFD) is a desirable trait for drought adaptive breeding (Nakhforoosh *et al.*, 2015). While screening for drought tolerant wheat genotypes, Mwadzingeni *et al.* (2016b) demonstrated a reduction of 0 to 4 days in days to heading (DTH) and 2-10 days in days to maturity (DTM) under drought conditions. GFD was longer in high yielding genotypes than low yielding ones and also showed positive correlation with kernel weight.

2.2. Water-soluble carbohydrates

Accumulation of water-soluble carbohydrates (WSCs) in various plant parts is a distinct feature for grain producing grasses (wheat [*Triticum aestivum*], barley [*Hordeum vulgare*] and oats [*Avena sativa*]) which evolved with adaptation to temperate environment. In these crops, developing grain completes its demand for carbon from current photosynthetic assimilates and stored carbohydrate sources. In wheat, WSCs accumulate as reservoirs mainly in stem and leaf sheath from stem elongation to early grain filling phase (Blum, 2011). Carbohydrate reserves function as a source of monosaccharides which are used in plant metabolism for growth and developmental activities (Slewinski, 2011). In wheat, glucose, fructose, sucrose and fructans are components of stem WSCs, among which fructans share a major part ranging between 10-80% (Zhang *et al*., 2015).

Fructans are major and the most important component of stem WSCs as it is the third most abundant (present in nearly 15% angiosperm species) metabolizable storage carbohydrate after starch and sucrose (Avigad and Dey, 1997). Fructans are derived from sucrose in cell vacuoles (Valluru, 2015 and Xue *et al*., 2006). Structurally, these water-soluble fructosyl-oligosaccharides might be found in linked or branched forms. In grass cereals, 'Graminan' type of fructans is pre-dominantly present, particularly between shoot elongation to early stages of grain development, which are branched in form and can be classified into two basic structures *viz*. inulin (pre-dominant with β-2,1- linkage) and levan (pre-dominant with β-2,6- linkage) (Chalmers *et al.*, 2003). In vacuoles, sucrose is transformed to fructans by fructosyl transferases activities. Two key enzymes *viz*. sucrose:sucrose-1-fructosyltransferase (*1-SST*) and sucrose:fructose-6-fructosyltransferase (*6-SFT*) catalyze synthesis of inulin and levan forms, respectively (Cortés-Romero *et al.*, 2012 and Lasseur *et al*., 2009). Up-regulation of these two genes (*1-SST* and *6-SFT*) has been found significantly associated with drought tolerance (Xue *et al.*, 2008). When carbon demand of developing grain increases with shortage of sucrose under drought stress condition, fructans hydrolyze to simpler forms to meet carbon demand which allows remobilization of stored sugars (Zhang *et al*., 2016). This process is catalyzed by fructans-1-exohydrolase (*1-FEH*) and fructosyltransferase enzymes (Zhang *et al*., 2015). These enzymes are supposed to be controlled at transcriptional level (Yáñez *et al.*, 2017). However, up-regulation of these genes depends on the degree of drought stress (Zhang *et al*., 2009). *1-FEH w3* has been identified as a major responsible gene for remobilization of stem fructans (Yáñez *et al*., 2017 and Zhang *et al*., 2015). Moreover, inverse role of invertase activities with fructans content has also been reported in vacuoles (Chibbar *et al.*, 2015). Primary role of invertase enzyme, in sucrose partitioning and modulation of sucrose gradient between phloem and sink tissues, is to facilitate long distance transportation of sucrose as an essential component of grain filling process (Braun *et al*., 2014 and Lalonde *et al*., 2003). Alteration in invertase activities under drought stress has been reported at transcriptional and post-transcriptional levels (Albacete *et al*., 2015 and Bhargava and Sawant, 2013). Plasma membrane sucrose transporters, which are regulated at transcriptional and post-transcriptional levels, also play crucial role in carbon partitioning by translocating sucrose between sink and source (Griffiths *et al.*, 2016).

Variations among wheat genotypes for accumulation and remobilization of water-soluble carbohydrates lay within the differential capacity of photosynthesis, respiration and carbon use efficiency under drought stress conditions (Tricker *et al.,* 2018). Therefore, drought tolerant varieties presumably accumulate and remobilize more WSCs as a secondary source of carbon and maintain a better harmonious relationship between source (CO_2 assimilation) and sink (developing grains) under water limiting conditions (Ruuska *et al.*, 2006 and Gebbing, 2003). Studies have shown relatively higher WSCs content in wheat stem under water stressed than non-stressed condition (Zhang *et al*., 2016 and Zhang *et al*., 2014). In a similar study, Goggin and Setter (2004) reported an increase of 2.5 folds in content of stems' fructans of three high yielding Australian cultivars *viz*. Kauz, Westonia and Attila-A under rainfed conditions. High yielding representative cultivars associated with increased WSCs have been released in Australia and United Kingdom (Dong *et al.*, 2016). Dreccer *et al.* (2009) evaluated a set of 194 Seri/Babax RILs under complete drought, rainfed and irrigated conditions and reported increase in grain filling rate, grain weight and yield by 41%, 34% and 10%, respectively in high WSCs content RILs relative to lower ones. Contribution of 10-20% and 30-50% in kernel weight due to remobilization of WSCs under optimum and water stress conditions, respectively has been advocated by Rebetzke *et al.* (2008) and Goggin and Setter (2004).

2.3 Genetic variability and correlation studies

Genetic variability is a core component of all crop improvement programs. Study on parameters of genetic variability *viz.* genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), genetic advance as percent of mean (GAM) and heritability (h^2) generates important data which serves as a basis of selection in base population for an efficient breeding program (Lira *et al.*, 2017). Till date, numerous studies to estimate the genetic variability for yield and yield attributing traits in wheat under optimal and drought conditions have been conducted but limited in reference to WSCs.

A study to evaluate genetic variability under irrigated and drought stress condition in 78 wheat breeding lines was conducted by Shamuyarira *et al.* (2019). They reported low GCV (<10%) for traits *viz*. days to 50% heading (DTH), days to maturity (DTM), number of productive tillers per plant (NOT) and plant height (PH) whereas, it was high (>20%) for number of spikelet per spike (SPS), grains per spike (GPS), thousand kernel weight (TKW), grain yield (GY) and biomass (BY) under both conditions. Interestingly, GCV for NOT and SPS under irrigated condition and TKW under drought was zero. DTH, DTM, PH, SL and TKW exhibited low PCV (<10%) under both conditions whereas, BY demonstrated low PCV under drought and moderate PCV (10-20%) under irrigation. NOT and GPS were recorded with moderate PCV under both conditions whereas, SPS exhibited low PCV under drought and high (>20%) PCV under irrigated conditions. Moderate and high PCV for GY was reported under drought and irrigated conditions, respectively. High heritability (>60%) was reported for DTM, SL and BY under drought and for DTH and SL under irrigated conditions. Moderate heritability (30-60%) was observed for PH under both conditions and for GPS and TKW under irrigated conditions. Rest of the studied traits showed low heritability (<30%) under both conditions. Low GAM (<10%) was observed for all the traits.

Arya *et al.* (2017) estimated parameters of genetic variability for 11 yield and its attributing traits in 49 bread wheat genotypes under irrigated condition and reported moderate GCV and PCV for DTH, peduncle length (PL), DTM and harvest index (HI) whereas, high for PH, NOT, TKW, SPS, GPS, GY and BY. They reported low heritability for DTM and NOT and moderate heritability for SL whereas, rest of the studied traits showed high heritability. DTM showed low and PL and HI showed moderate (11-20%) GAM. Other studied traits exhibited high (>20%) GAM. Genetic variability among 24 bread wheat genotypes under rainfed condition was studied by Yaqoob (2016). He reported low GCV and PCV for DTH, DTM and PH, low GCV and moderate PCV for SL and TKW, moderate GCV and PCV for GY and moderate GCV and high PCV for SPS. High heritability was recorded for DTH and GY only. PH, DTM, SL and TKW showed moderate heritability whereas, GPS and NOT showed low heritability. High GAM was reported for only GY.

Correlation studies help in identifying yield favouring and non-favouring traits providing a direction for direct and indirect selection of combination of traits for higher yield potential. Habti *et al.* (2020) identified positive correlation of GY and TKW with WSCs, glucose, fructose, sucrose and fructans in bread wheat genotypes under drought and combined stress of drought and heat. They also concluded that in contrast to old wheat varieties, this association was more rigid in modern wheat varieties.

While evaluating different agro-physiological traits under optimum and drought conditions of a bread wheat RIL population of SeriM82/Babax, Sobhaninan *et al.* (2019) reported positive correlation of GY with PH, SPS, BY, TKW (non-significant) and HI under irrigated condition whereas, GY was found positively associated with PH, SPS (non-significant), BY and HI under rainfed condition. Peduncle length showed positive correlation under stress condition and negative correlation under irrigated condition with GY but the association was non-significant at $p<0.05$. DTH did not show any correlation with GY under irrigated condition but they exhibited significantly negative correlation in rainfed condition. With 96 bread wheat genotypes, Mwadzingeni *et al.* (2016b) reported positive association of GY with DTH, DTM, NOT, PH, SL, SPS and TKW, correlation coefficient (r) ranging from 0.11 to 0.54. However, correlation of GY with DTH and DTM was non-significant.

Khan and Naqvi (2012) conducted a correlation study with 11 bread wheat genotypes by imposing drought stress at tillering, anthesis and grain filling stages and reported a highly significant and positive correlation of GY with NOT, SL, SPS and GPS with r ranging from

0.31 to 0.91 at different stages. All the studied traits showed significant and positive direct effect on GY under controlled conditions, except SL. GPS was the most influencing trait under drought at all the growth stages as it showed maximum direct effect on GY. NOT and SL showed significant and positive direct effect on GY when genotypes were exposed to drought at tillering stage. SPS was found as an influencer to GY when drought was executed at tillering and anthesis stages.

Ovenden *et al.* (2017) reported significantly negative correlation of WSCs with grain yield, grains per m^2 and tillers per m^2 under irrigated and rainfed conditions in bread wheat genotypes. This trait showed significantly positive correlation with TKW under both water regimes.

While studying the association between different physiological traits and yield potential of 384 bread wheat genotypes under rainfed, mild water stress and irrigated conditions, del Pozo *et al.* (2016) reported a non-significant negative correlation (r= 0.07) in first year trial and significant positive correlation (r= 0.15) in second year trial between WSCs and GY at anthesis under water stress condition. While in irrigated conditions, this correlation was significantly negative and insignificantly positive in first- and second-year trials, respectively. In all the trials, WSCs showed significantly positive correlation with TKW (r=0.22-0.49). In a multi-environment trial (n = 6) Ruuska *et al.* (2006) studied genetic variation in WSCs accumulation in a set of 22 diverse bread wheat genotypes and reported positive correlation of WSCs with GY (r=0.34) and TKW (r=0.46).

2.4 Multivariate analysis of genetic divergence

Genetic diversity is a key factor for success of any crop improvement program. Diversity in the base population provides opportunities for selection, development of new varieties with higher yield potential and correction in the genetic architecture of released varieties. Furthermore, it helps in identifying superior allelic combinations and different underlaying mechanisms governing expression of various trait(s) of interest. Parameters of genetic variability those were discussed in section 2.3 are univariate tools and give basic idea on genetic diversity for traits of interest whereas, multivariate tool like cluster and principal component analysis (PCA) provide reliable information on genetic diversity and genetic distance between genotypes (Bhanu, 2017). Cluster analysis classifies the subjected study material in different groups by calculating genetic distance between them on the basis of provided information. On the other hand, PCA is used to reduce dimensionality of data by producing a new linear set of variables by means of transforming correlated variables into uncorrelated variables. PCA provides information about the contribution of each trait in genetic diversity and associated genotypes.

Arifuzzaman *et al.* (2020) used multivariate techniques to screen drought tolerance in 25 wheat genotypes on the basis of plant height, flag leaf collar height, flag leaf length, flag leaf breadth, chlorophyll a, chlorophyll b, proline content, number of tillers per plant, root fresh weight, shoot fresh weight and root–shoot ratio. Hierarchical clustering based on Ward's agglomerative method with Euclidean distance grouped these genotypes in three major clusters under control (Cluster I) and drought (Cluster III) conditions. PCA revealed that first three principal components (PC) were explaining 76.3% and 68.9% variability in control and drought conditions, respectively. Eigen values in these first three components ranged from -0.475 (root fresh weight) to 0.403 (chlorophyll a) and -0.649 (flag leaf length) to 0.470 (chlorophyll b), respectively for control and drought conditions.

A core germplasm set of durum wheat was developed by Ambati *et al.* (2020) using Modified Rogers' distance (weight 0.7) and Shannon's diversity index (weight 0.3) on the basis of agronomical and quality traits. Sixty most diverse genotypes were extracted from a set of 600 genotypes. PCA was used to validate the extent of contribution of genotypes and studied traits in core set. PCA revealed scattered distribution of all genotypes representing complete genetic diversity. First 5 PCs showed 81.09% contribution. The loading vectors in these 5 PCs ranged from -0.69 to 0.91 for different traits. Devesh *et al.* (2019) used PCA to study genetic diversity in 17 newly developed CMS lines of bread wheat and contribution of different traits (DTH, DTM, PH, PL, NOT, relative water content, canopy temperature and chlorophyll content). In this study, first 5 PCs explained 84.5% variability. First PC dominated with positive loadings whereas, rest of the PCs were having mixed proportion of positive and negative loadings revealing almost equal contribution of studied traits in genetic diversity. Kandel *et al*. (2018) used single linkage method with Euclidean distance in 41 bread wheat genotypes to estimate genetic diversity on the basis of 17 morpho-physiological traits contributing to grain yield. Studied genotypes were grouped into 4 clusters among which cluster I explained nearly 92% genetic diversity. In PCA, first 6 PCs explained 77.5% variation and loading values for studied traits ranged between -0.527 (PH) and 0.510 (HI).

Survey of literature revealed that various studies have been conducted to identify variation for WSCs in bread wheat genotypes; however, none of them used multivariate approaches to estimate genetic diversity. Li *et al.* (2020) evaluated 120 RIL population developed from Longjian19/Q9086 for WSCs at different growth stages under irrigated and drought stress. They reported a range of 71.36-257.92 mg g^{-1} and 81.82-254.85 mg g^{-1} at mid grain filling stage (12-15 DAA) under drought and irrigated conditions, respectively. In an association mapping (AM) panel consisting of 144 bread wheat genotypes Dong *et al.* (2016) recorded a range of 6.1 to 19.6% w/w WSCs content at 14 days after anthesis (DAA). In another set of 262 bread wheat genotypes Li *et al.* (2015) recorded a range of 72.5-298.5 mg g^{-1} for drought stress, 49.4-229.5 mg g^{-1} for potassium iodide (KI) treated plants + drought stress, 50.8-256.9 mg g^{-1} for well irrigated and 52.2-146.6 mg g^{-1} for KI treated plants + well irrigated conditions for WSCs in wheat peduncle at 14 DAA and identified significant phenotypic variability among genotypes.

Suneja *et al.* (2015) studied differential response of three *T. dicoccum* and two *T. aestivum* drought adaptive genotypes for WSCs accumulation at anthesis, 10 DAA, 20 DAA and 30 DAA under irrigated and rainfed conditions. They reported peak accumulation of WSCs at 10 DAA under both irrigated (379.84-131.78 mg g^{-1}) and rainfed (364.34-201.55 mg g^{-1}) conditions. In general, value of WSCs in rainfed was higher than irrigated ones except for EC-14004 (*T. dicoccum*). WSCs content in all genotypes reduced with time and found lowest at 30 DAA in all genotypes under both the conditions. Maximum remobilization under water stress was shown by C-306 (*T. aestivum*), a drought tolerant genotype. In an earlier study, Reynolds *et al.* (2007) evaluated a drought adapted core set consisting of 12 synthetic lines and landraces of wheat and reported a range of 9.0 to 26.1% w/w WSCs in stem at 7 DAA.

2.5 Genome wide association mapping

Increased frequency of favorable alleles and/or allelic combinations brings desirable genetic improvements (Ødegård *et al.*, 2009). Gene pools are the morgues of several favorable allele and allelic combinations for many biotic and abiotic stress associated traits. Transfer of these favorable genes into modern cultivars is hampered by linkage drags (within primary pool) and reproductive barriers (between gene pools) (Prohens *et al.*, 2017). However, this hidden treasure can be exploited with deep information on genomic regions significantly associated with desirable traits by means of deploying recent genomic techniques and advanced molecular marker systems. Molecular markers are unaffected by environmental factors and therefore successfully eliminate effects of genotype x environment interaction during selection of polygenic traits (Mwadzingeni *et al*., 2016a). This enables plant breeders to improve their phenotypic selection efficiency in complicated breeding programs such improvement for drought tolerance which is vulnerable to high GXE interaction and low heritability (Sallam *et al*., 2019 and Gupta *et al*., 2017).

Development of molecular marker system has revolutionized crop improvement programs. Among various molecular markers, single nucleotide polymorphism (SNPs) based markers have gained significant popularity among plant scientists due to their genome-wide abundance (as much as twice of SSR), stability, amenability to automation, fast detection, high precision and cost-effectiveness (Guichoux *et al.*, 2011). Furthermore, SNPs can be directly linked to phenotypic expression and can also find functional and regulatory sites in non-coding regions (Kim *et al.*, 2007). SNP markers have significantly improved the pace and precision of refined genetic mapping, marker trait association analysis, high density QTL mapping, assessment of genetic variations and population structure (Mammadov *et al.*, 2012).

Different molecular marker systems have proved promising in identifying several QTLs for drought tolerance in more than 50 biparental mapping studies on bread wheat and related species (Gupta *et al*., 2017 and Mwadzingeni *et al*., 2016a). The major drawbacks of these studies are their dependency on limited recombination events, genetic variations and resolution power (Rasheed and Xia, 2019). These limitations can be overcome with genome wide association mapping studies (GWAS) (Zhu *et al.*, 2008). GWAS exploits the available genetic variations and historical recombination events within and/or across gene pools by genotypic and phenotypic association which depend on random association between alleles of different loci (LD: linkage disequilibrium) of GWAS panel (McCarthy *et al.*, 2008). The power of GWAS is influenced by population size, extent of genetic diversity, type of molecular marker, genome wide coverage of marker, statistical model and LD (Alqudah, *et al*., 2020). Different statistical models are used to study population structure and avoidance of false discovery rates (Nordborg and Weigel, 2008). Mixed linear model is most acceptable model for GWAS in which association between each individual marker and phenotype is tested. Generalized linear model (GLM) is used for GWAS for case verses control (Gupta *et al*., 2019). These methods can account for population structure by grouping individuals through principal component analysis or STRUCTURE analysis and/or by accounting for relationships through a kinship matrix that can be estimated from pedigree information and molecular marker data (Novembre, 2016; Lipka *et al.*, 2012 and Bradbury *et al.*, 2007). Instead of simply testing whether a particular locus has effect on phenotype, this approach tests if a locus has any effect on phenotype which is not explained by population structure or genetic background (Garcia *et al.*, 2019). In last five years, number of association studies targeting yield and various yield contributing traits under various environmental conditions have significantly increased in wheat using different SNP discovery techniques, such as genotyping by sequencing (GBS) and SNP chips (15K, 35K, 90K and 660K) which have helped in identifying significant marker trait associations (MTAs) and development of high throughput allele specific markers (Sun *et al*., 2020; Allen *et al*., 2017; Winfield *et al*., 2016 and Akhunov *et al*., 2009). However, to date very limited studies have been conducted under drought stress conditions for assessing functional loci related to yield and attributing trait(s) especially with reference to stem WSCs and its major components. Recent relevant studies have been reviewed in **Table 2.1**.

2.6 *In silico* gene identification

Bioinformatics resources and web-based database provide a platform to accelerate new gene discoveries and their structural and functional analysis through comparative genomics and simulation models. Till date no bioinformatic study has been conducted with an aim to identify genes involving in fructans metabolism but reviews on similar bioinformatic studies may be referred to strengthen the present investigation.

Guo *et al*., (2018) used extensive bioinformatic approaches to identify and characterize sugar transporter gene families (SWEET) in *Triticum aestivum* using *Arabidopsis thaliana* and

Oryza sativa. They identified 59 SWEET genes in wheat genome (*TaSWEETs*) and analyzed their amino acid and protein sequences for TMHs, exon/ intron, molecular weight and PI using web-based database and different bioinformatic tools which were further supported by study of phylogeny. In another study, Kumar *et al*. (2018) identified and characterized RWP-K gene families in wheat using *Brachypodium distachyon*. They identified nearly 37 RWP-K gene and further characterized gene structure and protein sequences using bioinformatic tools like GSDS v2.0, ProtParam and CDD database. 24 SSR markers were further developed by them with BatchPrimer v3.0 followed by *in silico* expression analysis of identified gene using WheatExp database.

Mitogen activated protein kinase kinase kinase (MAPKKK) gene family in bread wheat (*Triticum aestivum* L.) was identified by Wang *et al*. (2016). They retrieved 155 genes with the complete kinase domain in the wheat genome using *Arabidopsis thaliana*, *Oryza sativa*, *Zea mays* and *Brachypodium distachyon* as model species. They reported conserved evolutionary relationships between model species and wheat MAPKKK genes. They reported varying size of intron and exons ranging between 1 and 22 while demonstrating the structural conservation of gene with in a clade. They further predicted *cis*-regulatory elements (CREs) in 1.5Kb upstream and downstream of the identified genes and advocated the presence of elements involved in abiotic stress (SLAC1, FMA, CHX20, MYB and NAC transcription factor) and light responsiveness. Database available on gene ontology resources was further used to identify various functions of identified genes.

Muthusamy *et al*. (2017) identified 163 heat shock protein (*HSP20*) genes in bread wheat genome while considering *Oryza sativa*, *Sorghum bicolor*, *Zea mays*, *Brachypodium distachyon* and *Setaria italica* as reference and used web-based database and bioinformatics to analyze the structure, location and function of nucleotide and amino acid sequences. They used *in silico* gene expression analysis from WheatExp database to validate the role of identified genes under heat stress conditions.

Table 2.1: Brief review of recent association mapping studies relevant to present investigation

Sr. No.	Traits	AM	Water regime	Genotyping	MTAs	Reference
1	PH, SL, SPS, GPS, NOT, TKW, GWS, GY	384	IR	55K SNP	460	Li *et al.* (2020)
2	DTH, DTA, DTM, PH, SL, SPS, NOT, PH, PR, SD, SW, SI, GWS, TKW, GPS, SSNS, FSNS, GNFS	710	IR	15K SNP	118	Alqudah *et al*. (2020)
3	DTH, DTM, PH, TKW, GY	320	IR, RF	GBS	27(IR), 26(RF)	Gahlaut *et al.* (2019)
4	DTE, DTH, DTA, DTM, GFD, SPAD, NDVI, CT, SW, SL, SPS, TKW, GY	298	IR	GBS	313	Rahimi *et al.* (2019)
5	DTH, DTA, PH, SL, SPS, GPS, NOT, TKW, GY	277	IR, DT, HT	660K SNP	189	Li *et al.* (2019)
6	DTH, GFD, PH, NOT, GPS, TKW, GY	125	IR (ES and LS)	GBS	139	Jamil *et al.* (2019)
7	DTA, PH, SL, SPS, GPS, TKW, GP, DSI	111	DT	90K SNP	263	Tarawneh *et al.* (2019)
8	DTH, DTA, GFD, NOT, PH, PL, PEL, SL, SPS, GY, BY, HI, TKW	108	IR, DT, HT, HD	15K SNP	112(IR), 115 (DT), 104 (HT), 172 (HD)	Qaseem *et al.* (2018)
9	PH, SL, SPS, GPS, GWPS, TKW	215	IR	90K SNP	117	Guo *et al.* (2018)
10	GY, TKW, TNG	287	IR	90K SNP	41	Sukumaran *et al.* (2018a)
11	DTH, DTM, PHT, SPL, SPS, GPS, TKW, GY	93	IR, DT	38.6K DArT	334	Mwadzingeni *et al.* (2017)
12	PH, PL, SL, FSNS, SSNS, SPS, FLBA, FLD	163	IR	90K SNP	1769	Sun *et al.* (2017)
13	DTH, DTM, PH, NOT, GPS, BY, GY, HI, TKW	123	RF	90K SNP	44	Ain *et al.* (2015)
14	TKW	372	IR	775 SSR + 90K SNP	342	Zanke *et al.* (2015)
15	DTH, DTA, DTM, PH, PL, GY, BY, TKW, HI, TNG, SPADvg, SPADLLg, CTvg, CTLLg, NDVIvg, NDVILLg,	287	IR	90K SNP	31	Sukumaran *et al.* (2014)
16	WSCs	166	IR	90K SNP	52	Dong *et al.* (2016)
17	TKW, WSCs	262	IR, DT, HT, HD	209 SSR	7	Zhang *et al.* (2014)
18	TKW, WSCs	262	IR, KI-IR, DT, KI-DT	209 SSR	16	Li *et al.* (2015)

BY: Biological yield; **CT:** Canopy temperature; **DTE:** Date of emergence; **DTH;** Days to heading; **DTA:** Days to anthesis; **DTM:** Days to maturity, **DSI:** Drought susceptibility index; **FSNS:** Number fertile spikes per spike; **FLBA**: Flag leaf base angle; **FLD**: Flag leaf direction; **GFD**: Grain filling duration; **GP**: Germination percentage; **GNFS**: Grain number per fertile spikelet; **GPS**: Grain per spike; **GY**: Grain yield; **GWPS**: Grain weight per spike; **HI**: Harvest index; **Llg**: Grain filling stage **NOT**: Number of tillers; **NDVI**: Normalized differential vegetative index; **PH**: Plant height; **PL**: Peduncle length; **PEL**: Extruded peduncle length; **PR**: Protein content; **SD**: Sedimentation unit; **SPAD**: chlorophyll index; **SL**: Spike length; **SI**: Spike index; **SPS**: Spikelet per spike; **SSNS**: Number of sterile spikelet per spike, **SW**: Spike weight; **TKW**: Thousand kernel weight; **TNG**: Total number of grains, **WSCs**: Water-soluble carbohydrates; **vg**: Vegetative stage

CHAPTER-III

MATERIALS AND METHODS

Present investigation entitled as ‘Genome wide association mapping for total stem water-soluble carbohydrates in bread wheat (*Triticum aestivum* L.) under terminal water stress’ materials and methods used in the present investigation are as follow:

3.1. Plant material

3.2. Field experiments

3.3. Meteorological observations

3.4. Phenotyping

3.5. Statistical analysis

3.6. Association mapping

3.7. *In silico* genome wide identification of fructans genes

3.1. Plant material

A set of 302 bread wheat (*Triticum aestivum* L.) genotypes comprising of indigenous collection, landraces, released varieties, genetic stocks and improved wheat genotypes were used to constitute a genetically diverse association mapping panel for this study. These genotypes were selected from a predefined core set which was developed on the basis of Shennon index with DUS traits from a collection of 7000 genetically diverse germplasm lines at ICAR-IIWBR, Karnal. The basis of selection of these genotypes was the pedigree information (**Annexure-1; pp: I**) and available passport data to minimize the associations of erroneous markers as it provides a buffer against skewness in terms of the environmental effects. The seeds were procured from germplasm unit of ICAR-IIWBR, Karnal.

3.2. Field experiments

Field trails were conducted in two replications following alpha lattice design at two locations, Hisar and Karnal, for two consecutive cropping seasons *Rabi 2017-18* and *Rabi 2018-19*. An additional location Baramati, Pune (Maharashtra) was added to the plan in *Rabi* 2018-19. Crop was raised under three different water regimes irrigated (control), rainfed and complete drought. Each genotype was planted with a dibbling tool named as IIWBR-Dibbler (Sharma *et al.*, 2016) to ensure maximum homogeneity in the experiment. Crop was raised as per the recommended package of practices (POP); however, irrigation was completely checked for rainfed and drought treatments. Complete details of field trials are given in **Table 3.1**.

Table 3.1: Details of field experiment

Experimental Sites	1. ICAR-IIWBR, Karnal (Haryana) (*Rabi 2017-18* and *2018-19*) 2. CCS HAU, Hisar (Haryana) *(Rabi 2017-18* and *2018-19*) 3. Agharkar Research Institute, Baramati, Pune (Maharashtra) (*Rabi* 2018-19)	
Design of Experiment	Alpha lattice; Two Replications	
Layout	16 Blocks (15 Blocks with 20 Plots/Block and 1 Block with 6 plots)	
Plot Size	120x60 cm	
Method of Sowing	Dibbling	
Spacing	Plant to Plant	10 cm
	Row to Row	20 cm
	Plot to Plot	100 cm
	Block to Block	150 cm
Depth of Sowing	10 cm	
Treatments	1. Irrigated (Control)	In field (at all locations)
	2. Complete Drought	In Rain Out Shelter (Karnal)
	3. Rainfed	In field (at Hisar and Pune)
Agronomic Practices	As per package of practices except for the irrigation schedule	

3.3. Meteorological observations

Meteorological data for both cropping seasons was procured from Department of Agricultural Meteorology, CCS HAU, Hisar for Hisar location, Resource Management, ICAR-IIWBR, Karnal for Karnal and Baramati location. The temperature inside rain out shelter (ROS) at Karnal was recorded with the help of an automatic temperature recorder.

Soil moisture in each field was recorded one day prior to each irrigation schedule using gravimetric method. For this purpose, the soil was sampled with a screw auger from the depth of 15, 30 and 50 cm and stored in aluminum soil moisture boxes. Fresh weight of samples was recorded and then samples were kept for drying in hot air oven at 105°C for 48 hours. Dry weight of samples was recorded and the soil moisture of field was determined using following equation:

$$\text{Soil Moisture} = \frac{W_i - W_f}{W_i} - W_b$$

Where, W_i = fresh weight of soil with moisture box, W_f = weight of soil with moisture box after drying and W_b = weight of soil moisture box.

3.4. Phenotyping

3.4.1. Agro-phenological traits

Fourteen agro-phenological traits were recorded to characterize the study material by following Zadoks scale (**Figure 3.1**). For this purpose, ten plants were randomly selected and tagged at jointing stage (Zadoks Scale = 30-39) and mean values of the respective trait were used in further analyses.

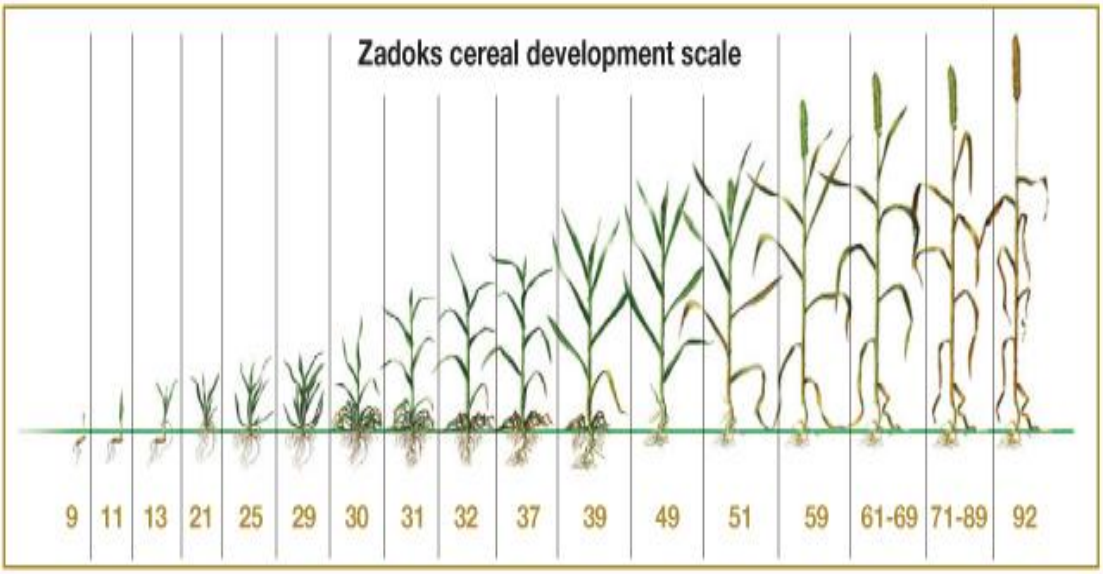


Figure 3.1 Zadok's scale of wheat growth and development

i. **Days to heading (DTH)**

Number of days taken by plant to reach at Zadoks scale = 50 from the date of sowing.

ii. **Days to anthesis (DTA)**

Date of extraction of anthers from the spikelet covering at least 75% of spike (Zadoks scale = 60) considered as date of anthesis. The number of days between date of sowing and date of anthesis recorded as DTA.

iii. **Days to maturity (DTM)**

For each tagged plant days to maturity recorded as number of days from date of sowing to reach it at Zadoks Scale = 90.

iv. **Grain filling duration (GFD)**

Number of days between anthesis and maturity recorded as grain filling duration.

v. **Plant height (PH)**

Plant height recorded at maturity (Zadoks scale = 90) in centimeters (cm) from ground level to top of the ear (except awn) of main shoot.

vi. **Number of tillers (NOT)**

NOT counted on per plant basis between Zadoks scale 60 and 90 (flowering to maturity).

vii. **Spike length (SL)**

Spike length measured in cm from base of first fertile spikelet to the tip of spike excluding awns at Zadoks scale = 90.

viii. **Peduncle length (PL)**

Distance between first internode and first rachis recorded as peduncle length and expressed in cm. The trait was observed at Zadoks scale = 90.

ix. **Number of spikelet per spike (SPS)**

Number of florets in each main spike counted in a fully developed spike.

x. **Biological yield plant^{-1} (BY):**

From each plot all the tagged plants manually harvested and bundled, separately. Each bundle was then separately weighed on an electronic balance. Weight of each bundle was then divided by total number of harvested plants and recorded as BY. The trait expressed in grams (g).

xi. **Grain yield plant^{-1} (GY):**

Each bundle was carefully hand-threshed and cleaned. Total grain weight taken on an electronic balance and later divided by total number of harvested plants from the respective plot for calculating yield per plant in grams (g).

xii. **Harvest index (HI)**

Harvest index of each genotype was calculated with following formula and expressed in percentage.

$$\mathrm{HI} = \frac{\text{Grain Yield Plant}^{-1}}{\text{Biological Yield Plant}^{-1}} \times 100\ \%$$

xiii. **Number of grains plant^{-1} (TNG)**

Total number of grains harvested from each plot counted separately on seed counter and then fractioned by total number of harvested plants in respective plot to record number of grains per plant.

xiv. **Thousand kernel weight (TKW)**

For each genotype test weight or thousand kernel weight (TKW) was calculated mathematically using the underwritten formula and expressed in grams (g):

$$\mathrm{TKW} = \frac{\text{Grain Yield per Plot (g)}}{\text{Total Number of Grains per Plot}} \times 1000\ \mathrm{g}$$

3.4.2. Water-soluble carbohydrates and free sugars:

Total water-soluble carbohydrates (WSCs) and free sugars (glucose, fructose, sucrose and fructans) estimated in peduncle of each genotype under stressed and non-stressed conditions after fifteen days of anthesis using Fourier transform near infrared (FT-NIR) spectroscopy. For this experiment, five plants from each plot were separately tagged and observed. Sampling was done by cutting peduncle of main shoot fifteen days after anthesis (15 DAA). Samples were collected in waterproof seed envelope and immediately stored under -20°C. Further, analysis was conducted in following steps:

3.4.2.1. Spectral acquisition:

Samples were dried at 60°C for 72 hours by keeping them in a pre-heated air oven. Samples were then chopped into 1-2 mm size with the help of a 'five blade' scissor. Moisture was controlled by keeping samples at 100°C for 30 minutes just prior to spectroscopy. NIR spectrum was then obtained using PerkinElmer's Frontier$^{\mathrm{TM}}$ FT-NIR spectroscope fitted with near infrared assembly (NIRA^{TM}; L1280450). Samples were placed in a cell holder (L9001029) and reflectance spectra (represented as log 1/R, where R is reflectance) of wave number 10000 cm^{-1} and 4,000 cm^{-1} collected at resolution 8 cm^{-1} and 2 cm^{-1} data intervals using Spectrum software^{TM} (PerkinElmer). Average of 32 spectra for each sample was obtained and mean spectrum was (raw data) used for analysis.

3.4.2.2. Biochemical analysis

I. Sample preparation and extraction

Random allocation of samples (n = 150) was done using R function *Sample()* in R studio (https://rstudio.com/). These allocated samples used for chemical determination of WSCs and free sugars for model development and calibration. Samples were finely ground with pastel and motor. Extraction was done with 150 mg of finely ground sample boiled at 80°C with 1.5 ml MerckMillipore^{TM} distilled water (*dd*H_2O) for 1 hour in a 2 ml eppendorf tube. It was then cooled down and centrifuged at 10000 rpm for 15 minutes. Supernatant was then collected in a 5 ml eppendorf tube followed to this storage was done at 1°C.

II. Total water-soluble carbohydrates (WSCs)

WSCs quantified with anthrone method originally published by Yemm and Willis (1954) with slight modification in following steps.

i. Reagents:

A. Sugar extract

B. D-Glucose

C. Anthrone reagent:

A freshly prepared (not more than 6 hours) reagent was made by dissolving anthrone in pre-chilled concentrated sulfuric acid (*conc* H_2SO_4) at the rate of 0.1 mg anthrone per 100 ml of *conc* H_2SO_4.

ii. Standard curve:

For preparation of a standard curve, a stock standard solution was prepared by dissolving 100 mg of D-Glucose in 100 ml of *dd*H_2O and stored at 4°C. The working standard solution was then prepared by diluting 10 ml of stock standard solution in 100 ml of *dd*H_2O and stored at 4°C. Now, 0.1 ml to 1 ml of working standard solution was pipetted out in different test tubes in three replications. In each test tube the volume was made up to 1 ml. For control, 1 ml of *dd*H_2O was poured in another test tube. To each test tube 2 ml of pre-chilled anthrone reagent was added and heated up in a water bath at 60°C for 15 minutes. The test tubes were then cooled down to room temperature simultaneously shaking on an orbital shaker. Optical density of solution was measured at 620 nm using a Thermo Scientific^{TM} Evolution 200 Series UV-Visible Spectrophotometer. The standard curve was developed in

MS-Excel v. 2013. The standard curve was re-developed each time when new anthrone reagent was prepared.

iii. WSCs

To determine WSCs, 100 μl of sugar extract pipetted out in a test tube and 2 ml of anthrone reagent added and heated up at 60°C for 15 minutes. The test tubes then cooled down to room temperature simultaneously shaking on an orbital shaker. Optical density of solution was measured at 620 nm using a Thermo Scientific™ Evolution 200 Series UV-Visible Spectrophotometer.

iv. Calculations

WSCs concentration in samples was calculated against standard curve and expressed in mg g^{-1}.

III. Free sugars:

i. Sugars *viz*. glucose, fructose and sucrose were estimated in the extracts using Megazymes commercial kit (K-SUFRG™). D-glucose concentration was determined before and after hydrolysis of sucrose by *β*-fructosidase (invertase). D-fructose content of sample was determined subsequent to the determination of D-glucose, after isomerization by phosphoglucose isomerase. Sucrose content was calculated by difference in D-glucose concentration before and after hydrolysis by *β*-fructosidase. The amount of the three sugars was calculated as followed and were expressed in mg g^{-1},

$$c = \frac{V \times M_w}{\varepsilon \times d \times v} \times \Delta A$$

where:

V = final volume (ml)

M_w = molecular weight of the substance assayed (g/mol)

ε = extinction coefficient of $NADPH^+$ at 340 nm *i.e.* 6300 L X mol^{-1} X cm^{-1}

d = light path (cm)

v = sample volume (ml)

ΔA = Sample absorbance (nm)

Fructans concentration in the extracts was estimated using Megazymes K-FRUC™ kit. In this assay, sucrose, starch and maltosaccharides were hydrolyzed to D-glucose and D-fructose using sucrase, pullulanase, *β*-amylase and maltase enzymes. D-glucose, D-fructose and residues of D-fructosyl were then reduced to corresponding sugar alcohols *viz*. D-sorbitol, D-mannitol and fructo-oligosaccharides by sodium borohydride. Followed to this, fructans and fructo-oligosaccharides were hydrolyzed to D-glucose and D-fuctose under the activity of inulinase (exo- and endo-) and endo-levanase. Finally, these sugars were reduced by *þ*-hydroxybenzoic acid hydrazide to form a colored PAHBAH complex. The absorbance of colored complex was measured at 410 nm and quantity of fructans (mg g^{-1}) was calculated as follow:

$$fructans\ = \Delta\mathrm{A}\ \times \frac{\mathrm{F}}{\mathrm{W}} \times \mathrm{D}\ \times 61.9$$

where:

ΔA = Sample absorbance (nm)

F = factor to convert absorbance values to µg of D-fructose

D = Dilution factor

W = Sample weight

3.4.2.3. Pre-processing and model development

Pre-processing of spectral data was done using Cameo Unscrambled©, before the model development. Pre-processing of spectral data included normalization, smoothing, differentiation and pre-treatment. Normalization was done using methods multiplicative scatter correction (MSC) and standard normal variant transformation (SNV). Median filter, Savitzkey-Golay and wavelet methods were used for spectral smoothing. Differentiation was done using 1st and 2nd derivatives followed by mean-centered pre-treatment.

3.4.3. Model development and cross validation

The calibration model was developed with the help of Cameo Unscrambled© tool. Best fitted partial least square regression was extracted by cross validation with leave-one-out method. Correct numbers of factors in each model were determined by calculating root mean square error of cross validation (RMSECV) and prediction (RMSEP) and plotting them against corresponding r^2 values. The model with minimum factors, high r^2, high relative estimation error (RPD) and low RMSEP was chosen for further analysis. To improve the model accuracy, outliers in laboratorial data were identified with Cook's distance in R tool using the following linear model before the development of calibration model:

```
model   ←  lm(x_reading ~., data = x)
cooksd  ←  cooks.distance (model)
```

Where,

x = data frame.

Variables showing Cook's distance more than 4 were considered non-influencer and removed.

3.4.4. External validation

Twenty samples which were not included in the calibration and cross validation were randomly selected for external validation. The predicated value of those samples was compared with the laboratorial values. The efficacy of models was determined on the basis of RPD and RSMEP and RMSECV values.

3.5. Statistical analysis

3.5.1. Data treatment

Prior to statistical analysis raw data was treated for outlier detection and missing values. The outliers in the data was detected using multivariate approach *viz*. Cook's distance in R tool using the following linear model:

```
model    ←   lm(x_reading ~., data = x)
cooksd   ←   cooks.distance (model)
```

Where,

x = data frame.

Variables showing Cook's distance more than 5 were considered non-influencer and removed.

Followed to the deletion of outliers, missing values were predicted in the data set using *mice* (multivariate imputation by chained equations) package of R and developing a multiple regression model. Subsequently, the missing values were replaced with the corresponding mean values obtained from these two methods.

3.5.2. Analysis of Variance (ANOVA)

Variances were calculated for per environment and across management (irrigated, rainfed, drought). For this purpose, following linear mixed models were implicated in *lme4* package using, restricted maximum likelihood (REML) approach where environment and management were fitted as fixed effect and genotypes, blocks, replicates and genotype interaction with management were fitted as random effect:

i. Per environment:

$$Y_{ijk} = \mu + Rep_i + Block_j \times Rep_i + Gen_k + \varepsilon_{ijk}$$

ii. Across managements:

$$Y_{ijkl} = \mu + Env_i + Rep_j \times Env_i + Block_k \times Env_i \times Rep_i + Gen_l + Env_i \times Gen_l + \varepsilon_{ijkl}$$

iii. Pooled:

$$Y_{ijkl} = \mu + Mang_i + Loc_i + S_i + \mathrm{Env}_i + Rep_i + Gen_l + Env_i \times Gen_l + Mang_i \times Gen_l + \varepsilon_{ijkl}$$

The type III sum of squares (SS), mean sum of squares (MSS) and *F*-value (>0.05%) of fixed effects was computed by fitting above models in *anova()* function. Best linear unbiased predictor (BLUP) and Best linear unbiased estimate (BLUE) values were then calculated for each genotype against per environment and across management.

Least significant difference (LSD) at 5% significance level was calculated as

$$\mathrm{LSD} = \overline{\mathrm{SE}} \times \mathrm{t}_{(1-0.05,\mathrm{df_e})}$$

where:

$\overline{\mathrm{SE}}$ = average standard error of the differences between pairs of means

t = cumulative Student's t distribution

0.05 = selected level of significance to 5%

df_e = degrees of freedom for variance of error

Coefficient of variation in percentage was calculated as

$$\mathrm{CV} = \frac{\overline{\mathrm{SE}}}{\overline{\mathrm{X}}} \times 100$$

where:

$\overline{\mathrm{SE}}$ = average standard error of the differences between pairs of means

$\overline{\mathrm{X}}$ = grand mean

3.5.3.Test of homogeneity of variance

For this purpose, based on the nature of distribution of the data either of the two *viz.* Bartlett test or Leven's test of homogeneity of variance was carried out in R studio using appropriate functions.

3.5.4.Descriptive statistics

For each set of mean and BLUP/BLUE values minimum, maximum, mean, standard deviation and standard error of mean were estimated using ADEL-R package. Interactive visualization of data was done in R environment using ggplot2, lattice and plotly packages.

i. Drought susceptibility indices (DSI)

Following stress indices were calculated from the best linear unbiased estimated (BLUE) values calculated pooled over managements (IR, RF, and DT) for yield as per Fischer and Maurer (1978)

$$\mathrm{DSI} = \frac{1-\left(\mathrm{Y_S}/\mathrm{Y_P}\right)}{1-\left(\bar{\mathrm{Y}}_\mathrm{S}/\bar{\mathrm{Y}}_\mathrm{P}\right)}$$

where,

Y_p = Yield under non-stress and Ys = Yield under stress

3.5.5. Components of genetic variability and heritability

i. Genotypic and phenotypic variances were estimated for each environment (σ_g^2,σ_p^2) and across the managements ($\sigma_{g\times m}^2, \sigma_{p\times m}^2$) with the help of corresponding mean square values (MS) and residual variance (σ_e^2). In each case, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as a percentage ratio between under root of corresponding variance ($\sigma_{g\ or\ p}^2$) and grand mean ($\overline{\mathrm{X}}$).

ii. Broad sense heritability (h^2) for each trait was calculated using underwritten formulae and expressed in percentage:

a. for each environment: $h^2 = \dfrac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_e^2}{r}} \times 100$

b. for across managements or environments: $h^2 = \dfrac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gy}^2}{y} + \frac{\sigma_e^2}{(y \times r)}} \times 100$

where σ_g^2, σ_e^2 and σ_{gy}^2 are genetic variance, residual variance and variance due to interaction between genotype and environment/management, respectively. 'y' and 'r' is total number of environments/managements and replications, respectively.

iii. Genetic advance

Genetic advance and genetic advance over grand mean were calculated for each individual environment and pooled over managements as per Johnson *et al*. (1955):

a. Genetic advance (GA)

$$\mathrm{GA} = \mathrm{k.h^2.\sigma^2}$$

b. Genetic advance over mean (GAM)

$$\mathrm{GAM} = \frac{\mathrm{GA}}{\overline{\mathrm{X}}}$$

Where: k is standardized selection differential at 5% selection intensity (2.06), h^2 is broad sense heritability for the trait, $\overline{\mathrm{X}}$ is population mean for the trait.

iv. Categorization of GCV and PCV was done as suggested by Shivasubramaniam and Menon (1973) and for heritability and GAM% categorization suggested by Johnson *et al*. (1955)

Category	**GCV and PCV**	**Heritability**	**GAM**
Low	<10%	<30%	<10%
Moderate	11-20%	31-60%	11-20%
High	>20%	60>	>20%

3.5.6. Correlations

Pearson's rank correlation for phenotypic (r_p) values among variables was calculated for using *rcorr()* function of R followed by the calculation of *p* values with significance level 0.001% (***), 0.01% (**) and 0.05% (*) using Hmisc package.

3.5.7. Multivariate analysis

Cluster and principal component analysis were carried out in R environment using required dependencies to estimate the genetic variability in population at phenotypic level and contribution of each phenotypic trait in it.

3.6. Association mapping

3.6.1. Genomic DNA isolation

The genomic DNA isolation was carried as per Murray and Thompson (1980). Seeds of all genotypes were grown for 3 weeks. About 5-10 cm young and actively growing fresh leaves were harvested for genomic DNA extraction. Fresh leaf material was taken and ground to fine powder in liquid nitrogen in pestle and mortar. 1 ml of pre-heated (65°C for 30 minutes) extraction buffer was then added to the ground powder and was homogenized. The homogenized material was transferred to 2 ml eppendrof tubes and then incubated for one hour with occasional stirring. Subsequently an equal amount of Chloroform:Isoamyloalcohol (24:1) was added to the tube and mixed by tilting and inverting the tube for 2-3 minutes. The samples were then subjected to centrifugation at 12,000 rpm for 8 minutes with the temperature maintained at 4ºC in a cooling centrifuge. The supernatant was then transferred to another tube to which 2/3rd volume of pre-chilled isopropanol (-2 to 0ºC) was added and stored at 4˚C overnight. On the next day, again the centrifugation was done at 10,000 rpm for 5 minutes at 4˚C. The supernatant was carefully discarded and the pellets were washed with 70% ethanol (200µl) to remove the contaminations and air dried on blot paper. DNA was then dissolved in 100µl TE buffer and stored at 4˚C. For purification of DNA, 2µl RNase (10mg/ml) was added to samples and incubated for one hour at 37°C.

Quantification of DNA was done with Nanodrop 1000 spectrophotometer (Biodrop Touch PC+125) at absorbance of 260nm.

3.6.2. SNP genotyping and filtering

The DNA was subjected to SNP genotyping with a 35K Axiom Wheat Breeders' Array (Affermetix UK Ltd., United Kingdome). SNP calling and filtering was done with PLINK software (Purcell *et al.*, 2007). In filtering process, markers with missing values more than 5%, minor allele frequency (MAF) less than 5% and/or no known chromosomal position in high density consensus map generated by Allen *et al.* (2017) were removed. Duplicate markers were identified and filtered out by R/QTL software (Arends *et al.*, 2010; Broman *et al.*, 2003). Furthermore, genotypes with more than 15% missing SNP calls were also eliminated from further analysis.

3.6.3. Genetic diversity and population structure

Descriptive statistics of extracted SNP markers was done by PowerMarker v3.2.5 (Liu and Muse, 2005). A population structure based on Bayesian algorithm was inferred by implementing admixture model with correlated allele frequency in STRUCTURE software v2.3.4 (Hubisz *et al.*, 2009). To identify the optimal sub-population (K), K-value between 1 and 10 were tested with a total of 10^5 burn-in periods Markov Chain Monte Carlo (MCMC) iterations. Each K-value was analyzed in three replications. Subsequently, optimal sub-population was identified by estimating log probability of data [LnP(D)] and an adhoc statistics (ΔK; rate of change in LnP(D) value between successive K values) (Evanno *et al.*, 2005) as implicated in Structure Harvester tool (Earl and vonHoldt, 2012). A Q-Q matrix representing population membership coefficients for each member was obtained from the inferred numbers of sub-population. Population stratification was then validated using Principal component analysis (PCA) and Neighbor-joining (NJ) based cluster analysis was performed with R based GAPIT v2.0 (Genomic Association and Prediction Integrated Tool) (Tang *et al.*, 2016) and DARwin v6.0 (Dissimilarity Analysis and Representation for Windows) (Perrier and Jacquemoud-Collet, 2006), respectively.

3.6.4. Marker and trait(s) association analysis

The marker and trait(s) association analysis (MTA) were conducted by using R based tool namely GAPIT v2.0 (Genomic Association and Prediction Integrated Tool) (Tang *et al.*, 2016) for each environment and pooled over water management. For this purpose, BLUPs/BLUEs values for each trait was used and implemented with different regression models from GAPIT, where first 3 principal components (PC) were used as covariates with kinship (K) information (K-PC model) (Zhao *et al.*, 2007). Additionally, the VanRaden method (VanRaden, 2008) was used to calculate K-matrix and a best fit model was chosen by evaluating Q-Q plots. *P-values* thresholds were determined by adjusting false discovery rate (FDR) to 10% and MTA with value $log_{10}P$ > 2.89 were considered significant.

3.6.5. Putative Candidate Gene Analysis and Expression Data

Candidate genes or putative related proteins of SNP flanking-regions (1KB upstream and downstream) were identified using BLAST algorithm. For this purpose tBLASTx search was performed for each significant MTA with cut off value (E) $1e^{-10}$ against *T. aestivum* L. reference genome *viz.* IWGSC RefSeq v.1.09 in EnsemblPlants (https://plants.ensembl.org/index.html) for *T. aestivum*10. Number of tightly linked genes adjacent to significant MTAs was looked by using the RefSeq v1.0 Gene Ontology (GO) annotation of the potential candidate genes in Blast2GO pro tool v.3.1.3 (Conesa and Götz, 2008). A reference physical map of significant and stable MATs was then prepared using Phenogram tool (Wolfe *et al.*, 2013).

3.7. *In silico* genome wide identification of fructans genes

3.7.1. Database search and retrieval of genes

Enzymes actively involved in metabolic processes of fructans in *T. aestivum* were identified by retrieving fructans biosynthesis pathway accessible from MetaCrop (http://metacrop.ipk-gatersleben.de/apex/f?p=269:111). Genes responsible for coding of peptide for these enzymes belonging to 13 model plant species *viz. Arabidopsis thaliana*, *Arabidopsis lyrata*, *Beta vulgaris*, *Brachypodium distachyon*, *Brassica oleracea*, *Brassica rapa*, *Glycine max*, *Helianthis annus*, *Hordeum vulgare* and *Medicago trancatula*, *Oryza sativa* sub. *Japonica*, *Setaria italica* and *Sorghum bicolor* were retrieved from database of National Center for Biotechnology Information (NCBI, https://www.ncbi.nlm.nih.gov/gene). A local database of these genes was thus developed with complete gene transcript, coding DNA sequences (CDS), cDNA sequences and amino acid sequences. The peptide sequences were then used as query for searching homologous amino acid sequences (AA) using BLAST algorithm by performing BLASTP search against recently released *T. aestivum* genome assembly (IWGSC RefSeq v1.1) with E=$1e^{-10}$ in Ensembl Plants (https://plants.ensembl.org/index.html). Sequences of wheat genomes with high sequence identity (≥70%) were retrieved with complete gene transcript, location in IWGSC RefSeq v1.0, CDS, cDNA, and protein sequences and a local wheat database was developed for further analysis. Genes with duplicate stable gene IDs were identified and eliminated from the further analysis.

3.7.2. Gene structure, gene statistics and phylogenetic analysis

The gene structure (exon and intron boundaries) of each gene available in the local database was defined by aligning CDS and the corresponding complete gene script by using a gene features visualizing server namely Gene Structure Display Server (GSDS v.2.0) developed at Perkin University, China (Hu *et al.*, 2015). Multiple sequence alignment (MSA) of all unspliced gene transcripts, CDS and AA sequences of genes available in the local data base was then performed in MEGA-X (Kumar *et al.*, 2018) by using ClustalW as third party with default settings. General statistics of these sequences like nucleotide composition, nucleotide pair frequency (16 pair bi-directional) and amino acid composition were calculated in MEGA-X. Followed to this a maximum likelihood (MLk) phylogenetic tree showing the evolutionary relationship among all the genes under study was obtained.

3.7.3. Gene localization

MapInspect software (http://www.softsea.com/download/MapInspect.html) was employed to visualize the distribution of *TaFruc* genes (*Triticum aestivum fructans* gene) in the wheat genome according to their initial position on chromosome and length of chromosome.

3.7.4. Identification of gene duplication and divergence rate

Gene duplication in *TaFruc* genes were identified by using BLAST algorithm. All the CDS of identified genes of were BLASTn ($E = 1e^{-10}$, sequence similarity >90%) to each other in Blast2go tool (Conesa and Götz, 2008). Gene duplication was further classified as per Liu and Ekramoddoullah (2009): (i) Tandem duplicates (TD): adjacent duplicate genes on the same chromosome, and (ii) Segmental duplicates (SD): duplicate genes separately located on a same or different chromosome.

Followed to this, synonymous (K_s) and non-synonymous (K_a) substitutions in those duplicate genes were identified by using DNasp v6.0 software (Librado and Rozas, 2009) and on the basis of ratio between K_s and K_a (K_a/K_s) selection pressure was defined as stabilizing selection ($K_a/K_s < 1$), neutral selection ($K_a/K_s = 1$), and positive selection ($K_a/K_s > 1$) (Gautam *et al.*, 2019). Furthermore, considering the rate of synonymous substitutions 6.5×10^{-9} substitutions per year time of divergence, time of divergence (T_{div}) among duplicate genes was calculated with following formula and expressed in millions of years (MY):

$$\mathrm{T_{div}} = \frac{\mathrm{K_s}}{(2 \times 6.5 \times 10^{-9})} \times 10^{-6}\ \mathrm{MY}$$

3.7.5. Identification of *cis*-regulatory elements

1.5 kb downstream and upstream sequence of *TaFruc* genes were annotated with PlantCARE database (Lescot, 2002) to identify *cis*-regulatory elements (CREs).

3.7.6. Analysis of amino acid sequences

Conserved domains (CD) in protein sequences coded by *TaFruc* genes were identified by using NCBI Batch CDD-search (Marchler-Bauer *et al.*, 2017). Sequence properties of motifs were retrieved with MEME suite (Bailey *et al.*, 2009). Physicochemical properties *viz.* peptide length (PL), molecular weight (MW), isoelectric point (pI), instability index (II) and grand average of hydropathy (GRAVY) were calculated by using ProtParam server of Expasy tool (Gasteiger *et al.*, 2005). Sub-cellular localization of these proteins was then predicted using PLANT-mPLoc (Chou and Shen, 2010).

3.7.7. Functional enrichment analysis

A singular enrichment analysis (SEA) in combination with hyper statistical method and Bonoferroni multi-test adjustment method were used to predict the gene ontology of the identified wheat *TaFruc* genes at significance level (p) 0.05 by using AgriGO server v2.0 (Tian *et al.*, 2017). To identify relation of *TaFruc* proteins KEGG pathway enrichment analysis was conducted with default parameters (Du *et al.*, 2014). Chemical-Protein interaction (CPI) networking analysis was conducted by BLASTing the *TaFruc* protein sequences in STITCH v.5.0 (http://stitch.embl.de/) database, while considering *Hordeum vulagare* and *Arabidopsis thaliana* as model species.

3.7.8. *In silico* expression profiling of Ta*Fruc* genes

An *in silico* expression profiling of identified candidate genes was performed using two online wheat expression databases *viz.* WheatExp (a wheat RNA-seq expression database of polyploid wheat11) and expVIP (Borrill *et al.*, 2016; Pearce *et al.*, 2015).

3.7.9. Targeting simple sequence repeats (SSR) and miRNA

SSRs were identified in the complete gene script of each identified wheat *TaFruc* genes and for them SSR molecular markers were developed using BatchPrimer3v1.0 (http://probes.pw.usda.gov/batchprimer3/). To identify the potential miRNA targets in these *TaFruc* genes a web based psRNATarget server was used with default parameters (Dai *et al.*, 2018).

CHAPTER-IV

RESULTS

The results obtained from present study ‘Genome wide association mapping for stem water-soluble carbohydrates in bread wheat (*Triticum aestivum* L.) under terminal water stress condition’ have been presented in this chapter under following headings:

4.1. Meteorological observations
4.2. Mean performance of genotypes
4.3. Drought susceptibility index (DSI)
4.4. Analysis of variance (ANOVA)
4.5. Estimates of genetic components
4.6. Correlation studies
4.7. Multivariate analysis of genetic divergence
4.8. Genome wide association mapping
4.9. *In-silico* identification of fructans metabolic genes

4.1. Meteorological observations

Meteorological observations reveled significant difference in weather conditions across experimental sites and seasons which signify (**Figure 4.1**) the suitability of multilocational trial for exploiting maximum phenotypic variations among the study material. During *Rabi 2017-18* for Hisar location minimum and maximum temperature ranged between 1.0-23.0°C and 12.4-37.4°C whereas, at Karnal location the rang was 2.2-19.4°C and 10.0-36.0°C, respectively. Likewise, during *Rabi 2018-19* range of minimum temperature at different experimental site was, -0.3-19.0°C (Hisar), 2.00-19.60 °C (Karnal), 5.1-22.2°C (Pune). Similarly, the range of maximum temperature was 13.0-37.0 °C (Hisar), 6.4-36.0 °C (Karnal) and 23.6-40.0 °C. Furthermore, in both cropping seasons, Karnal had maximum (31) number of rainy days followed by Hisar (7) and Pune (1). In *Rabi 2017-18*, maximum rainfall welcomed at different experimental sites was 34.20 mm (Karnal, 8 rainy days) and 10.9 mm (Hisar, 3 rainy days) whereas, in *Rabi 2018-19* it was 10.20 mm (Karnal, 31 rainy days), 8.80 mm (Hisar, 7 rainy days) and 0.16 mm (Pune, 1 rainy day). Average soil moisture percentage (w/w) in water stressed field during *Rabi 2017-18* and *2018-19* was 15.5% and 13.8% at Hisar, 8.2% and 9.6% Karnal (ROS), respectively and 13.10% at Pune in *Rabi* 2018-19.

Figure 4.1: Weather data for *Rabi* 2017-18 and 2018-19 taken at all three locations. In figure, solid lines indicate maximum temperature (ºC), dashed lines indicate minimum temperature (ºC) and bars indicate rainfall (mm)

4.2 Mean performance of genotypes

Total 302 bread wheat genotypes were evaluated for 14 phenological and agronomical traits and 6 biochemical traits at three locations under three different water regimes *viz.* irrigated, rainfed and drought for two consecutive cropping seasons *i.e.*, *Rabi* 2017-18 and *Rabi* 2018-19 consisting of total 10 environments (**Table 4.1**).

Data has been analyzed for individual environments and environments pooled over three different water regimes. Henceforth in the results, E01-E10 will denote individual environments and notations IR, RF and DT will be used for pooled results. Results of mean performance are as follow:

Table 4.1: Description of ten environments considered for the evaluation of study material

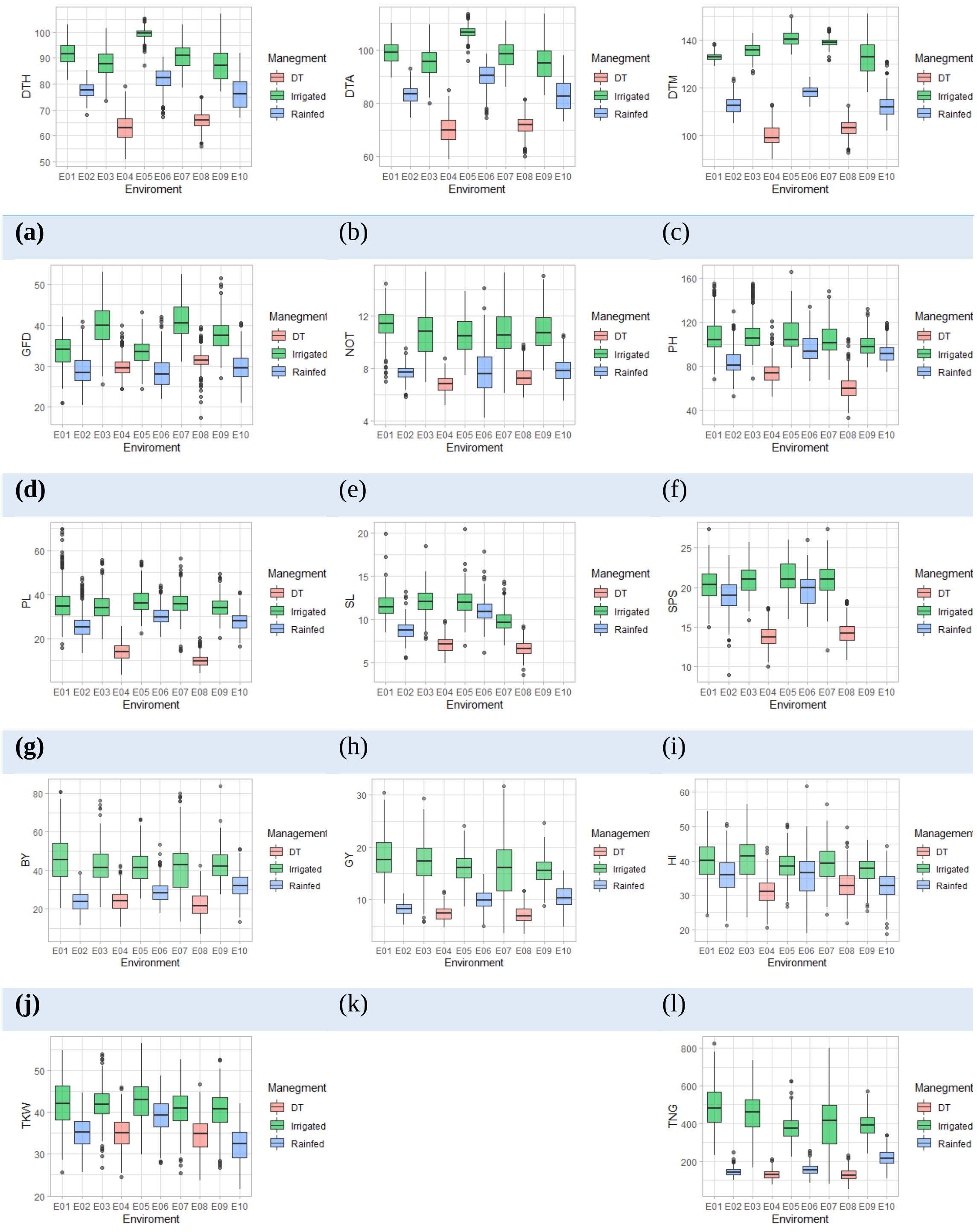
Environment code	Location	Water regime	Cropping season
E01	Hisar	Irrigated (IR)	*Rabi* 2017-18
E02	Hisar	Rainfed (RF)	*Rabi* 2017-18
E03	Karnal	Irrigated (IR)	*Rabi* 2017-18
E04	Karnal	Drought (DT)	*Rabi* 2017-18
E05	Hisar	Irrigated (IR)	*Rabi 2018-19*
E06	Hisar	Rainfed (RF)	*Rabi 2018-19*
E07	Karnal	Irrigated (IR)	*Rabi 2018-19*
E08	Karnal	Drought (DT)	*Rabi 2018-19*
E09	Baramati, Pune	Irrigated (IR)	*Rabi 2018-19*
E10	Baramati, Pune	Rainfed (RF)	*Rabi 2018-19*
IR	Hisar, Karnal, Baramati	Irrigated (IR)	Pooled
RF	Hisar, Baramati	Rainfed (RF)	Pooled
DT	Karnal	Drought (DT)	Pooled

4.2.1 Mean performance for agro-phenological traits

Box plots shown in **Figure 4.2** give a comparative overview of the mean performance of 302 wheat genotypes for four phenological ten and agronomical traits under environments E01-E10 whereas, density curves in **Figure 4.3** give an idea about distribution of different traits under three different water regimes *viz.* irrigated (IR), rainfed (RF) and drought (DT) on pooled mean basis. Detailed descriptive statistics for all the traits has been given in **Annexure 2 (pp: XI)**.

4.2.1.1 Phenological traits

The study material evaluated for four phenological traits *viz.* days to heading (DTH), days to anthesis (DTA), days to maturity (DTM) and grain filling duration (GFD). In all the environments, DTH, DTA, DTM and GFD ranged from 51.0 (E04) to 107.0 (E09), 59.0 (E04) to 113.5 (E05 and E09), 90.0 (E04) to 151.0 (E09) and 20.5 (E02) to 53.0 (E03) days, respectively. In well-watered environments (irrigated conditions), DTH, DTA, DTM and GFD ranged between 73.5 (E02) and 107.0 (E09), 80.0 (E03) and 113.5 (E05 and E09), 118.0 (E09) and 151.0 (E09) and 21.0 (E01) and 53.0 (E03) days, respectively. In rainfed environments values for ranged from 67.0 (E06) to 92.0 (E10), 73.0 (E10) to 98.0 (E10), 102.0 (E10) to 131.0 (E10) and 20.5 (E02) to 42.0 (E06) days for DTH, DTA, DTM and GFD, respectively. Among complete drought stress environments the earliest and latest heading (51.0-79.0 days), anthesis (59.0-85.0 days) and maturity (90.0-113.0 days) were reported in E04. Furthermore, minimum GFD was reported in E08 (17.5 days) whereas, maximum in E04 (40.0 days).



(a) (b) (c)

(d) (e) (f)

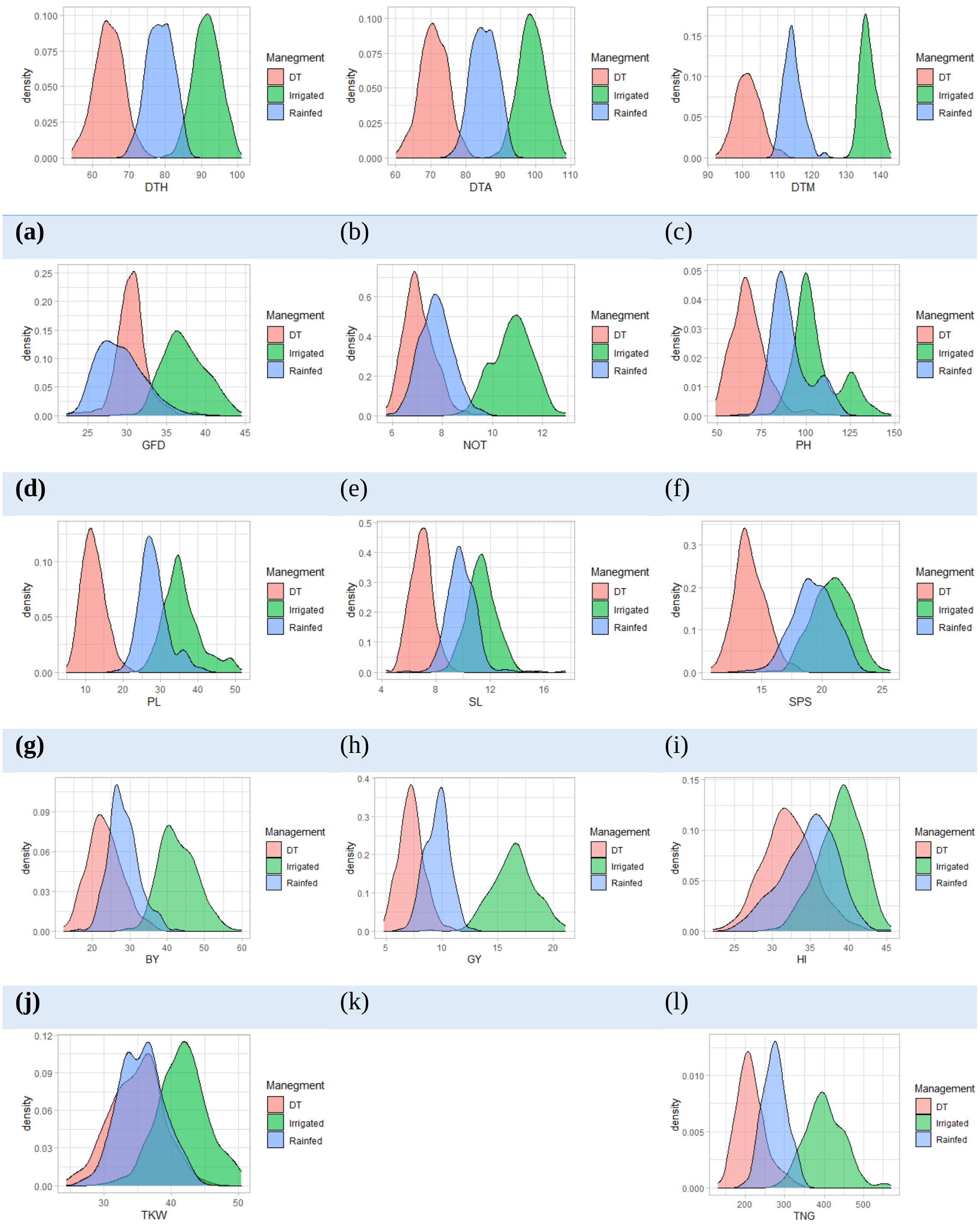
(g) (h) (i)

(j) (k) (l)

(m) (n)

Figure 4.2 (a-n): Mean performance of bread wheat genotypes for studied agro-phenological traits under different environments

[In figure, DTH: days to heading; **DTA:** days to anthesis; **DTM:** days to maturity; **GFD:** grain filling duration; **NOT:** number of tillers; **PH:** plant height (cm); **PL**: peduncle length (cm); **SL:** spike length (cm), **SPS:** spikelet per spike; **BY:** biological yield (g plant^{-1}); **GY:** grain yield (g plant^{-1}); **HI:** harvest index (%); **TKW:** thousand kernel weight (g); **TNG:** number of grains plant^{-1}; **DT:** drought**]**



(a) (b) (c)

(d) (e) (f)

(g) (h) (i)

(j) (k) (l)

(m) (n)

Figure 4.3 (a-n): Density curves of studied agro-phenological traits under different environments in bread wheat genotypes

[In figure, DTH: days to heading; **DTA:** days to anthesis; **DTM:** days to maturity; **GFD:** grain filling duration; **NOT:** number of tillers; **PH:** plant height (cm); **PL**: peduncle length (cm); **SL:** spike length (cm), **SPS:** spikelet per spike; **BY:** biological yield (g plant^{-1}); **GY:** grain yield (g plant^{-1}); **HI:** harvest index (%) **TKW:** thousand kernel weight (g); **TNG:** number of grains plant^{-1}; **DT:** drought**]**

Population mean for DTH, DTA, DTM and GFD ranged between 87.7 (E09) and 99.5 (E05), 95.2 (E09) and 106.8 (E05), 132.8 (E01) and 140.0 (E05), and 33.6 (E01) and 41.3 (E07) days, respectively in environments consisting of irrigated conditions, 76.3 (E10) and 81.9 (E06), 82.7 (E10) and 89.8 (E06), 112.6 (E02) and 118.3 (E06), and 29.1 (E02) and 28.4 (E06) days, respectively in environments with rainfed water regimes and 62.8 (E04) and 66.0 (E08), 69.9 (E04) and 71.9 (E08), 99.7 (E04) and 103.2 (E08), and 29.8 (E04) and 31.2 (E08) days, respectively under zero water regime (complete drought stress) **(Figure 4.2a-d)**.

For pooled data set *viz.* irrigated (IR), rainfed (RF) and drought (DT) population mean values were recorded as 914 (80.5-101.0), 78.5 (69.5-86.5) and 64.7 (54.2-75.5) days, respectively for DTH, 98.8 (88.6-108.7), 83.3 (75.6-93.5) and 70.9 (60.2-81.0) days, respectively for DTA, 136.2 (130.9-142.7), 114.4 (109.0-123.8) and 101.5 (92.2-112.0) days, respectively for DTM, and 37.3 (29.7-44.5), 29.1 (22.3-39.6) and 30.5 (23.0-38.7) days, respectively for GFD **(Figure4.3a-d)**.

4.2.1.2 Agronomical traits

A total of 10 agronomical traits including yield were recorded to evaluate the study material under different environments (E01-E10) and water regimes (IR, RF and DT), results of which are as follow:

i) Number of tillers plant^{-1} (NOT)

Among environments, minimum 4.2 tillers plant^{-1} recorded in E06 whereas, maximum 15.3 tillers plant^{-1} in E03. Population mean of different environments ranged between 6.8 (E04) and 11.3 (E01) tillers plant^{-1}. Among environments with complete irrigation, NOT ranged between 10.8 (E01) and 11.3 (E09) tillers plant^{-1} whereas, among environments pertaining to rainfed and complete drought it was 7.8 and 7.6 tillers plant^{-1}, respectively. The pooled population mean for NOT under different water regimes *viz.* IR, RF and DT was 10.7 (8.6-12.9), 7.7 (5.8-9.6) and 7.0 (5.7-9.6) tillers plant^{-1}, respectively **(Figure 4.2e and 4.3e).**

ii) Plant height (PH)

Shortest PH was recorded in E08 (33.6 cm) whereas, tallest in E05 (165.1 cm). Population mean for PH in different environments ranged between 61.1 (E08) and 109.0 cm (E03). PH ranged from 67.5 (E07) to 165.0 cm (E05) among irrigated environments for individual genotypes and population mean ranged between 99.3 (E09) and 109.0 cm (E03). Likewise, among rainfed environments, PH for individual genotype ranged between 52.9 (E02) and 133.9 cm (E06) and 52.4 (E04) and 120.4 cm (E04) among drought environments. Population mean ranged between 119.3 (E10) and 133.9 cm (E06) for rainfed environments and 61.1 (E08) and 74.5 cm (E04) for drought environments. Pooled population mean of PH under IR, RF and DT was 105.9 cm (76.0-147.6 cm), 91.3 cm (64.5-120.2 cm) and 67.7 cm (49.3-112.6 cm), respectively **(Figure 4.2f and 4.3f).**

iii) Peduncle length (PL)

Length of peduncle ranged from 3.6 (E04) to 69.6 cm (E01) among environments whereas, population mean ranged between 10.14 (E08) and 36.2 cm (E07). Under different environments pertaining to IR, RF and DT conditions values for PL ranged from 14.2 (E07) to 69.6 cm (E01), 13.2 (E02) to 47.5 cm (E02) and 3.6 (E04) to 25.1 cm (E04), respectively. Likewise, population mean ranged from 34.2 (E09) to 36.2 cm (E07), 26.4 (E02) to 30.4 cm (E06) and 10.1 (E08) to 14.0 cm (E04) in IR, RF and DT conditions, respectively. Pooled population mean under IR, RF, and DT was 35.6 cm (24.6-51.4 cm), 28.1 cm (18.2-42.0 cm) and 12.0 cm (5.0-24.6 cm), respectively **(Figure 4.2g and 4.3g).**

iv) Spike length (SL)

Among environments minimum and maximum values for SL were recorded in E08 (3.6 cm) and E05 (20.4 cm), respectively. Likewise, population mean for SL among environments ranged between 7.1 (E04) and 12.1 cm (E03). Furthermore, SL varied from 6.9 (E07) to 20.4 cm (E05), 5.5 (E02) to 17.8 cm (E06) and 3.6 (E08) to 19.8 cm (E04) among environments characterized by irrigated, rainfed and drought conditions, respectively. Overall population mean for SL under different water regimes *viz.* IR, RF and DT was 11.3 cm (8.4-17.6 cm), 9.8 cm (5.8-14.8 cm) and 6.9 cm (4.3-9.4 cm), respectively **(Figure 4.2h and 4.3h).**

v) Spikelet spike^{-1} (SPS)

Number of spikelet per spike varied from 9.0 (E02) to 27.0 (E01) among environments whereas, population mean ranged between 13.8 (E04) and 20.9 (E07). Among irrigated environments, SPS laid between 15.0 (E01) and 27.3 (E01) and among rainfed and drought environments it was between 9.0 (E02) and 26.0 (E06), and 9.8 (E04) and 18.2 (E08), respectively. Population mean ranged from 20.2 to 21.4 among irrigated environments, 18.9-19.7 among rainfed environments and 13.8 and 14.2 among drought environments. Pooled mean was recorded as 20.8 (15.8-25.6), 19.3 (13.5-23.1) and 14.0 (10.8-17.8) under IR, RF and DT conditions, respectively **(Figure 4.2i and 4.3i).**

vi) Biological yield (BY)

BY varied from 3.2 (E08) to 83.6 g plant^{-1} (E09) and population mean was between 10.3 (E08) and 46.2 g plant^{-1} (E01) among environments. Furthermore, among environments pertaining to irrigated conditions, it ranged from 13.2 (E07) to 8.6 g plant^{-1} (E09) with population mean ranging from 41.2 (E07) to 46.2 g plant^{-1} (E01) and from 6.6 (E02) to 35.6 g plant^{-1} (E10) and population mean between 1.8 (E02) and 21.6 g plant^{1} (E10) for environments pertaining to rainfed conditions. Under drought stressed environments, range of 3.2 (E08)-28.3 g plant^{-1} (E04) with range of population mean 10.3 (E08)-16.1 g plant^{-1} (E04) was recorded. Pooled population mean under IR, RF and DT water regimes was recorded as 42.9 g plant^{-1} (28.5-60.9 g plant^{-1}), 18.2 g plant^{-1} (1.4-27.4 g plant^{-1}) and 13.2 g plant^{-1} (3.6-6.8g plant^{-1}), respectively **(Figure4.2j and 4.3j).**

vii) Grain yield plant^{-1} (GY)

A range of 3.4 (E08)-31.6 (E07) g plant^{-1} with population mean ranging between 7.1 (E08) and 18.2 (E01) g plant^{-1} was reported among environments. The range for this trait among environments provided with irrigation laid between 3.5 (E07) and 31.6 (E07) g plant^{-1} with a population mean ranging from 15.7 (E09) to 18.2 (E01) g plant^{-1} whereas, among rainfed environments and drought conditions it ranged from 4.8 (E10) to 15.5 (E10) g plant^{-1} and 3.4 (E08) to 11.6 (E08) g plant^{-1} with population mean 8.2 (E02)-10.5 (E10) g plant^{-1} and 7.1 (E08)-7.4 (E04) g plant^{-1}, respectively. Pooled population mean of GY was recorded as 16.4 g plant^{-1} (8.99-21.1 g plant^{-1}), 9.6 g plant^{-1} (6.2-13.8 g plant^{-1}) and 7.2 g plant^{-1} (4.8-10.9 g plant^{-1}) for IR, RF and DT, respectively **(Figure 4.2k and 4.3k).**

viii) Harvest index (HI)

Mean values for different genotypes among environments ranged from 18.8% (E10) to 61.7% (E06) with population mean from 32.8% (E10) to 40.5% (E04). Environments pertaining to IR, RF and DT showed range of mean values for different genotypes between 23.6% (E03) and 56.6% (E07), 18.8% (E10) and 61.7% (E06), 20.6% (E04) and 49.8% (E08) with range of population mean 37.3% (E09)-40.2% (E01), 32.8% (E10)-35.9% (E02), and 31.2% (E04)-33.0% (E08), respectively. However, pooled population mean under IR, RF and DT was 38.8% (29.8-45.0%), 32% (22.2-41.6%) and 34.8% (25.4-45.5%), respectively **(Figure 4.2l and 4.3l).**

ix) Thousand kernel weight (TKW)

Among environments, for different genotypes TKW ranged from 21.9 (E10) to 56.3 g (E05) with population mean ranging between 32.3 (E10) and 42.9 g (E05). Mean value of TKW for genotypes among different environments provided with irrigated, rainfed and drought conditions laid from 25.4 (E07) to 56.3 g (E05), 21.6 (E10) to 48.2 g (E06) and 23.5 (E08) to 46.6 g (E08) with population mean 40.4 (E09)-42.9 g (E05), 32.3 (E10)-39.2 g (E06) and 34.6 (E08)-35.1 g (E04), respectively. Pooled population mean for different water regimes *viz*. IR, RF and DT was recorded as 41.7 g (30.4-50.3 g), 35.6 g (26.6-44.4 g), and 34.8 g (24.4-45.3 g), respectively **(Figure 4.2m and 4.3m).**

x) Total number of grains plant^{-1} (TNG)

Among all the environments TNG for different genotypes ranged from 80.5 (E07) to 874.7 grains plant^{-1} (E07) with population mean range of 212.4 (E08)-438.2 grains (E01). Mean value of genotypes among different environments provided with irrigated, rainfed and drought conditions laid from 80.5 (E07) to 238.0 grains (E09), 138.3 (E06) to 171.1 grains (E02) and 86.3 (E08) to 388.2 grains (E08) with population mean range of 378.3 (E05)-438.2 (E01) grains, 240.0 (E02)-328.3 grains (E10) and 212.4 (E08)-408.5 (E04) grains, respectively. Pooled population mean for different water regimes *viz*. IR, RF and DT was

401.7 grains (284.4-468.8 grains), 274.7 grains (192.2-353.1 grains), and 214.5 grains (130.7-336.5 grains), respectively **(Figure 4.2n and 4.3n).**

4.2.2 Mean performance for biochemical traits

Content of glucose, fructose, sucrose, fructans, total water-soluble sugars (WSCs) and total non-structural carbohydrates was estimated in all the genotypes under 8 environments (E01-E08) using Fourier-transform near infrared spectroscopy (FT-NIR). Partial least square regression (PLS) assisted calibration models (**Table 4.2**) were developed from FT-NIR spectra acquired between wave numbers (v) 10000 cm^{-1} and 4000 cm^{-1} on wheat peduncles sampled from 150 genotypes (**Figure 4.4a**). Among various mathematical pre-treatments, single derivative base line correction followed by 2nd order Savitzkey-Golay derivation with 15 points significantly reduced noises and redundancies of raw spectra (**Figure 4.4b**).

Figures 4.5 (a-e) revealed the highest regression coefficients for glucose, fructose, sucrose, fructans and WSCs associated with wave numbers 5282-5278 cm^{-1}, 4362-4364 cm^{-1}, 5270-5264 cm^{-1}, 5182 cm^{-1} and 4418 cm^{-1}, respectively. Values for glucose, fructose, sucrose, fructans and WSCs in reference set ranged from 11.9 to 14.8 mg g^{-1}, 8.7 to 13.9 mg g^{-1}, 32.5 to 38.8 mg g^{-1}, 41.0 to 154.0 mg g^{-1} and 26.6 to 135.1 mg g^{-1}, respectively**.** Predicted values for glucose, fructose, sucrose, fructans and WSCs ranged from 11.8 to 14.7 mg g^{-1}, 8.7 to 14.1 mg g^{-1}, 32.1 to 38.2 mg g^{-1}, 37.5 to 152.7 mg g^{-1} and 22.0 to 136.2 mg g^{-1}, respectively in calibration set whereas, for full validation set these values were 11.7-14.5 mg g^{-1}, 8.6-14.3 mg g^{-1}, 32.1-38.1 mg g^{-1},

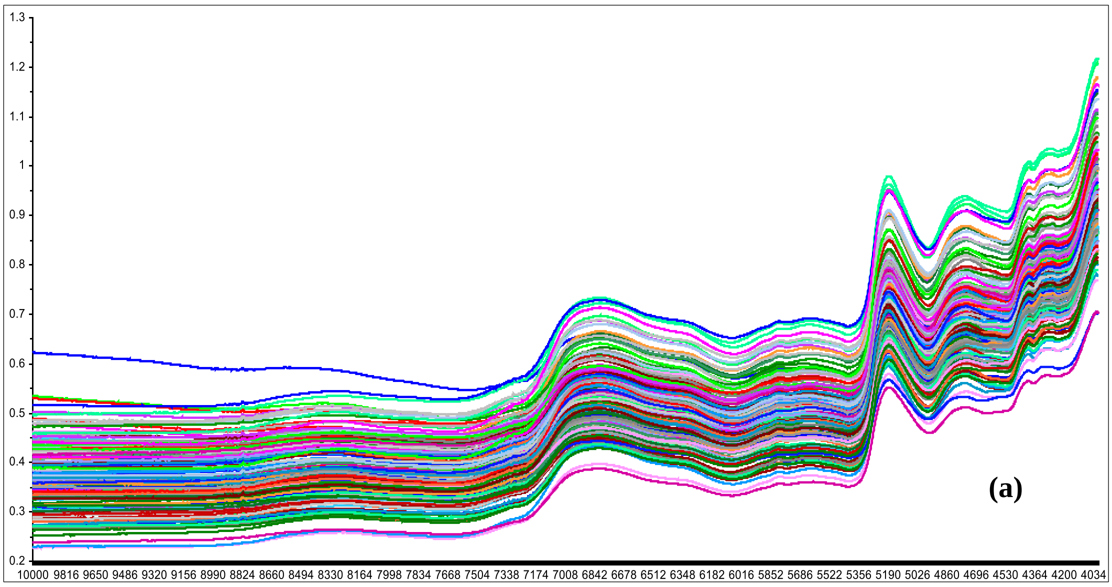


Figure 4.4 (a): Raw spectra of modelling set acquired between 10000cm^{-1} and 4000cm^{-1} near infrared red (NIR)

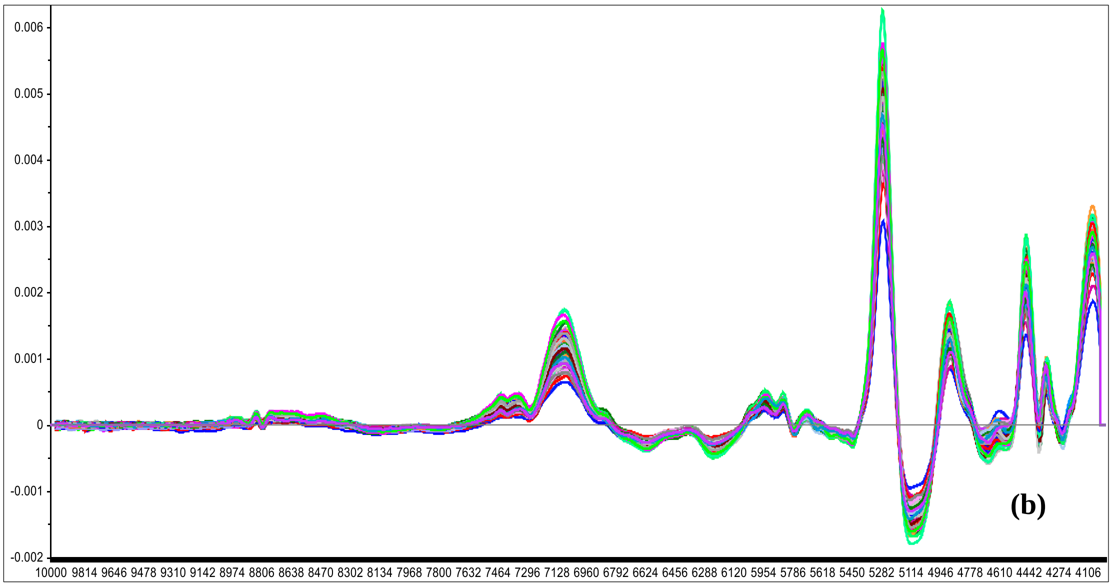


Figure 4.4 (b): **Processed spectra of modelling set acquired between 10000cm^{-1} and 4000cm^{-1} near infrared red (NIR)**

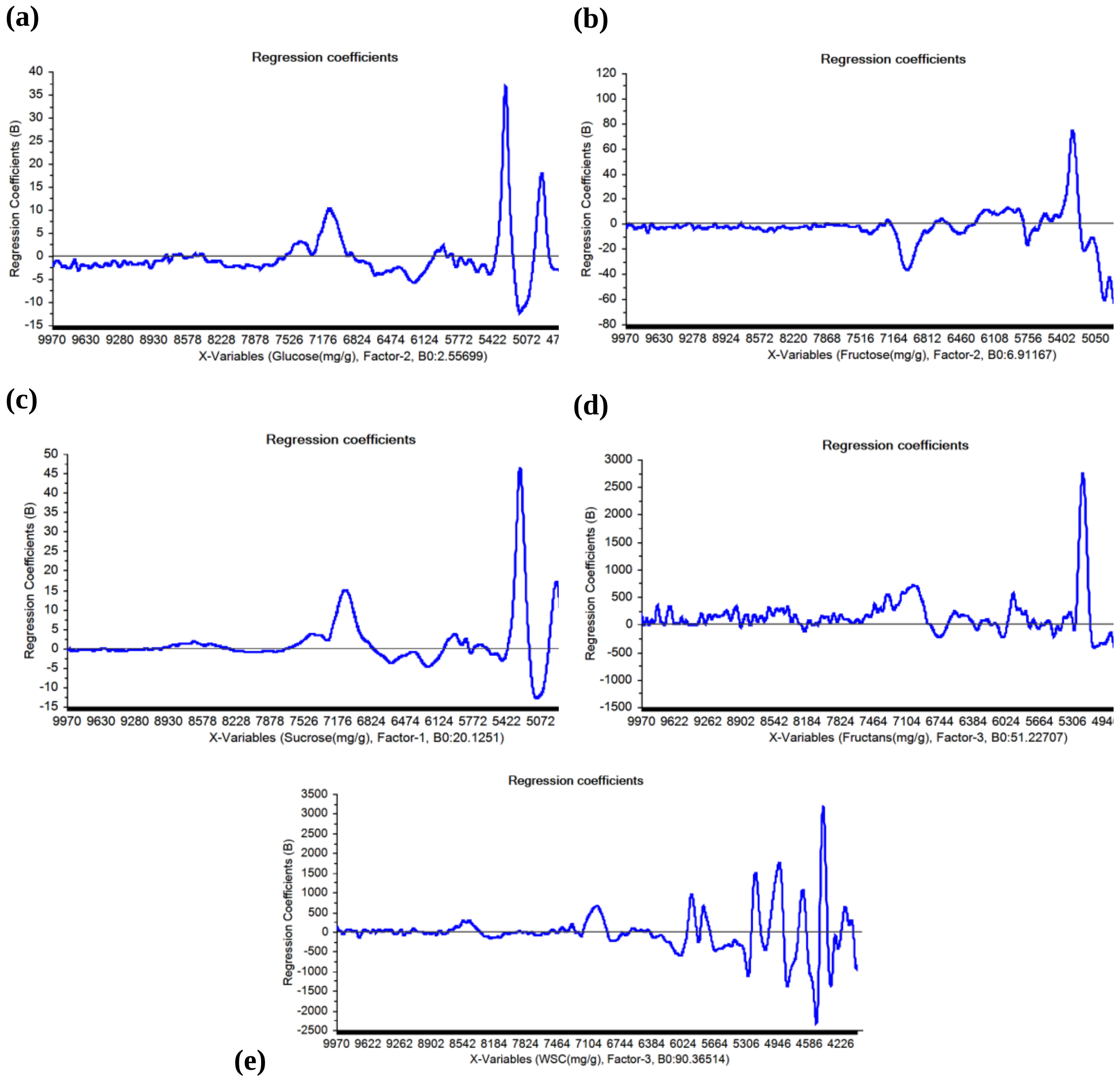


Figure 4.5 (a-e): **Regression coefficients and peaks associated with different biochemical traits**

39.4-142.1 mg g^{-1} and 20.9-132.7 mg g^{-1}, respectively. In calibration set, values for root mean square error for prediction (RMSEP) ranged between 0.12 (glucose) to 6.5 mg g^{-1} (fructans), 3.7 (sucrose) to 5.1 (glucose) for ratio of standard error of performance to standard deviation (RPD) and 0.81 (fructose) to 0.96 (glucose) for R^2. In contrast to this, in validation set range of 0.18 (glucose) to 11.5 mg g^{-1} (fructans), 2.4 (fructans) to 3.5 (glucose) and 0.71 (fructose) to 0.93 (glucose) was recorded for RMSEV, RPD and R^2, respectively.

These models were used to quantify the amount of glucose, fructose, sucrose, fructans and WSCs in study material. Content of TNSC was calculated as an addition of glucose, fructose, sucrose and fructans. Detailed results are shown in **Table 4.3**.

i) Total non-structural carbohydrates (TNSC)

TNSC content varied from 57.0 (E08) to 397.3 mg g^{-1} (E08) whereas, population mean was between 128.3 (E05) and 209.2 mg g^{-1} (E08) among all the environments. Among environments pertaining to irrigated conditions, it ranged from 57.0 (E07) to 312.5 mg g^{-1} (E07) with population mean ranging from 128.3 (E05) to 157.1 mg g^{-1} (E03) and from 93.0 (E06) to 259.7 mg g^{-1} (E06) with population mean between 154.5 (E02) and 160.2 mg g^{1} (E06) for environments pertaining to rainfed conditions. Under drought stressed environments range of 90.9 (E08)-397.3 (E08) mg g^{-1} (E08) with population mean of range 197.7 (E04)-209.2 (E08) mg g^{-1} was recorded. Pooled population mean under IR, RF and DT water regimes was 139.3 mg g^{-1} (102.9-181.9 mg g^{-1}), 157.3 mg g^{-1} (110.5-205.2 mg g^{-1}) and 198.5 mg g^{-1} (128.2-304.4 mg g^{-1}), respectively.

ii) Glucose

Glucose content ranged from 2.9 (E07) and 18.9 mg g^{-1} (E08) whereas, range of population mean was 11.0 (E07)-13.9 mg g^{-1} (E04) among all the environments. It ranged from 3.6 (E07) to 15.7 mg g^{-1} (E05) with population mean 11.0 (E07)-12.0 mg g^{-1} (E01) in irrigated environments and from 18.3 (E06) to 11.2 mg g^{-1} (E06) with population mean between 13.92 (E02) and 13.95 mg g^{1} (E03) in rainfed environments. Range of 3.0 (E08 and E04)-18.9 mg g^{-1} (E08) with population mean range 23.9 (E08)-13.9 mg g^{-1} (E04) was recorded under drought stressed environments. Pooled population mean under IR, RF and DT water regimes was recorded as 11.5 mg g^{-1} (8.9-13.6 mg g^{-1}), 13.9 mg g^{-1} (11.6-17.6 mg g^{-1}) and 13.9 mg g^{-1} (8.6-16.9 mg g^{-1}), respectively.

Table 4.2: Summary statistics of selected partial least square regression models for prediction of five biochemical traits

Traits	Reference			Calibration						Validation					
	Mean	Min	Max	Mean	Min	Max	RMSEP	RPD	R^2	Mean	Min	Max	RMSEV	RPD	R^2
WSC	86.30	26.69	135.15	86.30	22.04	136.26	6.49	4.45	0.94	86.21	20.93	132.70	8.64	3.35	0.91
Fructans	73.26	41.08	154.07	73.26	37.57	152.79	6.59	4.34	0.94	74.73	39.41	142.11	11.50	2.48	0.84
Sucrose	34.96	32.52	38.83	34.96	32.15	38.29	0.50	3.75	0.92	34.94	32.15	38.15	0.56	3.31	0.91
Glucose	13.12	11.90	14.81	13.12	11.85	14.71	0.12	5.15	0.96	13.12	11.79	14.58	0.18	3.58	0.93
Fructose	11.15	8.72	13.96	11.15	8.75	14.13	0.69	3.76	0.81	11.12	8.66	14.34	0.92	2.83	0.71

RMSEP/V: root mean square error of prediction/validation; **RPD:** ratio of standard error of performance to standard deviation

Table 4.3: Descriptive statistics of soluble sugars estimated in bread wheat genotypes (*Triticum aestivum* L.) under different environments and water regimes during *Rabi* 2017-18 and *Rabi* 2018-19

Traits (mg/g)	Statistics	Environments								Pooled		
		E01	E02	E03	E04	E05	E06	E07	E08	IR	RF	DT
TNSC	*Min*	78.08	106.01	77.34	127.37	76.97	93.00	57.00	90.91	102.92	110.51	128.83
	Max	184.49	234.84	267.45	339.01	204.61	259.76	312.59	397.33	181.97	205.23	304.42
	Mean	131.01	154.55	157.11	197.78	128.36	160.23	140.80	209.25	139.32	157.39	198.59
	σ	17.82	20.38	37.09	40.53	21.55	25.63	45.92	48.45	16.63	15.99	29.29
Fructans	*Min*	25.91	44.56	26.83	64.48	23.80	32.63	12.73	31.70	50.22	48.62	65.82
	Max	125.31	161.53	211.58	266.51	143.78	185.17	251.00	315.47	125.40	136.74	236.05
	Mean	76.94	91.99	104.61	133.40	74.33	96.80	89.13	144.84	86.25	94.39	134.34
	σ	16.93	18.61	35.62	38.18	20.12	23.57	43.69	45.22	15.81	14.66	27.78
Fructose	*Min*	6.94	8.70	7.67	8.68	6.55	8.18	5.17	6.12	8.03	9.11	9.21
	Max	12.91	13.82	14.80	17.88	14.06	15.28	18.11	20.57	12.73	13.74	16.86
	Mean	10.03	11.48	10.58	12.28	10.22	12.27	9.91	12.28	10.19	11.88	12.24
	σ	1.02	1.04	1.48	1.79	1.22	1.23	2.65	3.13	0.87	0.83	1.40
Glucose	*Min*	9.96	11.69	9.02	3.00	8.49	11.24	2.69	3.00	8.91	11.61	8.60
	Max	14.99	18.80	14.83	18.48	15.72	18.93	14.93	18.98	13.62	17.63	16.96
	Mean	12.07	13.92	11.13	13.99	11.96	13.95	11.08	13.97	11.56	13.93	13.95
	σ	0.80	1.20	0.98	1.51	1.00	1.33	1.18	1.52	0.52	0.87	1.03
Sucrose	*Min*	28.94	34.11	27.68	22.67	26.91	33.50	18.79	22.67	27.52	34.06	30.36
	Max	36.16	43.71	36.27	44.30	37.24	44.03	36.60	45.74	34.29	42.11	42.47
	Mean	31.97	37.16	30.78	38.11	31.84	37.21	30.68	38.16	31.32	37.18	38.06
	σ	1.11	1.66	1.41	2.11	1.38	1.85	1.73	2.21	0.73	1.21	1.45
WSC	*Min*	76.77	85.07	96.59	99.85	56.39	65.69	63.95	68.26	112.73	84.76	118.77
	Max	208.87	216.45	213.49	243.50	220.32	233.26	236.48	260.98	194.96	214.91	224.10
	Mean	154.72	152.64	160.42	180.52	141.67	144.85	160.47	170.19	154.32	148.75	178.58
	σ	26.31	28.76	22.40	28.96	29.93	34.53	30.75	37.31	14.35	22.91	20.92

TNSC: total non-structural carbohydrates; **WSC:** total water-soluble carbohydrates **IR:** irrigated; **RF:** rainfed; **DT:** Drought; **σ:** standard deviation

iii) Fructose

Among environments, fructose ranged from 5.1 (E07) to 20.5 mg g^{-1} (E08) with population mean 9.9 (E07) to 12.2 mg g^{-1} (E04 and E08). Mean values ranged from 5.1 (E07) to 18.1 mg g^{-1} (E07), 11.2 (E06) to 18.9 mg g^{-1} (E06) and 6.1 (E08) to 20.5 mg g^{-1} (E08) with population mean of 9.9 (E07)-10.5 mg g^{-1} (E03), 11.4 (E02)-12.2 mg g^{-1} (E06) and 12.2 mg g^{-1} (E04 and E08) among different environments provided with irrigated, rainfed and drought conditions, respectively. Pooled population mean for different water regimes *viz*. IR, RF and DT were 11.5 mg g^{-1} (8.9-13.6 mg g^{-1}), 13.9 mg g^{-1} (11.6-17.6 mg g^{-1}) and 13.9 mg g^{-1} (8.6-16.9 mg g^{-1}), respectively.

iv) Sucrose

A range of 18.7 (E07)-34.1 (E02) mg g^{-1} with population mean ranging between 30.6 (E07) and 38.1 mg g^{-1} (E08) was reported among environments. Range of sucrose among environments pertaining to irrigation laid between 18.7 (E07) and 36.6 mg g^{-1} (E07) with a population mean ranging from 30.6 (E07) to 31.9 mg g^{-1} (E01) whereas, among environments provided with rainfed and drought conditions it ranged from 33.5 (E06) to 44.0 mg g^{-1} (E06) and 22.6 (E04 and E08) to 44.3 mg g^{-1} (E08) with population mean range as 37.16 (E06)-37.21 mg g^{-1} (E02) and 38.11 (E04)-38.16 mg g^{-1} (E08), respectively. Pooled population mean for IR, RF and DT was recorded as 31.3 mg g^{-1} (27.5-34.2 mg g^{-1}), 37.1 mg g^{-1} (34.0-42.1 mg g^{-1}) and 38.0 mg g^{-1} (30.3-42.4 mg g^{-1}), respectively.

v) Fructans

Among environments, minimum and maximum values for fructans were recorded in E07 (12.7 mg g^{-1}) and E08 (315.4 mg g^{-1}), respectively. Population mean for fructans among environments ranged between 74.3 (E05) and 144.8 mg g^{-1} (E08). Furthermore, mean values for fructans varied from 12.7 (E07) to 251.0 mg g^{-1} (E07), 32.6 (E06) to 185.1 mg g^{-1} (E06) and 31.7 (E08) to 266.5 mg g^{-1} (E04), population mean ranged from 74.3 (E05) to 89.1 mg g^{-1} (E07), 91.9 (E05) to 96.8 mg g^{-1} (E06) and 133.4 (E04) to 144.8 mg g^{-1} (E08) among environments characterized by irrigated, rainfed and drought conditions, respectively. Overall population mean for fructans under different water regimes *viz*. IR, RF and DT was 86.2 mg g^{-1} (50.2-125.4 mg g^{-1}), 94.3 mg g^{-1} (48.6-136.7 mg g^{-1}) and 134.3 mg g^{-1} (65.8-236.0 mg g^{-1}), respectively.

vi) Total water-soluble carbohydrates (WSCs)

Among environments, minimum and maximum values for WSCs were recorded in E05 (56.3 mg g^{-1}) and E04 (243.5 mg g^{-1}), respectively. Population mean for WSCs among environments ranged between 14.6 (E05) and 180.5 mg g^{-1} (E04). WSCs ranged between 56.3 (E05) to 96.5 mg g^{-1} (E03), 45.6 (E06) to 234.2 mg g^{-1} (E06) and 68.2 (E08) to 260.9 mg g^{-1} (E08) among environments characterized by irrigated, rainfed and drought conditions, respectively. Range of population mean for IR, RF and DT environments was recorded as

141.6 (E05)-160.4 mg g^{-1} (E07), 154.8 (E06)-162.6 mg g^{-1} (E02) and 170.1 (E08)-180.5 mg g^{-1} (E04), respectively. Overall population mean for WSCs under different water regimes *viz*. IR, RF and DT was recorded as 154.3 mg g^{-1} (112.7-194.9 mg g^{-1}), 158.7 mg g^{-1} (94.7-224.9 mg g^{-1}) and 178.5 mg g^{-1} (118.7-224.1 mg g^{-1}), respectively.

4.3. Drought susceptibility index (DSI)

DSI for grain yield was estimated from best linear unbiased estimates (BLUE) pooled on the basis of water regimes *viz*. IR, RF and DT. DSI for grain yield under rainfed condition ranged between -0.20 (UAS-304) and 1.68 (HD-2687) with a standard deviation of ±0.36 from mean value. Under complete drought stress condition, it varied from 0.07 (LGM-245) to 1.45 (HD-2687) with a standard deviation of ±0.22 from mean value. Furthermore, **Table 4.4** depicted that in top 20 genotypes ranked on the basis of lowest to highest value of DSI, only seven genotypes *viz*. VL-907, IC-311988, LGM-245, C-306, FLW-11, MACS-6145 and MACS-6222 were common. Ranks of these genotypes were different under RF and DT water regimes except for IC-321988 which gained constant rank 4 with DSI -0.10 and 0.33 under rainfed and drought stressed conditions, respectively. Additionally, LGM-245 showed relatively constant ranks in top 20 genotypes by getting rank 5 (DSI = -0.06) under rainfed and rank 1 (DSI = 0.07) under drought condition.

4.4. Analysis of variance (ANOVA)

ANOVA was done using restricted maximum likelihood model for each trait in each environment and pooled across environments. Results from individual environments (**Annexure 3, pp: XIII**) and pooled data (**Table 4.5**) revealed substantial genetic variability among genotypes for the aimed traits. Furthermore, significant effects of genotype x environment and genotype x management interactions were also seen on all the traits. Test for homogeneity revealed that most of the varieties were stable across environments laying in similar water managements for all the traits except for BY, GY and TNG.

4.5. Estimates of genetic components

Genetic components *viz*. genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), genetic advance (GA), genetic advance as percentage of mean (GAM%) and broad sense heritability (h^2%) were estimated for individual environments and pooled environments on the basis of water regimes. Results from pooled analysis are mentioned in **Table 4.6-4.8** whereas, detailed results for individual environments are shown in **Annexure 4 (pp: XV)**.

Table 4.4: List of top 20 bread wheat (*Triticum aestivum* L.) genotypes ranked on the basis of drought susceptibility index (from lowest to highest) for grain yield under rainfed and drought conditions estimated from pooled BLUE

Rank	**Rainfed**						**Drought**		
	Genotype	**Yp**	**Ys**	**DSI**		**Genotype**	**Yp**	**Ys**	**DSI**
1	UAS-304	10.44	11.09	-0.20		LGM-245*	11.36	10.97	0.07
2	NI-5439	10.5	11.08	-0.18		IC-321899	11.57	10.73	0.15
3	VL-907*	11.08	11.57	-0.14		GL-6	11.31	10.34	0.18
4	IC-321988*	7.5	7.73	-0.10		IC-321988*	7.5	6.32	0.33
5	LGM-245*	11.36	11.58	-0.06		DBW-98	12.25	9.59	0.46
6	Lok-54	12.83	12.47	0.09		MACS-6145*	10.68	8.17	0.49
7	KB-2012-03	10.86	10.49	0.11		PBW-660	12.85	9.63	0.53
8	C-306*	12.24	11.64	0.16		Pusa-2019A	13.17	9.67	0.56
9	Hindi-62	11.05	10.31	0.22		IC-321905A	13.02	9.53	0.56
10	IC-322011A	10.77	10	0.23		PBW-697	12.1	8.66	0.60
11	HI-1500	12.95	11.85	0.28		C-306*	12.24	8.75	0.60
12	WH-1164	12.38	11.31	0.28		HD-2987	13.81	9.85	0.60
13	MACS-6145*	10.68	9.66	0.31		DBW-51	12.94	9.2	0.61
14	GL-11	11.4	10.29	0.32		LGM-191	9.21	6.54	0.61
15	HUW-12	10.59	9.56	0.32		L-5(AL)	12.02	8.51	0.61
16	FLW-11*	12.43	11.08	0.35		HUW-598	14.56	10.31	0.61
17	IC-212145	10.38	9.24	0.36		VL-907*	11.08	7.82	0.62
18	K-68	11.61	10.32	0.36		FLW-11*	12.43	8.76	0.62
19	MACS-6222*	12.52	11.11	0.36		Bageshwar local	12.47	8.73	0.63
20	PBW-704	11.62	10.29	0.37		MACS-6222*	12.52	8.75	0.63
Summary	*Minimum*	7.50	6.27	-0.20		*Minimum*	7.50	4.80	0.07
	Maximum	18.67	12.86	1.68		*Maximum*	18.67	10.97	1.45
	Sd (±)	1.73	1.08	0.36		*Sd (±)*	1.73	1.10	0.22

Yp: Grain yield (g plant^{-1}) under non stressed condition, **Ys**: Grain yield (g plant^{-1}) under water stressed condition; **DSI:** drought susceptibility index; ***:** genotypes common in rainfed and drought conditions; **Sd**: standard deviation from mean

Table 4.5: Pooled analysis of variance for agro-phenological traits in 302 bread wheat genotypes

Variable	Stat	Management	Loc	Season	Env	Rep	Block	Genotype	G X M	G X E
	DF	1.00	2.00	1.00	2.00	1.00	1.00	301.00	301.00	1503.00
DTH	MSS	8.63	0.79	1.73	0.11	429.97***	3.38	156.18***	14.98***	21.90***
	Error	9.22	9.19	9.23	9.24	9.23	9.23	9.23	9.23	9.23
DTA	MSS	824.03***	70.78**	141.23***	418.05***	428.04***	3.18	155.09***	16.58	24.08***
	Error	15.29	15.29	15.29	15.29	15.29	15.29	15.29	15.29	15.29
DTM	MSS	164.22	2.91	20.52	1.03	500.19***	0.00	78.08***	13.89***	19.31***
	Error	9.63	9.63	9.63	9.63	9.63	9.63	9.63	9.63	9.63
GFD	MSS	52.97	10.55	0.15	0.70	1533.68***	11.86	42.46***	17.06***	21.20***
	Error	10.61	10.61	10.61	10.61	10.61	10.61	10.61	10.61	10.61
NOT	MSS	0.40	0.61	0.00	0.08	285.98***	3.52	3.65***	1.88	3.69***
	Error	2.04	2.04	2.04	2.04	2.04	2.04	2.04	2.04	2.04
PH	MSS	232.71	14.38	2.17	5.47	6297.57***	53.83	1164.33***	276.80***	109.97***
	Error	76.57	76.57	76.57	76.57	76.57	76.57	76.57	76.57	76.57
PL	MSS	979.13***	28.72	7.15	375.51***	610.09***	39.93*	161.91***	67.20***	34.85***
	Error	10.12	10.12	10.12	10.12	10.12	10.12	10.12	10.12	10.12
SL	DF	1.00	1.00	1.00	2.00	1.00	1.00	301.00	301.00	1202.00
	MSS	1.70	0.01	0.08	0.12	24.92***	0.20	6.71***	2.35***	1.67***
	Error	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24
SPS	DF	1.00	1.00	1.00	2.00	1.00	1.00	301.00	301.00	1201.00
	MSS	3.53	0.74	0.74	0.03	478.20***	0.01	16.80***	4.34**	2.45
	Error	3.50	3.50	3.50	3.50	3.50	3.50	3.50	3.50	3.50
	DF	1.00	2.00	1.00	2.00	1.00	1.00	301.00	301.00	1503.00
BY	MSS	8.02	17.70	35.68	0.26	2010.40***	0.05	179.55***	188.87***	184.37***
	Error	46.33	46.33	46.33	46.33	46.33	46.33	46.33	46.33	46.33
GY	MSS	0.06	34.50**	11.09	37.84***	292.21***	0.28	19.75***	20.48***	25.35***
	Error	5.30	5.30	5.30	5.30	5.30	5.30	5.30	5.30	5.30
HI	MSS	56.06	20.44	22.96	1.83	5.50	23.22	71.80***	47.01***	39.50***
	Error	24.99	24.99	24.99	24.99	24.99	24.99	24.99	24.99	24.99
TKW	MSS	0.02	19.37	17.97	304.80***	22.23	24.91	132.57***	26.90***	22.19***
	Error	16.10	16.10	16.10	16.10	16.10	16.10	16.10	16.10	16.10
TNG	MSS	187.83	2478.31	166.54	238.07	160506.53***	303.72	16159.63***	13110.81***	16039.35***
	Error	4488.76	4488.76	4488.76	4488.76	4488.76	4488.76	4488.76	4488.76	4488.76

DF: degree of freedom, **MSS:** mean sum of square, '*******': *p>0.001*, '******': *p>0.01*, '*****': *p>0.05*

4.5.1. Pooled over irrigated

Minimum value of GCV and PCV was recorded for days to maturity (DTM, 1.3% and 1.6%, respectively) and maximum for peduncle length (PL, 12.6% and 13.8%, respectively). Days to heading (DTH), days to anthesis (DTA), days to maturity (DTM), grain filling duration (GFD), number of tillers (NOT), spike length (SL), spikelet per spike (SPS), harvest index (HI) and thousand kernel weight (TKW) showed low GCV (<10%) and PCV (<10%). Low GCV with moderate PCV (11-20%) was recorded for biological yield (BY), grain yield (GY) and total number of grains (TNG) whereas, plant height (PH) and peduncle length (PL) exhibited moderate GCV (11-20%) and PCV (11-20%).

GA ranged between 0.43 (NOT) and 38 (TNG) whereas, GAM between 2.1% (DTM) and 23.95% (PL). Most of the studied traits (DTH, DTA, DTM, GFD, NOT, BY, GY, HI and TNG) possessed low GAM (<10%). Traits with moderate GAM (11-20%) were SL, SPS and TKW and with high GAM (>20%) were PH and PL.

Range for h^2 was recorded between 25.2% (BY) and 92.5% (PH). DTH, DTA, DTM, GFD, PH, PL, SL, SPS and TKW showed high heritability (>60%). Contrarily, HI and TNG exhibited moderate (31-60%) and NOT, BY and GY exhibited low (<30%) heritability (**Table 4.6**).

4.5.2. Pooled over rainfed

DTM was recorded with minimum GCV (1.5%) and PCV (2.3%) whereas, maximum GCV (11.3%) and PCV (13.8%) was recorded for PL and BY, respectively. Traits DTH, DTA, DTM, GFD, NOT, SPS and TKW demonstrated low GCV and PCV. In contrast to these traits, SL, BY, GY, HI and TNG showed low GCV with moderate PCV, and PH and PL showed moderate GCV and PCV.

Minimum values of GA (0.07) and GAM (0.87%) were recorded for NOT and TNG and PH were recorded with maximum values of GA (13.7) and GAM (22.0%), respectively.

Table 4.6: Genetic component estimation in studied population of bread wheat genotypes pooled over irrigated environments

Regime	Statistic	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
Irrigated	Mean	91.47	98.89	136.28	37.34	10.79	105.96	35.69	11.40	20.87	42.99	16.63	39.19	41.70	403.69
	σ^2_g	10.89	10.70	3.21	4.61	0.16	151.06	20.51	0.99	2.27	7.04	1.25	4.23	10.51	994.33
	$\sigma^2_{g\times e}$	8.95	9.46	7.92	7.78	1.72	36.83	14.79	0.68	0.59	79.84	12.29	9.34	7.87	7381.57
	σ^2_e	5.44	6.84	4.72	9.08	0.98	42.94	9.50	0.61	1.75	48.87	5.79	24.68	9.78	4170.93
	σ^2_p	13.22	13.28	5.27	7.07	0.60	162.72	24.42	1.24	2.64	27.90	4.29	8.56	13.06	2887.74
	GCV	3.61	3.31	1.31	5.75	3.73	11.60	12.69	8.75	7.23	6.17	6.72	5.25	7.77	7.81
	PCV	3.98	3.68	1.68	7.12	7.20	12.04	13.84	9.77	7.78	12.29	12.45	7.47	8.66	13.31
	GA	6.17	6.05	2.88	3.57	0.43	24.40	8.55	1.84	2.88	2.75	1.24	2.98	5.99	38.12
	GAM	6.74	6.12	2.11	9.56	3.98	23.02	23.95	16.14	13.81	6.39	7.48	7.59	14.36	9.44
	h^2	82.35	80.60	60.97	65.15	26.84	92.83	84.00	80.18	86.15	25.25	29.17	49.37	80.46	34.43
	LSD	4.24	4.45	3.99	4.37	1.85	9.51	5.50	1.38	1.68	12.71	4.84	5.80	4.46	121.04
	CV	2.55	2.64	1.59	8.07	9.18	6.18	8.63	6.86	6.35	16.26	14.46	12.68	7.50	16.00

Table 4.7: Genetic component estimation in studied population of bread wheat genotypes pooled over rainfed environments

Regime	Statistic	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
Rainfed	Mean	78.61	85.35	114.49	29.14	7.75	91.36	28.18	9.87	19.31	28.34	9.61	34.82	35.60	274.71
	σ^2_g	8.99	9.13	2.95	5.81	0.02	106.72	10.19	0.76	1.55	6.42	0.21	4.81	7.62	199.43
	$\sigma^2_{g\times e}$	6.29	4.44	8.75	3.70	0.85	0.00	9.21	0.25	1.34	15.23	1.98	12.64	4.72	1133.93
	σ^2_e	7.11	11.12	8.08	9.22	0.68	74.90	9.77	0.65	2.50	23.75	1.58	21.18	9.77	1906.41
	σ^2_p	12.27	12.46	7.21	8.58	0.42	119.21	14.89	1.05	2.84	15.45	1.13	12.55	10.82	895.14
	GCV	3.81	3.54	1.50	8.27	1.88	11.31	11.33	8.83	6.44	8.94	4.77	6.30	7.75	5.14
	PCV	4.46	4.14	2.35	10.05	8.33	11.95	13.69	10.36	8.73	13.87	11.08	10.18	9.24	10.89
	GA	5.29	5.33	2.26	4.09	0.07	20.14	5.44	1.53	1.89	3.36	0.41	2.80	4.77	13.73
	GAM	6.72	6.24	1.98	14.02	0.87	22.04	19.30	15.50	9.80	11.87	4.24	8.03	13.40	5.00
	h^2	73.25	73.27	40.88	67.70	5.09	89.53	68.44	72.60	54.49	41.54	18.56	38.31	70.41	22.28
	LSD	5.09	5.14	5.76	4.68	1.75	10.03	6.06	1.50	3.17	8.40	2.69	7.77	4.99	73.56
	CV	3.39	3.91	2.48	10.42	10.66	9.47	11.09	8.20	8.18	17.20	13.08	13.22	8.78	15.89

σ^2_g: genotypic variance; **$\sigma^2_{g\times e}$**: genotypic × environment interaction; **σ^2_e**: residual variance; **σ^2_p**: phenotypic variance; **GCV**: genotypic coefficient of variance; **PCV**: phenotypic coefficient of variance; **GA**: genetic advance; **GAM**: genetic advance over mean (%); **h^2**: broad sense heritability (%); **LSD**: least significant difference; **CV**: coefficient of variation (%)

Low GAM was displayed by DTH, DTA, DTM, GFD, NOT, SPS, GY, HI and TNG. Traits PL, SL, BY and TKW possessed moderate GAM whereas, PH exhibited high GAM. Among studied traits, NOT and PH showed minimum (5.0%) and maximum (89.5%) heritability, respectively. Traits like DTH, DTA, GFD, PH, PL, SL and TKW exhibited high heritability, while others exhibited low (NOT, GY and TNG) and moderate (DTM, SPS, BY and HI) (**Table 4.7**).

4.5.3. Pooled over drought

GCV ranged between 3.0% (DTM) and 18.9% (PL) and PCV between 3.5% (DTM) and 24.9% (PL). Low GCV and PCV was recorded for DTH, DTA, DTM, GFD, NOT and SPS. Traits SL, BY, GY, HI and TNG demonstrated low GCV and moderate PCV. PH and TKW exhibited moderate GCV and PCV. PL was the only trait which exhibited moderate GCV and high PCV. Range of GA and GAM recorded as 0.43 (GY)-25.83 (TNG) and 5.4% (DTM)-29.6% (PL), respectively. Most of the studied traits (DTH, DTA, DTM, GFD, NOT, BY and GY) had low GAM. Moderate GAM was recorded for SL, SPS, HI and TNG. However, PH, PL and TKW had high GAM. Range of heritability laid between 13.5% (BY) and 91.1% (TKW). Most of the traits (DTH, DTA, DTM, GFD, PH, SL, SPS and TKW) showed high heritability. NOT, PL, HI and TNG were recorded with moderate heritability but BY and GY with low (**Table 4.8**).

Table 4.8: Genetic component estimation in studied population of bread wheat genotypes pooled over drought environments

Traits	**Drought**											
	Statistical parameters											
	Mean	σ^2_g	$\sigma^2_{g\times e}$	σ^2_e	σ^2_p	**GCV**	**PCV**	**GA**	**GAM**	h^2	**LSD**	**CV**
DTH	64.46	11.10	5.33	5.46	15.13	5.17	6.03	5.88	9.12	73.36	5.61	3.63
DTA	70.93	10.61	4.45	8.39	14.93	4.59	5.45	5.66	7.97	71.05	5.82	4.08
DTM	101.49	9.75	3.68	6.15	13.12	3.08	3.57	5.54	5.46	74.27	5.13	2.44
GFD	30.57	2.44	1.90	2.28	3.97	5.12	6.52	2.53	8.27	61.63	3.45	4.94
NOT	7.06	0.19	0.20	0.24	0.35	6.11	8.36	0.65	9.20	53.46	1.13	6.96
PH	67.81	79.98	11.36	49.79	98.11	13.19	14.61	16.63	24.53	81.52	12.02	10.41
PL	12.11	5.26	4.85	5.64	9.10	18.95	24.91	3.59	29.68	57.83	5.48	19.61
SL	6.90	0.47	0.16	0.41	0.65	9.92	11.69	1.20	17.32	71.93	1.19	9.33
SPS	14.07	1.38	0.02	0.96	1.63	8.35	9.06	2.23	15.84	84.85	1.39	6.95
BY	23.36	2.85	26.82	18.75	20.94	7.22	19.59	1.28	5.48	13.59	11.89	18.54
GY	7.27	0.23	1.44	0.99	1.20	6.60	15.04	0.43	5.97	19.26	2.75	13.66
HI	32.12	5.53	5.52	10.75	10.98	7.32	10.32	3.44	10.70	50.37	6.53	10.21
TKW	34.88	13.49	0.00	5.26	14.81	10.53	11.03	7.22	20.71	91.11	3.20	6.58
TNG	214.55	459.75	1149.24	1241.62	1344.77	9.99	17.09	25.83	12.04	34.19	83.09	16.42

σ^2_g: genotypic variance; $\sigma^2_{g\times e}$: genotypic × environment interaction; σ^2_e: residual variance; σ^2_p: phenotypic variance; **GCV:** genotypic coefficient variance; **PCV:** phenotypic coefficient of variance; **GA:** genetic advance; **GAM:** genetic advance over mean (%); h^2: broad sense heritability (%); **LSD:** least significant difference; **CV:** coefficient of variation (%)

4.6. Correlation studies

Pearson's correlation was estimated for all the studied traits from data pooled over water regimes (**Table 4.9 and Table 4.10**). Blended results of correlation coefficients obtained with varied enormity at three significance levels *viz*. 0.001, 0.01 and 0.05 from data pooled over different water regimes are as follow:

4.6.1 Association of agro-phenological traits with grain yield

Grain yield was positively correlated with BY, HI, TKW and TNG at significance level $p>0.001$ and GFD at significance level $p>0.05$ but negatively correlated with DTH, DTA and DTM at significance level $p>0.001$ under pooled irrigated environment. Similarly, positive correlation of GY with GFD, NOT, BY, HI, TKW and TNG at significance level $p>0.001$, PH and PL at significance level $p>0.01$ and negative correlation with DTH and DTA at significance level $p>0.01$ was reported under pooled rainfed environment. Under pooled drought environment, NOT, PH, PL, BY, TKW and TNG at $p>0.001$ and SL, SPS and HI at $p>0.01$ exhibited positive correlation with grain yield.

4.6.2 Association among yield contributing agro-phenological traits

Correlation of all the traits was studied to have a better understanding of effect of traits over one another. Although all the traits had significant effects on grain yield but correlation of directly contributing traits like NOT, SL, SPS, BY, HI, TKW and TNG is mentioned here.

Under pooled irrigated environment (**Table 4.9**), NOT showed positive correlation with GFD, PH and PL at $p>0.001$, BY ($p>0.01$) and TNG ($p>0.05$) but negative with DTH, DTA, SPS, HI at $p>0.001$ and TKW ($p>0.01$). SL exhibited strong positive correlation with SPS ($p>0.001$) and HI ($p>0.01$) and negative with PH ($p>0.01$) and DTM ($p>0.05$). Positive correlation of SPS was observed with DTH and DTA at $p>0.001$ and DTM ($p>0.01$) while a negative correlation with GFD and NOT at $p>0.001$, PL and TKW at ($p>0.01$). BY showed positive association with PH, PL, GY, TKW and TNG at $p>0.001$, with GFD and NOT at $p>0.01$ whereas, negative association with DTH and DTA at $p>0.05$. HI was observed to have positive TNG ($p>0.001$) and TKW ($p>0.01$) and negative with DTH, DTA and DTM at significance level $p>0.001$. Likewise, with PL ($p>0.01$), and GFD ($p>0.05$) TWK had positive correlation whereas, it had negative correlation with DTH, DTA, and TNG at significance level $p>0.001$ and with DTM at significance level $p>0.05$. TNG was observed to have positive association PL ($p>0.001$) and PH ($p>0.01$).

Results from Pearson's correlation analysis among pheno-agronomical traits pooled over

Table 4.9: Pearson correlation between agro-phenological traits of bread wheat pooled over irrigated environments

IR	**DTH**	**DTA**	**DTM**	**GFD**	**NOT**	**PH**	**PL**	**SL**	**SPS**	**BY**	**GY**	**HI**	**TKW**
DTH													
DTA	0.99***												
DTM	0.71***	0.70***											
GFD	-0.76***	-0.78***	-0.10										
NOT	-0.26***	-0.25***	-0.03	0.32***									
PH	0.16**	0.16**	0.38***	0.10	0.19***								
PL	-0.22***	-0.21***	0.11	0.39***	0.24***	0.72***							
SL	-0.05	-0.06	-0.14*	-0.05	-0.07	-0.18**	-0.08						
SPS	0.36***	0.34***	0.18**	-0.32***	-0.20***	-0.05	-0.16**	0.40***					
BY	-0.13*	-0.12*	-0.01	0.15**	0.19**	0.29***	0.21***	-0.01	-0.11				
GY	-0.24***	-0.22***	-0.21***	0.13*	0.03	-0.10	-0.05	0.08	-0.09	0.82***			
HI	-0.24***	-0.24***	-0.37***	0.01	-0.20***	-0.60***	-0.39***	0.16**	-0.03	-0.07	0.49***		
TKW	-0.19***	-0.19***	-0.15*	0.14*	-0.15**	0.09	0.19**	0.10	-0.16**	0.21***	0.27***	0.15**	
TNG	-0.08	-0.08	-0.10	0.01	0.12*	-0.17**	-0.19***	0.01	0.03	0.62***	0.76***	0.37***	-0.40***

Table 4.10: Pearson correlation between agro-phenological traits of bread wheat pooled over rainfed (below diagonal) and drought (above diagonal) environments

		Drought													
		DTH	**DTA**	**DTM**	**GFD**	**NOT**	**PH**	**PL**	**SL**	**SPS**	**BY**	**GY**	**HI**	**TKW**	**TNG**
Rainfed	**DTH**	1	0.99***	0.87***	-0.34***	-0.08	0.01	-0.33***	0.03	0.09	0.04	-0.07	-0.16**	-0.17**	0.06
	DTA	0.99***	1	0.86***	-0.37***	-0.07	0.01	-0.33***	0.04	0.07	0.05	-0.06	-0.15**	-0.18**	0.07
	DTM	0.57***	0.58***	1	0.15**	-0.06	0.04	-0.24***	0.02	0.11*	0.09	-0.01	-0.19***	-0.08	0.05
	GFD	-0.68***	-0.67***	0.21***	1	0.03	0.05	0.19***	-0.04	0.06	0.07	0.10	-0.05	0.19***	-0.03
	NOT	-0.20***	-0.20***	-0.10	0.15**	1	0.24***	0.22***	0.02	0.02	0.52***	0.49***	-0.07	-0.09	0.51***
	PH	0.16**	0.17**	0.45***	0.20***	0.19**	1	0.49***	0.35***	0.05	0.30***	0.21***	-0.26***	0.15*	0.09
	PL	-0.28***	-0.27***	0.11*	0.42***	0.24***	0.65***	1	0.20***	-0.07	0.25***	0.21***	-0.13*	0.20***	0.04
	SL	-0.06	-0.06	0.02	0.07	0.00	-0.05	-0.02	1	0.21***	0.27***	0.15**	-0.24***	0.05	0.11
	SPS	0.17**	0.17**	0.15**	-0.07	-0.10	0.06	-0.06	0.47***	1	0.19***	0.15**	-0.05	-0.15**	0.25***
	BY	0.02	0.04	0.26***	0.18**	0.27***	0.57***	0.39***	0.04	0.08	1	0.85***	-0.31***	0.17**	0.65***
	GY	-0.18**	-0.17**	0.01	0.22***	0.27***	0.16**	0.16**	0.07	0.08	0.66***	1	0.18**	0.23***	0.74***
	HI	-0.24***	-0.25***	-0.34***	0.00	-0.07	-0.56***	-0.32***	0.03	-0.02	-0.57***	0.20***	1	0.03	0.13*
	TKW	-0.23***	-0.23***	0.02	0.29***	0.06	0.18**	0.32***	0.07	-0.15*	0.29***	0.46***	0.13*	1	-0.48***
	TNG	0.01	0.02	-0.01	-0.03	0.23***	0.01	-0.11	0.00	0.20***	0.45***	0.63***	0.07	-0.38***	1

DTH: days to heading; **DTA:** days to anthesis; **DTM:** days to maturity; **GFD:** grain filling duration; **NOT:** number of tillers; **PH:** plant height (cm); **PL**: peduncle length (cm); **SL:** spike length (cm), **SPS:** spikelet per spike; **BY:** biological yield (g plant^{-1}); **GY:** grain yield (g plant^{-1}); **HI:** harvest index (%) **TKW:** thousand kernel weight (g); **TNG:** number of grains plant^{-1}, **p>0.05, **p>0.01, ***p>0.001* rainfed environments revealed that NOT exhibited significant positive correlation with PL, BY and TNG at $p>0.001$, with GFD and PH at $p>0.01$ and negative correlation with DTH and DTA at $p>0.001$. SL showed strong positive association with SPS ($p>0.001$). Furthermore, SPS found to be positively correlated to DTH, DTA and DTM at $p>0.01$ but negatively correlated with TKW ($p>0.05$). DTM, PH, PL, GY, TKW and TNG at $p>0.001$, and GFD at $p>0.01$ had positive correlation with BY. HI was observed to have strong positive correlation with TKW ($p>0.05$) but negative correlation with DTH, DTA, DTM, PH, PL and BY at significance level $p>0.001$. TKW showed positive correlation with GFD and PL at $p>0.001$ and PH at $p>0.01$. Negative correlation of TKW was recorded with DTH, DTA and TNG at significance level $p>0.001$.

Under drought conditions, NOT was observed to have positive association with PH, PL, BY and TNG at significance level $p>0.001$. SL showed positive correlation with PH, PL, SPS and BY at $p>0.001$ and negative correlation with HI ($p>0.001$). SPS had positive correlation with BY and TNG at significance level $p>0.001$ and DTM at significance level $p>0.05$ whereas, negative with TKW at significance level $p>0.01$. NOT, PH, PL, and TNG at $p>0.001$ and TKW at $p>0.01$ had positive association with BY. Correlation between BY and HI was strongly negative ($p>0.001$). HI showed significantly positive correlation with TNG ($p>0.05$) whereas, exhibited negative correlation with DTM and PH at $p>0.001$, DTH and DTA at $p>0.01$ and PL at $p>0.05$. TKW showed positive correlation with GFD and PL with significance level $p>0.001$ and PH with $p>0.05$ significance whereas, with TNG significant negative correlation at $p>0.001$ and with DTH, DTA and SPS at $p>0.01$ was reported.

4.6.3 Association between soluble sugars and agro-phenological traits

Association of soluble sugars with studied agro-phenological traits under pooled environments was done in two experiments. In first experiment (**Table 4.12**) association was estimated with the help of all 302 genotypes while in second experiment (**Table 4.13**) partitioning of genotypes was done on the bases of drought susceptibility index and correlation was recalculated among studied traits with the help of selected top twenty genotypes (**Table 4.4**). Results from both of the experiments are as follow

A. Based on 302 bread wheat genotypes

Study of association between soluble sugars and yield and its contributing traits in complete set of genotypes under irrigated environment revealed that TNSC (total non-structural carbohydrates) had significant positive correlation with DTM ($p>0.01$), DTH and DTA ($p>0.05$). Similarly, fructans showed positive association with DTM ($p>0.01$), DTH and DTA ($p>0.05$). GFD, GY and TNG were found to have positive correlation with fructose at significance level $p>0.01$. Glucose and sucrose did not show significant association with any agro-phenological trait. WSC (water-soluble carbohydrates) showed positive association with DTH and DTA ($p>0.01$) and negative with BY ($p>0.01$) and GY ($p>0.5$).

Correlation coefficients of soluble sugars with yield and yield contributing traits under different environments in complete set of genotypes showed that TNSC and fructans exhibited similar patterns of association with different agro-phenological traits. They were positively correlated with DTH, DTA and TNG at $p>0.01$ and DTM at $p>0.05$ and negatively correlated with TKW ($p>0.01$). Fructose showed significantly positive association with TNG ($p>0.05$) and negative with PL and TKW at significance level $p>0.01$. Furthermore, glucose and sucrose did not show significant correlation with any of the traits. Significantly positive correlation of WSC was observed with DTH and DTA at significance level $p>0.01$ whereas, with GFD ($p>0.01$), PL ($p<0.05$) and TKW ($p<0.05$) it was significantly negative.

Correlation pattern between soluble sugars and agro-phenological with complete set of genotypes under pooled drought environment was quite similar to that of pooled rainfed. TNSC and fructans were positively associated with DTH and DTA at significance level $p>0.01$, and DTM at $p>0.05$ whereas, in significantly negative association with GFD and PL at $p>0.01$, PH at $p>0.05$. Glucose, fructose and sucrose did not exhibit any significant association with studied agro-phenological traits. WSC had significant correlation only with DTH, DTA and DTM at $p<0.01$ that too in negative direction (**Table 4.11**).

B. Based on drought tolerant bread wheat genotypes

Analysis of correlation coefficients of soluble sugars with yield and its contributing traits in drought tolerant genotypes in all three pooled environments *viz.* IR, RF and DT was performed. Under pooled irrigated environment TNSC and fructans exhibited non-significant positive correlation with BY, GY, TKW and TNG. Fructose had positive association with GFD at significance level $p>0.01$ and non-significant positive association with BY, GY, TKW and TNG. On the other hand, non-significant positive association was reported for glucose and sucrose with TKW however, both glucose and sucrose had significantly negative correlation with GY and TNG at $p>0.05$ and a non-significant negative association with BY. Contrarily, WSC showed non-significant positive association with GY, TKW and TNG but significantly negative correlation with PH and SL at $p>0.01$ whereas, with BY at negative and non-significant.

Table 4.11: Pearson correlation between soluble sugars with yield and contributing traits for environments pooled over irrigated, rainfed and drought calculated using 302 bread wheat genotypes

	Traits	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
Irrigated	**TNSC**	0.12*	0.12*	0.19**	0.03	-0.02	0.04	0.03	-0.04	0.05	-0.05	-0.04	0.02	-0.03	0.01
	Glucose	0.04	0.04	0.01	-0.05	-0.04	0.06	0.04	-0.01	0.02	-0.05	-0.07	-0.05	-0.06	-0.02
	Fructose	-0.04	-0.05	0.05	0.13*	0.08	-0.05	0.01	-0.01	-0.06	0.1	0.14*	0.06	0.03	0.12*
	Sucrose	0.03	0.04	0.02	-0.03	-0.04	0.06	0.05	-0.02	0.01	-0.04	-0.06	-0.05	-0.06	-0.01
	Fructans	0.12*	0.13*	0.19**	0.03	-0.03	0.04	0.03	-0.04	0.06	-0.06	-0.04	0.02	-0.03	-0.01
	WSC	0.14*	0.14*	0.08	-0.13*	-0.1	-0.04	-0.08	0.05	0.04	-0.16**	-0.11*	0.08	0.01	-0.1
Rainfed	**TNSC**	0.15**	0.16**	0.13*	-0.09	-0.05	0.01	-0.06	-0.09	-0.01	0.03	0.01	-0.01	-0.19**	0.18**
	Glucose	0.07	0.08	0.03	-0.07	-0.07	-0.02	0.04	-0.1	-0.04	0.02	-0.01	-0.02	-0.06	0.04
	Fructose	0.03	0.05	0.04	-0.03	-0.03	-0.1	-0.19**	0.02	0.05	-0.01	-0.07	-0.03	-0.2**	0.14*
	Sucrose	0.05	0.07	0.03	-0.05	-0.08	-0.01	0.05	-0.09	-0.04	0.03	0.01	-0.02	-0.06	0.05
	Fructans	0.15**	0.17**	0.13*	-0.08	-0.05	0.02	-0.06	-0.08	-0.01	0.03	0.02	-0.01	-0.19**	0.18**
	WSC	0.22**	0.22**	0.05	-0.22**	0.01	-0.08	-0.15*	-0.03	0.05	-0.06	-0.03	0.05	-0.12*	0.07
Drought	**TNSC**	0.20**	0.22**	0.13*	-0.19**	-0.02	-0.12*	-0.20**	-0.03	0.05	-0.04	-0.03	0.02	-0.06	0.01
	Glucose	-0.05	-0.03	-0.07	-0.08	0.11	-0.03	0.07	-0.02	-0.05	0.08	0.09	-0.01	0.09	0.02
	Fructose	-0.03	-0.03	-0.05	-0.04	0.06	-0.01	0.01	0.05	0.04	-0.01	0.01	0.05	-0.01	0
	Sucrose	-0.02	0	-0.05	-0.09	0.1	-0.03	0.06	-0.02	-0.04	0.07	0.08	-0.01	0.09	0.02
	Fructans	0.21**	0.24**	0.14*	-0.19**	-0.04	-0.13*	-0.22**	-0.03	0.05	-0.05	-0.04	0.02	-0.07	0.01
	WSC	-0.20**	-0.18**	-0.17**	0.05	-0.02	0.07	0.01	-0.09	0.01	0.02	0.03	0.01	0.04	-0.02

Table 4.12: Pearson correlation between soluble sugars with yield and contributing traits under IR, RF and DT in identified drought tolerant genotypes

	Traits	N	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
Irrigated	**TNSC**	32	-0.09	-0.03	0.1	0.13	0.14	0.02	-0.11	-0.03	-0.1	0.1	0.1	0.01	0.07	0.05
	Glucose		0.06	0.05	0.08	0.01	-0.17	0.16	-0.03	-0.05	-0.27	-0.15	-0.39*	-0.33	0.03	-0.44*
	Fructose		-0.35	-0.33	0.1	0.48**	0.32	0.04	0.33	0.09	-0.1	0.15	0.25	0.1	0.24	0.03
	Sucrose		0.04	0.04	0.1	0.05	-0.14	0.17	-0.02	-0.07	-0.28	-0.12	-0.37*	-0.32	0.03	-0.40*
	Fructans		-0.08	-0.01	0.09	0.1	0.14	0.01	-0.13	-0.04	-0.08	0.11	0.11	0.03	0.06	0.09
	WSC		0.12	0.12	-0.24	-0.35	-0.28	-0.40*	-0.41*	0.28	0.24	-0.13	0.17	0.35	0.14	0.03
Rainfed	**TNSC**	20	0.13	0.15	0.14	-0.05	-0.25	-0.04	0.06	-0.34	-0.59**	0.16	0.17	-0.05	-0.09	0.27
	Glucose		-0.28	-0.24	0.21	0.48*	-0.36	-0.08	0.09	-0.15	0.04	-0.14	0.11	0.19	0.18	-0.15
	Fructose		0.13	0.17	0.38	0.17	-0.27	0.07	-0.36	0.04	0.23	-0.21	-0.44	-0.14	-0.29	-0.2
	Sucrose		-0.3	-0.27	0.21	0.51*	-0.38	-0.06	0.11	-0.16	0.02	-0.09	0.14	0.17	0.2	-0.14
	Fructans		0.16	0.18	0.1	-0.12	-0.2	-0.04	0.07	-0.34	-0.64**	0.19	0.19	-0.06	-0.09	0.31
	WSC		0.28	0.26	-0.33	-0.64**	0.08	-0.34	-0.03	-0.16	-0.58**	-0.1	0.21	0.28	-0.16	0.43
Drought	**TNSC**	20	0.08	0.13	0.12	0.01	-0.18	-0.13	-0.13	0.21	0.15	0.14	-0.08	-0.26	0.15	-0.11
	Glucose		-0.2	-0.18	0.15	0.61**	0.08	-0.58**	-0.35	-0.17	0.06	0.33	0.28	0.03	0.21	0.13
	Fructose		-0.04	-0.03	0.04	0.14	0.29	-0.11	-0.23	-0.38	-0.12	0.19	0.23	0.16	0.02	0.22
	Fructans		0.1	0.15	0.1	-0.06	-0.2	-0.07	-0.09	0.25	0.15	0.1	-0.11	-0.27	0.13	-0.13
	Sucrose		-0.17	-0.14	0.17	0.58**	0.05	-0.57**	-0.34	-0.17	0.07	0.31	0.24	-0.01	0.22	0.1
	WSC		-0.61**	-0.60**	-0.47*	0.15	0.29	0.14	0.22	0.07	0.19	0.21	0.39	0.34	0.02	0.3

**p>0.05, **p>0.01, ***p>0.001*

Under pooled rainfed environment, TNSC and fructans showed non-significant and positive relation with BY, GY and TNG whereas, significantly negative relation with SPS at *p>0.01*. With TKW both TNSC and fructans had non-significant association with negative magnitude. Fructose was reported to have non-significant negative association with BY, GY, TKW and TNG. Glucose and fructose showed significantly positive association with GFD (*p>0.01*) and with GY and TKW non-significant and positive. Relationship of glucose and fructose with and BY and TNG was negative but non-significant. Non-significant positive association of WSC was seen with GY and TNG. Furthermore, WSC showed significant negative correlation with GFD and SPS at *p>0.01* whereas, with BY and TKW it was non-significant.

Pearson's correlation coefficients estimated between soluble sugars and agro-phenological traits with identified drought tolerant genotypes revealed that under pooled drought environment TNSC and fructans were positively associated with BY and TKW and negatively with GY and TNG but they did not have significance level. Fructose showed non-significant positive correlation with BY, GY, TKW and TNG. Glucose and sucrose exhibited similar correlation pattern. They were observed to have positive correlation with GFD (*p>0.01*) and with BY, GY, TKW and TNG non-significant whereas, with PH they had significantly (*p>0.01*) negative correlation. Likewise, WSC showed non-significant positive correlation with BY, BY, TKW and TNG but significantly negative correlation with DTH and DTA at *p>0.01* and DTM at *p>0.05* (**Table 4.12**).

4.7. Multivariate analysis for genetic divergence

Multivariate approaches *viz* principal component analysis and hierarchical clustering was used to estimate genetic divergence in association mapping panel. Both of these analyses performed on data pooled over different water regimes in question. Results on multivariate analysis are as follow

4.7.1. Principal component analysis (PCA)

Out of 20 principal components (PCs) extracted from original variables (**Table 4.13**), first 8 components under irrigated conditions and first 7 components under rainfed and drought conditions exhibited latent eigenvalue above one which accounted for 84.5% (irrigated), 80.1% (rainfed) and 76.4% (drought) of the total variation. First three factors (PC1-PC3) retained maximum information of original variables under all three water regimes.

Under irrigated condition eigenvalue (EV), individual proportion (IP) and cumulative proportion (CP) ranged from 1.1 to 3.8, 5.6% to 19.4% and 19.4% to 84.5%, respectively for extracted principal components (PC1 to PC8). PC1 retained maximum information from original variables with the highest eigenvalue (3.8) and individual proportion (19.4%). First four PCs retained valuable information as each of them exhibited more than 10% individual proportion with a cumulative proportion of 59.3% whereas, rest four components contributed with an individual proportion of less than 10.0% and cumulative proportion of 25.1%. Vector loadings shown in **Table 4.14** indicated that the highest loadings contained by DTH (-0.45, PC1), TNSC (-0.43, PC2), PH (0.43, PC3), TNG (-0.57, PC4), TKW (0.62, PC5), SPS (-0.52, PC6), fructose (0.67, PC7) and WSC (0.54, PC8) as major contributing traits. Relative distribution of genotypes on first two components is shown in **Figure 4.6**.

PCA for variables pooled over rainfed environments (**Table 4.13**) revealed that first seven principal components can effectively summarize all the original variables. Range for EV, IP and CP for these extracted PCs (PC1-PC7) recorded as 1.1-3.9, 5.9-19.7% and 19.76-8.1%, respectively. First three were components found to be more important than others as they were explaining 50.2% of total variation form original variables with an IP of 19.7%, (PC1), 16.3% (PC2) and 14.0% (PC3). Cumulative proportion of remaining four PCs was 29.9%. PC1 retained information contained in 3.9 of original variables. Traits with largest absolute value under different PCs (**Table 4.14**) were fructans (0.38, PC1), BY (-0.47, PC2), DTH and DTA (0.42, PC3), TNG (0.59, PC4), SL (-0.62, PC5), fructose (-0.57, PC6) and WSCs (-0.43, PC7).

Table 4.13: Total variance explained by different principal components in bread wheat genotypes extracted pooled over different water regimes

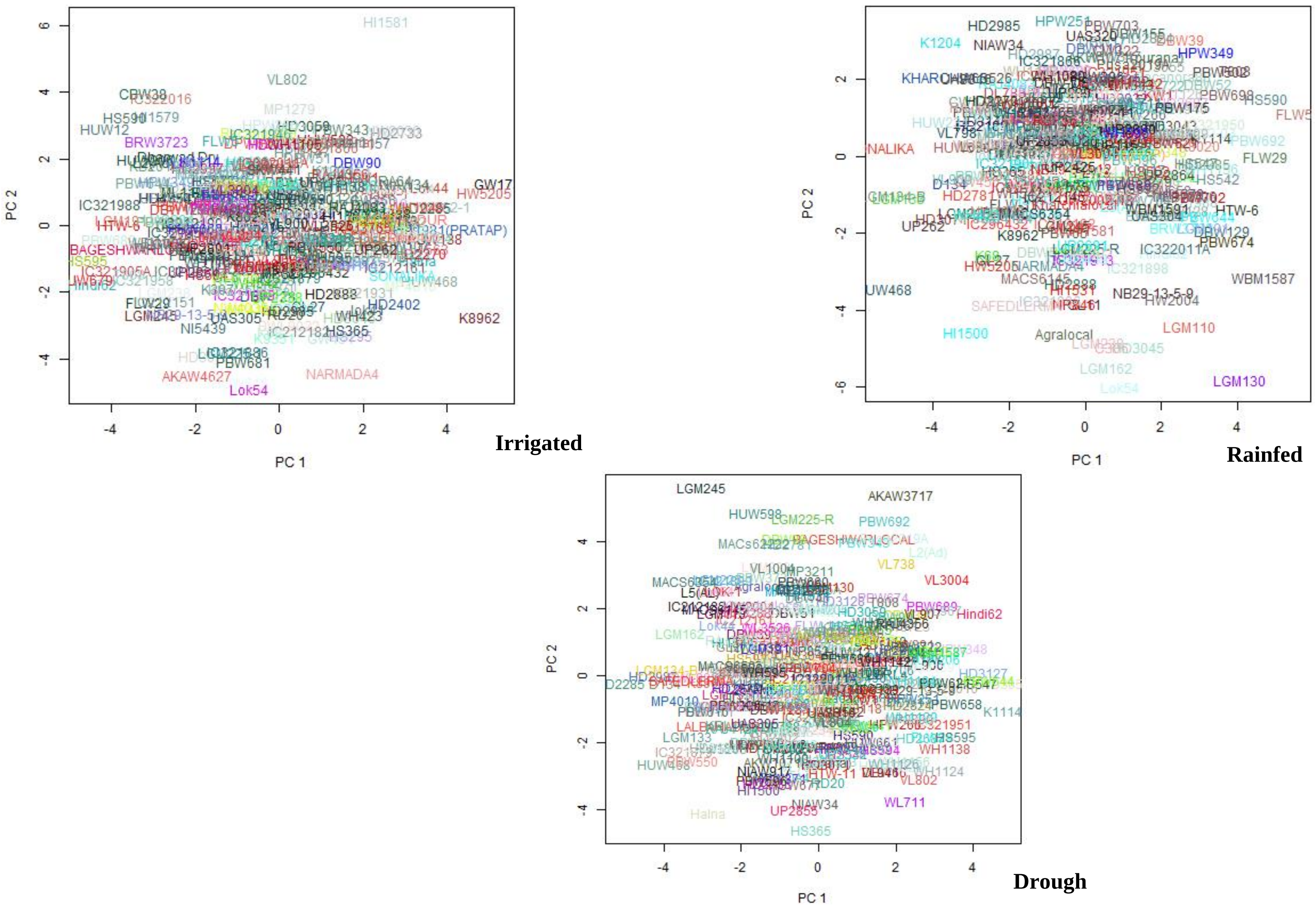
Components	**Irrigated**			**Rainfed**			**Drought**		
	EV	**IP**	**CP**	**EV**	**IP**	**CP**	**EV**	**IP**	**CP**
PC1	3.89	19.43	19.43	3.95	19.76	19.76	3.66	18.29	18.29
PC2	2.97	14.86	34.29	3.27	16.37	36.13	3.50	17.50	35.79
PC3	2.74	13.72	48.01	2.81	14.07	50.20	2.82	14.10	49.89
PC4	2.27	11.37	59.38	1.98	9.90	60.10	1.69	8.46	58.35
PC5	1.47	7.36	66.74	1.42	7.08	67.18	1.35	6.76	65.10
PC6	1.25	6.25	72.98	1.39	6.95	74.13	1.20	6.00	71.11
PC7	1.18	5.91	78.89	1.19	5.96	80.10	1.08	5.39	76.49
PC8	1.13	5.64	84.54	0.99	4.94	85.04	0.96	4.80	81.29
PC9	0.75	3.74	88.27	0.77	3.83	88.86	0.80	3.99	85.28
PC10	0.61	3.07	91.35	0.72	3.60	92.46	0.75	3.73	89.01
PC11	0.56	2.81	94.16	0.55	2.76	95.22	0.72	3.58	92.60
PC12	0.50	2.49	96.64	0.43	2.14	97.36	0.58	2.92	95.52
PC13	0.45	2.23	98.87	0.29	1.44	98.80	0.50	2.49	98.01
PC14	0.20	0.98	99.85	0.20	1.01	99.81	0.36	1.79	99.80
PC15	0.01	0.06	99.92	0.02	0.09	99.90	0.02	0.09	99.89
PC16	0.01	0.04	99.96	0.01	0.05	99.95	0.01	0.06	99.96
PC17	0.01	0.03	99.99	0.01	0.04	99.99	0.01	0.04	99.99
PC18	0.00	0.01	100.00	0.00	0.00	100.00	0.00	0.01	100.00
PC19	0.00	0.00	100.00	0.00	0.00	100.00	0.00	0.00	100.00
PC20	0.00	0.00	100.00	0.00	0.00	100.00	0.00	0.00	100.00

PC: principal component; **EV:** eigenvalue; **IP**: individual proportion (%); **CP:** cumulative proportion (%)

Table 4.14: Vector loading of first 8 principal components estimated in studied bread wheat population for various traits pooled over water regimes

	PC	*DTH*	*DTA*	*DTM*	*GFD*	*NOT*	*PH*	*PL*	*SL*	*SPS*	*BY*	*GY*	*HI*	*TKW*	*TNG*	*TNSC*	*Glu*	*Fru*	*Suc*	*Fruc*	*WSC*
Irrigated	**PC1**	-0.45	-0.44	-0.36	0.28	0.14	-0.13	0.06	0.05	-0.17	0.14	0.26	0.18	0.15	0.13	-0.21	-0.17	0.03	-0.17	-0.21	-0.13
	PC2	0.18	0.17	0.03	-0.23	-0.14	-0.13	-0.21	0.05	0.12	-0.13	-0.11	0.04	-0.06	-0.06	-0.43	-0.42	-0.17	-0.44	-0.41	0.00
	PC3	-0.08	-0.08	-0.25	-0.16	-0.23	-0.49	-0.40	0.17	0.11	-0.31	-0.02	0.43	-0.05	0.01	0.16	0.16	0.00	0.16	0.15	0.13
	PC4	-0.18	-0.19	-0.12	0.16	0.00	0.07	0.19	-0.03	-0.13	-0.44	-0.51	-0.11	0.12	-0.57	-0.04	0.03	-0.15	0.02	-0.03	0.08
	PC5	0.03	0.03	-0.09	-0.15	-0.29	0.13	0.16	0.43	0.26	0.23	0.22	-0.02	0.62	-0.25	0.00	0.04	-0.14	0.03	0.01	0.15
	PC6	0.09	0.11	0.10	-0.05	-0.20	-0.08	-0.11	-0.50	-0.52	0.03	0.15	0.19	0.41	-0.15	0.14	-0.18	0.14	-0.17	0.15	0.14
	PC7	0.03	0.01	0.15	0.14	-0.05	-0.06	0.01	0.23	0.21	-0.11	-0.09	0.03	0.10	-0.16	0.15	-0.23	0.67	-0.19	0.14	-0.46
	PC8	-0.04	-0.05	0.17	0.28	0.16	0.01	0.09	0.18	0.16	-0.05	0.01	0.10	-0.12	0.09	0.28	-0.37	-0.15	-0.36	0.33	0.54
Rainfed	**PC1**	0.33	0.33	0.14	-0.27	-0.13	-0.05	-0.18	-0.06	0.06	-0.07	-0.12	-0.02	-0.22	0.06	0.39	0.31	0.08	0.30	0.38	0.28
	PC2	0.01	0.00	-0.23	-0.21	-0.19	-0.41	-0.35	0.01	-0.03	-0.47	-0.31	0.31	-0.16	-0.18	-0.16	-0.15	0.04	-0.16	-0.16	-0.03
	PC3	0.42	0.42	0.32	-0.21	-0.07	0.23	-0.02	0.05	0.15	0.11	-0.10	-0.25	-0.06	-0.05	-0.27	-0.30	-0.01	-0.30	-0.25	-0.10
	PC4	0.01	0.01	-0.13	-0.13	0.16	-0.20	-0.28	0.21	0.30	0.20	0.43	0.19	-0.17	0.59	-0.01	-0.15	0.13	-0.15	0.00	0.06
	PC5	0.09	0.08	-0.17	-0.25	0.26	-0.01	-0.06	-0.62	-0.56	0.10	0.14	0.01	0.01	0.14	-0.03	-0.12	-0.18	-0.13	0.00	0.14
	PC6	0.09	0.08	0.06	-0.04	-0.09	-0.05	0.00	0.21	0.10	-0.04	0.23	0.28	0.47	-0.19	0.05	-0.09	-0.57	-0.11	0.10	0.41
	PC7	0.15	0.15	0.07	-0.12	-0.26	-0.12	-0.14	-0.09	-0.11	0.10	0.33	0.22	0.41	-0.02	-0.15	0.30	0.17	0.32	-0.22	-0.43
	PC8	-0.01	0.00	0.52	0.48	-0.21	-0.04	-0.15	-0.21	-0.18	-0.09	0.10	0.25	0.04	0.05	0.15	-0.25	0.29	-0.24	0.19	0.05
Drought	**PC1**	0.37	0.37	0.29	-0.19	-0.15	-0.17	-0.28	-0.08	0.01	-0.18	-0.19	0.07	-0.12	-0.09	0.36	0.15	0.09	0.17	0.36	-0.21
	PC2	0.17	0.17	0.17	-0.03	0.32	0.20	0.11	0.19	0.16	0.46	0.40	-0.32	-0.03	0.38	0.13	0.13	0.05	0.14	0.12	-0.09
	PC3	-0.34	-0.33	-0.34	0.02	0.06	-0.04	0.13	-0.04	-0.09	-0.02	0.05	0.10	0.13	-0.05	0.31	0.43	0.17	0.44	0.28	-0.10
	PC4	-0.13	-0.12	-0.20	-0.12	0.18	-0.39	-0.31	-0.27	0.13	-0.01	0.13	0.18	-0.50	0.46	0.03	-0.11	0.04	-0.11	0.04	0.06
	PC5	-0.12	-0.13	-0.14	-0.01	-0.09	0.16	0.11	0.40	0.27	-0.07	-0.12	-0.04	-0.14	-0.02	0.18	-0.35	0.47	-0.31	0.20	-0.35
	PC6	-0.04	-0.07	0.28	0.64	-0.01	-0.25	-0.14	-0.28	0.04	0.11	0.25	0.13	0.35	-0.01	0.09	-0.15	0.17	-0.13	0.09	-0.21
	PC7	0.08	0.09	-0.05	-0.27	0.31	0.11	0.17	-0.28	-0.70	0.01	0.08	0.09	0.07	0.02	0.00	-0.19	0.24	-0.17	0.00	-0.26
	PC8	-0.03	0.00	-0.25	-0.44	-0.19	-0.27	-0.36	0.11	-0.01	0.25	0.23	-0.18	0.49	-0.13	0.08	-0.15	0.03	-0.15	0.09	0.16

PC: Principal component; **DTH:** days to heading; **DTA:** days to anthesis; **DTM:** days to maturity; **GFD:** grain filling duration; **NOT:** number of tillers plant^{-1}; **PH:** plant height (cm); **PL:** peduncle length (cm); **SL:** spike length (cm); **SPS:** spikelet per spike; **BY:** biological yield (g plant^{-1}); **GY:** grain yield (g plant^{-1}); **HI:** harvest index (%); **TKW:** thousand kernel weight (g); **TNG:** total number of grains plant^{-1}; **Glu:** glucose (mg g^{-1}); **Fru:** fructose (mg g^{-1}); **Suc:** Sucrose (mg g^{-1}); **Fruc:** fructans (mg g^{-1}); **WSC:** total water-soluble carbohydrates (mg g^{-1}); **TNSC:** total non-structural carbohydrates (mg g^{-1})



Irrigated

Rainfed

Drough

Figure 4.6: Coordinates of 302 bread wheat genotypes under study on first two principal components (PC1 and PC2)

Results of PCA for variables pooled over drought environment (**Table 4.13**) were similar to the results of rainfed conditions. First 7 PCs contributed to 76.4% of total variability where PC1 retained maximum information contained in 3.66 of original variable with highest individual contribution of 18.29%. First three PCs explained 49.39% variations for original variables in studied traits whereas, remaining four PCs (PC4-PC7) retained lesser information on variability for original variables as they contributed only 26.60% of variation. **Table 4.13** explains vector loading of studied traits in extracted PCs. Traits with the highest vector loadings under first 7 principal components were DTH and DTA (0.37, PC1), BY (0.46, PC2), sucrose (0.44, PC3), TKW (-0.50, PC4), fructose (0.47, PC5), GFD (0.64, PC6) and SPS (-0.70, PC7). Furthermore, Figure 5 depicts the relative position of wheat genotypes in first two components under rainfed and drought conditions.

4.7.2. Agglomerative hierarchical clustering analysis

Agglomerative clustering with Ward's minimum method extracted 8 clusters at Euclidian distance 400 (13.3% similarity level), 398 (13.2% similarity level) and 433 (14.3% similarity level) for data pooled over IR, RF and DT, respectively. Distribution of studied bread wheat population in 8 extracted clusters along with their distance from main centroid is shown in **Table 4.15** and **Table 4.16** depicts inter-cluster distance from centroid of each cluster. Summary statistics of each cluster for studied variables under IR, RF and DT is given in **Annexure 5 (pp: XX)**. Cluster membership detail of genotypes is given in **Annexure 6 (pp: XXIV)** Clustering patterns revealed that for pooled over IR environments average distances of clusters from centroid were between 22.8 (cluster II) and 33.1 (cluster I) whereas, for RF and DT these were from 18.4 (cluster VI) to 31.2 (cluster I) and 27.7 (cluster III) to 40.7 (cluster II). Maximum distances between the centroid of clusters for different clusters observed under IR, RF and DT 63.3 (cluster- I), 65.6 (cluster I) and 106.6 (cluster II), respectively. For IR, RF and DT inter-cluster distances were 29.2 (Cluster V and VII) to 238.6 (Cluster II and VIII), 25.1 (Cluster IV and VI) to 93.9 (Cluster I and VII), and 41.2 (Cluster IV and V) to 135.0 (Cluster I and VI), respectively**.** Furthermore, under pooled irrigated environment, cluster V contained highest number of 61 (20.19%) genotypes and cluster II was the smallest one with only 5 (1.65%) genotypes. Clusters IV and V were identified as the largest cluster under pooled rainfed and pooled drought environments with 60 (19.86%) and 84 (28.00%) genotypes, respectively. On the other hand, cluster VIII with only 18 (5.96%) genotypes was the smallest cluster under pooled rainfed and drought environments. Interestingly cluster VIII exhibited 18 genotypes in all three pooled environments.

Table 4.15: Distribution of bread wheat genotypes and distance statistics from centroid recorded for observed clusters extracted from hierarchical clustering analysis of data set pooled over different water regimes

Clusters	Irrigated			Rainfed			Drought		
	n	*ADC*	*MDC*	*n*	*ADC*	*MDC*	*n*	*ADC*	*MDC*
I	42	33.12	63.39	37	31.24	65.66	19	33.24	58.62
II	05	22.84	33.26	46	26.69	56.76	35	40.73	106.62
III	52	31.04	61.77	27	25.71	45.97	32	27.74	53.76
IV	36	25.17	50.71	60	23.39	45.21	49	30.05	74.10
V	61	28.87	51.02	30	26.72	46.06	84	29.42	60.27
VI	41	26.90	48.83	33	18.43	32.01	27	39.63	80.67
VII	47	22.95	42.12	51	29.65	60.07	38	28.12	59.47
VIII	18	31.36	58.54	18	28.54	41.39	18	28.02	54.38

n: number of genotypes, **ADC:** average distance from centroid, **MDC:** maximum distance from centroid

Table 4.16: Distance between centroids of observed clusters extracted from hierarchical clustering analysis of bread wheat data set pooled over different water regimes

	Clusters	*I*	*II*	*III*	*IV*	*V*	*VI*	*VII*	*VIII*
Irrigated	*I*	0.00	164.65	78.05	66.17	53.60	61.85	33.48	79.33
	II	164.65	0.00	88.35	118.44	160.43	208.05	162.43	238.63
	III	78.05	88.35	0.00	38.29	77.41	121.68	75.62	151.08
	IV	66.17	118.44	38.29	0.00	42.68	92.31	51.26	125.04
	V	53.60	160.43	77.41	42.68	0.00	52.36	29.27	86.40
	VI	61.85	208.05	121.68	92.31	52.36	0.00	47.36	39.37
	VII	33.48	162.43	75.62	51.26	29.27	47.36	0.00	79.53
	VIII	79.33	238.63	151.08	125.04	86.40	39.37	79.53	0.00
Rainfed	*I*	0.00	52.61	84.37	57.51	51.08	37.70	93.99	89.93
	II	52.61	0.00	74.83	41.01	65.86	32.01	49.77	64.26
	III	84.37	74.83	0.00	35.95	41.37	55.17	59.84	43.19
	IV	57.51	41.01	35.95	0.00	37.12	25.16	45.39	43.70
	V	51.08	65.86	41.37	37.12	0.00	40.01	78.75	58.27
	VI	37.70	32.01	55.17	25.16	40.01	0.00	60.12	62.88
	VII	93.99	49.77	59.84	45.39	78.75	60.12	0.00	42.23
	VIII	89.93	64.26	43.19	43.70	58.27	62.88	42.23	0.00
Drought	*I*	0.00	56.70	67.19	114.80	82.20	135.00	114.48	130.55
	II	56.70	0.00	74.92	100.29	59.57	78.75	67.87	95.00
	III	67.19	74.92	0.00	58.45	44.06	131.08	92.47	85.61
	IV	114.80	100.29	58.45	0.00	41.16	122.79	72.16	47.21
	V	82.20	59.57	44.06	41.16	0.00	94.45	50.04	49.83
	VI	135.00	78.75	131.08	122.79	94.45	0.00	52.66	86.81
	VII	114.48	67.87	92.47	72.16	50.04	52.66	0.00	42.57
	VIII	130.55	95.00	85.61	47.21	49.83	86.81	42.57	0.00

Mean values of clusters identified under pooled irrigated environment revealed that cluster I exhibited the highest mean values for days to maturity (DTM), peduncle length (PL), spikelet per spike (SPS), total non-structural carbohydrates (TNSC), glucose, fructose and sucrose. Cluster II had the lowest mean values for grain filling duration (GFD), spike length (SL), and thousand kernel weight (TKW) and the highest mean values for days to heading (DTH), days to anthesis (DTA), biological yield (BY), grain yield (GY), harvest index (HI) and the total number of grains (TNG). Cluster III exhibited the lowest values of DTH and DTA and the highest values of GFD and number of tillers (NOT). Cluster IV was identified with the highest mean value for SL and the lowest for glucose, sucrose and WSCs. Cluster V had minimum values for DTM, SPS, TNSC and fructans and cluster VI for NOT. These clusters did not show maximum values for any of the studied traits. Cluster VII showed the lowest mean values for PH, PL and fructose whereas, the highest mean values of WSCs. Cluster VIII exhibited the lowest mean values of BY, GY, HI and TNG and the highest mean values of PH, TKW and fructose.

Under pooled rainfed environment the highest mean value of NOT, SPS, BY, GY, TNG and fructose was recorded in cluster I along with the lowest mean of TKW. Cluster II characterized minimum mean of WSCs. Cluster III had minimum value for GFD and PL and maximum value for WSCs. The lowest mean of fructose was recorded in cluster IV. Cluster V showed the highest mean of TNSC, glucose, fructose, sucrose and fructans. Cluster VI exhibited the shortest DTM, PH and PL and the longest SL and highest HI. The lowest mean values of DTH, DTA, SPS, TNSC, glucose, sucrose and fructans along with the highest mean values of GFD, PL and TKW were characterized in cluster VII. Cluster VIII had minimum mean values of NOT, SL, SPS, BY, GY, HI and TNG and maximum mean values of DTH, DTA, DTM and PH.

Under pooled drought environment, cluster I had the highest mean of NOT, PH, SL, SPS, BY, GY, TNG and WSCs and the lowest mean of HI and TKW. The highest mean values of DTH, DTA and TNG were recorded in cluster II. Cluster III was identified with minimum mean values of TNSC, glucose, sucrose, fructose and fructans and maximum means values of GFD and PL. The lowest mean of DTH, DTA, DTM, SL and SPS were recorded in cluster IV. Cluster V did not have any minimum and maximum values. Cluster VI had the highest mean of TNSC, glucose, fructose, sucrose and fructans whereas, the lowest means of GFD, PL and WSCs. Cluster VII was characterized by minimum and maximum means of PH and PL, respectively. Cluster VIII had the lowest mean of NOT, BY, GY and TNG and the highest mean of DTM.

4.8. Genome wide association mapping

Genome wide association mapping was performed to identify significant marker traits associations (MTAs) between polymorphic SNPs and 20 studied traits. Each environment was considered as an individual data set thus generating 13 data sets (10 individual environments + 3 pooled environments) for the study of association mapping. Results for GWAS are as follow:

4.8.1. Marker statistics and population structure

Association mapping panel was genotyped with 35K Axiom Breeders SNP chip generating an unprocessed data of 35143 SNPs. Out of these, 14571 SNPs were extracted after test for monomorphism, test for missingness (>0.05), minor allele frequency test (MAF<0.05), marker duplication and lack of physical position. Furthermore, RD20 was discarded from this analysis for being a *Triticum durum* genotype. Thus, present investigation included 301 *Triticum aestivum* genotypes with 14571 polymorphic SNPs.

Polymorphic markers covered genetic distance of 1288986.92 centiMoragn (cM) across the *Triticum aestivum* genome with an average density of 88.46 cM. It is evident form **Table 4.17** and **Figure 4.7** that maximum 7357 SNPs were distributed on genome ‘B’ covering genetic distance of 643957.26 cM with an average density of 87.53 cM. Minimum coverage of SNPs was on genome ‘D’ followed by genome ‘A’. For individual chromosomes, SNPs distribution ranged between 61 (4D) and 1360 (2B). The shortest genetic distance was covered on chromosome

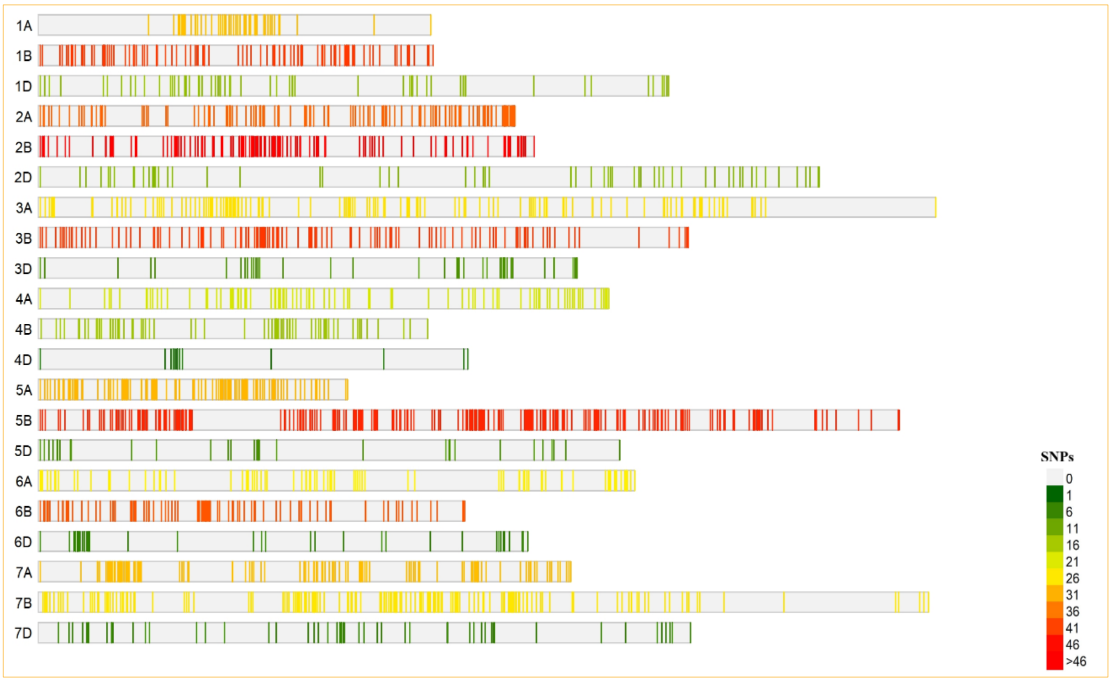


Figure 4.7: Distribution pattern of 14571 polymorphic SNPs on 21 chromosomes of *T. aestivum*

Table 4.17: Basic statistical analysis of SNP markers used for genome-wide association study (GWAS) of 301 wheat genotypes

Chromosome	No. of Markers	Marker Position(cM)			Marker Density	Minor allele frequency			Heterozygosity			PIC		
		Min	**Max**	**Sum**		**Min**	**Max**	**Mean**	**Min**	**Max**	**Mean**	**Min**	**Max**	**Mean**
1A	846	41.03	148.06	60580.63	71.61	0.05	0.50	0.26	0.10	0.50	0.35	0.09	0.25	0.21
1B	1213	0.00	148.84	49451.81	40.77	0.05	0.50	0.26	0.10	0.50	0.36	0.09	0.25	0.22
1D	388	0.00	238.14	51250.93	132.09	0.05	0.50	0.32	0.10	0.50	0.39	0.09	0.25	0.22
2A	1097	0.00	179.99	89668.60	81.74	0.05	0.50	0.26	0.10	0.50	0.36	0.09	0.25	0.22
2B	1360	0.00	187.28	125457.46	92.25	0.05	0.50	0.27	0.10	0.50	0.36	0.09	0.25	0.22
2D	365	0.00	295.13	76527.78	209.67	0.05	0.50	0.23	0.10	0.50	0.33	0.09	0.25	0.21
3A	760	0.00	339.45	71384.42	93.93	0.05	0.50	0.26	0.10	0.50	0.35	0.09	0.25	0.21
3B	1215	0.00	245.57	111673.39	91.91	0.05	0.50	0.29	0.10	0.50	0.38	0.09	0.25	0.22
3D	206	0.00	203.45	19785.46	96.05	0.05	0.50	0.27	0.10	0.50	0.36	0.09	0.25	0.21
4A	579	0.00	215.51	74461.22	128.60	0.05	0.50	0.25	0.10	0.50	0.35	0.09	0.25	0.21
4B	426	0.37	146.87	35316.91	82.90	0.05	0.50	0.23	0.10	0.50	0.32	0.09	0.25	0.20
4D	61	0.00	162.13	3279.41	53.76	0.06	0.49	0.28	0.11	0.50	0.36	0.10	0.25	0.21
5A	875	0.00	116.44	54897.46	62.74	0.05	0.50	0.27	0.10	0.50	0.36	0.09	0.25	0.22
5B	1261	0.00	325.55	171403.38	135.93	0.05	0.50	0.31	0.10	0.50	0.39	0.09	0.25	0.23
5D	192	0.00	219.57	6045.84	31.49	0.05	0.48	0.16	0.10	0.50	0.26	0.09	0.25	0.18
6A	718	0.00	225.31	72094.60	100.41	0.06	0.50	0.28	0.11	0.50	0.36	0.10	0.25	0.22
6B	1136	0.00	160.89	72602.11	63.91	0.05	0.50	0.28	0.10	0.50	0.37	0.09	0.25	0.22
6D	130	0.00	184.72	7770.30	59.77	0.06	0.50	0.26	0.11	0.50	0.36	0.10	0.25	0.22
7A	853	0.00	201.13	46397.43	54.39	0.05	0.50	0.27	0.10	0.50	0.36	0.09	0.25	0.22
7B	746	0.94	336.69	78052.20	104.63	0.05	0.50	0.28	0.10	0.50	0.37	0.09	0.25	0.22
7D	144	6.96	246.43	10885.58	75.59	0.05	0.50	0.25	0.10	0.50	0.34	0.09	0.25	0.21
A Genome	5728	0.00	339.45	469484.36	81.96	0.05	0.50	0.26	0.10	0.50	0.36	0.09	0.25	0.22
B Genome	7357	0.00	336.69	643957.26	87.53	0.05	0.50	0.28	0.10	0.50	0.37	0.09	0.25	0.22
D Genome	1486	0.00	295.13	175545.30	118.13	0.05	0.50	0.26	0.10	0.50	0.34	0.09	0.25	0.21

4D (3279.41 cM) whereas, the longest genetic distance was covered on 5B (171403.38 cM). In contrast to other chromosomes markers were densely distrusted on chromone 5D with an average marker density of 31.49 cM. However, density of markers was quite loose on chromosome 2D (209.67 cM), 5B (135.93 cM), 1D (132.09 cM), 4A (128.6 cM), 7B (104.63 cM) and 6A (100.41 cM). Furthermore, mean values for MAF, heterozygosity and polymorphic information content (PIC) ranged from 0.16 (5D) to 0.32 (1D), 0.26 (5D) to 0.39 (1D) and 0.18 (5D) to 0.23 (5A), respectively.

Population structure of AM panel was done using STRUCTURE tool. These results showed no extensive subpopulation structure separation of 301 genotypes. Principal component analysis was applied to summarize the genetic diversity and population structure in AM panel (**Table 4.8**). Top three principal components explained 25.16% (PC1: 15.33%; PC2: 5.33% and PC3: 4.49%) of genetic variance. The study material stratified in two major subpopulations. Subpopulation-I (SP1) consisted of 51 genotypes which were mainly landraces or indigenous collection or genetic stocks registered with abiotic stresses (such as C-306, Kharchia local, Bageshwer local, Hind-62, and HI-1500). In addition to this, some varieties which were recommended for north-western zone clustered in this population. In contrast to SP1, larger number of genotypes (251) grouped in subpopulation-II (SP2) and had all six categories *i.e.* indigenous collection (IC), landraces, genetic stocks (GS), varieties and improved varieties (IV). Cluster analysis was further conducted to learn genetic structure of SP2 which revealed that genotypes having similar lineage were placed in same cluster **(Figure 4.8c)**.

4.8.2. Marker trait associations (MTAs)

Among various tested models for efficient association mapping, compressed mixed linear model (CMLM) showed minimum deviation in estimated *p*-values from observed ones and thus advocated minimal effects of population structure and relatedness (K-kinship). Therefore, CMLM was selected as a method for association mapping in present study. All 14751 polymorphic SNPs produced nearly 38.3 lacs of MTAs for 20 traits in 13 data set. Out of these, 3423 MTAs produced by 1987 SNPs found to be significant at cutoff $-\log_{10}p > 2.89$ while explaining phenotypic variation (PEV) between 2.93% and 52.71% and -76.54 to 71.87 SNP effect. Genome ‘A’, ‘B’ and ‘D’ covered 41%, 48% and 11% of significant SNPs, respectively. Among linkage groups (LG) maximum MTAs were covered by 5B (309) whereas, minimum by 4D (15). On top of, since not all traits were evaluated in all 13 data set, comparison of MTAs distribution was done on the basis

Figure 4.8: **(a) PCA, (b) kinship matrix and (c) neighbor-joining dendrogram depicting the population structure of GWAS panel consisting of 301 *Triticum aestivum* genotypes**

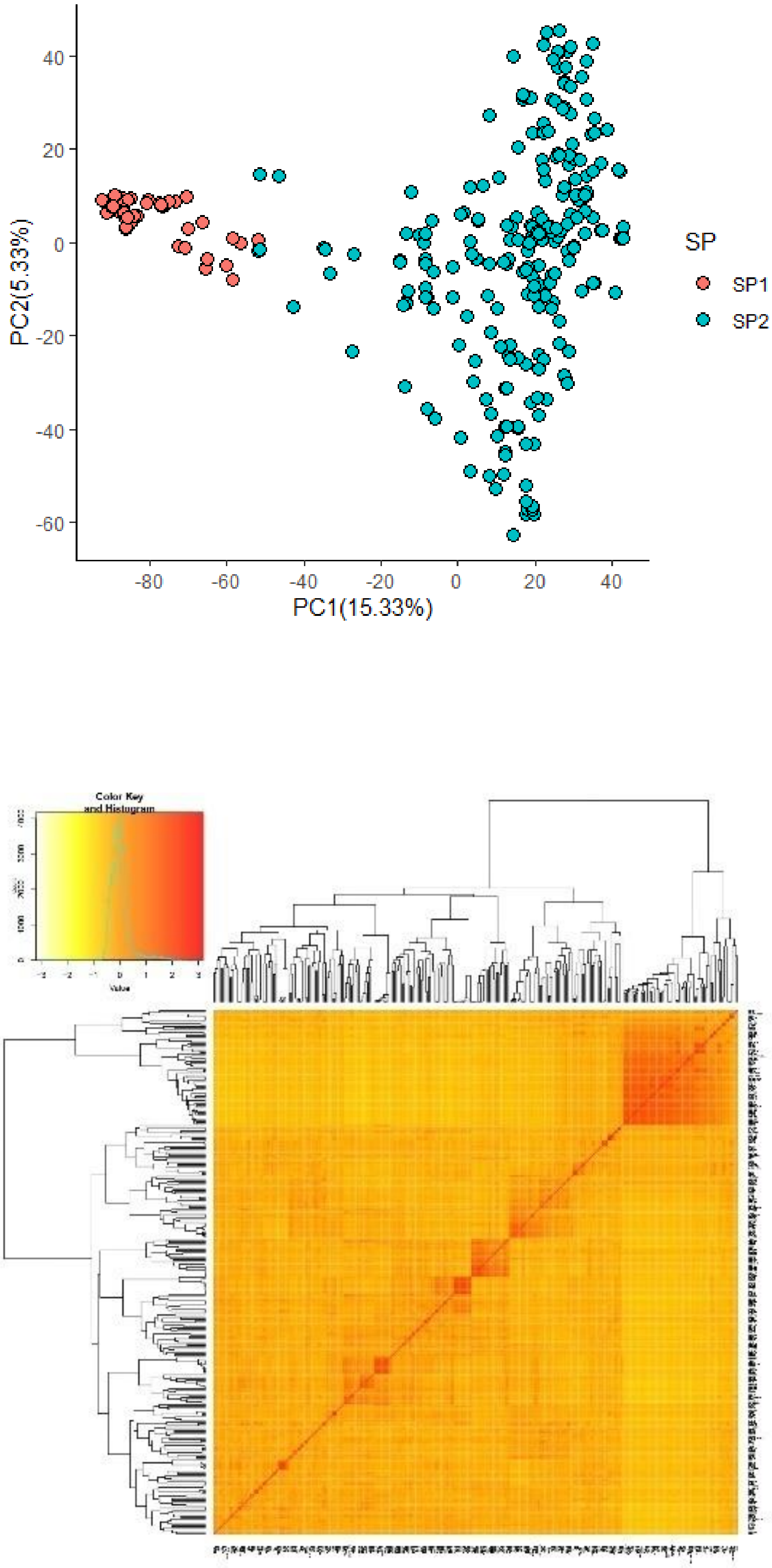
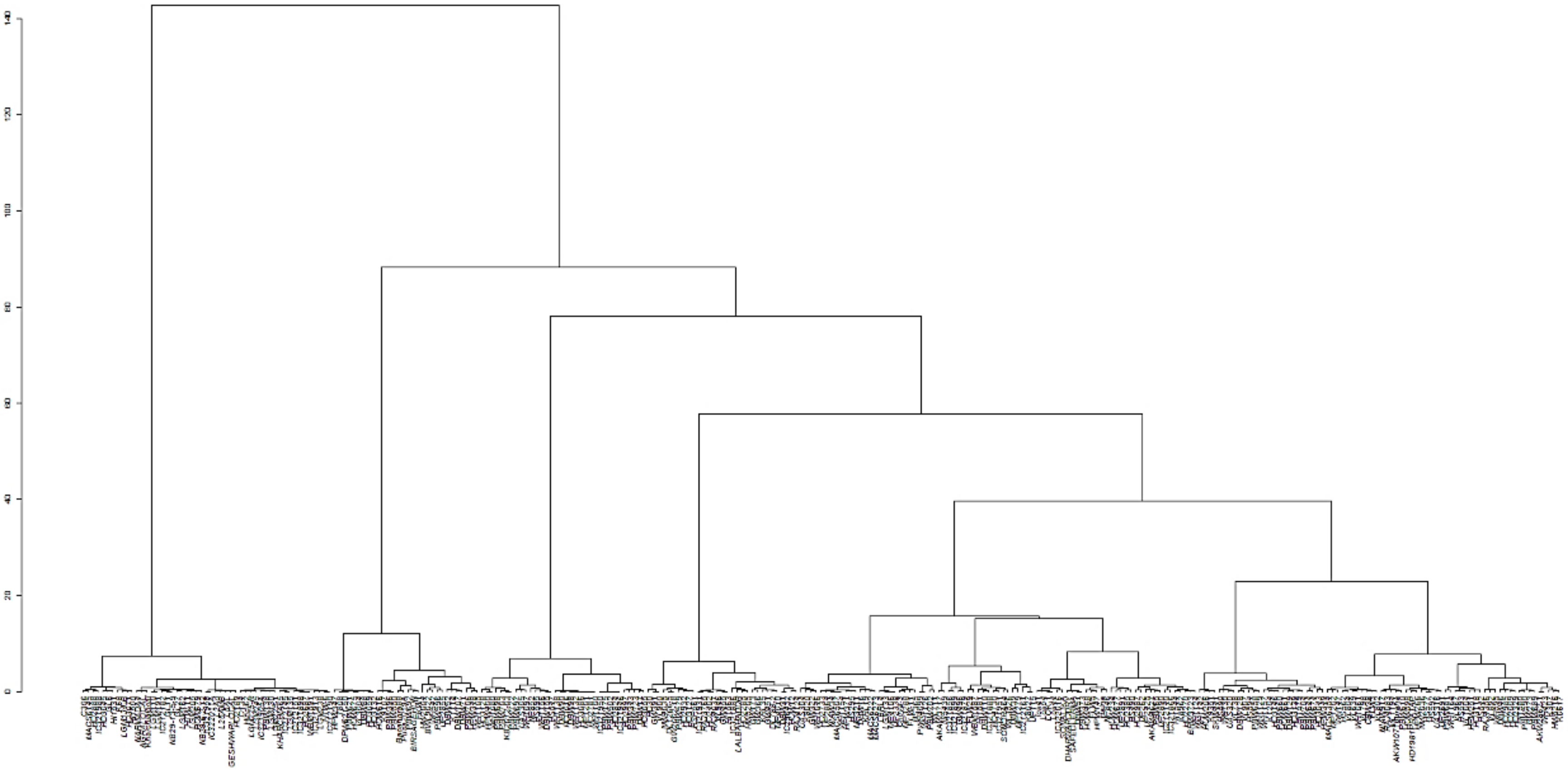


Figure 4.8c:



of MTAs per trait. Maximum 17.5 MTAs per trait were recorded in IR and minimum 12.0 MTAs per trait in (E01). For three different water managements, distribution of MTAs on ‘A’, ‘B’ and ‘D’ genomes was 707, 718 and 168 for IR, 509, 388 and 137 for RF, and 297, 422 and 81 for DT, respectively. **Table 4.18** reveals that linkage group 5B possessed maximum 80 MTAs for E04 data set whereas, minimum 1 MTA was observed in data set E01 (2D), E03 (7D), E04 (1D), E06 (2D,4D), E08 (4D, 6D), E10 (3D), IR (2D, 6D and 7D), RF (1D) and DT (1B).

It is evident from **Table 4.19** and **Table 4.20** that there were substantial MTAs for each of the studied traits. However, distribution of these MTAs on linkage groups and data set was quite random *i.e.* not all traits were linked to all linkage groups and not all data sets had significant MTAs for all the studied traits. Among all data sets, maximum 269 and minimum 113 significant MTAs were identified for PH and sucrose, respectively. For individual traits, maximum number of significant MTAs identified in any data set were 22 (DTH: E09, E10, RF), 30 (DTA: E10), 34 (DTM: RF), 31 (GFD: E09), 51 (NOT: IR), 42 (PH: DT), 30 (PL: RF), 29 (SL: E5), 21 (SPS: E05), 31 (BY: E03), 38 (GY: E07), 25 (HI: E01), 24 (TKW: E02), 18 (TNG: E07), 22 (TNSC: E02), 32 (Glucose: E04), 21 (Fructose: E04), 14 (Sucrose: E02, E04, E06), 27 (Fructans: E02) and 31 (WSC: E06). Interestingly, no significant MTA was identified for GY and TKW in E10 data set and for WSC in E01 data set.

Table 4.18: Distribution of significant MTAs on 21 linkage groups in 13 data set

LG	E01	E02	E03	E04	E05	E06	E07	E08	E09	E10	IR	RF	DT
1A	10	37	20	9	27	23	17	28	14	15	40	33	1
1B	6	23	19	12	14	10	16	10	5	10	14	21	33
1D	-	2	6	1	4	5	6	7	3	9	10	1	4
2A	12	3	52	17	5	15	18	7	5	5	57	34	18
2B	11	13	17	9	8	11	32	29	3	6	31	38	22
2D	1	3	2	9	5	1	5	14	4	-	1	2	5
3A	5	29	18	17	13	17	6	17	9	8	19	6	28
3B	27	20	16	26	36	25	19	22	22	3	16	8	9
3D	15	9	3	10	15	16	21	5	-	1	14	16	5
4A	6	3	2	21	5	6	16	3	9	6	5	4	8
4B	16	10	11	6	4	-	7	10	19	9	14	12	7
4D	-	2	2	-	-	1	3	1	2	-	2	2	-
5A	33	28	27	6	13	5	17	13	25	48	25	24	9
5B	20	19	27	80	7	5	30	28	3	8	11	14	57
5D	-	-	3	2	7	11	2	-	-	-	2	5	2
6A	-	10	8	12	11	10	7	11	7	6	43	24	12
6B	35	23	22	5	19	24	20	15	13	10	14	21	6
6D	7	5	-	-	3	17	-	1	3	-	1	20	-
7A	5	33	23	9	19	50	30	21	7	6	19	21	30
7B	29	21	13	5	31	17	7	25	23	-	11	7	6
7D	2	2	1	1	2	4	4	9	-	-	1	3	5
Total	**240**	**295**	**292**	**257**	**248**	**273**	**283**	**276**	**176**	**150**	**350**	**316**	**267**

Table 4.19: Trait wise distribution of significant MTAs $(-log_{10}P>2.89)$ on 21 linkage groups of genomes of 301 *Triticum aestivum* genotypes

Traits	1A	1B	1D	2A	2B	2D	3A	3B	3D	4A	4B	4D	5A	5B	5D	6A	6B	6D	7A	7B	7D
DTA	7	8	7	4	15	1	11	10	1	9	1	-	58	4	1	4	25	1	7	3	2
DTH	7	10	7	3	17	1	12	11	1	11	1	-	65	6	1	7	27	-	10	8	2
DTM	14	1	-	38	26	2	9	10	-	6	-	-	31	2	1	2	16	1	15	7	10
GFD	14	4	12	3	4	2	1	20	14	10	10	-	31	9	1	29	26	-	8	5	-
NOT	10	8	2	73	22	6	3	17	1	7	12	1	3	24	1	6	7	5	13	7	2
PH	54	14	-	-	5	8	28	4	22	7	20	-	1	61	5	-	7	14	9	7	3
PL	45	6	-	7	4	11	9	31	15	6	44	-	19	19	-	1	6	-	13	8	1
SL	19	9	12	10	10	-	4	15	6	6	1	-	8	3	6	2	10	-	16	5	1
SPS	6	2	6	5	17	1	2	3	5	-	-	-	2	9	-	15	16	-	46	4	-
BY	3	19	1	23	27	2	1	14	17	4	-	1	5	10	2	15	20	5	12	8	1
HI	3	6	-	4	15	-	14	14	24	8	1	-	9	36	-	2	9	4	13	4	2
GY	6	9	5	9	11	2	13	10	10	7	1	1	4	20	4	14	20	1	15	27	-
TKW	6	5	2	9	7	-	3	-	-	5	13	10	7	3	2	23	1	1	32	16	7
TNG	8	13	1	12	6	1	1	7	2	3	5	2	3	17	1	10	10	1	10	23	-
TNSC	13	21	-	1	3	3	30	12	1	-	1	-	4	14	3	5	4	3	11	9	-
Glucose	3	11	1	19	2	-	3	10	1	2	-	-	4	26	1	10	8	4	3	19	1
Fructose	30	14	-	5	17	2	4	26	-	-	-	-	5	22	-	-	2	-	16	2	1
Sucrose	5	10	1	20	1	-	3	11	1	2	-	-	4	9	2	9	8	4	3	19	1
Fructans	14	18	1	1	2	3	30	11	-	-	1	-	8	13	3	6	2	2	10	10	-
WSC	7	5	-	2	19	7	11	13	9	1	14	-	2	2	-	1	3	11	11	4	-
Total	**274**	**193**	**58**	**248**	**230**	**52**	**192**	**249**	**130**	**94**	**125**	**15**	**273**	**309**	**34**	**161**	**227**	**57**	**273**	**195**	**34**

Table 4.20: Trait wise distribution of significant MTAs (-$log_{10}P$>2.89) in 13 data set

Trait	**DTA**	**DTH**	**DTM**	**GFD**	**NOT**	**PH**	**PL**	**SL**	**SPS**	**BY**	**HI**	**GY**	**TKW**	**TNG**	**TNSC**	**Glucose**	**Fructose**	**Sucrose**	**Fructans**	**WSC**	**Total**
E01	10	11	7	10	7	24	16	11	15	12	25	22	15	14	6	6	16	6	7	-	**240**
E02	9	13	4	11	6	25	40	11	3	19	6	21	24	11	22	10	16	14	27	3	**295**
E03	16	22	7	15	35	14	9	14	13	31	14	11	22	17	13	6	9	4	12	8	**292**
E04	12	11	21	2	12	30	10	6	10	14	21	7	4	2	8	32	21	14	10	10	**257**
E05	8	14	7	13	6	13	25	29	21	12	18	10	8	9	8	13	11	13	6	4	**248**
E06	15	13	21	7	4	22	11	11	13	13	9	20	4	11	17	12	9	14	16	31	**273**
E07	16	12	15	22	8	17	11	17	7	23	7	38	15	18	8	10	5	13	8	13	**283**
E08	2	5	14	12	75	19	24	1	13	4	8	8	4	9	21	5	17	5	22	8	**276**
E09	22	25	16	31	5	6	21	-	-	6	7	8	15	14	-	-	-	-	-	-	**176**
E10	22	30	24	23	1	16	11	-	-	6	11	-	-	6	-	-	-	-	-	-	**150**
IR	21	24	3	46	51	19	15	20	16	13	8	15	22	2	2	17	16	13	1	26	**350**
RF	22	25	34	8	6	22	30	20	16	29	13	20	14	17	4	7	11	6	3	9	**316**
DT	4	2	18	3	14	42	22	3	12	8	21	9	5	6	29	10	15	11	23	10	**267**
Total	**179**	**207**	**191**	**203**	**230**	**269**	**245**	**143**	**139**	**190**	**168**	**189**	**152**	**136**	**138**	**128**	**146**	**113**	**135**	**122**	**3423**

Figure 4.9 depicts the genome wise distribution of studied traits. For individual traits, maximum number of MTAs identified on any genome was 115 (DTH: A), 100 (DTA: A), 115 (DTM: A), 96 (GFD: A), 115 (NOT: A), 118 (PH and PL: B), 65 (SL: A), 76 (SPS: A), 98 (BY and GY: B), 85 (HI: B), 85 (TKW: A), 81 (TNG: B), 64 (TNSC: A and B), 76 (Glucose: B), 83 (Fructose: B), 58 (Sucrose: B), 69 (Fructans: A) and 60 (WSCs: B). Likewise, maximum number significant MTAs on different linkage groups was 58 (DTA: 5A), 65 (DTH: 5A), 38 (DTM: 2A), 31 (GFD: 5A), 73 (NOT: 2A), 61 (PH: 5B), 45 (PL: 1A), 19 (SL: 1A), 46 (SPS: 7A), 27 (BY: 2B), 36 (HI: 5B) ,27 (GY: 7B), 32 (TKW: 7A), 23 (TNG: 7B), 30 (TNSC: 3A), 26 (Glucose: 5B), 30 (Fructose: 1A), 20 (Sucrose: 2A), 30 (Fructans: 3A) and 19 (WSC: 2B). Detailed distribution pattern of MTAs for each trait with individual data set is tabulated in **Annexure 7 (pp: XXVI)**.

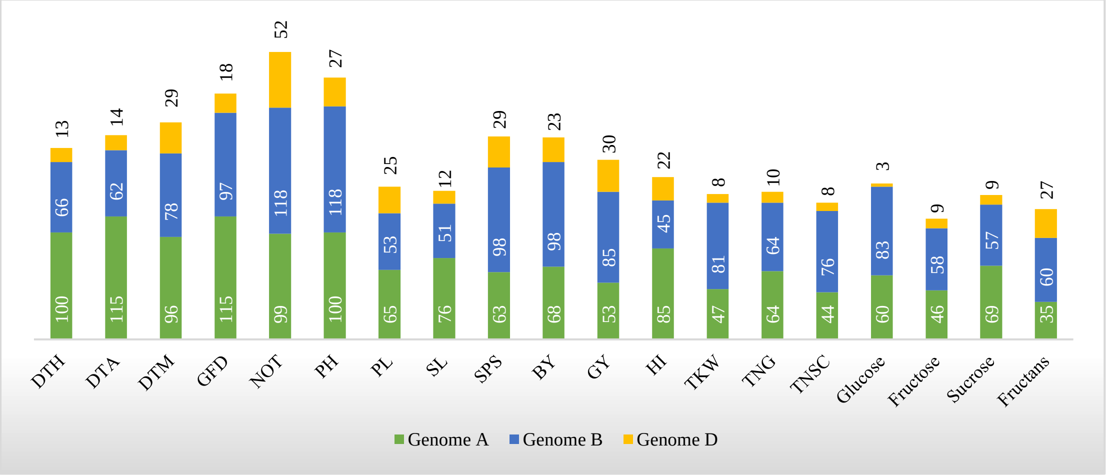


Figure 4.9: Distribution pattern of significant MTAs on the genome of 301 bread wheat genotypes

Percentage phenotypic variation (PEV%) explained by significant SNPs for individual trait was 5.4-32.4% (DTH), 3.9-31.3% (DTA), 4.5-22.5% (DTM), 5.0-26.8% (GFD), 3.8-26.3% (NOT), 9.4-52.7% (PH), 8.3-37.3% (PL), 4.0-25.7% (SL), 4.6-17.3% (SPS), 3.0-23.8% (BY), 3.9-16.3% (GY), 3.7-34.2% (HI), 6.5-14.3% (TKW), 3.9-16.1% (TNG), 2.9-9.7% (TNSC), 3.1-6.6% (Glucose), 3.3-7.7% (Fructose), 3.3-7.0% (Sucrose), 2.9-10.3% (Fructans) and 4.3-7.1% (WSC) with SNP effect -2.7-3.0 (DTH), -2.8-2.7 (DTA), -3.4-3.2 (DTM), -2.4-2.2 (GFD) , -0.80-0.78 (NOT), -9.8-9.1 (PH), -5.6-3.9 (PL), -0.75-0.99 (SL), -0.96-0.93 (SPS), -7.6-7.6 (BY), -2.9-2.8 (GY), -3.5-4.4 (HI), -2.2-2.7 (TKW), -76.5-71.8 (TNG), -24.5-16.9 (TNSC), -0.61-0.72 (Glucose), -3.6-3.2 (Fructose), -0.87-1.03 (Sucrose), -23.1-17.7 (Fructans) and -16.6-13.8 (WSC).

SNPs producing significant MTAs with 20 studied traits in 13 data set were further grouped in two classes *viz*., non-repeating SNPs (SNPs showing only one significant MTA) and repeating SNPs (SNPs showing MTAs for one or multiple traits in one or more data set). Repeating SNPs were further classified as stable SNPs (associated with one trait in more than one data set), common and stable SNPs (stable SNPs associated with more than one trait), unstable SNPs (those showing association with one or more traits only in one data set). Out of 1987 significant SNPs, 1264 SNPs were found to be non-repeating thus producing 1264 MTAs for 20 traits with 13 data set. Further, 723 SNPs were repeating which produced 2159 MTAs for 20 traits with 13 data set. Reference linkage map **(Figure 4.10)** drawn for identifying stable and common SNPs revealed that out of 723 repeating SNPs, 431 were stable SNPs which were producing 1124 MTAs, of which 77 SNPs found common for 518 MTAs. Furthermore, 501 of 723 repeating SNPs were producing 1035 unstable MTAs for different traits. Of these 501 unstable SNPs 74 were non-repeating whereas, 427 unstable SNPs were common for 961 unstable MTAs. Detailed results on stable and unstable SNPs are given in **Annexure 8 (pp: XXX)**.

4.8.3. Functional annotation of MTAs

Significant SNPs were annotated for putative genes in IWGSC reference assembly. A total of 1225 genes were reported in close association with identified significant SNPs, however only 249 genes found to be associated with 354 stable MTAs and considered for annotation (**Annexure 9; pp: XLI**). 250 conserved domains were identified in the protein sequences of these genes in CDD batch search. Furthermore, curation from InterPro and Pfam database revealed that most of the genes were involved in kinase activity, protein binding, transferase activities and cation (Ca and Zn) binding (**Figure 4.11 and 4.12**). Furthermore, out of 249 putative genes, enzymatic activities of 125 genes were identified by searching against KEGG pathway database. The KEGG annotation revealed that majority of genes was involved in genetic information processing followed by carbohydrate metabolism (Figure 4.13). The *in silico* gene expression analysis revealed differential expression of identified genes in different plant tissues at different growth and development stages. GoSlim annotation revealed that genes *TraesCS1A02G009900*, *TraesCS1D02G178000*, *TraesCS1D02G178000*, *TraesCS2B02G431400*, *TraesCS2D02G047900*, *TraesCS2D02G502600* and *TraesCS5B02G236400*, *TraesCS7D02G543400* were actively involved in drought response due to the presence of WH_DNA-bd_sf, HSF_DNA_bd, Haem_peroxidase_sf, Scorpion_toxin-like, Scorpion_toxin-like, WD40_repeat, P-loop_NTPase, DNA_mismatch_repair_MutS_sf, MutS2, NB-ARC,NAC_dom and Rx_N domains. *TraesCS7D02G433100* gene associated with SNP namely AX-94583229 caused the major variations in fructans and was directly involved in carbohydrate metabolism due to the presence of FucosylTrfase_pln domain which falls under Glycosyltransferases and Hexosyltransferases classes. Curated results from functional analysis of putative genes are tabulated in **Annexure 9 (pp: XLI)**.

Figure 4.10: Reference genotype-phenotype map of stable and common SNPs showing significant MTAs aligned with the reference genome of *Triticum aestivum* (RefSeq v.1.0)

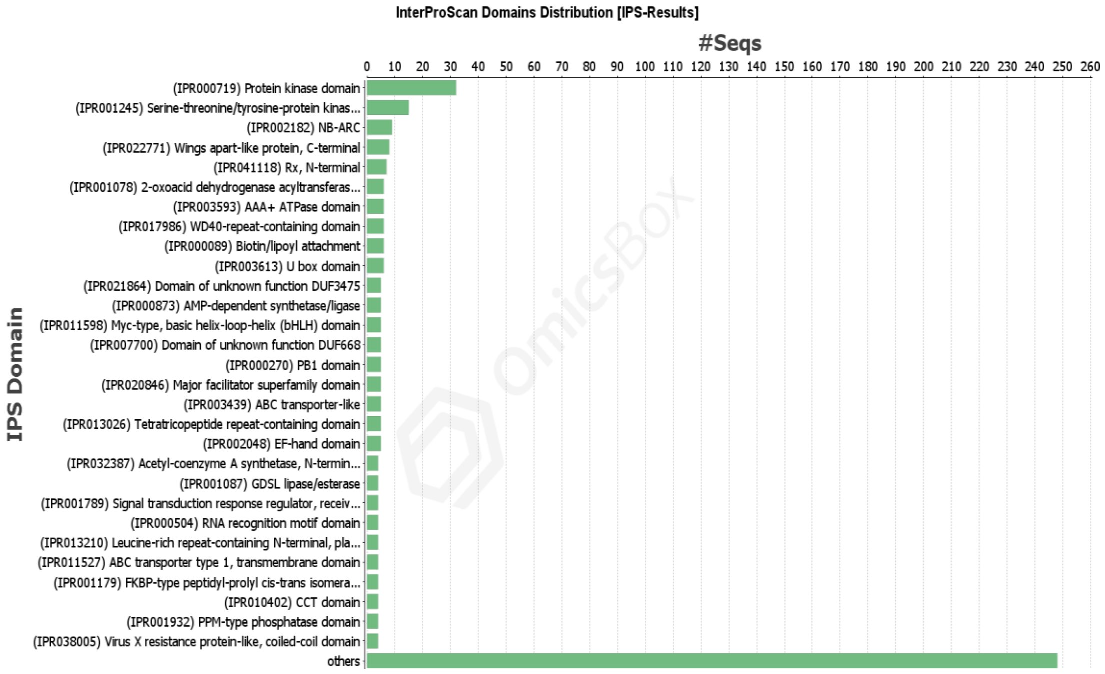


Figure 4.11: Distribution of major InterPro domains in the putative genes associated with significant and stable SNPs

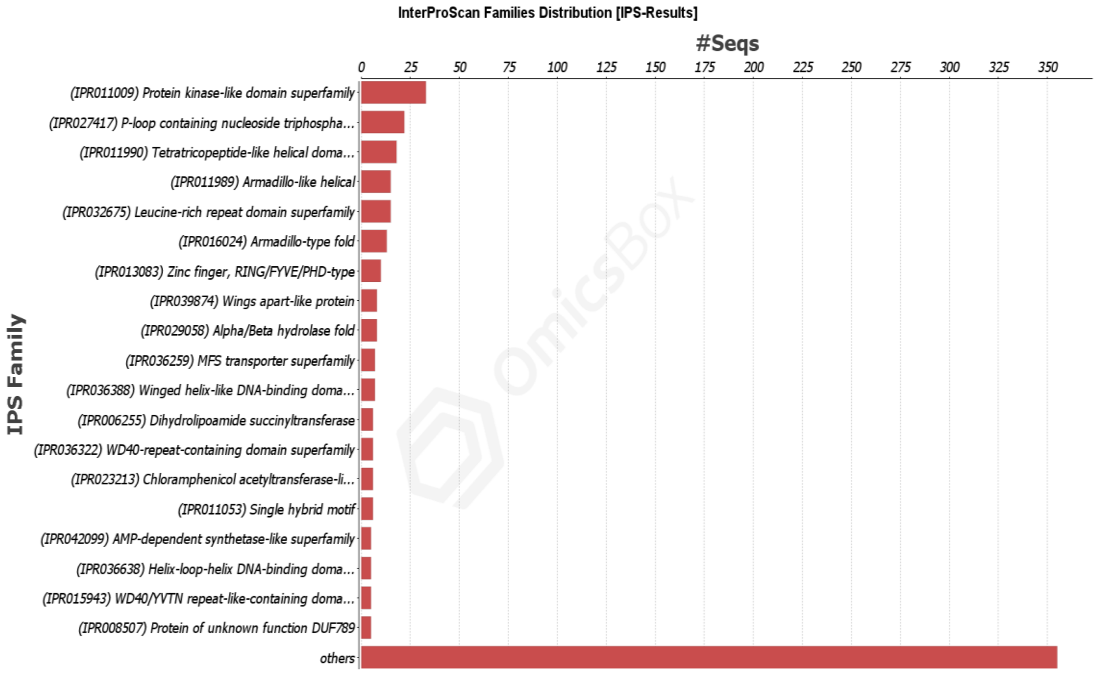


Figure 4.12: Distribution of major InterPro family in the putative genes associated with significant and stable SNPs

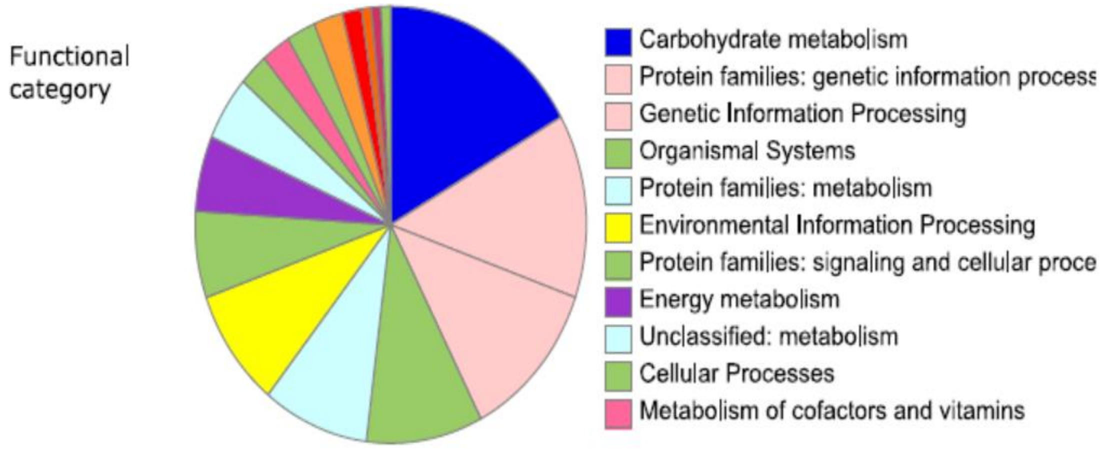


Figure 4.13: Functional categories identified in KEGG annotation of 249 putative genes

4.9. *In-silico* identification of fructans metabolic genes

An *in silico* genome wide study carried out to explore the *Triticum aestivum* genome to identify potential genes involved fructans biosynthesis. Results from this study are as follow

4.9.1. Pathway analysis

Fructans metabolic activities take place in vacuoles as shown in **Figure 4.14**. Sucrose is transported to vacuoles by various vacuolar sucrose transporters. In vacuoles, two fructosyltransferase enzymes *viz.* Sucrose:sucrose-1-fructosyltransferase (1-SST) and Sucrose:fructans-6-fructosyltransferase (6-SFT) catalyze the conversion of sucrose to 1-Kestotriose and 6-Kestotriose. Sucrose and 1-Kestotriose form 1,6-Kestotetrarose in the presence of 6-SFT. Newly formed 1-Kestotriose leads to two anabolic activities. In first one with, 1-Ketotriose with sucrose works as substrate for 6-SFT to synthesize 1,6-Kestotetraose (tetrasaccharide bifrucose) and in second one it solely works as substrate to form 1,1-Kestotetraose under the catalytic activity of for 1-FFT. In catabolic part of pathway exohydrolase enzymes *viz.* Fructan-1-exohydrolase (1-FEH) and Fructan-6-exohydrolase (6-FEH) remove terminal fructose from fructans chain thus re-releasing fructose and sucrose in cell compartments.

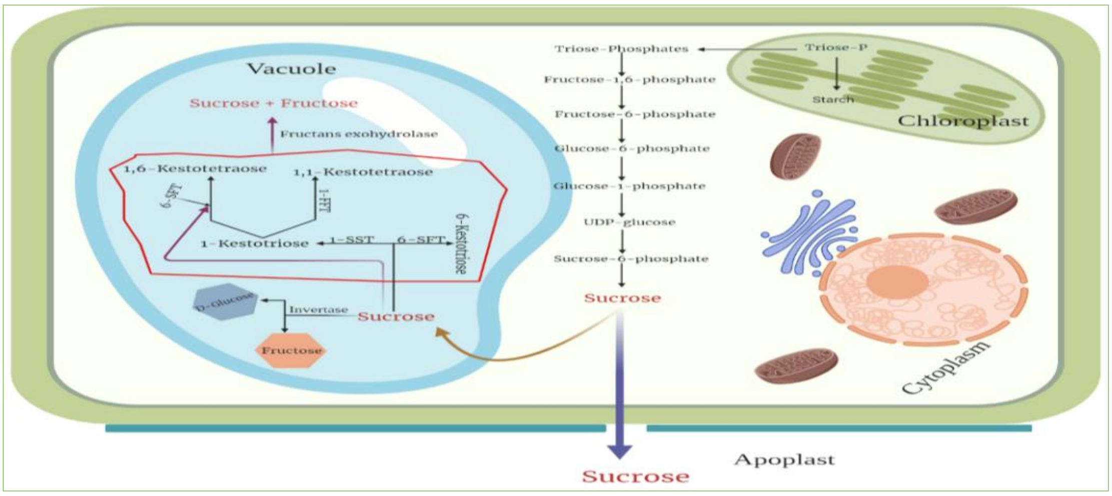


Figure 4.14: Metabolic pathway of fructans in wheat plant cells

4.9.2. Gene retrieval and genome wide identification

A total of 29 genes from 13 reference plant species were retrieved from NCBI and Ensmble (**Table 4.21**). These genes were involved in transferase or exohydrolase activities during fructans metabolism. Maximum number of genes were retrieved from the genome of *Helianthus annus*. Using 29 retrieved genes, BLASTP algorithm identified a total of 7,458 homologues in bread wheat genome (**Figure 4.15**) with similarity percentage ranging from 24.10 to 96.70% and E-value from 0.00E+00 to 1.20E-01(**Annexure 10; pp: LIII, and 11; pp: LIV**). Maximum number of homologues was identified against *Helianthus annus* (1271) and minimum against *Medicago truncatula*. Out of 7,458 homologous *T. aestivum* genes only 1,138 genes passed first criterion of selection *i.e.* similarity percentage above 70%. Maximum (307) homologues with more than 70% similarity queried with *Brachypodium distachyon* and minimum (21) with *Medicago truncatula*. Further filtering on the basis of sequence duplicates, similarity of more than 95% and the lowest E-value, extracted only 104 *aestivum* genes (**Annexure 12; pp: LV**) suitable for further study.

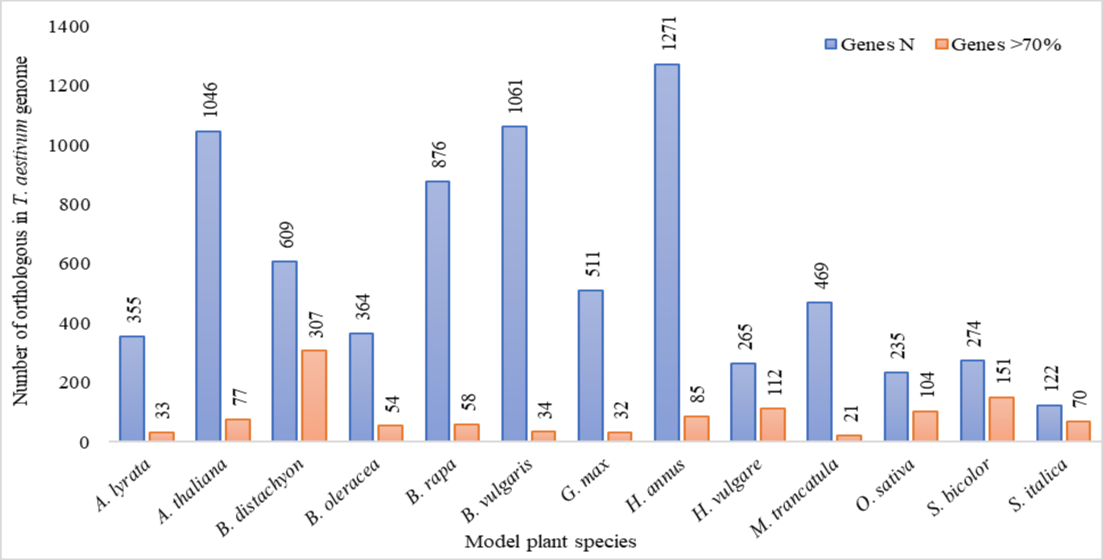


Figure 4.15: Number of homologous genes identified in bread wheat genome against query sequences

Renaming of selected genes was done by designating prefix *TaFruc* (*Triticum aestivum fructans*) to chromosome number followed by sequence of gene on chromosome (*i.e.* gene on upper distal end was designated ‘1’ and so on).

4.9.3. Chromosomal distribution and structural analysis

Figure 4.16a and **4.16b** depicts non-random distribution of *TaFruc* on 7 groups of homologues and 21 individual chromosomes. Genomes ‘A’, ‘B’ and ‘D’ exhibited 41, 24 and 34 *TaFruc* genes, respectively. Among homologous groups maximum (21) number of *TaFruc* genes were located on group 6 and 7 chromosomes (6A, 6B, 6D, 7A, 7B and 7D) while minimum (3) number of *TaFruc* belonged to group 1 chromosomes (1A, 1B and 1D). On individual chromosome basis maximum 14 *TaFruc* genes were located on chromosome 4A whereas, minimum 1 *TaFruc* gene was located on chromosomes 1A, 1B, 1D and 5A.

Table 4.21: Fructans metabolic genes retrieved from model plant species

Organism	Nomenclature	Gene stable ID	Transcript stable ID	Chr	Coordinates (bp)		Function
					Start	End	
Arabidopsis lyrata	*ALFEH6.1*	scaffold_601221.1	scaffold_601221.1	6	4821085	4823895	*6,1-FEH*
Arabidopsis thaliana	*ATBF1.1.4*	AT1G55120	AT1G55120.4	1	20566030	20569322	*BFD*
	ATBF3.1.5	AT3G13790	AT3G13790.5	3	4532762	4535914	
	ATBF3.1.3	AT5G11920	AT5G11920.3	5	3839316	3842409	
Beta vulgaris	*BVFEH7.1*	BVRB_7g170560	KMT04889	7	37678122	37683442	*6-FEH*
	BVFEH7.2	BVRB_7g170580	KMT04891	7	37698363	37703692	
	BVFEH8.1	BVRB_8g185370	KMT04083	8	6851129	6853674	
	BVFEH8.2	BVRB_8g185380	KMT04084	8	6871664	6873964	
Brachypodium distachyon	*BDSFT3.1*	BRADI_3g00910v3	KQJ92819	3	507449	511126	*1-SST*
	BDSFT1.1	BRADI_1g52210v3	KQK20061	1	50739522	50743956	
	BDSFT1.2	BRADI_1g52210v3	KQK20062	1	50739522	50743956	
Brassica oleracea	*BOFEH9.1*	Bo9g169760	Bo9g169760.1	C9	50110086	50112407	*6-FEH*
Brassica rapa	*BRFEH3.1*	Bra006129	Bra006129.1	A03	2133594	2139231	*6,1-FEH/HOG /Inulinase/Levanase*
	BRFEH3.2	Bra006130	Bra006130.1	A03	2139997	2141566	
	BRFEH10.1	Bra008926	Bra008926.1	A10	14448927	14450810	
Glycine max	*GMFEH17.1.2*	GLYMA_17G227800	KRH05440	17	38275485	38278808	*6-FEH*
	GMFEH17.2.2	GLYMA_17G227900	KRH05442	17	38284476	38287851	
Helianthus annus	*HAGEH3.1*	HannXRQ_Chr03g0081811	OTG32000	3	1.32E+08	1.32E+08	*GH*
	HAGEH7.1	HannXRQ_Chr07g0187971	OTG19983	7	12038262	12038624	
	HAGEH7.2	HannXRQ_Chr07g0187981	OTG19984	7	12038833	12039298	
	HAFEH17.1	HannXRQ_Chr17g0538391	OTF85292	17	17083549	17089293	*6-FEH*
	HAGEH17.1	HannXRQ_Chr17g0538401	OTF85293	17	17093509	17096643	*GH*
	HAFEH17.2	HannXRQ_Chr17g0538411	OTF85294	17	17096694	17099980	*6-FEH*
Hordeum vulgare	*HVSFT7.8*	HORVU7Hr1G001040	HORVU7Hr1G001040.8	7H	2257283	2260447	*6-SST*
Medicago truncatula	*MTFEH1.1*	MTR_1g015940	AES59227	1	4127132	4130009	*FEH*
	MTFEH1.2	MTR_1g015970	AES59229	1	4135963	4139183	*FEH*
Oryza sativa japonica	*OSJSST2.1*	Os02g0106100	Os02t0106100-01	2	343057	346875	*FT*
Setaria italica	*SISST1.1*	SETIT_016887mg	KQL27737	I	309764	313288	*1-SSFT*
Sorghum bicolor	*SBSST4.1*	SORBI_3004G004800	OQU84152	4	418239	423162	

1-SST: *1-Sucrose:sucrose fructosyl transferase;* ***6-FEH****: 6-Fructosyl exohydrolase;* ***6-SSFT****: 6-Sucrose:sucrose fructosyl transferase;* ***6,1-FEH:*** *6,1-Fructosyl exohydrolase;* ***BFD:*** *Beta-fructofuranosidase;* ***Chr:*** *Chromosome number;* ***FEH:*** *Fructosyl exohydrolase;* ***GH:*** *Glycoside hydrolase;* ***HOG:*** *Hydrolyzing O-glycosyl*

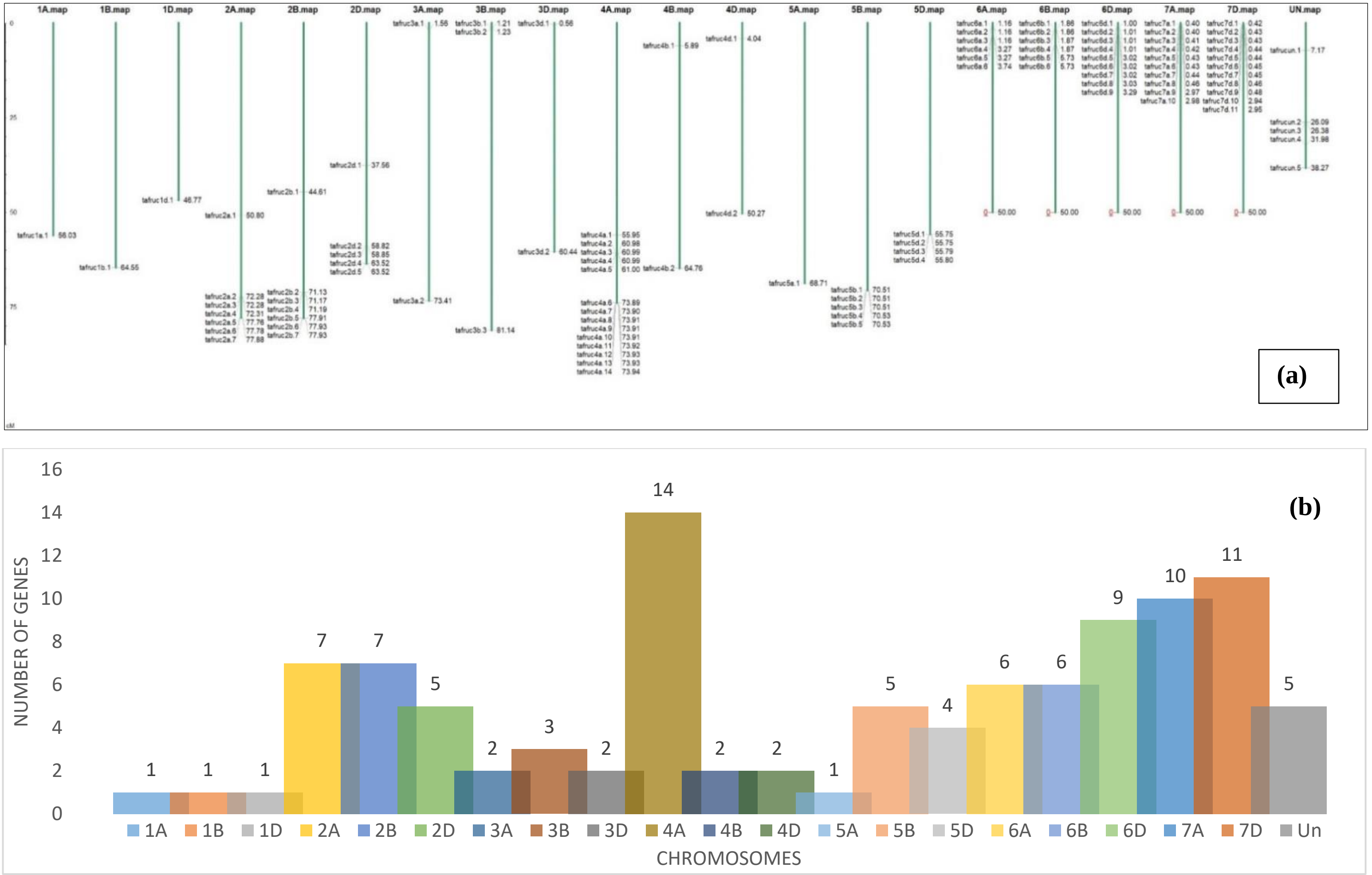


Figure 4.16: Chromosomal location (a) and distribution (b) of 104 *TaFruc* genes in *T. aestivum* genome

Among reference plant species transcript length varied between 309 (*HAGEH7.2*) and 3198 bp (*SBSST4.1*) with GC content (%) ranging from 39.10% (*BVFEH7.2*) to 57.99% (*SISST1.1*). Furthermore, maximum 8 transcripts were reported for gene *HVSFT7.8* from *Hordeum vulagre*. In contrast to model plant species, range of full-length transcript among *TaFruc* genes was obtained from 300 (*TaFruc2B.5*) to 4022 bp (*TaFruc4A.2*) with GC (%) ranging between 38.52% (*TaFruc5D.4*) and 62.03% (*TaFruc2A.4*). Range of CDS length among these genes was 300 (*TaFruc2B.5*)-2271 bp (*TaFruc7D.5*). Most of the *TaFruc* genes exhibited 1 or 2 transcripts except for genes *TaFruc4A.7, TaFruc6B.5*, *TaFruc7A.4*, *TaFruc7A.5*, *TaFruc7A.9* and *TaFruc7D.10* which exhibited maximum (3) number of transcripts.

Results from gene structure display server (**Annexure 13; pp: LX**) revealed that gene structure had substantial differences between reference genes and identified *TaFruc* genes. Exon numbers ranged between 1 *(HAGEH7.1)* and 9 (*BRFEH3.1)* among reference plant species. Exceptionally, gene structure of *HAGEH7.1* did not show any intron phase in upstream and/or downstream sequence. Gene *BRFEH3.1* had maximum (8) number of introns. Phase P0 types of introns were dominatingly present among reference genes (26) followed by P2 (21) and P1 (19). Most of the genes exhibited three P0 types of introns except *SISST1.1*, *BDSFT3.1*, *BDSFT1.2*, *HAGEH7.2*, *OSJSST2.1* and *SBSST4.1* which exhibited only one P0 type of intron. Genes *HAGEH3.1*, *GMFEH17.1.2* and *GMFEH17.2.2* exhibited two P0 introns. *BRFEH3.1* had maximum (4) number of P1 type of introns. All reference genes had only one P2 type of intron. Gene *BDSFT1.2* had the longest downstream sequence whereas, *SBSST4.1* had the longest upstream sequence. Gene *BVFEH7.1* exhibited the longest intron (~4 kb) followed by *BVEH7.2* and *HAFEH17.1* (~3 kb) among all reference genes.

Number of exons ranged from 2 to 8 and number of introns ranged from 1 to 7 among identified *TaFruc* genes. Genes *TaFruc2B.5*, *TaFruc4A.9* and *TaFruc7D.6* had minimum number of exons and introns while *TaFruc4A.3*, *TaFruc4A.4*, *TaFruc5B.2*, *TaFruc5B.3*, *TaFruc5D.1* and *TaFruc5D.2* had maximum number of exons and introns. Range of different types of introns was 0-4 (P0) and 0-2 (P1 and P2). *TaFruc4A.8* had only P1 and P2 types of introns and maximum (4) number of P0 type of introns was found in *TaFrucUn.1*, *TaFruc5B.1*, *TaFruc5D.3*, *TaFruc4A.3, TaFruc4A.4*, *TaFruc5B.2*, *TaFruc5B.3*, *TaFruc5D.1* and *TaFruc5D.2*. Additionally, out of 104 *TaFruc* genes, 29 genes didn’t exhibit any P1 intron, contrarily 44 genes and 31 genes exhibited one and two P1 introns, respectively. Likewise, number of genes exhibiting 0, 1 and 2 P2 type of intron was 45, 39 and 20, respectively. *TaFruc4A.2* had the longest upstream (~3 kb) and downstream (~6 kb) sequence. The longest intron of nearly 13 kb was found in *TaFruc6D.5*. Genes *TaFruc3A.1* and *TaFrucUn5* were the shortest in all aspects of gene structure.

4.9.4. Phylogenetic and evolutionary study

Phylogenetic relationship between all 132 fructans gene was assessed with maximum likelihood method considering all sites as subset. As shown in **Figure 4.17**, all genes grouped into six major clades *viz*. C-I (red), C-II (blue), C-III (green), C-IV (pink), C-V (orange) and C-VI (turquoise). 22, 20, 28, 23, 16 and 14 genes were distributed in C-I, C-II, C-III, C-IV, C-V and C-VI, respectively. Most of the reference genes were grouped in C-I and were characterized with exohydrolase activities. Reference genes exhibiting transferase activities were grouped under C-II (*SISST1.1*, *BDSFT1.1*, *BDSFT1.2*, *BDSFT3.1*, *OSJSST2.1*, and *SBSST4*.1) and C-III (*HVFSFT7.8*). Clades C-IV, C-V and C-VI had only *TaFruc* genes.

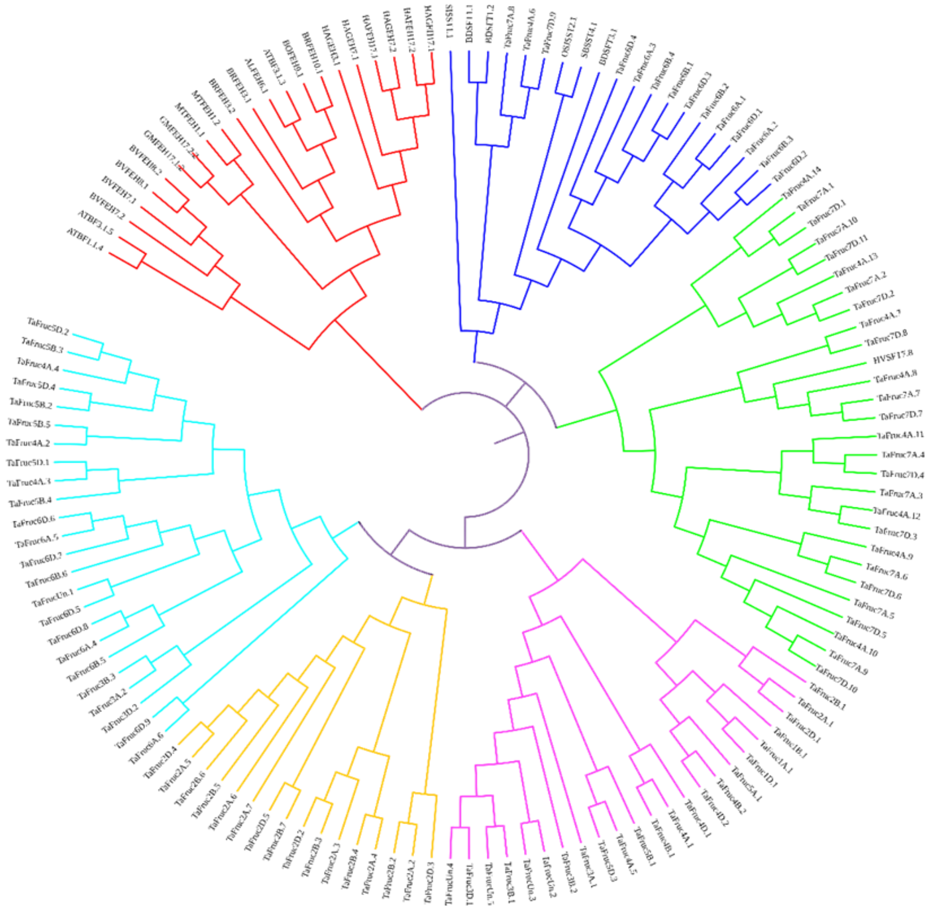


Figure 4.17: Phylogenetic tree of fructans metabolic genes constructed by maximum likelihood method

TaFruc genes with ≥90% similarity were considered as duplicate genes. Thus, total 106 gene duplicate pairs were identified in this study (**Annexure 14; pp: LXIII**). All the identified duplicate pairs were segmental duplicates (SD) except for pairs *TaFruc3B.1-TaFruc3B.2*, *TaFruc6B.1-TaFruc6B.2*, *TaFruc6D.1-TaFruc6D.2*, *TaFruc6D.1-TaFruc6D.4*, *TaFruc6D.2-TaFruc6D.3*, *TaFruc6D.2-TaFruc6D.4*, *TaFruc6D.3-TaFruc6D.4*, *TaFrucUn.2-TaFrucUn.5*, *TaFrucUn.3-TaFrucUn.5* and *TaFrucUn.4-TaFrucUn.5* which were tandem duplicates (TD). Rate of synonymous and non-synonymous substitution was also estimated among duplicate gene pairs. The highest and the lowest number of potential synonymous substitution (S) were reported for gene pairs *TaFruc6B.4-TaFruc6D.3* (485.33) and *TaFruc3B.1-TaFrucUn.5* (66.33), respectively. Similarly, the highest and the lowest number of potential non-synonymous substitutions (N) were reported for gene pairs *TaFruc6A.3-TaFruc6B.4* (1487.67) and *TaFruc2B.5-TaFruc2D.4* (220.83). However, average value for S and N was 360.85 and 1163.66, respectively. Furthermore, considering a constant rate of 6.5 $\times 10^{-9}$ substitutions per year time of divergence (Td) between duplicate gene pairs ranged from 3.76 (*TaFruc1A.1-TaFruc1D.1*) to 54.48 (*TaFruc3A.1-TaFruc5B.1*) million years (MYA) with an average Td of 22.33 MYA.

4.9.5. *Cis*-regulatory elements

A total of 108 *cis*-regulatory elements (CREs) were extracted within 1.5 kb downstream and upstream regions of 104 *TaFruc* genes. These motifs were grouped in 10 different classes depending up on their general functions *viz*. abiotic stress (ABS), anaerobic induction (AI), biotic stress (BS), cellular growth and development (CGD), circadian rhythm (CR), distinct functions or function is not properly known (DF), essential regulatory element (ER), hormonal regulation (HR), light responsive (LR) and tissue specific elements (TSE). **Figure 4.18** clearly indicates that majority of CRE*s* belonged to class light responsive (30) followed by abiotic stress (29). One *cis* regulatory element falls into classes AI (ARE) and HR (Unnamed-1) each. On the basis of classes, CREs belonging to class abiotic stress (35%) were the most widely distributed followed by light responsive CREs (19%). On individual basis TATC-box was dominatingly distributed followed by CAAT-box. Both these motifs are highly conserved across eukaryotes and considered as an essential regulatory element important for cellular growth and development. Furthermore, AACA-motif, GRA, LS7 and Unnamed-1 were least frequent CREs occurring only once. **Figure 4.19** gives an overview on the distribution of detected CREs on individual *TaFruc* and their adjacent genes laying within 1.5 kb upstream or downstream regions. A quick view on **Figure 4.19** reveals that the majority of genes exhibited different types and numbers of CREs belonging to different classes except for the gene *TraesCS4A02G485700.0* which exhibited only one CRE namely CAAT-box which is a common *cis*-acting element in promoter and enhancer regions with essential role in gene translation and regulation.

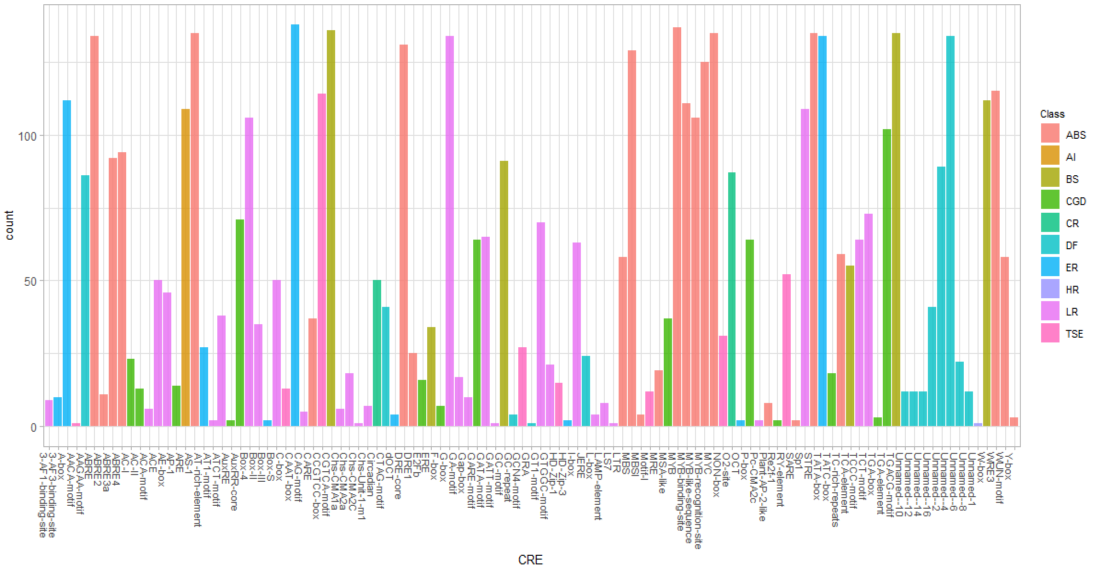


Figure 4.18: Occurrence of identified *cis*-regulatory elements within 104 *TaFruc* genes

4.9.6. Physicochemical analysis of amino acid sequences

All nucleotide triplicates were translating to amino acids as per the universal codon system. Polypeptide chains of different length and compositions were translated by *TaFruc* genes (**Annexure 15; pp: LXX**). Gene *TaFruc7D.5* translated to the longest polypeptide chain whereas, the shortest chain was translated by gene *TaFruc2B.5*. **Figure 4.20** depicts that the most abundant amino acid ratio was of glycine (8.43%) followed by alanine (8.18%) and minimum amino acid ratio was of cysteine (1.21%). Molecular weight (Mw) of different proteins ranged between 10.85 KDa and 84.89 KDa with an average of 65.09 KDa. The highest molecular weight was reported for the protein translated by *TaFruc7D.5* and the lowest was reported for the protein translated by *TaFruc2B.5*. **Table 4.22** depicts physicochemical properties of polypeptide chains translated by different *TaFruc* genes. The most acidic protein was translated by *TaFruc4A.2* with isoelectric point (pI) 4.48 and the most basic protein was translated by *TaFrucUn.4* with pI 9.7. Average value of pI was 6.33. Instability index (II) ranged between 26.75 (*TaFrucUn.2*) and 45.51 (*TaFrucUn.1*) with an average of 36.97. Protein translated by gene *TaFruc2B.3* was thermostable as it showed the highest aliphatic index (AI) 84.83 whereas, protein with AI 31.26 translated by *TaFruc4A.1* was the most thermolabile. Average value of AI was 78.83. Grand average of hydropathy value (GRAVY) for different *TaFruc* proteins ranged from -0.49 and -0.15 and with average of -0.28.

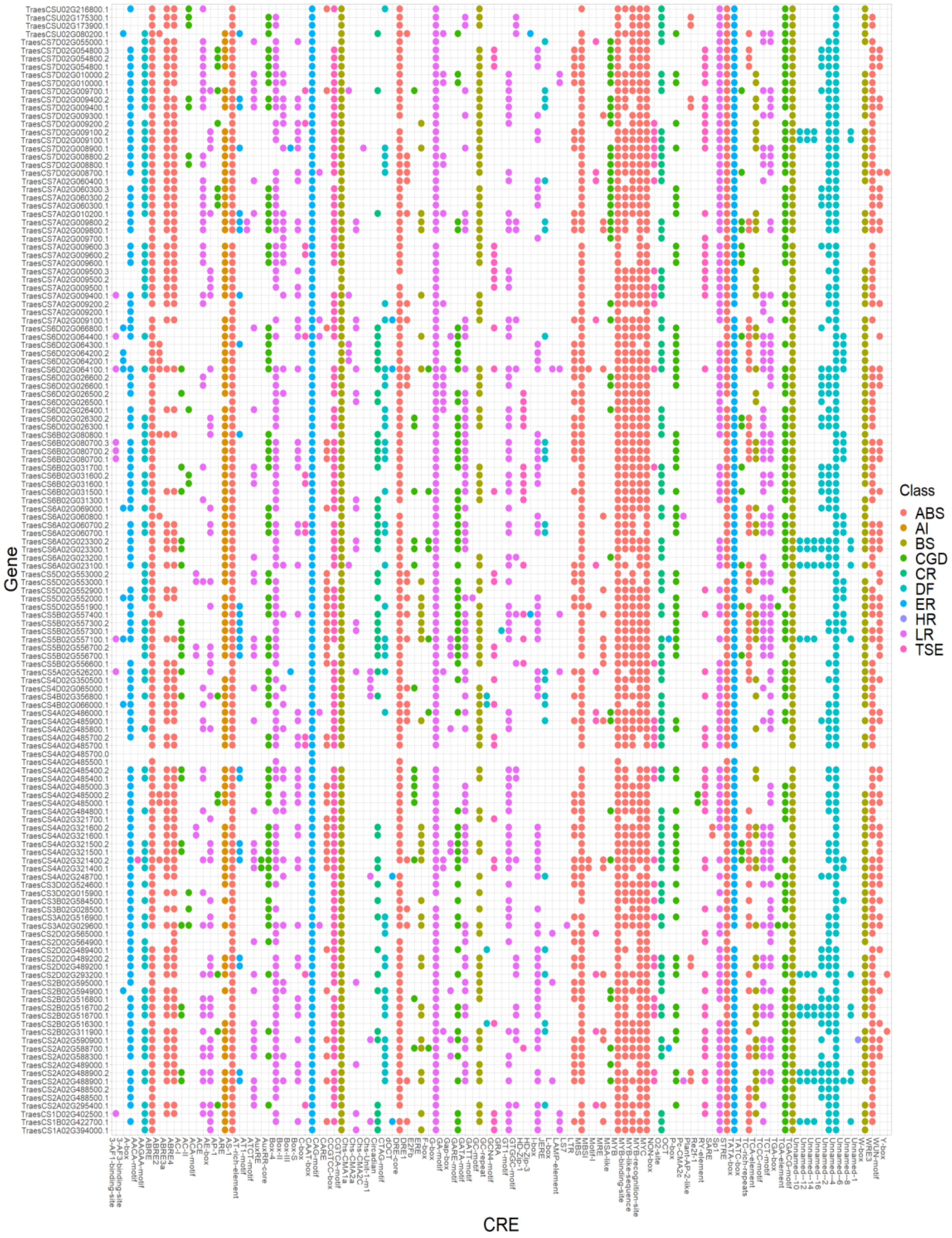


Figure 4.19: Distribution of *cis*-regulatory elements on individual *TaFruc* gene and the adjacent gene lying within ±1.5kb region.

[In figure, ABS: abiotic stress; **AI:** anaerobic induction; **BS:** biotic stress; **CGD:** cell growth and development; **CR:** circadian rhythm; **DF:** distinct function/unknown function; **ER:** essential regulatory element; **HR:** hormone regulation; **LR:** light responsiveness; **TSE:** tissue specific expression]

Table 4.22: Physicochemical properties of different *TaFruc* proteins

TaFruc	**Mw**	**GRAVY**	**pI**	**II**	**AI**	**ST**	**TaFruc**	**Mw**	**GRAVY**	**pI**	**II**	**AI**	**ST**
TaFruc1A.1	64.35	-0.38	8.03	29.63	81	S	*TaFruc4A.8*	68.47	-0.299	5.16	36.27	76.93	S
TaFruc1B.1	64.66	-0.37	8.83	30.5	82.43	S	*TaFruc4A.9*	56.62	-0.316	6.46	34.95	76.99	S
TaFruc1D.1	64.31	-0.382	9.21	32.59	81.49	S	*TaFruc4B.1*	65	-0.267	6.7	33.13	80.91	S
TaFruc2A.1	73.91	-0.295	9.28	38.41	81.74	S	*TaFruc4B.2*	64.55	-0.288	8.67	31.53	79.74	S
TaFruc2A.2	59.85	-0.366	5.6	37.84	74.16	S	*TaFruc4D.1*	64.88	-0.242	6.47	33.72	81.74	S
TaFruc2A.3	64.54	-0.16	4.91	41.41	83.08	U	*TaFruc4D.2*	64.59	-0.309	8.96	29.35	79.57	S
TaFruc2A.4	64.76	-0.29	5.58	38.56	77.62	S	*TaFruc5A.1*	64.56	-0.304	8.82	30.65	79.05	S
TaFruc2A.5	65.48	-0.3	7.05	40.35	80	U	*TaFruc5B.1*	66.27	-0.392	9.12	30.38	78.78	S
TaFruc2A.6	65.56	-0.286	7.14	43.55	79.68	U	*TaFruc5B.2*	65.83	-0.236	5.57	44.15	81.8	U
TaFruc2A.7	68.62	-0.336	7.11	38.62	74.65	S	*TaFruc5B.3*	70.42	-0.201	4.99	42.88	80.39	U
TaFruc2B.1	69.74	-0.28	9.57	33.42	84.19	S	*TaFruc5B.4*	59.56	-0.32	4.97	36.23	81.1	S
TaFruc2B.2	60.05	-0.405	5.26	37.4	72.91	S	*TaFruc5B.5*	58.63	-0.382	4.56	44.93	80.04	U
TaFruc2B.3	65.05	-0.157	4.98	39.66	84.83	S	*TaFruc5D.1*	66.91	-0.263	5.08	40.19	81.45	U
TaFruc2B.4	64.45	-0.246	5.45	36.44	77.73	S	*TaFruc5D.2*	66.85	-0.239	4.86	42.74	80.15	U
TaFruc2B.5	10.85	-0.234	9.18	42.07	82.53	U	*TaFruc5D.3*	66.24	-0.379	9.28	31.59	78.12	S
TaFruc2B.6	65.71	-0.276	7.02	44.53	82.5	U	*TaFruc5D.4*	63.37	-0.303	5.23	45.1	81.37	U
TaFruc2B.7	58.64	-0.273	6.95	42.97	79.22	U	*TaFruc6A.1*	73.41	-0.272	5.09	33.68	75.42	S
TaFruc2D.1	69.31	-0.288	9.44	34.39	83.66	S	*TaFruc6A.2*	72.68	-0.224	4.89	33.67	76.73	S
TaFruc2D.2	64.7	-0.161	4.98	39.81	83.41	S	*TaFruc6A.3*	73.3	-0.259	5.55	33.72	76.08	S
TaFruc2D.3	60.69	-0.405	5.75	34.1	71.12	S	*TaFruc6A.4*	66.35	-0.285	4.8	43.67	78.48	U
TaFruc2D.4	65.37	-0.281	7.21	41.5	80.64	U	*TaFruc6A.5*	67.41	-0.145	5.99	42.04	83.38	U
TaFruc2D.5	64.36	-0.225	7.79	41.86	80.6	U	*TaFruc6A.6*	66.22	-0.356	5.86	40.42	75.81	U
TaFruc3A.1	37.89	-0.423	8.44	29.14	76.9	S	*TaFruc6B.1*	73.31	-0.275	5.7	36.87	74.81	S
TaFruc3A.2	64.8	-0.263	6.11	35.11	80.97	S	*TaFruc6B.2*	73.63	-0.261	5.35	34.71	76.2	S
TaFruc3B.1	11.55	-0.304	9.2	31.91	83.24	S	*TaFruc6B.3*	71.29	-0.232	5.32	30.53	78.35	S
TaFruc3B.2	65.96	-0.366	8.77	29.41	77.24	S	*TaFruc6B.4*	73.27	-0.242	5.24	33.92	76.09	S
TaFruc3B.3	64.84	-0.273	5.93	35.7	81.31	S	*TaFruc6B.5*	66.85	-0.269	4.67	42.24	80.5	U
TaFruc3D.1	61.35	-0.432	8.63	29.21	73.09	S	*TaFruc6B.6*	61.61	-0.294	5.62	43.35	80.98	U
TaFruc3D.2	64.46	-0.303	6.11	35.93	80.75	S	*TaFruc6D.1*	73.62	-0.269	5.01	34.24	74.76	S
TaFruc4A.1	64.72	-0.259	6.64	31.26	31.26	S	*TaFruc6D.2*	73.14	-0.233	5.16	32.87	78.81	S
TaFruc4A.10	72.4	-0.277	7.16	39.59	80.83	S	*TaFruc6D.3*	73.72	-0.208	5.56	36.02	79.54	S
TaFruc4A.11	72.49	-0.224	6.63	36.34	79.49	S	*TaFruc6D.4*	72.87	-0.249	5.55	36.17	75.9	S
TaFruc4A.12	71.66	-0.166	5.69	37.39	83.23	S	*TaFruc6D.5*	51.38	-0.318	4.92	34.53	78.44	S
TaFruc4A.13	71.36	-0.208	4.9	34.61	79.77	S	*TaFruc6D.6*	68.15	-0.21	6.23	44.79	80.3	U
TaFruc4A.14	72.72	-0.277	5.03	39.29	76.52	S	*TaFruc6D.7*	69.16	-0.226	6.61	44.07	80.83	U
TaFruc4A.2	52.86	-0.346	4.48	45.51	83.7	U	*TaFruc6D.8*	66.61	-0.285	4.68	43.59	80.18	U
TaFruc4A.3	67.3	-0.218	5.16	39.59	82.69	S	*TaFruc6D.9*	66.03	-0.375	6.31	39.74	75.9	S
TaFruc4A.4	65.59	-0.271	4.82	42.64	80.34	U	*TaFruc7A.1*	72.52	-0.261	5.11	40.96	77.76	U
TaFruc4A.5	66.06	-0.37	9.37	28.96	77.92	S	*TaFruc7A.10*	70.73	-0.202	5.23	34.3	79.13	S
TaFruc4A.6	71.47	-0.192	4.55	38.8	81.69	S	*TaFruc7A.2*	71.12	-0.211	4.72	34.85	80.68	S
TaFruc4A.7	42.98	-0.355	4.7	42.6	80.13	U	*TaFruc7A.3*	71.74	-0.155	6.14	37.1	84.31	S
TaFruc7A.4	70.89	-0.224	5.99	33.71	79.75	S	*TaFruc7D.4*	73.06	-0.248	6.23	38.16	78.66	S
TaFruc7A.5	72.91	-0.314	7.34	40.72	77.59	U	*TaFruc7D.5*	84.89	-0.262	7.36	43.33	80.22	U
TaFruc7A.6	67.59	-0.309	6.89	33.59	75.73	S	*TaFruc7D.6*	56.71	-0.32	6.96	31.24	78.7	S
TaFruc7A.7	68.92	-0.286	5.08	33.98	76.76	S	*TaFruc7D.7*	69.01	-0.29	4.95	35.92	75.7	S
TaFruc7A.8	71.49	-0.2	4.55	38.12	81.07	S	*TaFruc7D.8*	70.89	-0.195	4.72	38.15	79.33	S
TaFruc7A.9	70.4	-0.291	6.21	39.98	77.73	S	*TaFruc7D.9*	71.51	-0.202	4.55	38.3	81.08	S
TaFruc7D.1	72.62	-0.255	4.79	41	77.95	U	*TaFrucUn.1*	68.64	-0.251	5.63	45.51	77.16	U
TaFruc7D.10	78.51	-0.276	6.23	42.18	77.22	U	*TaFrucUn.2*	60.17	-0.444	8.57	26.75	74.58	S
TaFruc7D.11	71.07	-0.212	5.57	34.16	78.83	S	*TaFrucUn.3*	60.17	-0.444	8.57	26.75	74.58	S
TaFruc7D.2	70.89	-0.202	4.95	33.37	80.54	S	*TaFrucUn.4*	45.3	-0.491	9.7	28.31	72.83	S
TaFruc7D.3	71.66	-0.182	5.93	37.99	81.27	S	*TaFrucUn.5*	11.56	-0.301	9.2	31.07	83.24	S

Mw: *molecular weight (Kda);* ***GRAVY:*** *grand average hydropathy;* ***pI:*** *isoelectric point;* ***II****: instability index;* ***ST:*** *stability;* ***U:*** *unstable;* ***S:*** *stable*

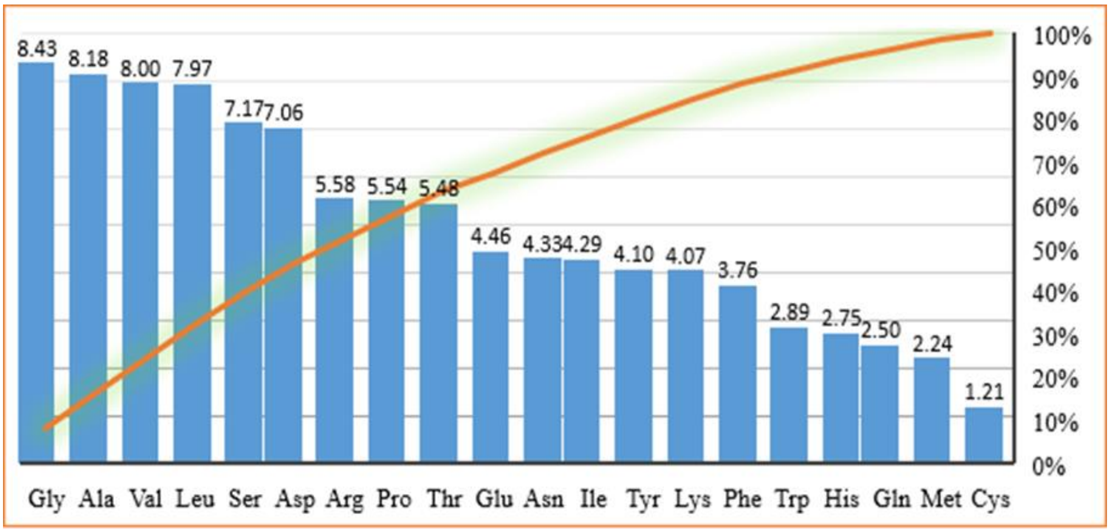


Figure 4.20: Average frequency of amino acids occurred in 104 polypeptide chains translated by *TaFruc* genes

Proteins translated by *TaFrucUn.4* and *TaFruc6A.5* showed the highest and the lowest values of GRAVY, respectively. Also, out of 104 *TaFruc* proteins, 73 were stable and 39 were unstable.

4.9.7. Conserved domains and motifs

Search for conserved domain identified presence of glycosyl hydrolase family members in all *TaFruc* proteins. Interestingly, few novel conserved sequences were also present in some of the *TaFruc* proteins. Novel domains like DEP_RGS7 of DEP superfamily and Methyltr_RsmF_N were found in polypeptide chain translated by gene *TaFruc6D.4* and *TaFruc4A.11*, respectively. *TaFruc3A.1* and *TaFruc7D.2* proteins exhibited primitive sequences of family Phage_T4_Ndd and Trp_oprn_chp, respectively. Additionally, Kelch-4 repeats were also present in proteins translated by genes *TaFruc4A.10*, *TaFruc7A.5*, *TaFruc7A.9*, *TaFruc7D.10* and *TaFruc7D.6*.

In MEME analysis, total 20 motifs were identified **(Table 4.23)**. Sequence length of these motifs ranged from 11 to 50 AA. M-3 motif had the upmost width (50 AA) and M-9 had the shortest width (11 AA). These motifs were distributed non-randomly among all *TaFruc* proteins. Minimum and maximum occurrence was reported for motifs M-2 and M-17, respectively. **Figure 4.21** revealed that distribution pattern of motifs was almost similar within a clade except in clade-I and II. In clade-I, polypeptide chains were translated by genes *TaFruc2B.1* and *TaFrucUn5* and in clade-II polypeptide chain of *TaFruc2B.5* exceptionally exhibited only two motifs (M-2 and M-15).

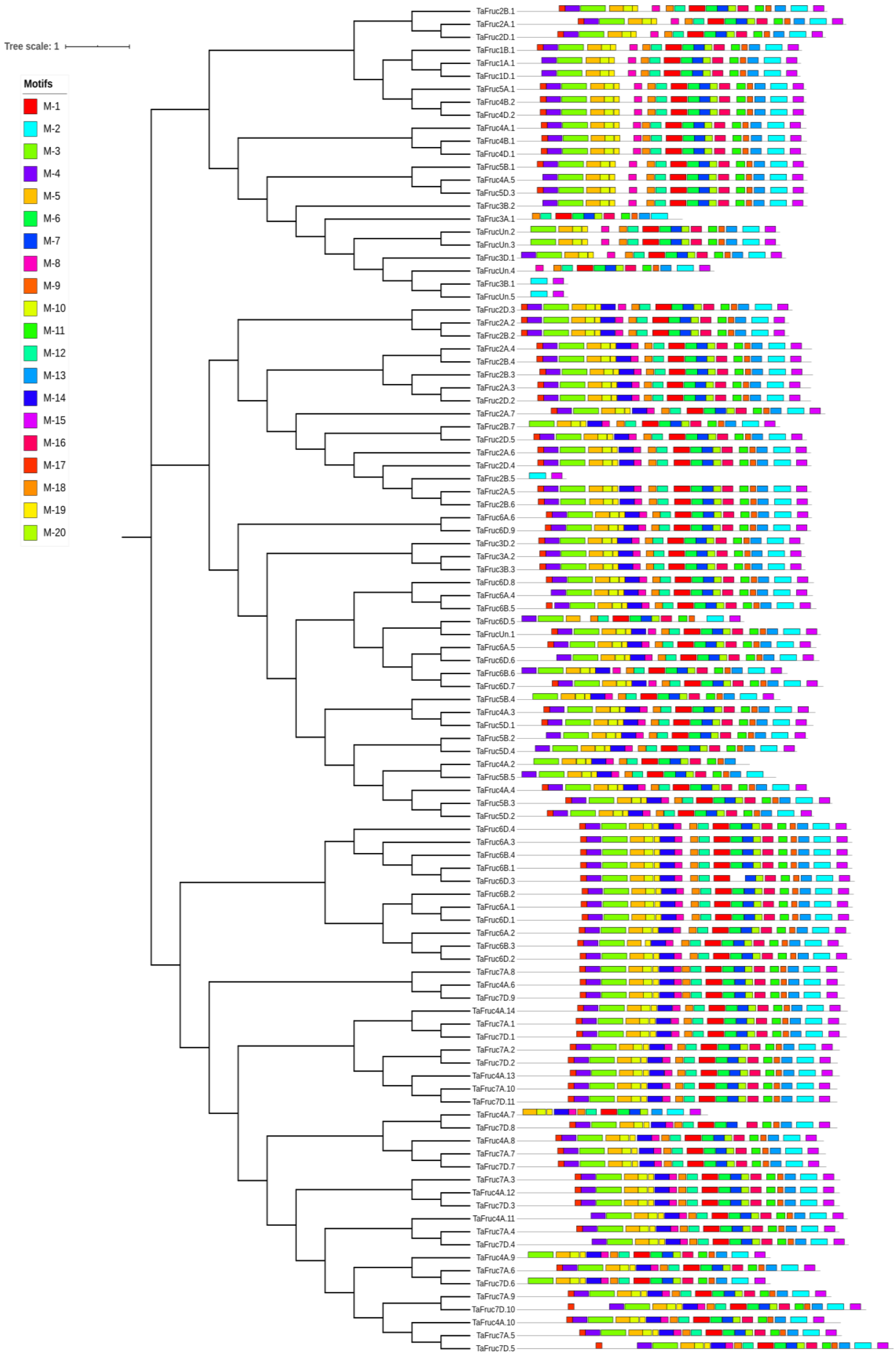


Figure 4.21: Comparative view of motifs in *TaFruc* protein sequences

Table 4.23: Description of 20 motifs identified in proteins translated by *TaFruc* genes

Motif	Motif sequence	Width	Sites	E-Value
M-1	RYDYGKFYASKSFYDPAKKRRVLWGWVNETDS	32	101	3.0e-2522
M-2	KGEKISLRTLIDHSIVESFGMGGRTCITSRVYP	33	103	1.9e-2544
M-3	SWGHSVSRDLVNWRHLPPAMVPDQPYDINGCWSGSATIL PDGRPVILYTG	50	98	2.2e-3532
M-4	WMNDPNGPMYYKGWYHLFYQYNPKGAVWG	29	91	6.5e-2136
M-5	QVQNLAFPKBPSDPLLREWTKPPNNPVI	28	99	9.0e-2093
M-6	DDVAKGWAGJQAIPRTIWLDEKG	23	100	1.3e-1538
M-7	KQLLQWPVEEIETLRTNETNL	21	101	9.4e-1458
M-8	VNGTGMWECPDFFPV	15	99	1.0e-934
M-9	EHTAVYFRVFK	11	100	3.1e-702
M-10	PPPPGINSKDFRDPTTAW	18	97	4.1e-972
M-11	ASVRGGLGPFGLLVLAS	17	100	5.1e-958
M-12	RHDYYALGRYDAAABTFTPDD	21	101	2.2e-1124
M-13	KYRTLMCHDETRSSLAPDVYK	21	100	2.8e-1147
M-14	ADLNHAGIALLYKTKDFJNWELVPGPLYR	29	79	3.4e-1203
M-15	FNNGSATVKVEKLVAWEMDSA	21	101	3.0e-1088
M-16	QADVEASFEJDSLDIAEPFEP	21	100	6.6e-1091
M-17	QRTGYHFQPEKN	12	77	1.0e-652
M-18	AISEGVKHVLKMSLD	15	101	1.3e-585
M-19	GSDGTWRIAVG	11	98	1.0e-492
M-20	SGITVKKGSVFEIKG	15	100	8.6e-394

4.9.8. Functional enrichment analysis of *TaFruc* genes

Cellular localization analysis revealed that majority of *TaFruc* genes (89) were acting on cell wall whereas, only one gene *TaFruc2B.5* was acting in chloroplast. Genes *TaFruc3B.1* and *TaFrucUn.5* were acting in nucleus and chloroplast, respectively in addition to cell wall. Thirteen genes *viz*. *TaFruc6A.1*, *TaFruc6A.2*, *TaFruc6B.1*, *TaFruc6B.2*, *TaFruc6B.3*, *TaFruc6B.4*, *TaFruc6D.1*, *TaFruc6D.2*, *TaFruc4A.6*, *TaFruc6D.3*, *TaFruc6D.4*, *TaFruc7A.8* and *TaFruc7D.9* were found to be acting in vacuoles.

Gene ontology revealed that identified *TaFruc* genes exhibited catalytic functions which play important role in hydrolase and transferase activities of various glycosyl groups of non-structural sugars **(Figure 4.22)**. To gain deep knowledge on activities of each identified *TaFruc* gene, their amino acid sequences (AA) were annotated against Koyto encyclopedia of gene and genome database (KEGG-database) using global metabolic pathway of family *Poaceae* (4479). Results from KEGG-database revealed that 39 out of 104 identified *TaFruc* genes were functionally involved in carbohydrate metabolism **(Figure 4.23)** by means of translating into three different types of enzymes *viz*. β-fructofuranosidase (INV; EC:3.2.1.26), sucrose:sucrose fructosyltransferase (SST; EC:2.4.1.99) and fructan beta-(2,1)-

fructosidase (1FEH/inulinase; EC:3.2.1.153). From **Figure 4.24**, it can be observed that identified genes are involved in thirteen different processes *viz*. carbohydrate storage (CS), cellular response to gibberellin stimulus (CRGS), defense response to bacteria (DRB), defense response to fungi (DRF), nectar secretion (NS), plasma membrane (PM), primary root development (PRW), response to wounding (RW),

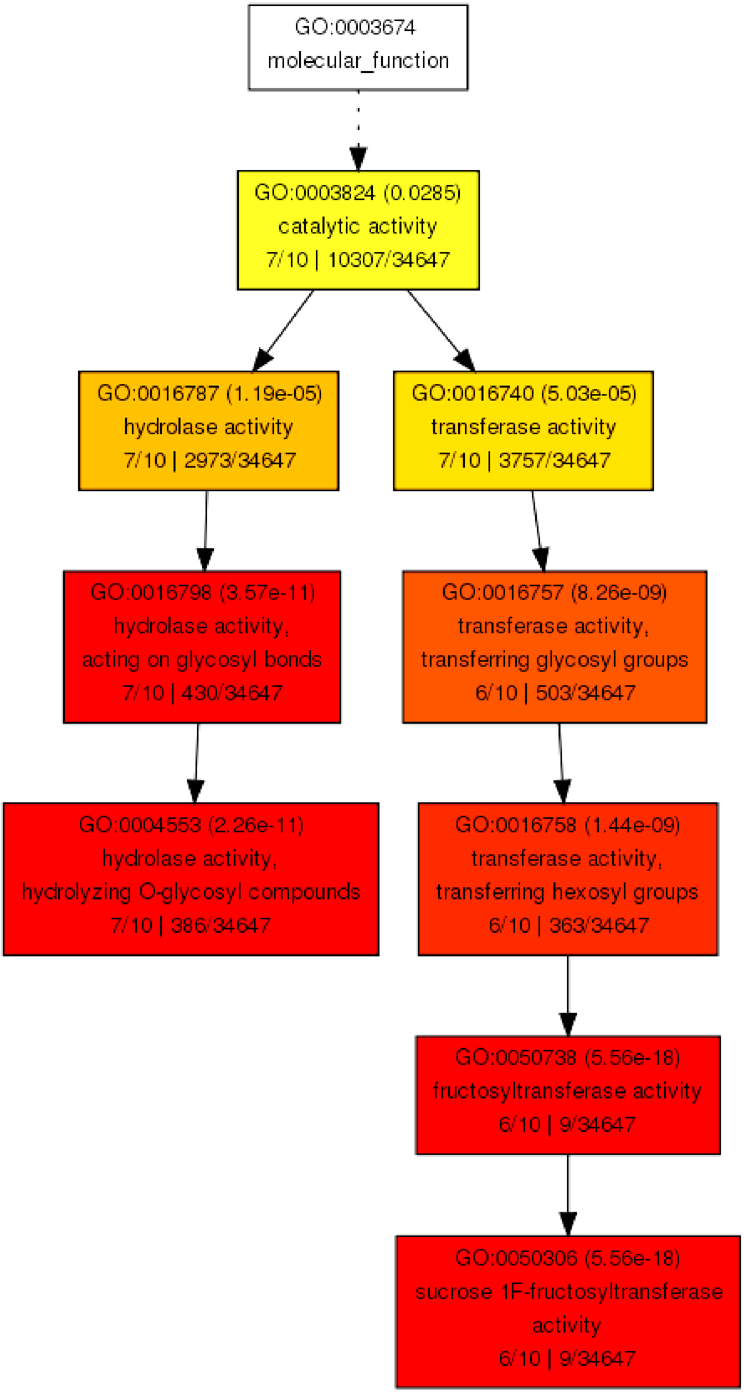


Figure 4.22: Gene ontology of 104 *TaFruc* genes

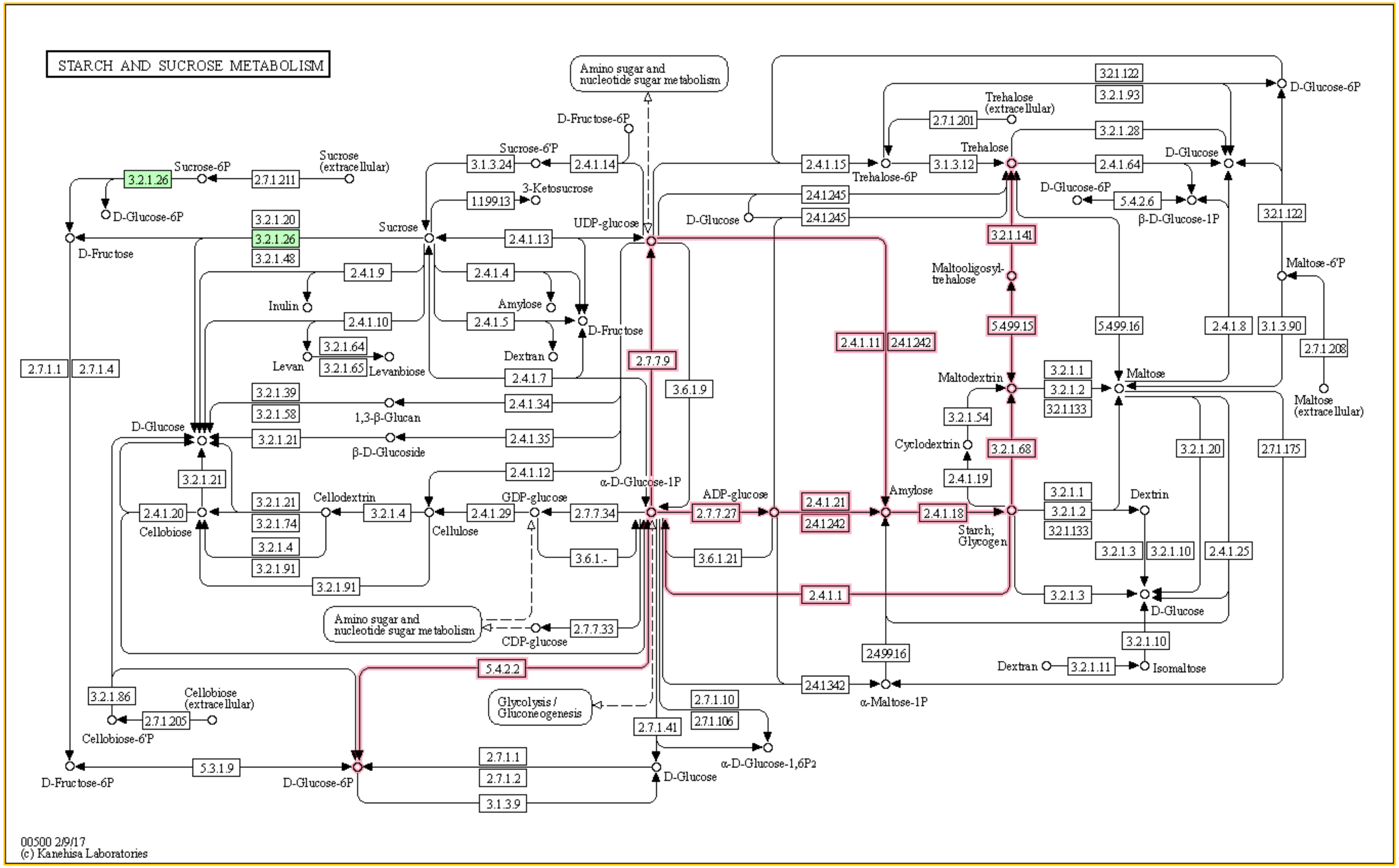


Figure 4.23: Starch and sucrose metabolic pathway retrieved from KEGG-database [In figure, green boxes show identified enzymes**]**

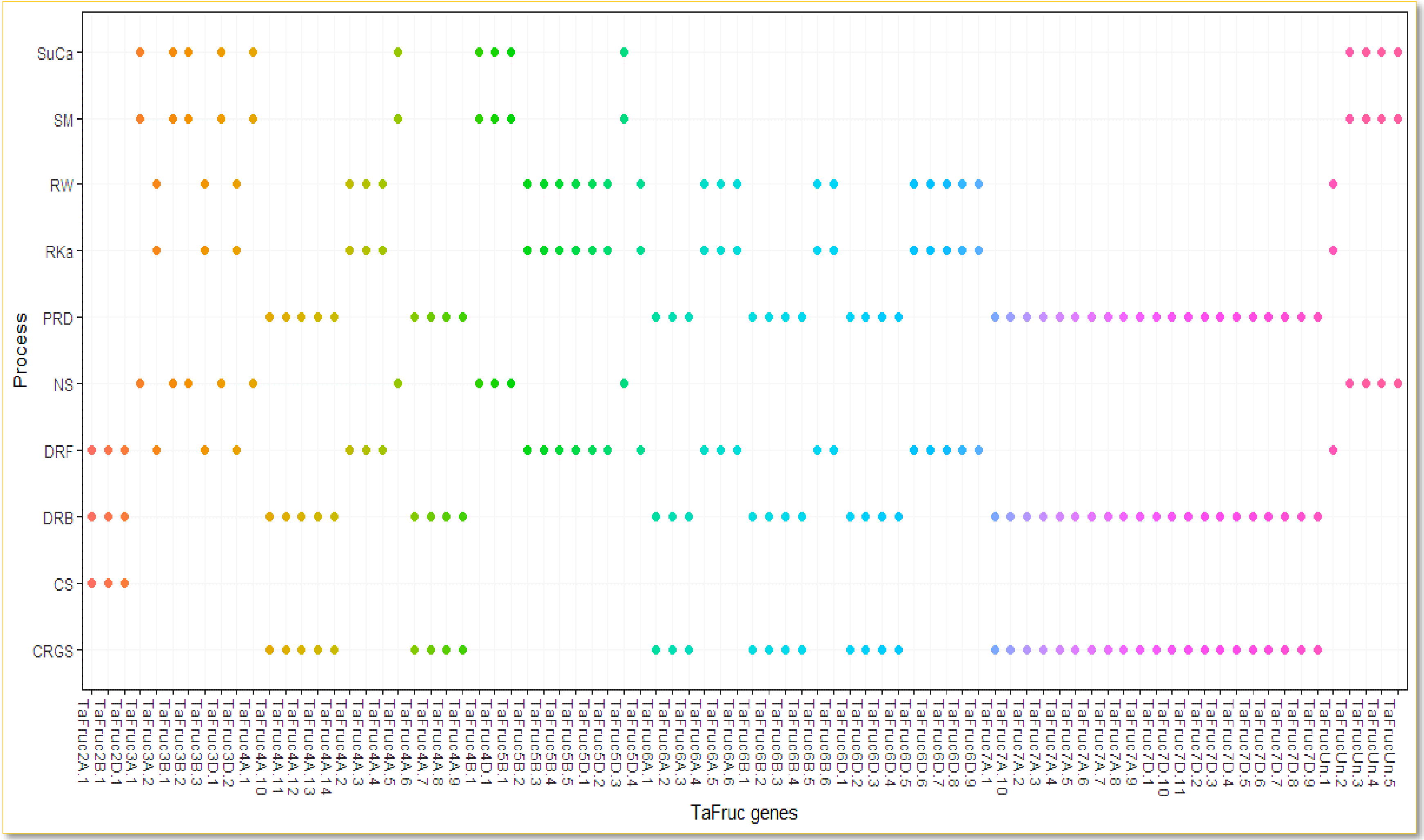


Figure 4.24: Involvement of 104 *TaFruc* genes in different biological processes

starch metabolism (SM), sucrose catabolic activity (SuCa) and response to Karrikin (RKa). These genes were simultaneously involved in multiple biological processes through their transferase and/or exohydrolase activities. **Figure 4.25** depicts the number of genes involved in various processes; maximum 44 *TaFruc* genes were working as defense response against bacterial attacks, 41 *TaFruc* genes were involved in cellular response to gibberellin stimulus and primary root development (PRD). Only three *TaFruc* genes *viz. TaFruc2A.1*, *TaFruc2B.1* and *TaFruc2D.1* were showing their involvement in carbohydrate storage. Detailed results on KEGG database annotation are mentioned in **Annexure 16 (pp: LXX)**.

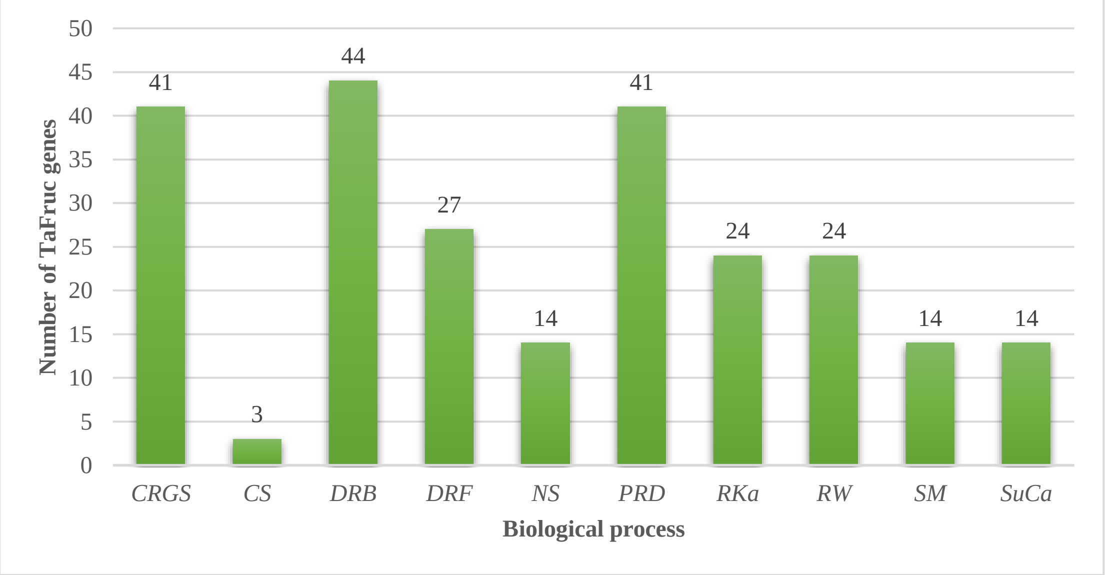


Figure 4.25: Number of identified *TaFruc* genes by process on the basis of KEGG database

Since data for *Tritcum aestivum* interactome is not available in STITCH database interactome data of *Arabidopsis thaliana* and *Hordeum vulgare* was used as reference for chemical-protein interaction (CPI) analysis **(Figure 4.26)**. At least fifty characterized and uncharacterized homologous proteins were identified for each *TaFruc* genes in both of the database. These proteins shared common domains from family glycol hydrolase. The major predicted proteins were beta-fructofuranosidase, 6-fructan exohydrolase, 1-fructanexohydrolase, cell wall invertase-2, sucrose:sucrose-1-fructosyltransferase, sucrose:fructan-6-fructosyltransferase. Additionally, a series of proteins prefixed with MLOC and characterized by the presence of superfamily GH-32 was also predicted with *H. vulgare* database. Major predicted functional partners (chemicals) of these proteins common in both databases were sucrose, fructose, glucose and sucrose-6-phosphatase. All of the predicted proteins were interacting with these chemicals with high confidence values.

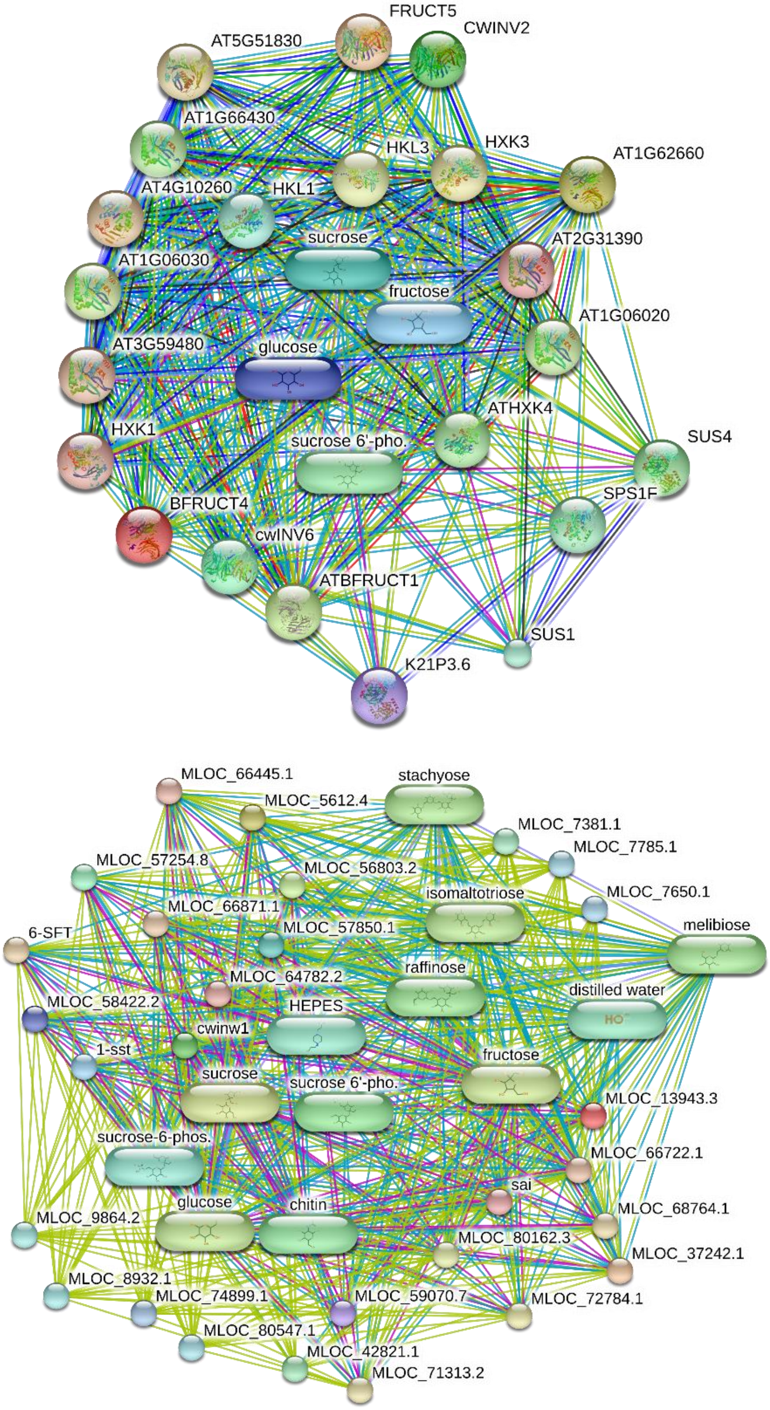


Figure 4.26: Chemical-protein interaction (CPI) network depicting the chemical partners of translated *TaFruc* proteins annotated against (a) *Arabidopsis thaliana* and (b) *Hordeum vulgare* database

4.9.9. *In silico* expression analysis of *TaFruc* genes

Differential expression of all the *TaFruc* genes was checked in tissues of root, leaves/shoot, grain and spike sampled from chinease spring and Azhurnaya at different growth and development stages combinied with different conditions such as normal, drought, salinity and diseased using WheatExp and expVIP databse **(Figure 4.27)**. Among different

TaFruc genes expressing in different tissues, gene *TaFruc4B.2* in diseased tissue of chinease spring leaves sampled at vegetative stage and gene *TaFruc7D.*7 in tissues of chinease spring spike under optimal conditions had highest expression (15.97 counts). At seedling and reproductive stages, genes *TaFruc2A.3* (leaves, abiotic condtions, 13.83 count) and *TaFruc7A.7* (spike, optimum conditions, 14.31 count) had highest expression, respectively. Under abiotic stress, maximum expression was shown by gene *TaFruc2A.3* (13.83 counts) in leaves of seedlings and gene *TaFruc4B.2* showed maximum expression among diseased tissues.

Furthermore, herarichical clustering based on expression data of genes in various tissues grouped the genes in two major clusters which further divided into four subculters **(Figure 4.27)**. Genes grouped into cluster I had highest expression under different plant tissues as compared to cluster II. More specifically, genes of cluster C-IA showed higher degree of gene expression in all tissues than cluster C-IB. In cluster II, genes of C-IIA were more expressive than that C-IIB. In C-IIB, only few genes which are clutered in C-IIB.1 showed some considerable amount of expression.

4.9.10. Simple sequence repeats (SSR) and miRNAs

Using computational approach, a total of 203 SSR primers for 104 *TaFruc* genes was obtained. Out of these 203 SSRs, only 189 primers paired successfully with 72 *TaFruc* genes **(Annexure 17; pp: LXXIII)**. Range of SSRs laid between 12 and 52 bp with product size and motif lengths ranging from 106 to 298 bp and 3-4 bp, respectively. The most frequent motif was CATG (13) followed by TTG (9), GGC (8) and ATGG (8). Number of SSR markers detected with di-, tri-, tetra-, penta- and hexa- nucleotides was 12, 62, 114, 13 and 2, respectively. Average GC% for detected SSRs was 42.67% (30-61.11%). Melting temperature (T_m) of SSRs was between 50.56 and 59.9°C with an average of 55.15°C. For 104 *TaFruc* genes, 60 miRNA of length 19 to 24 bp were detected **(Annexure 18; pp: LXXXIV)**. Most of the detected miRNAs were targeting more than one *TaFruc* genes. Expectation value (E) for detected miRNAs ranged between 1.5 and 5 with UPE (maximum energy to unpair the target site) values from 5.12 to 24.92. Most of the detected miRNAs exhibited cleavage type of inhibition with multiplicity of 1. The only miRNA with maximum multiplicity of 2 was tae-miR5086 which was targeting *TaFruc6A.3*.

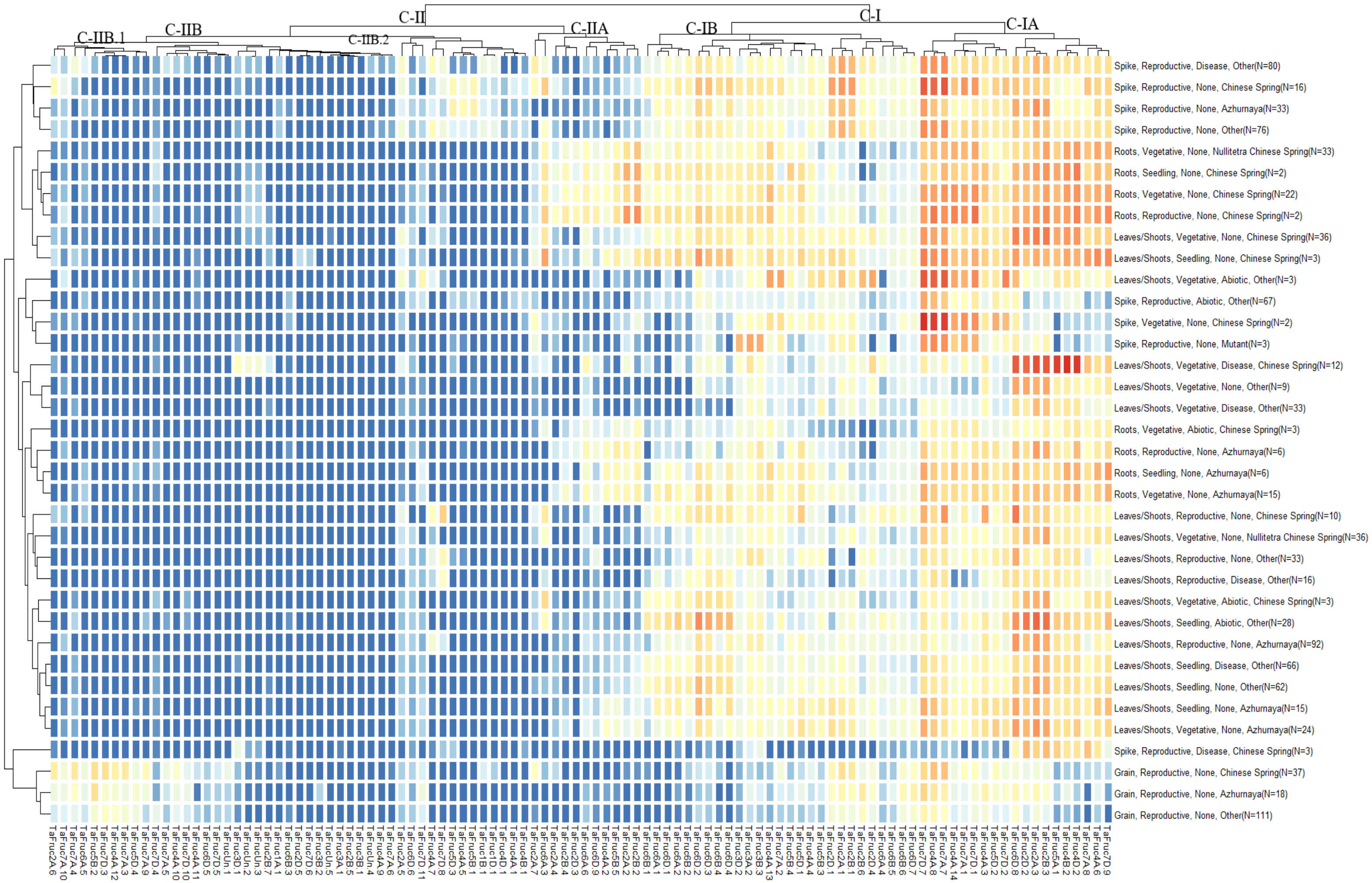


Figure 4.27: Heatmap of differential expression of 104 *TaFruc genes* in different tissues and conditions

CHAPTER-V

DISCUSSION

Water stress is a huge challenge to scientists and global food security. Multifaceted behavior of plants under water deficit conditions brings complexities in breeding for high yielding drought tolerant wheat varieties. However, identification of underlaying genomic regions for yield and yield contributing traits may facilitate breeding programs by means of improving selection efficiency through marker assisted selection (MAS). Therefore, the present investigation 'Genome wide association mapping for stem water-soluble carbohydrates in bread wheat (*T. aestivum* L.) under terminal water stress' has been designed.

This study was conducted on 302 bread wheat genotypes evaluated under irrigated, rainfed and complete drought stressed environments at three different locations (*viz.* Hisar, Karnal and Pune) consisting a total of ten environments. Results of the present study have been discussed under the following headings:

5.1. Water stress and performance of genotypes
5.2. Genetic components and trait association
5.3. Multivariate analysis
5.4. Genome wide association mapping
5.5. Identification of fructans genes

5.1. Water stress and performance of genotypes

5.1.1. Agro-phenological traits

The present investigation was conducted under three water managements *viz.* irrigated, rainfed and drought. In irrigated trials, six irrigations through flooding were given whereas, irrigation was completely checked in rainfed trails. Trials were conducted under a rain out shelter for artificialization of drought stress. Weather conditions and soil moisture throughout the trials were satisfying enough to achieve the objectives of present investigation. Furthermore, ANOVA revealed substantial genetic variability among genotypes for all the studied traits.

In a plant, water stress leads to various malfunctions at morphological, physiological and biochemical levels (Valliyodan and Nguyen, 2006). Degree of damage to a plant due to water stress depends on three major factors *viz.* severity of drought, growth and developmental stage of plant at which water scarcity occurs and genetic architecture of plant (Nezhadahmadi *et al.*, 2013). Water stress affects wheat plant at all growth and developmental stages which ultimately affects the grain yield (Ali, 2019). Results from this study completely satisfy these previous findings. Depending on the trial conditions significant effects of water stress on wheat growth and development habits. In general, significant reduction was recorded for all the traits under both rainfed and drought stressed trials as compared to irrigated ones. However, these reductions were considerably high in drought as compared to rainfed trails. Among rainfed trials, maximum reduction in individual traits in contrast to their corresponding optimum trails was 31% (DTH: E05 vs E06), 28% (DTA: E05 vs E06), 26% (DTM: E09 vs E10), 49% (GFD: E09 vs E10), 58% (NOT: E05 vs E06), 42% (PH: E01 vs E02), 64% (PL: E01 vs E02), 55% (SL: E01 vs E02), 52% (SPS: E01 vs E02), 74% (BY: E01 vs E02), 75% (GY: E01 vs E02), 56% (HI: E05 vs E06), 44% (TKW: E09 vs E10) and 70% (TNG: E05 vs E06). In contrast, maximum reduction for different traits among drought trails was 41% (DTH: E04 vs E03), 39% (DTA: E04 vs E03), 34% (DTM: E04 vs E03), 47% (GFD: E04 vs E03), 62% (NOT: E04 vs E03), 66% (PH: E07 vs E08), 90% (PL: E04 vs E03), 60% (SL: E04 vs E03), 53% (SPS: E04 vs E03), 80% (BY: E04 vs E03), 80% (GY: E07 vs E08), 52% (HI: E04 vs E03), 41% (TKW: E04 vs E03) and 78% (TNG: E07 vs E08). Reduction on the basis of data pooled over managements was also estimated and compared. Maximum reduction under rainfed condition for different traits was 21% (DTH), 20% (DTA), 19% (DTM), 39% (GFD), 48% (NOT), 28% (PH), 42% (PL), 31% (SL), 26% (SPS), 57% (BY), 60% (GY), 37% (HI), 28% (TKW) and 52% (TNG) whereas, it was 37% (DTH), 34% (DTA), 32% (DTM), 39% (GFD), 52% (NOT), 65% (PH), 85% (PL), 59% (SL), 53% (SPS), 74% (BY), 74% (GY), 48% (HI), 41% (TKW) and 69% (TNG) under drought conditions. The extent of reduction in various traits are in agreement with various studies (Ding *et al*., 2018; Mwadzingeni *et al*., 2016a and Dhanda and Sethi, 2002).

Different genotypes showed exceptionally higher values for different traits at different locations and years under stressed condition than that of their corresponding checks however, when data was pooled and compared only few exceptions were reported indicating the existence of higher genotype (G) and genotype x environment (GXE) interaction which further advocate linear responses of individual genotype with environments leading to unstable performance for various traits under stressed conditions (Kumar *et al*., 2018). Thus, while supporting the statements of previous scientists (Sallam *et al*., 2019; Kumar *et al*., 2018; and El-Rawy and Hassan, 2014) results from present study advocate the multi environment screening for selection of drought tolerant wheat genotypes or identifying any genetic stock related to drought tolerance. On the basis of pooled data under rainfed and drought conditions, major exceptions were reported for harvest index (HI). Twenty-seven and twelve genotypes showed higher values for HI under rainfed and drought stress, respectively. However, only three genotypes *viz.*, Bacanora-88, HD-3071 and RD-20 were common exceptions in both conditions. Tracking of passport data of exceptional genotypes revealed that all these were improved genotypes and were resistant to either abiotic or biotic stresses or recommended for late sowing (except RD-20). The most probable explanations for exceptions in HI value may be: 1) most of the breeding programs are orientated towards higher biomass and harvest index, 2) space planting may have allowed balanced production of biomass (BY) and grain (GY) even under stressed conditions as in all of these varieties percentage reduction of BY and GY was virtually similar and/or 3) higher water use efficiency due to their genetic architecture. Although, reaching to a final conclusion behind these exceptions is quite difficult due to complex nature of harvest index, a deep insight into the trend of reduction in harvest index in present study reveals: 1) harvest index is stable and less affected by water stress, and 2) despite significant reduction in BY and GY, considerable reduction in harvest index under water stress needs a large difference between reduction observed for BY and GY. These outcomes are in agreement with Fereres and González-Dugo, (2009) and Hay, (1995) who reviewed various studies on harvest index in detail.

Pooled data was used to identify drought tolerant genotypes. On the basis of drought susceptibility index (DSI) top 20 genotypes (**Table 4.4**) were selected for rainfed and drought conditions. Genotypes C-306, FLW-11, IC-3211988, MACS-6145, MACS-6222and VL-907 were common for both rainfed and drought conditions. Among these genotypes, C-306 and VL-907 are pre-identified drought tolerant varieties whereas, MACS-6145 had genetic background of C-306 providing it a polygenic drought tolerance ability. Exceptionally, FLW-11 and MACS-6222 are mainly rust resistant varieties but pedigree information revealed that FLW-11 had genetic background of WH-542 which is highly responsive to fertile lands and may be correlated with high fertility maintenance of experimental sites whereas, MACS-6222 probably has nuclear genes related to drought and heat tolerance coming from its parent MACS-2496. Furthermore, IC-3211988 is an indigenous local collection from northern Himalayan hills of Uttarakhand region and is still unexplored therefore presumably its genetic architecture here under stressed conditions may be the reason for maintaining grain yield. Other than these genotypes, 14 uncommon genotypes were also identified, most of these genotypes were either tolerant to heat or drought or both or otherwise had tolerant parent somewhere in their pedigree. Unfortunately, pre-identified drought tolerant genotypes *viz.* AKAW-3717, AKAW-4627 and Dharwad dry were not identified as drought tolerant on the basis of DSI which might be due to GXE interaction. However, reduction in GY of these genotypes was considerably low as compared to other genotypes. These genotypes may be identified as promising drought tolerant genotypes with the help of other drought indices as proper calculation and interpretation of different drought indices is needed for error-less selection, since no single drought index is considered complete (El-Rawy and Hassan, 2014). Reasons for heat tolerant genotypes showing good DSI may be: 1) Drought stress induces heat stress due to increased soil temperature, 2) Many cellular, molecular and physiological responses are common in wheat against drought and heat stress.

A major misleading result from present study was mimicry of drought tolerance by genotype ‘Agra Local’ which is a landrace from western Uttar Pradesh and highly susceptible to all three type of rust due to this reason it was infected with rust even after recommended sprays against rusts in all environments, however the incidence of rust under stressed condition was comparatively lower than that of optimal environments due to early heading and anthesis. Therefore, extent of grain yield reduction for this genotype was higher under irrigated conditions than that of corresponding stressed conditions leading to improper calculation of DSI and misinterpretation.

5.1.2. Water-soluble carbohydrates

Water-soluble carbohydrates play important role in grain development under stressed conditions by means of serving as carbohydrate reservoir and a source of monosaccharides during stressed conditions (Slewinski, 2011). Under water stress conditions remobilization of WSCs and fructans helps in compensating the negative effects of drought on GY (Dreccer *et al*., 2009). In present study total water-soluble carbohydrates including its major components *viz*. glucose, fructose, sucrose and fructans were quantified in peduncle of wheat stem sampled 15 days after anthesis (DAA). For this purpose, Fourier-transform near infrared (FT-NIR) spectroscopy was used. In recent years FT-NIR spectroscopy has been used by many scientists as a rapid and non-destructive technique for quantifying several biochemicals in plant samples (Mishra *et al*., 2018 and Pandey *et al*., 2018). NIR spectrum processed with 1st derivative baseline correction followed by 2ndorder Savitzkey-Golay derivation with 15 points was found suitable to develop a rigid partial least square regression model (PLS) with high R^2 (>0.70), low RPD (2.8-3.4) and low RMSEV (9.2%-11.5%) which is in agreement with previous studies of Das *et al*. (2018), Miao *et al*. (2017) and Wang *et al*. (2011). Wave numbers with high regression points associated with WSC, glucose, fructose, sucrose and fructans ranged from 4362 to 5282 cm^{-1}. In addition to this, some peaks associated with H_2O, amides and NH combinatorial were also reported. The identified peaks were similar to those reported by Pandey *et al*., (2018). These calibration models further helped in rapid and non-destructive quantification of WSCs in wheat peduncle in all the studied genotypes sampled under eight environments (E01-E8).

A wide range of WSC, glucose, fructose, sucrose, fructans and total non-structural sugars (TNSC, sum of all WSC components) was obtained (**Table 4.3**). Range of WSC reported in present investigation was in agreement with experiment of Zhang *et al*., (2014). Studies have demonstrated that fructans are predominating sugars followed by sucrose and the maximum accumulation of soluble sugars take place by 16 DAA (Zhang *et al*., 2014). Furthermore, under water stress conditions plants tend to accumulate and remobilize more WSCs in contrast to non-stressed conditions (Yáñez *et al*., 2017 and Zhang *et al*., 2014). Similar results were reported in this study. Fructans was predominating sugar followed by sucrose. Nearly 70-75% of total WSCs and TNSC was constituted by fructans whereas, contribution of sucrose, glucose and fructose was nearly 19-21%, 7-8% and 6-7%, respectively. In contrast to irrigated conditions, amount of WSC and TNSC both significantly increased under water stressed conditions which was mainly due to increase in fructans and sucrose concentrations. However, concentration of glucose and fructose was also high in stressed conditions. Furthermore, this increment was much higher under drought condition as compared to rainfed one. Fructans, sucrose, glucose and fructose increased by 56%, 23%, 16% and 20%, respectively and increase in WSC and TNSC was 16% and 43%, respectively under drought conditions. Likewise, increase in WSC, TNSC, fructans, sucrose, glucose and fructose concentration were 10%, 12%, 9%, 19%, 18% and 9%, respectively under rainfed condition. Present study indicated that variability in TNSC and WSC among genotypes was mainly due to fructans and sucrose as their range was higher than glucose and fructose. The higher peaks of fructans content along with sucrose indicate the simultaneous accumulation and breakdown of fructans after anthesis as stress tolerance mechanism.

5.2. Genetic components and trait association

The ANOVA indicated significant variability of genotypes on all the studied traits. This is important because crop improvement programs and efficacy of GWAS depend on the relative importance of these genetic effects. Results from ANOVA were in accordance with Mathew *et al*., (2018).

Estimate of genetic components *viz.,* GCV, PCV, h^2 and GAM provide basic information about genetic architecture of the studied population which offers a strategy for future crop improvement programs. Similar to many previous studies estimates of genetic components were high in optimal conditions as compared to stressed conditions (Yacoubi *et al*., 2020 and Ghodke *et al*., 2019). In this study, higher PCV compared with GCV estimated for all the traits in individual and pooled analysis indicated the presence of other contributing factors to the total variations, this was similar to results of Shamuyarira *et al*. (2019). In pooled analysis (**Table 4.6-4.8**), all the studied traits exhibited low to moderate GCV and PCV under all of the three water managements, suggesting limited opportunities for improvement of these traits through selection and need of introducing new germplasm to widen the genetic base for future improvement programs. These results are in agreement with Shamuyarira *et al*., (2019), Mathew *et al*., (2018), Arya *et al*., (2017) and Bellundagi *et al*., (2013). Furthermore, narrow difference between GCV and PCV for DTH, DTA, DTM, PH, PL, SPS and TKW under all three conditions and for GFD under rainfed and drought condition indicates lesser influence of environment on these traits. Moderate difference between GCV and PCV for GFD and HI under irrigated condition and for NOT under both irrigated and rainfed conditions indicates cumulative effect of genetic and environmental factors in the expression of these traits. Wider difference between GCV and PCV of BY, GY and TNG under all three water regimes indicated strong influence of external factors on these traits. Similarly, NOT and HI under rainfed conditions and PL, SL and HI under drought condition had wider difference between GCV and PCV. Previous studies had also advocated that BY, GY and TNG are highly influenced by GXE interaction (Wardofa *et al*., 2019 and Quintero *et al*., 2018). These results further indicate that water stress significantly affects the traits which generally had positive correlation with BY and GY. Sharp and Davies (1989) also asserted strong influence of water stress on above ground biomass.

Broad sense heritability (h^2) is an important genetic component to measure the proportion of phenotypic variance attributed to genotypic variance and an important predictor for response of trait to natural or artificial selection. Broad sense heritability alone does not provide true breeding value of any trait as it contains both additive and non-additive effects. Heritability and genetic advance over mean (GAM) are complementary aspects of selection during crop improvement program. Estimates of GAM serve as degree of expected response of selection by a certain trait. Many previous studies had demonstrated low to high h^2 and GAM for studied traits under both irrigated and water stress conditions (El-Mouhamady and Ibrahim, 2020; Shamuyarira *et al*., 2019; Mathew *et al*., 2018 and Ramakrishnan *et al*., 2016). Trivia from these studies regarding heritability is that under optimal conditions traits shows higher estimates of heritability with respect to stressed environment which may be due to higher potential under favorable environments. In this study, DTH, DTA and GFD exhibited high h^2 and low GAM under both irrigated and water stressed conditions whereas, DTM exhibited high h^2 and low GAM under irrigated and drought conditions and moderate h^2 and low GAM under rainfed conditions which signify predominance of non-additive gene action in the expression of these genes. These results correlate with the molecular basis of phenology (DTH, DTA and DTM) in wheat crop. Phenological traits *viz*. DTH, DTA, GFD and DTM are strongly controlled by *Vrn* and *Ppd* genes which might be the reason for high and stable heritability of these traits (Bogard *et al.*, 2014). Regulation of these genes is highly influenced by light intensity and temperature thus indicates effect of environment on these traits. Therefore, selection for these traits should be done in later generations or after multi-environment screening (Behl *et al*., 2019 and Karsai, 2008). High h^2 and GAM were reported for PH under both optimal and stressed conditions which signify the presence of additive effect and indicate that early selection will be worthy for wheat improvement programs. The most presumable reason for high and stable heritability of PH may be its genetic control by major QTLs like *Rht* which is abundant in modern wheat varieties (Thomas, 2017). PL, SL and SPS exhibited moderate to high h^2 and low to moderate GAM indicating presence of epistasis and genetic control under minor QTLs, which get affected by external factors (QTL X Environment interaction), with some major QTLs. This further signifies that in present study material improvement of these traits is possible with recurrent selection (accumulation of favorable alleles). Previously, Zandipour *et al*. (2020), Farokhzadeh *et al*. 2020; Roncallo *et al*. (2017) and Ma *et al*. (2007) had advocated the genetic control of PL, SL and SPS under minor epistatic QTLs as well as presence of GXE, QXE and epistasis. Furthermore, TKW was recorded with high h^2 under all three condition, but moderate GAM under irrigated and rainfed conditions and high GAM under drought condition which advocates the further possibilities for improvement through selection. Bányai *et al*. 2020 identified TKW as stable trait under irrigated and water stressed conditions. BY, GY, HI and TNG were recorded with low to moderate h^2 and low GAM. This indicates low responsiveness of these traits to natural and artificial selection due to large influence of external factors. Therefore, improvement of these traits will require rigorous selection. Range of h^2 and GAM estimated for different traits under variable conditions is similar to Jatoi *et al*. (2012), Taheri *et al*. (2011) and Rebetzke *et al*. (2002).

Correlation studies are conducted to identify yield favouring and non-favouring traits providing a direction for direct and indirect selection of combination of traits for higher yield potential. In present study, grain yield was positively correlated with BY, HI, TKW and TNG at significance level $p>0.001$ and GFD at significance level $p>0.05$, but negatively correlated with DTH, DTA and DTM at significance level $p>0.001$ under pooled irrigated environment (**Table 4.9**). Similarly, positive correlation of BY with GFD, NOT, BY, HI, TKW and TNG at significance level $p>0.001$, PH and PL at significance level $p>0.01$ and negative correlation with DTH and DTA at significance level $p>0.01$ was reported under pooled rainfed environment (**Table 4.10**). Under pooled drought environment, NOT, PH, PL, BY, TKW and TNG at $p>0.001$ and SL, SPS and HI at $p>0.01$ exhibited positive correlation with grain yield (**Table 4.10**). Previously, Qaseem *et al*. (2019), Sukumaran *et al*., (2018b), Mia *et al*. (2017) and Li *et al*. (2011) and various other scientists demonstrated different magnitudes of association between grain yield and its attributing traits under stressed and non-stressed conditions closer to present study.

In this study, correlation of quantified biochemicals with yield and its attributing traits was calculated with complete set of genotypes and with identified drought tolerant genotypes. With complete set of genotypes, no clear correlation of WSC and TNSC with GY was seen (**Table 4.11 and 4.12**). The magnitude of correlation between these traits ranged from significantly negative to positive under different environments. In pooled analysis, a significantly negative trade-off between WSC and GY can be seen under irrigated conditions whereas, none of the other two water regimes showed any significant correlation of TNSC and WSC with GY. Similarly, no clear relation of other components (glucose, fructose and fructans) of WSC was noted with GY. Yield attributing traits like DTH, DTA and DTM showed significant positive correlation with TNSC and fructans under all three water regimes whereas, these traits were positively correlated with WSC under irrigated and rainfed but negatively under drought stress. On the other hand, TNSC showed positive correlation with TNG but the significant trade-off between these two traits was reported only under rainfed condition. Similar relationship was also reported between fructans and TNG under all three conditions. Trait association analysis between studied biochemicals and yield and its associated traits for drought tolerant genotypes completely changed the scenario. TNSC, WSC and fructans showed positive correlation with GY, BY, TKW and TNG under all three water managements. Due to very small population size this trade off was non-significant however, magnitude of correlation was considerable. These finding have strong support of del Pozo *et al*. (2016) who demonstrated unclear relationship between WSCs and GY under irrigated and water stress conditions with magnitude ranging between -0.37 to 0.11 in a diverse panel of 384 *Triticum aestivum* genotypes. Why magnitude of correlation changed with set of genotypes? The most appropriate answer to this question may be that soluble sugars accumulate in different parts of plant depending upon the photosynthetic capacity however, the remobilization of these sugars to grain is utmost important to contribute to grain yield which directly depend on the activities of fructosyltransferase and fructans exohydrolase enzymes. Presumably, the activities of these enzymes must be higher in drought tolerant genotypes. Yáñez *et al*. (2017) demonstrated that expression of fructosyltransferase and fructans exohydrolase genes differs in both drought tolerant and susceptible varieties under both stressed and non-stressed conditions which further significantly affect grain yield by means of affecting carbon flow to grain.

5.3. Multivariate analysis

Multivariate analysis was carried out to summarize the contribution of studied traits in variability and dissect the genetic diversity in present study material. It was performed with the BLUE values estimated for each water regime by pooling corresponding environments. Results showed significant effect of water management on both trait expression and genetic diversity. In PCA (**Table 4.13**), first eight components accounted for ca. 84.50% of total variance under irrigated conditions and first seven components accounted for ca. 80.10% and 76.40% of total existing variance under rainfed and drought stress conditions, respectively. Thus, the data can be summarized usefully by projecting the points on these axes (PC1-PC8). Results from PCA further signify that all the traits had considerable vector loading in some or the other extracted principal components under all three water regimes and substantial diversity was present for different traits in present population. Devesh *et al*. (2019) also extracted seven principal components and suggested due importance of all the studied traits in genetic diversity among sixty *Triticum aestivum* genotypes evaluated under irrigated conditions. Results of PCA from present study are in close agreement with findings of other researchers (Ambati *et al*., 2020; Shafi *et al*., 2020; Mwadzingeni *et al*., 2016b and Khodadadi *et al*., 2011).

Euclidean distance between genotypes was estimated based on all the studied traits and then clustering was done with Ward’s minimum variance method for all three water regimes (**Table 4.15 and 4.16**). Cluster analysis allowed grouping of studied genotypes in two major clusters which further sub-divided into eight clusters at ca. 14.00% similarity. Cluster II was identified as superior cluster due to high mean value of GY. In reference to drought tolerance favouring traits, cluster I, III and VIII were identified more important with irrigated data set as these clusters had high values of DTM, GFD NOT, PL, SPS, TNSC, glucose, sucrose, fructose, fructans and WSCs and shorter DTH, DTA and PH. Furthermore, majority of drought tolerant genotypes were distributed under cluster IV and VIII and were in proximity to each other. Among these clusters maximum number of drought tolerant genotypes was grouped in cluster VI followed by cluster VIII whereas, only five genotypes were grouped in cluster I. Cluster I was found to be superior and characterized by higher values of NOT, SPS, BY, GY, TNG and fructose and had maximum (9) number of identified drought tolerant genotypes followed by cluster II with six genotypes in RF data set. Similarly, cluster I was superior and characterized with higher values of NOT, SPS, BY, GY, TNG and WSC under drought stress. With this data set, cluster II had maximum (9) number of drought tolerant genotypes and it was characterized with highest mean for TNG followed by cluster I with 7 genotypes. Rest of the clusters had nearly equal frequency of drought tolerant genotypes under both rainfed and drought water regimes. Previously, Arifuzzaman *et al*. (2020) also used Ward’s minimum method with Euclidean distance to access genetic diversity among 25 *Triticum aestivum* genotypes on the basis of agro-phenological traits and identified three clusters under stressed and non-stressed conditions. Results from present investigation have concurrence with findings of many other scientists (Adilova *et al*., 2020; Grzesiak *et al*., 2019; Naghavi and Khalili, 2017; Mwadzingeni *et al*., 2016b and Singh and Salgotra, 2014).

5.4. Genome wide association mapping

Phenotypic and genotypic data of 301 wheat genotypes was used in this experiment. Genotyping was done with 35K Axiom Breeder chip which is an improved version of 820K SNP array and has been used by many researchers for association mapping studies in wheat (Alomari *et al*., 2017). In this study, a total of 14571 polymorphic SNPs were identified which was in agreement with Liu *et al*. (2017) however, difference in number of polymorphic SNPs between two studies is due to utilization of different association mapping panel (AMP) and SNP array. The high values of heterozygosity (0.39) and PIC (0.23) speculated the existence of substantial genetic diversity in the present AMP which has concurrence with results of Eltaher *et al* (2018). Moreover, genome D showed the highest heterozygosity and PIC which is consistent with previous reports of Ain *et al*., (2015). Results from population structure analysis revealed the existence of two major clusters with slight admixture which were coinciding with pedigree and geographic conditions. Sukumaran *et al*. (2014) also reported two sub-populations in their AMP for grain yield and associated traits. These results signify the existence of substantial genetic and allelic variability for conducting this experiment.

In present study AMP was characterized to identify genomic loci for 14 pheno-agronomical traits and WSCs and its 4 major components in 13 data set and 3423 MTAs (marker trait association) ($-log_{10}P>2.899$) were identified with 1987 SNPs which makes ca. 13 MTAs per trait (**Table 4.20**). Average number of MTAs per trait was higher than 8 MTAs/trait as reported by Qaseem *et al*., (2018) which might be due to the difference in threshold criterion, number of genotypes used and number of polymorphic SNPs identified. Significant MTAs common in more than one data set were termed as stable MTAs and have been discussed here. A total of 431 stable MTAs was reported and out of these, 77 showed pleotropic effect. Most commonly, SNPs associated with DTH showed pleiotropy with DTA, GFD and DTM, SNPs, associated with PH showed pleiotropy with PL, SPS and SL and SNPs associated with TKW showed pleiotropy for SPS, TNG and GY. Previously, Pradhan *et al*. (2019) had also identified pleiotropic MTAs affecting both TKW and TNG. Qaseem *et al*. (2018) reported pleiotropic MTAs for DTH, DTA, DTM, PH and SL. The distribution pattern of stable MTAs for different traits on individual linkage group and genome of wheat was in agreement with findings of Sheoran *et al*. (2019) and Ain *et al*. (2015). Discussing more particularly about WSCs and its components, 8 MTAs (AX-94384779, AX-94419960, AX-94560557, AX-94865722, AX-94916179, AX-95105243, AX-95135556 and AX-95685387) for glucose on 1B, 2A, 5B, 6A and 6D, 9 MTAs (AX-94384779, AX-94419960, AX-94490070, AX-94560557, AX-94865722, AX-94916179, AX-95105243, AX-95135556 and AX-95685387) for sucrose on 1B, 2A, 5B, 6A and 6D, 3 MTAs (AX-94504454, AX-94583506 and AX-94960090) for fructose on 1A, 4 MTAs (AX-94472299, AX-94923277, AX-95204178 and AX-95225454) for fructans on 1B and 3A, 3 MTAs (AX-94472299, AX-94923277 and AX-95204178) on for TNSC 1B and 3A and 5 MTAs (AX-94413225, AX-94426796, AX-94921095, AX-95111986 and AX-95120751) for WSCs on 6A and 7A were found stable in this study. No GWAS study has been conducted to identify individual components till now so no evidence is available to support present findings in reference to glucose, fructose, sucrose and fructans. For WSCs, identified MTAs did not coincide with previous findings of Fu *et al*. (2020) and Dong *et al*. (2016). Therefore, unstable MTAs were reviewed in which 4 SNPs *viz*. AX-94879209, AX-94759517, AX-94887053 and AX-94964616 were found common with Fu *et al*. (2020). All these SNPs were pleiotropic for fructans, TNSC and WSC in present study. Thus, rest of the identified stable MTAs may be considered novel for WSCs and its components. It is interesting to know that no marker was found polymorphic for previously known *1-FEH* and *6-SFT* genes in this study. Marker AX-94508292 was associated with DTH and DTA in this study but Sheoran *et al.* (2019)

identified this marker for DTM. Two noteworthy MTAs (AX-95257620 and AX-94456473) for DTH were found in proximity of *Vrn-1A* (89.0 cM) (Sukumaran *et al*., 2014). Significant SNPs were also identified in the previously reported QTL regions for DTA (1A:38.4 and 1A:59.6 cM) and PH (1A:69.4 and 1A:105.3 cM). MTA (AX-94412521) identified for PH on linkage group 7A at 29.9 cM was within the region of *Rht2* gene (for reduced plant height) which is reported as QTL for plant height previously by Peng *et al.* (2011). These evidences advocate authenticity of present study.

In putative candidate gene analysis 249 genes were identified. Most of these genes were involved in carbohydrate metabolism and repair mechanisms. However, only one gene namely *TraesCS7D02G433100* which transcribes glycosyltransferase and hexosyltransferase enzymes was associated with fructans (AX-94583229) indicating that WSCs biosynthesis must be affected by other metabolic processes also. Very few genes directly involved in stress mechanism were also reported. For example, presence of domains like NAC, NB_ARC, Scropian_toxin_like and P-lop-NTPase signifies identification of novel drought stress tolerance associated MTAs in this study. These results are in close agreement with many previous studies (Gahlaut *et al*., 2019; Ledesma-Ramírez *et al*., 2019 and Chao and Lin, 2018).

5.5. Identification of fructans genes

Fructans makes a large part of reserved WSCs and plays important role in compensating loss of grain yield under water stressed conditions (Yáñez *et al*., 2017). Accumulation and breakdown of fructans depend on upregulation and downregulation of fructan exohydrolase and fructosyltransferase genes (*TaFruc*). A total of 104 functional genes associated with fructans metabolism were retrieved from IWGSC reference sequence (IWGSC RefSeq.) database by *in silico* comparative genomic approach using the genomic information of 13 model plant species (*Arabidopsis thaliana*, *Arabidopsis lyrata*, *Brachypodium distachyon*, *Brassica oleracea*, *Brassica rapa*, *Beta vulgaris*, *Glycine max*, *Helianthus annus*, *Hordeum vulgare*, *Medicago trancatula*, *Oryza sativa*, *Sorghum bicolor* and *Setaria italica*). Previously, Gautam *et al*. (2019) and Muthusamy *et al*. (2017) also used these plant species as model organisms for retrieving orthologs of SWEET protein and HSP20, respectively from wheat genome (IWGSC RefSeq.). Newly identified *TaFruc* genes were distributed on all three genomes (A, B and D) indicating the evolution of all three genomes from a single progenitor in past (Feldman and Levy, 2012). Among genomes, ‘A’ genome had maximum (41) number of *TaFruc* genes whereas, among chromosomes, 4A chromosome had maximum (14) genes (Figure 4.16). *TaFruc* identified in this study had a considerable length of coding DNA sequence (300-2271 bp) which is in accordance with Kumar *et al*. (2018) who retrieved genes from IWGSC RefSeq with CDS ranging between 1266 and 1776 bp. Range of GC% (28.52-62.03%) was within the defined range of GC content present in monocots (Šmarda *et al*., 2014). Presence of higher GC content in these genes confirms thermostability to higher order structures of DNA and RNA transcripts due to stacking interaction of triple hydrogen bond (Biro, 2008). Structural analysis of complete *TaFruc* transcripts was done with GSDS v2.0 server which was also used by Jiang *et al*. (2020) to dissect gene structure of SRO genes in wheat. The gene structure results revealed presence of multi-exonic genes interrupted with at least one P0 type of intron. Maximum 8 exons were reported for genes *TaFruc4A.3*, *TaFruc4A.4*, *TaFruc5B.2*, *TaFruc5B.3*, *TaFruc5D.1* and *TaFruc5D.2* which indicates that in contrast to other *TaFruc* genes these genes undergo higher splicing events and allow formation of protein isoforms with different roles (Lim *et al*., 2018). Conserved position and non-randomness in intron phase distribution in *TaFruc* genes further signify multiple exon shuffling events during evolution (Fedorov *et al*., 1998). The number of reported P0, P1 and P2 introns were in agreement with Fedorov *et al*. (1992). Introns are of great evolutionary importance and play key role in gene expression. A longer length of intron conserves enormous evolutionary information within it and indicates insufficient purifying selection to remove InDels in a small population and longer transcribe duration. Besides, difference in lengths of introns signifies regulatory mechanisms of gene, gene with longer introns is generally tissue specific and has complex regulatory mechanism whereas, genes with shorter introns are generally housekeeping genes and have less complex regulation (Keane and Seoighe, 2016). In this study, the longest intron length (13Kb) was reported for gene *TaFrcu6D.5* whereas, the shortest for *TaFruc3A.1* and *TaFrucUn5*. Similar results for intron length were reported by Jiang *et al*. (2020).

Cis-regulatory elements (CREs) are non-coding motifs present in proximity or within the gene and required for its spatiotemporal expression. In plants, large number of studies have advocated the role of many specific CREs regulating gene expression under biotic and abiotic stress conditions (Alok *et al*., 2020; Li *et al*., 2019; Sahu *et al*., 2016). PlantCare database was used to annotate the CREs within 1.5 Kb downstream of each *TaFruc* genes. Most recently, Bai *et al*. (2019) used same approach to identify CREs regulating MYC family genes in wheat. A total of 108 different CREs was identified for 104 *TaFruc* genes. Of these, abiotic stress responsive CREs were most abundant (ca. 35%) followed by light responsive CREs (ca. 19%). This signifies responsiveness of identified *TaFruc* genes under water stress conditions. On individual basis TATC-box and CAAT-box were dominatingly distributed. TATC-box is gibberellin responsive CRE which indicates that most of the genes were responsive to abiotic stress (Colebrook *et al*., 2014). On the other hand, CAAT is common CRE in promoter and enhancer regions (Miao *et al*., 2020). Similar results for CREs were also reported by Gautam *et al*. (2019), Kumar *et al*. (2018) and Gahlaut *et al*. (2016).

Protein sequences translated by *TaFruc* genes were also studied. All polypeptide chains started with translation of methionine (Met) by start codon (ATG). Length of polypeptide chains ranged between 99 (*TaFruc2B.5*) to 756 (*TaFruc7D.5*) for amino acid residues with molecular weight 10.85 KDa to 84.89 KDa. Physicochemical properties of *TaFruc* genes revealed that majority of genes were thermostable, basic and hydrophilic in nature. These findings are in concurrence with Kumar *et al*. (2018). Furthermore, the transcribed proteins were mainly glycine rich. To identify functional domains, CDD search was conducted and results were confirmed with Pfam and ProtParam whereas, sequence and length of conserved domain was obtained using MEME v.5.0. Similar strategy was adopted by Tian *et al*. (2020) and Ye *et al*. (2019). In this study major occurrence was reported for glycosyl hydrolase (GH) family members. Enzymes of this family catalyze exohydrolase activities of soluble sugars which indicates that all the identified genes were involved in carbohydrate metabolism. Besides, GH family members, Kelch_4repeats (galactosidase activities), DEP_RGS7 (GTPase-activating) and Methyltr_RsmF_N (methyltransferase activity) were also identified which indicates that all identified genes were involved in carbohydrate metabolism. Cellular localization is necessary to identify the proper functioning of proteins. To predict subcellular location of *TaFruc* genes, mPLoc software was used which was also used by Li *et al*. (2020) in reference to ASR family genes. In this study, 89, 13, 2 and 1 genes were predicted to be in cell wall, vacuoles, nucleus and chloroplast, respectively which further confirms the role of *TaFruc* genes in carbohydrate metabolism.

Gene ontology annotation of *TaFruc* genes revealed two major molecular functions of identified *TaFruc* proteins were hydrolase and transferase activities of non-structural sugars. Furthermore, to identify role in different metabolic and signaling pathways KEGG pathway enrichment analysis was done which indicated that these proteins were primarily involved in starch and sucrose pathway. These genes were coding for three different types of enzymes *viz*. β-fructofuranosidase (INV; EC:3.2.1.26), sucrose:sucrose fructosyltransferase (SST; EC:2.4.1.99) and fructan beta-(2,1)-fructosidase (1FEH/inulinase; EC:3.2.1.153) which were further involved in 13 different biological processes among which carbohydrate storage, primary root development and defense response to bacterial/fungal were major. Besides abiotic stresses, fructans play key role in biotic stresses also. Response to Karrikin was also reported signifying the involvement in phytohormone signaling network and key role in seed dormancy and germination (Meng *et al*., 2017). Zhang *et al*. (2017) also adopted GO term and KEGG database for functional enrichment of newly identified proteins in wheat. Chemical-protein interaction networking with STITCH v2.0 database annotation supported the present findings and indicated that coded proteins had four major functional partners *viz*. sucrose, fructose, glucose and sucrose-6-phosphatase. Previously, McIntyre *et al*. (2011) also used STITCH database to annotate chemical-protein interaction network for differentially expressed genes in high and low WSC accumulating wheat lines and reported similar interaction. Other researcher who used STITCH database for chemical-protein interaction are Tyagi *et al*. (2020), Kumar *et al*. (2019) and Kalapos *et al*. (2016).

Complete protein sequences coded by *TaFruc* genes and reference genes were used to establish phylogenetic relationships using maximum likelihood method (MLk). Previously, Dubey *et al*. (2020) and Wang *et al*. (2019) also used MLkM for establishing phylogenetic relationship in wheat genes. Identified and predicted genes grouped into six clades. All the reference genes translating to functional exohydrolase genes grouped into clade-I. Interestingly this clade did not have any predicted *TaFruc* gene. Reference genes with transferase activities grouped under clade-II with few *TaFruc* genes having similar enzymatic activities. In addition to this, gene from *Hordeum vulgare* (*HVSFT7.8*) was grouped with *TaFruc* genes in clade-III. Clade IV-VII had exclusive *TaFrcu* genes most of them were duplicate gene pairs. These results clearly indicated the evolutionary pattern of fructans metabolic genes and were in agreement with evolutionary tree annotated from '*Tree of life*'. These results further, supported the results for gene structure and conserved domain sequences which were highly conserved within and between clades. Previously, Jiang *et al*. (2020) and Wang *et al*. (2019) reported similar results. In addition to phylogenetic relationship, gene duplication study between identified *TaFruc* genes was also done. In this study, 106 duplicate gene pairs were reported and out of which 96 were segmental duplicates and rest (10) were tandem duplicates which are supposed to diverged ca. 22.3 MYA. All duplicated gene pair showed Ka/Ks ratio <1 indicating their purifying selection during evolution which signifies that amino acid sequence and function did not alter under selection pressure (Kumar *et al*., 2018).

In silico tissue specific differential expression approach was used to explore the regulation of identified gene under specific conditions. These results indicated up-regulation of most of the *TaFruc* genes under both abiotic and biotic stress conditions signifying their important role in providing tolerance towards various stresses in wheat. Previously, Tyagi *et al*. (2020) and Yang *et al*. (2019) and several other scientists also used web based database to explore tissue specific gene expression in newly identified *Triticum aestivum* genes. A total of 189 SSR primer pairs for 72 *TaFruc* genes was designed using batch primer. Additionally, 60 miRNA targeting *TaFruc* genes were also identified. These miRNA were regulating gene expression under abiotic and biotic stresses for several growth and developmental activities for instance, miR156 and miR444 were involved in gene expression under abiotic (powdery mildew) and biotic stresses (heat and drought) (Liu *et al*., 2017 and Xin *et al*., 2010). These results are in closer association with findings of Jiang *et al*. (2020) and Kumar *et al*. (2018).

CHAPTER-VI

SUMMARY AND CONCLUSIONS

Water stress is a major constrain for wheat productivity across the globe. Unpredicted genotypic response and higher magnitude of GXE interaction makes wheat breeding for drought tolerance a complex trade to achieve. However, recent incorporation of genomics with plant breeding is a way to improve drought tolerance in wheat so the productivity. Therefore, present study entitled 'Genome wide association mapping for water-soluble carbohydrates under terminal water stress' was under taken to achieve following objectives:

1. To evaluate the germplasm for total stem WSCs
2. To identify genomic regions associated with stem WSCs under terminal water stress
3. *In silico* genome wide identification of genes involved in fructans metabolism

In this study, 302 bread wheat genotypes were evaluated for 14 agro-phenological traits and 6 biochemical traits in alpha-lattice block deign with two replications for two consecutive seasons (*Rabi* 2017-18 and *Rabi* 2018-19) at three locations Hisar, Karnal and Baramati (Pune). Data was analyzed for individual environments and pooled over water managements *viz.* irrigated (IR), rainfed (RF) and complete drought (DT) using mixed linear models fitted with best R^2 value. Along with agro-phenological traits, biochemical analysis for quantification of TNSCs, fructans, fructose, glucose, sucrose and WSCs was also performed. Genotyping was done using 35K SNP Breeder's array. Genome wide association mapping was perforemed for studied traits in an association mapping panel of 301 diverse bread wheat genotypes by applying compressed mixed linear model. Additionally, an *in silico* study was carried out to identify genes associated with fructans (*TaFruc*) metabolism in wheat. Salient findings of present study and conclusions drawn from them are summarized below:

- Significant effect of water regimes on phenotypic expression was reported. Significant reduction in all the studied agro-phenological traits was observed. As much as 80% of yield reduction was recorded under complete drought stress. Traits like harvest index and thousand kernel weight were found to be least affected by water stress. Exceptionally, as response to water stress, total WSCs and its components (glucose, fructose, sucrose and fructans) increased. As much as 56% increase in fructans was reported under complete water stress indicating a linear relation between water stress and quantity of soluble sugars in wheat which indicates differential expression of associated gene under water stress conditions.

- It is worthy to note that in present study a new rapid and non-destructive method using Fourier transform near infrared spectroscopy (FT-NIR) was developed and used to estimate glucose, fructose, sucrose and fructans in wheat stem.
- Twenty tolerant genotypes from each rainfed and drought conditions were identified on the basis of drought susceptibility index (DSI). Among them, C-306, FLW-11, IC-3211988, LGM-245, MACS-6145, MACS-6222, VL-907 were showing minimal reduction under both water regimes.
- Analysis of variance for individual environments, pooled over managements and overall pooled indicated significant variation in genotypes and effect of genotypes x environment and genotype x management interaction on each trait.
- High values of all the genetic components (GCV, PCV, heritability and GAM) were reported for all the traits within environments. But when pooled over management, these values ranged between low to moderate for most of the studied traits due to high GXE interaction. Generally, values were lower in stressed conditions than that of irrigated condition. Plant height, peduncle length, spikelet per spike and thousand kernel weight were under additive gene effect and least influenced by GXE interaction. These traits were suitable for indirect selection for grain yield under all three water managements or in a multi-location trial.
- Correlation between yield and studied traits largely varied with environmental and water conditions. From correlation matrix it could be interpreted that shorter plant height, longer grain filling duration, early days to heading, thousand kernel weight (35-40 grams) is the most favorable trait combination for achieving high grain yield under all three water conditions, simultaneously.
- Positive correlation of WSCs with grain yield, biological yield, thousand kernel weight and total number of grains was reported only for drought tolerant genotypes which indicated that higher amount of soluble sugars does not assure higher grain yield under irrigated conditions or in all genotypes with high WSCs. Therefore, opportunities to explore cellular and molecular mechanisms to understand role of WSCs in grain yield are widely open.
- Principal component analysis (PCA) and agglomerative hierarchical clustering by Ward's minimum variance method using Euclidean distance was carried out and significant effect of water managements on PCA and clustering was seen.
- In PCA, first eight components contained maximum information (84.5%) whereas, for rainfed (80.1%) and drought (76.4%) first seven components retained maximum information of original variables. Loading vectors further indicated that all traits were important for genetic variability.

- In cluster analysis genetic material distributed under two major clusters and further divided into eight sub clusters. This indicated a higher degree of genetic variability under all three studied water regimes. Clustering pattern was highly influenced by water managements.
- The most suitable cluster combination for obtaining maximum transgressive segregants was Cluster II and VIII for IR, Cluster I and VII for RF and Cluster I and VI for DT as they had maximum inter-cluster distance among themselves. More interestingly, all of these clusters have drought tolerant genotypes and can be used to improve susceptible genotypes laying within them to get superior allelic combinations.
- 1288986.92 cM of genomic region of bread wheat genome was covered by polymorphic SNPs. 431 stable SNPs for 20 studied traits were identified out of which 77 SNPs were pleotropic for different traits. For example, SNP associated with plant height also associated with peduncle length, spike length, spikelet per spike, biological yield and harvest index. Five SNPs (AX-94583229, AX-94879209, AX-94759517, AX-94887053 and AX-94964616) for fructans and total non-structural carbohydrates, three (AX-94508292, AX-95257620 and AX-94456473) for days to heading and one (AX-94412521) for plant height were most significant.
- In functional annotation of significant SNPs, 249 genes were identified in IWGSC RefSeq. V1.0. Most of these genes were indulged in carbohydrate metabolism and repair mechanisms. Only few genes had stress related domains *viz.* WH_DNA-bd_sf, HSF_DNA_bd, Haem_peroxidase_sf, Scorpion_toxin-like, Scorpion_toxin-like, WD40_repeat, P-loop_NTPase, DNA_mismatch_repair_MutS_sf, MutS2, NB-ARC, NAC_dom and Rx_N_dom.
- 104 *TaFruc* genes transcribing into stable proteins associated with fructans metabolism were identified in *in silico* study. All of these were involved in either hydrolase activities or transferase activities of glycosyl groups of soluble sugars.
- Structure and function of these genes were conserved during the evolution. 106 duplicate gene pairs were reported of which 96 were segmental duplicates. Divergence time of duplicate gene pairs is expected to be ca. 22 MYA. Most of the genes were having abiotic stress responsive *cis*-elements in their promotor regions indicating their importance in stress mechanisms.
- In functional enrichment analysis, major biological processes associated with these genes were carbohydrate storage and response to bacterial/fungal and seed germination. These genes were found to be expressive under different stress conditions, mainly water stress. To facilitate future breeding programs a total of 189 SSR molecular markers and 60 micro RNAs have been predicted successfully.

Conclusions:

All traits studied in the present investigation exhibited certain variability and results from present investigation will facilitate future wheat breeding programs. Genetically diverse genotypes can be used to make more favorable allelic combinations. SNPs identified in this study can be used in genomic assisted plant breeding and development of efficient KASP markers. Newly identified *TaFruc* genes have opened opportunities for researchers to expand their understanding with fructans metabolism in wheat. Henceforth, newly predicted SSR markers and miRNAs can directly be used in molecular breeding programs. The most instant opportunity that opens with this investigation is to validate newly designed SSR markers on different types of genetic materials.

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ANNEXURES

Annexure 1: Information on pedigree of 302 bread wheat genotypes included in present study

Genotypes	SP	Pedigree	Category	Zone	Season	Trait
Agralocal	SP1	Local landrace	IC	---	---	Susceptible to rust
AKAW3717	SP2	--	GS			
AKAW4627	SP2	WH 147/SUNSTAR*/C 80.1	Variety	Maharashtra	---	Drought tolerance
AKW1071	SP2	VEE'S'/ 3FLN/ACC// ANA	Variety	CZ	---	Heat tolerant stock
AKW2862-1	SP2	VEERI-6//DOVE(SIB)/(SIB)BUCKBUCK	GS	---	---	Early and late heat tolerance
Bacanora88	SP2	JUP/BJY//URES	Landraces	---	---	---
BAGESHW ARLOCAL	SP1	LOCAL COLL. UPHILLS	IC	---	---	---
BirsaGehun	SP2	Local collection	IC			
BRW3723	SP2	ACHYUT/BL1887	Variety	BIHAR	TS, RF	---
BWL9022	SP2	C591/PBW343	IG	---	---	---
C306	SP1	REGENT-1974/CH-23//2*C-591/3/P-19/C-281	Variety	NWPZ/NEPZ	---	Drought tolerant
CBW38	SP2	CNDO/R 143/ENTE/MEXI_2/3/Ae.SQUARROSA (TAUS)/4/WEAVER/5/2*PASTOR	Variety	---	---	---
Chirya-3	SP2	CS/AG.CU//GLEN/3/ALD/PVN/4/NINGMAI NO.4/OLESON//ALD/YANGMAI NO.4	Landraces	---	---	---
D134	SP1	RS31/WIS245'S'	Variety	CZ	---	---
DBW107	SP2	TUKURU/INQALAB91	Variety	---	---	---
DBW110	SP2	KIRITATI/4/2*SERI-82*2/3/KAUZ*2/BOBWHITE//KAUZ	Variety	---	---	---
DBW128	SP2	SITE/MO//PASTOR/3/TILHI	IG	---	---	---
DBW129	SP2	PFAU/MILAN/5/CHEN/A.SQUARROSA (TAUS)/BCN/3/VEE#7/BOW/4/PASTOR	IG	---	---	---
DBW155	SP2	HUW548/Mv231-98	IG	---	---	---
DBW16	SP2	RAJ 3765/WR 484//HUW 468	Variety	NEPZ	---	---
DBW17	SP2	CMH-79-A-95/3*CIANO-79//RAJ-3777	Variety	NWPZ	---	Terminal heat tolerance
DBW31	SP2	DBW14/PBW343	GS	---	---	---
DBW39	SP2	ATTILA/HUI	Variety	---	---	---
DBW46	SP2	PBW 343/INQ 21	GS	---	---	---
DBW51	SP2	SITELLA/MILAN	GS	---	---	---
DBW52	SP2	CAL/NH/H567.71/3/SERI/4/CAL/NH/H567.71/5/2*KAUZ/6/PASTOR	IG	---	---	---

DBW-71	SP2	PRINIA/UP-2425				
DBW88	SP2	KAUZ//ALTAR-84/AWNED-ONAS/3/MILAN/KAUZ,MEX/4/HUITES	Variety	---	---	---
DBW90	SP2	HUW-468/WH-730	Variety	---	---	---
DBW98	SP2	PBW65*2/PASTOR//PBW550	IG	---	---	---
Dharwad Dry	SP2	-	IC			
DL1266-5	SP2	SFW/VAISHALI	GS	---	---	---
DL788-2	SP2	K7537/HD2160/ HD2278//L24/K4.14	Variety	CZ	---	---
DPW621-50	SP2	KAUZ//ALTAR-84/(AOS)AWNED-ONAS/3/MILAN/KAUZ/4/HUITES	Variety	---	---	---
FKW1	SP2	UP2338*4/CHINA84-40022	GS	---	---	Resistance to yellow and black rust
FLW-11	SP2	WH 542*/Hobbit	GS	---	---	Multiple rust resistance
FLW29	SP2	PBW343/CAPPELLE DESPREZ/PBW343/Lr28(CS2D2M3/8)F7	GS	---	---	Resistance to brown,yellow and black rust
FLW3	SP2	UP 2338/ China 84-40022	GS	---	---	Resistance to yellow and black rust
FLW5	SP2	UP 2338/ ARKAN	GS	---	---	Resistance to brown and black rust
GL11	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
GL27	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
GL6	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
GW173	SP2	TW-275-7-6-10/LOK-1	Variety	CZ	---	---
GW2002-18	SP2	DL51-91/GW265	GS	---	---	---
GW273	SP2	CPAN-2084/VW-205	Variety	CZ	---	---
GW322	SP2	PBW-173/GW-196	Variety			
GW366	SP2	DL802-3/GW232	Variety	CZ	---	---
GW391	SP2	C-306/TR.SH//HW-2004	IG	---	---	---
GW451	SP2	GW324/4/CROC_1/AE.SQUARROSA(205)//JUP/JY/3/SKAUZ/4/KAUZ/5/GW339	Variety	---	---	---
GW455	SP2	J429/DL790-1//PBW510	IG	---	---	---
GW496	SP2	HD2285/4/CNO/NO//CC/INIA 66/3/KAL/BB	Variety	GUJARAT	---	---
Halna	SP2	Heat Tolerant Stock	GS	---	---	Heat Tolerant stock
HD1981	SP2	E 5557 /HD 845	Variety	NWPZ	---	---
HD2009	SP2	LERMA-ROJO-64-A/NAINARI-60	Variety	NWPZ	---	---
HD2189	SP1	HD1963/HD1931	Variety	PZ	---	---
HD2270	SP2	HD 1962/E4870/ K65/HD 2119 /247	Variety	NWPZ	---	---
HD2285	SP2	HD1912/H D1592/3/HD196211E4870/K65/4/HD2160/5/H D2186	Variety	NWPZ	---	Karnal bunt tolerant

HD2329	SP2	HD 1962/E 4870/3/K 65/5/HD1553/4/UP262	Variety	NWPZ	---	---
HD2385	SP2	HI 687/HD 2268	IG	---	---	---
HD2402	SP2	HD2177//CNO67/BB/3/HD2160/4/HD2236	Variety	NEPZ	---	---
HD2687	SP1	CPAN-2009/HD-2329	Variety	NWPZ	---	---
HD2733	SP2	ATTILA /3/ TUI /CARC // CHEN / CHTO /4/ ATTILA	Variety	NEPZ	TS, IR	---
HD2781	SP2	BOBWHITE/C-306/C-591/HW-2004	Variety	PZ	---	---
HD2824	SP2	PTO-1 / CNO 79 / PRL /GAA /3/HD 1951	Variety	NEPZ	TS, IR	---
HD2888	SP1	C 306/T.sphaerococcum//HW 2004	Variety	NEPZ	---	---
HD2932	SP2	KAUZ/STAR//HD 2643	Variety	CZandPZ	---	---
HD2985	SP2	PBW 343/PASTOR	Variety	---	---	---
HD2987	SP2	HI-1011/HD-2348//MENDOS//IWP-72/DL-153-2	Variety			
HD2997	SP2	BOBWHITE//HD-2285//HD-2444	IG	---	---	---
HD30	SP2	HD-2160/HD-1977//HD-7949/HD-1944/HD-2136	GS	---	---	Karnal bunt resistant
HD3016	SP2	PBW-65/2*PASTOR	IG	---	---	---
HD3043	SP2	PAJONAL/BOBWHITE//OPATA-85*2/3/CROC-1/TR.TA(224)//OPATA-85	Variety	---	---	---
HD3045	SP1	-	Variety			
HD3055	SP2	OASIS/SKAUZ//4*BCM/2*PASTOR	IG	---	---	---
HD3059	SP2	KAUZ//ALTAR-84/(AOS)AWNED-ONAS/3/MILAN/KAUZ/4/HUITE	Variety	---	---	---
HD3071	SP1	BOW/2*C306//HW2004/PBW175	IG	---	---	---
HD3086	SP2	DBW-14/HD-2733//HUW-468	Variety	---	---	---
HD3118	SP2	ATTILA*2/PBW-65//WEEBILL-1*2/TUKURU	Variety	---	---	---
HD3127	SP2	PBW343/CHOIX/Star/3/HEI/3*CNO79//2*SERI	IG	---	---	---
HD3128	SP2	VL849/HW5015	IG	---	---	---
HD3132	SP2	WH542/UP2425	IG	---	---	---
HD3139	SP2	WBLL1//UP2338*2/VIVITSI	IG	---	---	---
HD3146	SP2	HUW510/CBW17	IG	---	---	---
HD4730	SP2	ALTAR84/STINT//SILVER45	IG	---	---	---
HI1500	SP1	HW 2002*2//STREMPALLI/PNC 5	Variety	CZ	---	---
HI1531	SP1	HI 1182/CPAN 1990	Variety	CZ	---	---
HI1544	SP2	HINDI 62/BOBWHITE/CPAN 2099	Variety	CZ	---	---
HI1563	SP2	MACS 2496*2/MC 10	Variety	---	---	---
HI1579	SP2	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	IG	---	---	---

HI1580	SP2	-	Variety			
HI1581	SP2	-	Variety			
Hindi62	SP1	PBW-226/HW-1042//HD-2285	GS	---	---	Heat and drought tolerant
HPW147	SP2	CPAN-1869/HIM-10-BA	Variety	Himachal	---	---
HPW251	SP2	WW-24/LEMHI/P-2-II-149	Variety	NHZ	---	---
HPW266	SP2	CH-01-X/STAR/3/HE-1/3*CIANO-79/2*SERI-82	IG	---	---	---
HPW347	SP2	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	IG	---	---	---
HPW348	SP2	EFED/FINSI	IG	---	---	---
HPW349	SP2	OASIS/SKAUZ//4*BACANORA-88/3/PASTOR/4/KAUZ*2/YACO//KAUZ	Variety	---	---	---
HPW371	SP2	KIRTATI//HUW234+lr34/PRINA	IG	---	---	---
HPW400	SP2	PRL/*2PASTOR	IG	---	---	---
HS295	SP2	CINQUENTENARIO/AZTECA-67//IAS 55/ALONDRA/3/ALONDRA/NAOFEN/4/PAJONAL/PEL-1276.69	Variety	NHZ	LS, RF/LIR	---
HS365	SP2	HS 207 /SONALIKA	Variety	NHZ	---	---
HS490	SP2	HS-364/HPW-114//HS-240/HS-346	Variety	NHZ	---	---
HS542	SP2	MILAN/KAUZ,MEX//PRINIA/3/BABAX	Variety	---	---	---
HS547	SP2	CHIRYA3/HS396	IG	---	---	---
HS562	SP2	OASIS/SUPER-KAUZ//4*BACANORA-88/3/2*PASTOR	Variety	---	---	---
HS577	SP2	HW2045/HS435	IG	---	---	---
HS590	SP2	HS469/DL460	IG	---	---	---
HS592	SP2	CMH82A.1294/2*KAUZ//MUNIA/CHTO/3/MILAN	IG	---	---	---
HS593	SP2	BAVIS	IG	---	---	---
HS594	SP2	HS469/EC463658	IG	---	---	---
HS595	SP2	FRET*2/ELVIRA	IG	---	---	---
HTW-11	SP1	Heat Tolerant Stock	GS	---	---	Heat tolerant stock
HTW-6	SP1	Heat Tolerant Stock	GS	---	---	Heat tolerantstock
HUW12	SP2	NP 876 / CIANO 66	Variety	NEPZ	---	---
HUW206	SP2	KAVKAZ/(SIB)BUHO//KALYANSONA/BLUEBIRD	Variety	NEPZ	---	---
HUW234	SP2	HUW 12* 2 / CPAN 1666// HUW 12	Variety	NEPZ	LS, IR	---
HUW468	SP2	CPAN-1962 / TONI // LIRA's’ / PRL's'	Variety	NEPZ	TS, IR	---
HUW598	SP2	WH581/HUW395//RAJ3765	IG	---	---	---
HUW616	SP2	RAJ-3814/WH-283//HD-2402	IG	---	---	---

HUW661	SP2	W15.92/4/PASTOR/HXL7573/2*BAU/3/WBLL1	IG	---	---	---
HUW675	SP2	ALTAR84/KAUZ//MILAN/HUW510	IG	---	---	---
HUW677	SP2	HUW510/NW1012//HD2189	IG	---	---	---
HUW679	SP1	HUW510/HUW533//PBW476	IG	---	---	---
HW2004	SP2	C 306 *7 //TR 380-14 #7 /3 AG14	Variety	---	---	---
HW5205	SP2	CIANO-67/MARIS-FUNDIN//MONCHO(SIB)/3/SERI-82	IG	---	---	---
HW5216	SP2	PBW343//HW3083	Variety	---	---	---
IC212140	SP2	COLLECTED FROM BARMER	IC	---	---	---
IC212145	SP1	COLLECTED FROM JALOR	IC	---	---	---
IC212151	SP1	COLLECTED FROM BANASKANTHA	IC	---	---	---
IC212161	SP2	COLLECTED FROM JAMNAGAR	IC	---	---	---
IC212182	SP1	COLLECTED FROM SIROHI	IC	---	---	---
IC212190	SP1	COLLECTED FROM JODHPUR	IC	---	---	---
IC296432	SP2	WL 711* 4/ Aegilops geniculata Acc. 3547	GS	---	---	---
IC321856	SP2	SK 11,PISSILOCAL FROM GUNA,MP	IC	---	---	---
IC321866	SP2	SK 21,BROWN SPIKE LOCAL WHEAT,RAISEN,MPP	IC	---	---	---
IC321879	SP2	SK 34,LONG SPIKED LOCAL FROM KASHIPUR,MP	IC	---	---	---
IC321886	SP2	SK 41, LOCAL COLL. FROM BHOPAL,MP	IC	---	---	---
IC321888	SP2	SK 43,DROUGHT TOLERANT LOCAL FROM GUNA,MP	IC	---	---	Drought tolerant local
IC321898	SP1	SK 53,BLACK AWNED PISSI FROM SHIVPURI,MP	IC	---	---	---
IC321899	SP2	SK 54,RAIFED LOCAL WHEAT FROM BHATARWAR,MP	IC	---	---	---
IC321905A	SP1	SK 60,OLD CULTIVAR FROM GUNA,MP	IC	---	---	---
IC321913	SP1	SK 68,TALL BLACK AWNED DURUM FROM SIRSA VILL.MP	IC	---	---	---
IC321931	SP2	SK 86,LAL PISSI FROM ,GUNA,MP	IC	---	---	---
IC321946	SP2	SK 101,DWARF WHEAT FROM MORAGAON,ASSAM	Landraces	---	---	---
IC321950	SP2	SK 105,IMPROVED VAR. FROM DOLOIGAON,ASSAM	Landraces	---	---	---
IC321951	SP2	SK 106,OLD DURUM VAR. FROM SHILLOGNI,ASSAM	IC	---	---	---
IC321958	SP1	SK 113,DESI WHEAT FROM RAIBENGIA VILL.,ASSAM	IC	---	---	---
IC321988	SP1	SK 143,CHURI GEHUN FROM JOSHIMATH,UTTARANCHAL	IC	---	---	---
IC322011A	SP1	SK 166, DESI WHEAT FROM JOSHIMATH	IC	---	---	---
IC322016	SP2	SK 171, LOCAL WHEAT FROM JOSHIMATH	IC	---	---	---
K0617	SP2	HD 2733/K 9423/K 9351	IG	---	---	---

K1114	SP2	HP1731/HUW234	IG	---	---	---
K1204	SP2	K8464/PBW343	IG	---	---	---
K307	SP2	K 8321/UP 2003	Variety	NEPZ	---	---
K68	SP1	NP-773/K-13	Variety	Uttar Pradesh	---	---
K8020	SP2	KALYANSONA/HD 1982	Variety	NEPZ	---	---
K8027	SP2	NP875/4/N10B/Y53//Y50/3/KT54B/5/2*K852	Variety	NEPZ	TS, RF	---
K8962	SP2	K 7401 /HD 2160	Variety	NEPZ	---	---
K9107	SP2	K-8101/K-68	Variety	NEPZ	---	Karnal bunt tolerant
K9351	SP2	K72/K8027//K72	Variety	Uttar Pradesh	---	---
KB2012-03	SP2	PBW343*6/KBRL22	IG	---	---	---
KHARCHIA65	SP1	KHARCHIA LOCAL/ EG 953	Variety	ALL ZONES	---	---
KharchiaLocal	SP1	Salt Tolerant collection	IC	---	---	Salt tolerant collection
KRL19	SP2	PBW255/KRL 1-4	Variety	ALL ZONES	---	Salt tolerant collection
KRL35	SP2	HD-2160/KRL-1-4 (KHARCHIA-LOCAL/WL-711)	GS	---	---	Salt tolerant and water lodging tolerant
L2(Ad)	SP1	LOCALCOLL.LAHAUL/SPITI	IC	---	---	---
L25(AMB)	SP1	LOCALCOLL.LAHAUL/SPITI	IC	---	---	---
L5(AL)	SP1	LOCALCOLL.LAHAUL/SPITI	IC	---	---	---
LALBAHADUR	SP2	S-54723/RS-31-1	Variety	NWPZ	---	---
LBRL4	SP2	BREEDSEL-172/PC-OE-BW-22	GS	---	---	Leaf blight resistant
LGM110	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM130	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM133	SP2	LOCAL COLL.GUJARAT	Landraces	---	---	---
LGM134-B	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM135	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM162	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM191	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM205	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM225-1	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM225-R	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM238	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
LGM245	SP1	LOCAL COLL.GUJARAT	IC	---	---	---

LOK-1	SP2	S308 / S331	Variety	CZ	TS/LS, IR	---
Lok41	SP2	S308/S331	IG	---	---	---
Lok44	SP2	---	IG	---	---	---
Lok54	SP2	LOK1/J.24/SONALIKA"S"//HW2006/RW2358/HW2002	IG	---	---	---
MACS6145	SP1	C306+LR28	Variety	NEPZ	---	---
MACS6222	SP2	HD 2189*2//MACS 2496	Variety	PZ	---	---
MACS6273	SP2	KAUZ*2/CHEN//BCN/MILAN	IG	---	---	---
MACS6354	SP2	-				
MACS6507	SP2	WG2780/JB1002	IG	---	---	---
ML1194	SP2	BB-ND/NO 66-P1+C81	GS	---	---	Resistant to loose smut ,karnal bunt, stripe and leaf rust
MP1201	SP2	CMH-82-A-1294/2*KAUZ//MUNIA/CHORLITO/3/MILAN	Variety	---	---	---
MP1202	SP2	CMH-82-A-1294/2*KAUZ//MUNIA/CHORLITO/3/MILAN	Variety	---	---	---
MP1279	SP2	GW322/HW2451	IG	---	---	---
MP3211	SP2	SUPER-KAUZ/FLYCATCHER	Variety	---	---	---
MP3288	SP2	DOVE/BUC/DL 788-2	Variety	CZ	TS, RF	---
MP4010	SP2	ANGOSTURA 88	Variety	CZ	---	---
MP4106	SP2	CHIBIA//PRL11/CM65531	Variety	Madhya Pradesh	LS, IR	---
NARMADA4	SP1	GB-AVS/N14/3/PW5//TH/NP165	Variety	Madhya Pradesh	---	---
NB-29-13-5-9	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
NB-29-6-2-12	SP1	LOCAL COLL.GUJARAT	IC	---	---	---
NI5439	SP2	RFPM-80/3*NP-710	Variety	PZ	---	---
NIAW34	SP2	CNO 79/PRL “S”	Variety	MAH	---	---
NIAW917	SP2	GW 244/BOB WHITE	Variety	PZ	TS, IR	---
NP846	SP2	RIO-NEGRO/NP-760				
NP852	SP2	KENYA-FARMER/2*NP-761	Variety	NEPZ	---	---
NW2036	SP2	BOBWHITE/CROW/BUCKBUCK/PAVON-76	Variety	NEPZ	---	---
NW4035	SP2	WEAWER/WL-2926//SW-89-3064	IG	---	---	---
PBW138	SP1	WG-387/HD-2177	Variety	PUNJAB	---	---
PBW175	SP2	HD 2160 /WG 1025	Variety	NWPZ	---	---

PBW343	SP2	NORD-DESPREZ/VG-1944//KALYANSONA//BLUEBIRD/3/YACO(SIB)/4/VEERY-5	Variety	NWPZ	---	Tolerant to lodging
PBW373	SP2	ND/VG9144 //KAL/BB/3/YCO”S’/4/VEE#5 'S’	Variety	NWPZ	LS, IR	---
PBW396	SP2	CIANO-67/(MFD)MARIS-FUNDIN//MONCHO(SIB)/3/SERI-82	Variety	NWPZ	---	---
PBW502	SP2	W-485/PBW-343//RAJ-148	Variety	NWPZ	---	Resistant to karnal bunt
PBW550	SP2	WH-594/RAJ-3858//W-485	Variety	NWPZ	---	---
PBW579	SP2	W7554/PBW427	IG	---	---	---
PBW590	SP2	WH 594/RAJ3814//W 485	Variety	NWPZ	LS, IR	---
PBW596	SP2	PBW-343/DHARWAD-DRY//PBW-343	Variety	PZ	---	---
PBW610	SP2	W 13334/IBWSN 92//PBW 496	IG	---	---	---
PBW621	SP2	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	Variety	---	---	---
PBW644	SP2	PBW-175/HD-2643	Variety	---	---	---
PBW65	SP2	USA 255/K 816 /3/ WL 202	Variety	NWPZ	---	---
PBW658	SP2	CHINESE-SPRING/TH.SC//3*PAVON-76/3/MIRLO/BUCKBUCK/4/MILAN/5/TILHI	Variety	---	---	---
PBW660	SP2	WG 6761 / WG 6798	Variety	---	---	---
PBW674	SP2	-	Variety			
PBW681	SP2	UP2338/KALYANSONA	IG	---	---	---
PBW689	SP2	PBW442/WH576//DWR232	IG	---	---	---
PBW692	SP2	INQUALAB91*3/TUKURU//DBW18	IG	---	---	---
PBW697	SP2	DBW18/3WL711-AE. OVATA/CS(S)//WL711NN/4/DBW18	IG	---	---	---
PBW698	SP2	BW9250*3/YR10/6*AVOCET/3/BW9250*3//YR15/6*AVOCET	IG	---	---	---
PBW702	SP2	PBW533//YR15/6*AVOCET/3/PBW533	IG	---	---	---
PBW703	SP2	BW9250*3/YR10/6*AVOCET/3/BW9250*3//YR15/6*AVOCET	GS	---	---	---
PBW704	SP2	HP1887/PBW565	IG	---	---	---
PBW706	SP2	MINO/898.97	IG	---	---	---
PBW722	SP2	PBW343+Lr57/Yr40+Lr37+Yr17	IG	---	---	---
PBW723	SP2	PBW343+Lr57/Yr40+Yr15	Variety	---	---	---
Pusa2019A	SP2	CS CMS*7/HW2019	GS	---	---	---
PWR4099	SP2	CBHW-CHN-89-R-4294O-CHN-S-2BV-97-(EC-4141480)	GS	---	---	---
RAJ3765	SP2	HD 2402/VL639	Variety	NW/NEPZ	---	---
RAJ4037	SP2	DL 788-2/RAJ 3717	Variety	CZ	---	---
RAJ4083	SP2	PBW-343/UP-2442//WR-258/UP-2425	Variety	PZ	---	---
RAJ4124	SP2	BUCK-PANGARE(SIB)//CIANO-67(SIB)/GALLO/HD-30//VL-804	IG	---	---	---

RAJ4356	SP2	---	IG	NEPZ	---	---
RD20		PBW 34/DCB 25	GS	---	---	---
RSP561	SP2	HD2637/Ae. crassa// HD2687	Variety	---	---	---
SAFEDLERMA	SP2	Y50//N10B/3/LR 52/3*LR	Variety	NPZ	---	---
SKW441	SP2	RAYON/PASTOR	IG	---	---	---
SONALIKA	SP2	II-53-388/ANDES//(SIB)PITIC-62/3/LERMA-ROJO-64	Variety	NW/NEPZ	---	Salt tolerant
SONORA64	SP2	YAKTANA-54//NORIN-10/BREVOR/3/2*YAQUI-54	Variety	NEPZ/CZ	---	---
T808	SP2	Local Landrace	IC	---	---	---
UAS304	SP2	SERI/CEP80120//KAUZ/PBW343	Variety	---	---	---
UAS305	SP2	CMH-84-3379/CMH-78-578//MILAN/HD-2189	IG	---	---	---
UAS316	SP2	PASTOR/DHARWAD DRY/DWR39	IG	---	---	---
UAS320	SP2	UAS-257//GW-322/DWR-195	GS	---	---	---
UP115	SP2	NP-887/E-4870//UP-302	Variety	NEPZ	---	---
UP2338	SP2	UP 368 /VL 421//UP 262	Variety	NWPZ	TS/LS, IR	---
UP2425	SP2	HD 2320/UP 2263	Variety	NWPZ	---	---
UP262	SP2	SONALIKA(S-308)/BAJIO-66	Variety	NEPZ	---	---
UP2691	SP2	UP2377/HW1085	IG	---	---	---
UP2855	SP2	PBW565/UP2565	IG	---	---	---
UP2864	SP2	PBW573/UP2425	IG	---	---	---
UP2890	SP2	INQUALAB*2/TUKURU//UP2382	IG	---	---	---
UP2891	SP2	HUW562/(CROC_1/A.SQU(205)//BORL95/3/2*MILAN	IG	---	---	---
VL1004	SP2	RAJ3765/BLUEBOYII/RAJ3765	IG	---	---	---
VL3004	SP2	HD2844/PBW486	IG	---	---	---
VL639	SP2	VL421/CPAN1535	GS	---	---	Loose smut resistant
VL738	SP2	NS12.07 /LIRA”S” //VEE ‘S”	Variety	NHZ	---	---
VL798	SP2	CPAN-3004/CPAN-1922/PBW-65	GS	---	---	Hill bunt resistant
VL802	SP2	CPAN3018/CPAN3004//PBW65	Variety	---	---	---
VL804	SP2	CPAN 3018 /CPAN 3004 //PBW 65	Variety	NHZ	---	---
VL892	SP2	WH 542/PBW 226	Variety	NHZ	---	---
VL900	SP2	KAUZ/3/MYNA/BUL/FLK/4/MILAN	IG	---	---	---
VL907	SP2	DYBR-1982-83/842-ABVD-50/VW-9365//PBW-343	Variety	NEPZ	---	---

VL946	SP2	HW 2045/ VW 0185	IG	---	---	---
VL967	SP2	SHARP/3/PRL/SARA/TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ#4	IG	---	---	---
WBM1587	SP2	MILAN/SHA7	GS	---	---	Yellow rust resistant
WBM1591	SP1	PYN/BAU//MILAN	GS	---	---	Yellow rust resistant
WH1046	SP2	VEERY/PAJONAL//2*HUITLE/3/WH-756	IG	---	---	---
WH1061	SP2	WEAWER/WL 2926//SW 89.3064	IG	---	---	---
WH1080	SP2	21STSAWSN151	Variety	NWPZ	TS, RF	---
WH1097	SP2	ATILLIA/BABAX//PASTOR	IG	---	---	---
WH1100	SP2	PBW 65/ 2*PASTOR	IG	---	---	---
WH1105	SP2	MILAN/S-87230//BABAX	Variety	---	---	---
WH1124	SP2	MUNIA/CHORLITO//AMSEL	Variety	---	---	---
WH1126	SP2	WBLL 1*2/VIVITSII	IG	---	---	---
WH1129	SP2	CS/TH.CS//3*PVN/3/MIRLO/BUC/4/MILAN/5/TILHI	IG	---	---	---
WH1132	SP2	PBW65*2/PASTOR	IG	---	---	---
WH1138	SP2	PBW65*2/PASTOR	IG	---	---	---
WH1142	SP2	CHEN/TR.TA//FLYCATCHER/3/2*WEAVER	Variety	---	---	---
WH1154	SP2	WH337/HD2255//RAJ3077	IG	---	---	---
WH1156	SP2	TILHI/PASTOR	IG	---	---	---
WH1157	SP2	MUNIA/CHTO/AMSEL	IG	---	---	---
WH1164	SP2	RL6043/4*NAC//2*PASTOR	IG	---	---	---
WH147	SP2	E 4870/C286/C273 /4/S339/PV18	Variety	CZ	---	Salt tolerant
WH423	SP2	WL 371-M 164 x Raj 842	IG	---	---	---
WH542	SP2	JUPATECO-73/BLUEJAY//URES-81	Variety	NWPZ	---	---
WH595	SP2	PRL 6045/NAC 76	GS	---	---	Stripe rust resistant
WH730	SP2	CPAN 2092/Improved Lok-1	IG	---	---	Heat tolerantstock
WL3526	SP2	HD2009/WG 377	GS	---	---	Loose smut ,karnal bunt, stripe leaf resistant
WL711	SP2	SONALIKA/CHRIS//KALYANSONA	Variety	NWPZ	---	---

Annexure 2: Descriptive statistics of pheno- phenological traits observed in bread wheat (*Triticum aestivum* L.) under different environments and water regimes

Traits	**Statistics**	**Environments**										**Pooled**			**BLUEs**		
		E01	**E02**	**E03**	**E04**	**E05**	**E06**	**E07**	**E08**	**E09**	**E10**	**IR**	**RF**	**DT**	**IR**	**RF**	**DT**
DTH	*Min*	81.50	68.00	73.50	51.00	87.00	67.20	78.50	56.00	77.00	67.00	80.50	69.57	54.25	80.50	69.92	54.25
	Max	103.00	85.50	101.50	79.00	105.22	90.50	103.00	75.00	107.00	92.00	101.00	86.50	75.50	101.00	86.65	75.50
	Mean	91.74	77.53	87.93	62.89	99.52	81.97	90.44	66.02	87.69	76.25	91.47	78.58	64.47	91.47	78.61	64.46
	σ	3.97	3.03	5.16	4.83	2.04	4.34	5.25	3.87	6.21	5.51	3.64	3.51	3.89	3.64	3.51	3.89
DTA	*Min*	89.50	74.50	80.00	59.00	96.00	74.50	86.00	60.00	83.00	73.00	88.60	75.67	60.25	88.60	75.99	60.22
	Max	110.00	93.00	109.50	85.00	113.50	98.50	111.00	81.50	113.50	98.00	108.70	93.50	81.00	108.70	93.92	80.95
	Mean	99.20	83.43	95.38	69.90	106.81	89.88	97.85	71.94	95.21	82.73	98.89	85.35	70.93	98.89	85.35	70.93
	σ	4.18	2.96	5.29	4.81	2.28	4.40	5.26	3.93	6.29	5.56	3.64	3.53	3.87	3.64	3.54	3.86
DTM	*Min*	129.00	105.00	126.28	90.00	134.00	112.00	131.50	92.88	118.00	102.00	130.90	109.00	92.25	130.85	109.00	92.25
	Max	138.50	124.00	143.00	113.00	150.00	124.50	145.00	112.50	151.00	131.00	142.76	123.83	112.00	142.69	123.91	112.00
	Mean	132.78	112.62	135.64	99.76	140.79	118.33	139.18	103.21	133.04	112.50	136.29	114.48	101.50	136.28	114.48	101.49
	σ	1.60	3.60	3.01	4.39	3.10	2.53	1.96	3.71	6.54	5.33	2.30	2.68	3.63	2.30	2.70	3.62
GFD	*Min*	21.00	20.50	25.50	24.50	24.50	22.00	31.00	17.50	27.00	21.00	29.70	22.33	23.00	29.62	22.11	23.00
	Max	42.00	41.00	53.00	40.00	43.26	42.00	52.50	39.50	51.50	40.50	44.50	39.67	38.75	44.36	39.63	38.75
	Mean	33.58	29.19	40.26	29.86	33.71	28.46	41.32	31.27	37.83	29.77	37.34	29.14	30.57	37.34	29.14	30.56
	σ	3.81	3.91	4.79	2.27	3.24	3.77	4.75	2.42	3.84	3.58	2.66	2.91	1.99	2.66	2.95	1.99
NOT	*Min*	6.99	5.83	6.96	5.17	7.44	4.25	6.13	5.74	7.80	5.50	8.66	5.83	5.75	8.65	5.83	5.77
	Max	14.43	9.50	15.32	8.76	13.88	14.13	15.25	9.80	15.06	10.50	12.91	9.68	9.52	12.94	9.68	9.25
	Mean	11.35	7.64	10.65	6.80	10.55	7.74	10.57	7.31	10.85	7.87	10.79	7.75	7.06	10.79	7.75	7.06
	σ	1.16	0.58	1.80	0.65	1.43	1.55	1.75	0.78	1.49	0.95	0.78	0.65	0.60	0.78	0.65	0.60
PH	*Min*	68.48	52.92	69.25	52.41	77.85	66.15	67.65	33.64	78.39	74.52	76.01	64.53	49.32	76.07	64.58	49.36
	Max	154.77	129.60	155.00	120.44	165.15	133.95	148.05	104.80	132.06	119.34	147.67	120.24	112.62	147.66	120.41	112.66
	Mean	108.36	85.09	109.05	74.50	108.34	96.82	104.71	61.11	99.37	92.22	105.97	91.36	67.76	105.96	91.36	67.81
	σ	16.03	13.24	15.38	10.26	15.17	13.33	14.89	11.44	10.31	9.20	12.76	10.92	9.98	12.76	10.93	9.92
PL	Min	15.84	13.23	19.78	3.68	22.50	20.83	14.21	4.25	20.21	16.34	24.65	18.21	5.03	24.73	18.39	5.04
	Max	69.63	47.52	55.76	25.51	54.90	44.06	56.25	20.42	49.28	41.13	51.44	42.06	21.68	51.47	41.86	21.67
	Mean	36.05	26.40	34.86	14.08	37.04	30.47	36.24	10.14	34.28	27.69	35.69	28.18	12.09	35.69	28.18	12.11
	σ	8.70	6.18	6.25	4.26	5.89	4.33	5.78	2.79	4.38	4.08	4.95	3.87	3.03	4.94	3.86	3.02

DTH: days to heading; **DTA:** Days to anthesis; **DTM:** days to maturity; **GFD:** Grain filling duration; **NOT:** numbers of tillers; **PH:** plant height(cm); **PL:** peduncle length (cm); **SL:** spike length (cm); **IR:** irrigated; **RF:** rainfed; **DT:** Drought; **BLUEs:** best linear unbiased estimates; ***Mean*:** Mean; **σ:** standard deviation; **SEm**: standard error, **'-'**: data not recorded

Traits	Statistics	Environments										Pooled			BLUEs		
		E01	**E02**	**E03**	**E04**	**E05**	**E06**	**E07**	**E08**	**E09**	**E10**	**IR**	**RF**	**DT**	**IR**	**RF**	**DT**
SL	*Min*	8.53	5.54	7.75	4.97	7.01	6.15	6.98	3.63	-	-	8.41	5.84	4.30	8.40	5.77	4.30
	Max	19.97	13.23	18.52	9.84	20.46	17.85	14.40	9.21	-	-	17.60	14.87	9.43	17.62	14.80	9.43
	Mean	11.60	8.74	12.10	7.14	12.07	11.00	9.80	6.66	-	-	11.39	9.87	6.90	11.40	9.87	6.90
	σ	1.36	1.03	1.51	0.93	1.48	1.27	1.26	0.90	-	-	1.11	1.02	0.81	1.11	1.02	0.81
SPS	*Min*	15.00	9.00	15.83	9.98	16.00	15.00	12.12	10.83	-	-	15.80	13.50	10.83	15.80	13.51	10.83
	Max	27.33	24.00	25.67	17.40	26.00	26.00	27.32	18.27	-	-	25.63	23.17	17.82	25.63	23.16	17.82
	Mean	20.24	18.91	20.85	13.88	21.47	19.72	20.92	14.26	-	-	20.87	19.31	14.07	20.87	19.31	14.07
	σ	2.02	2.13	1.73	1.31	1.90	1.94	2.07	1.42	-	-	1.63	1.69	1.28	1.62	1.69	1.28
BY	*Min*	20.25	6.60	20.55	7.09	25.20	11.92	13.23	3.21	27.60	8.83	28.50	10.45	6.85	28.44	10.61	6.85
	Max	80.75	22.38	76.25	28.36	66.38	35.61	80.00	19.58	83.67	34.18	60.91	27.41	20.64	60.86	27.38	20.64
	Mean	46.27	13.86	42.51	16.11	42.25	19.13	41.23	10.36	42.71	21.60	42.99	18.20	13.23	42.99	18.20	13.24
	σ	12.30	3.08	9.44	3.86	8.63	3.79	13.76	3.07	7.74	4.35	5.29	2.55	2.55	5.29	2.55	2.55
GY	*Min*	9.24	5.24	5.80	4.68	8.70	4.89	3.50	3.47	8.85	4.88	8.98	6.27	4.80	8.94	6.23	4.81
	Max	30.43	11.09	29.31	11.53	24.04	14.93	31.69	11.66	24.70	15.50	21.11	12.86	10.97	22.50	12.84	10.97
	Mean	18.21	8.29	17.09	7.40	16.08	9.96	16.07	7.14	15.72	10.59	16.48	9.61	7.27	16.63	9.61	7.27
	σ	4.28	1.19	4.19	1.32	2.80	1.79	5.78	1.61	2.41	2.16	1.87	1.08	1.10	2.07	1.08	1.10
HI	*Min*	24.32	21.34	23.69	20.64	26.80	18.95	24.38	21.91	25.42	18.84	29.87	22.26	25.46	30.19	25.39	22.26
	Max	54.49	50.91	56.44	43.97	50.64	61.76	56.62	49.83	45.97	44.29	45.09	41.61	45.53	45.85	45.69	41.61
	Mean	40.27	35.95	40.51	31.25	38.68	35.63	39.13	33.00	37.38	32.88	38.89	32.13	34.82	39.19	34.82	32.12
	σ	5.62	5.32	6.13	3.79	4.53	6.34	5.22	4.30	3.73	4.01	2.80	3.31	3.54	2.93	3.55	3.31
TKW	*Min*	25.60	25.65	26.78	24.45	29.83	27.78	25.45	23.54	26.81	21.67	30.14	26.69	24.49	30.25	26.73	24.49
	Max	54.70	44.55	53.86	45.93	56.35	48.72	52.48	46.63	52.53	42.00	50.39	44.40	45.34	50.52	44.35	45.34
	Mean	42.03	35.24	42.07	35.13	42.93	39.21	41.01	34.65	40.48	32.36	41.70	35.60	34.88	41.70	35.60	34.88
	σ	5.35	4.00	4.34	4.04	5.07	4.25	4.79	3.96	4.79	4.26	3.63	3.30	3.85	3.62	3.30	3.85
TNG	*Min*	207.61	171.15	150.09	121.14	223.85	138.39	80.50	86.39	238.09	160.63	284.45	192.22	130.79	280.38	192.12	130.86
	Max	793.06	387.85	684.75	350.88	642.01	382.65	874.73	388.23	551.57	505.80	568.89	353.17	336.51	595.87	353.15	336.61
	Mean	438.21	240.07	408.50	216.35	378.33	255.74	401.54	212.40	391.92	328.32	401.74	274.71	214.53	403.69	274.71	214.55
	σ	105.12	34.90	97.60	41.37	63.60	44.24	155.97	52.44	62.66	61.61	48.99	30.07	36.78	53.89	30.06	36.80

SL: spike length(cm); **SPS**: numbers of spikelet per spike; **BY:** biological yield per plant (gm); **GY:** grain yield per plant; **HI:** harvest index (%); **TKW:** thousand kernel weight(gm); **TNG:** total number of grains per plant; **IR:** irrigated; **RF:** rainfed; **DT:** Drought; **BLUEs:** best linear unbiased estimates; ***Mean*:** mean; **σ:** standard deviation; **‘-‘**: data not recorded

Annexure 3: Analysis of variance for studied trait under individual environments (E01-E10)

ENV	Source	DF	DTA	DTH	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
E01	*Rep*	1	0.76	0.83	976.53	922.87	1148.62	817.46	1.14	668.88	1446.57	597.1	97.59	1.1	1.9	80542.55
	Block	29	26.13	23.04	6.69	25.69	3.84	218.59	140.67	3.15	6.5	359.32	48.71	67.05	107.22	38385.71
	Genotype	301	33.3**	29.92**	4.55**	27.77**	2.37**	499.7**	139.83**	3.49**	7.66**	276.7**	33.16**	60.85**	48.78**	19181.02**
	Error	272	7.08	5.47	1.25	8.37	0.55	45.6	12.42	0.87	1.83	59.26	9.45	32.41	9.75	6439.9
E02	*Rep*	1	21.74	16.92	4863.64	5535.78	148.72	59818.75	37.18	0.06	2328.56	6.79	0.04	35.69	7552.88	362115.4
	Block	29	55.2	1772.96	20.63	36.39	0.25	149.32	53.83	1.8	8.87	42.56	2.06	62.79	24.16	3007.34
	Genotype	301	15.03**	4573.72**	24.64**	31.18**	0.66**	342.54**	73.53**	2.05**	8.53**	53.86**	2.67**	55.09**	30.64**	2226.94**
	Error	272	4.51	1144.54	7.62	12.75	0.19	91.4	13.7	0.66	2.65	12.05	0.67	31.36	9.28	1079.06
E03	*Rep*	1	264.9	294.84	2442.52	4314.57	892.21	6.22	23.52	10.09	674.25	709.03	0.01	719.63	767.11	66812.4
	Block	29	20.84	24.08	9.12	21.44	3.19	241.01	32.27	1.01	3.58	90.52	16.07	66.42	31.08	10031.37
	Genotype	301	54.71**	51.42**	17.86**	45.14**	6.29**	453.56**	75.57**	4.52**	5.78**	177.55**	34.26**	72.58**	35.69**	18484.04**
	Error	272	7.38	5.9	4.04	10.95	1.27	41.59	8.31	0.39	1.45	58.73	8.25	29.69	9.44	5116.51
E04	*Rep*	1	3645.59	888.36	3489.65	856.61	133.03	26760.83	3341.3	228.08	946.35	628.12	697.67	6213.8	3740.68	1299527
	Block	29	27.95	24.18	14.03	6.77	0.76	143.04	22.56	1.38	2.15	39.71	1.88	22.62	19.11	2901.87
	Genotype	299	44.66**	44.5**	37.73**	9.76**	0.79**	200.06**	34.99**	1.6**	3.28**	64.1**	3.38**	27.35**	31.25**	3266.02**
	Error	270	6.48	7.81	6.1	1.2	0.22	35.95	6.8	0.34	0.78	13.97	0.91	7.8	6.28	1160.89
E05	*Rep*	1	487.97	530.11	268.66	401.82	582.05	31.74	56.1	3.57	1318.03	3480.24	1320.51	1063.29	15.38	770135
	Block	29	3.9	5.14	23.1	21.87	2.7	265.05	36.27	2.76	4.18	112.17	11.72	42.1	46.24	10469.17
	Genotype	301	10.17**	7.94**	17.56**	20.17**	3.92**	440.58**	67.47**	4.18**	7.02**	140.52**	14.85**	39.1**	48.77**	7475.54**
	Error	272	1.76	1.21	4.9	8.55	1.05	35.65	11.7	0.71	1.73	35.55	2.41	24.19	13.32	2561.68
E06	*Rep*	1	233.94	209.24	6.36	189.71	1020.17	405.42	14.93	7.74	0.24	0.5	1435.15	17676.26	30.35	863103.8
	Block	29	51.29	1339.7	33.55	13.7	2.49	323.58	28.35	1.44	3.91	48.19	5.4	25.63	30.58	3471.19
	Genotype	301	35.5**	10398.29**	11.29**	28.41**	4.69**	341.04**	36.05**	3.14**	7.36**	63.02**	6.05**	80.4**	34.22**	3758.32**
	Error	272	9.04	2117.15	3.54	8.41	1.42	96.26	8.17	0.66	2.32	28.76	1.78	21.16	10.58	1553.43

ENV	**Source**	**DF**	**DTA**	**DTH**	**DTM**	**GFD**	**NOT**	**PH**	**PL**	**SL**	**SPS**	**BY**	**GY**	**HI**	**TKW**	**TNG**
E07	*Rep*	1	174.02	200.73	512.16	89.1	1294.73	10.53	284.29	433.12	1665.94	1262.56	260.24	10.24	2960.72	20718.23
	Block	29	25.06	25.54	3.65	23.85	5.23	280.58	38.87	1.57	6.06	370.44	52.55	41.22	48.83	36232.79
	Genotype	301	53.81**	53.47**	7.51**	44.41**	5.77**	418.83**	63.86**	3.07**	8.28**	348.41**	62.19**	52.44**	42.84**	45536.39**
	Error	272	7.86	6.57	1.89	9.24	1.3	61.6	7.33	0.48	1.95	68.76	7.55	23.11	8.61	5412.12
E08	*Rep*	1	2488.54	13326.6	3715.24	2968.96	155.07	47808.37	1490.93	57.34	798.06	5370.16	365.79	420.36	5088.66	1012673
	Block	29	19.2	22.4	10.39	7.22	1.4	296.94	12.47	1.15	3.84	88.1	5.66	27.53	21.54	3796.1
	Genotype	301	28.58**	30.03**	27.38**	11.26**	1.11**	243.48**	14.79**	1.57**	3.83**	82.94**	4.79**	35.76**	29.63**	5259.65**
	Error	272	4.5	8.82	5.98	3.4	0.27	64.15	4.47	0.49	1.1	23.89	1.07	13.63	4.75	1319.45
E09	*Rep*	1	4230.47	4283.56	1313.31	6168.36	809.88	25028.25	341.66	-	-	12557.24	1083.38	444.95	2690.25	98963.94
	Block	29	36.99	33.19	55.51	46.55	8.37	192.69	44.93	-	-	227.82	22.72	26.14	27.69	11761.96
	Genotype	301	76.31**	74.65**	82.39**	25.89**	3.77**	197.05**	35.38**	-	-	100.62**	9.56**	26.81**	44.02**	6817.71**
	Error	272	10	8.06	10.75	7.73	0.73	32.93	7.88	-	-	25.1	1.79	14.37	7.67	1665.52
E10	*Rep*	1	294.49	5195.72	6755.63	4229.14	322.94	36469.47	4254.46	-	-	1467.87	1808.78	8953.41	7835.47	180692.3
	Block	29	26.32	32.68	31.79	21.27	2.8	264.43	32.7	-	-	166.28	18.35	46.92	46.29	10162.5
	Genotype	301	60.58**	58.9**	54.99**	24**	1.56**	149.49**	30.9**	-	-	72.19**	7.91**	29.07**	32.83**	6869.17**
	Error	272	19.94	9.07	13.1	5.63	0.45	48.37	7.41	-	-	31.69	2.35	10.41	9.55	3179.03

p>0.5, **p>0.01, ***p0.001

Annexure 4: **Estimates of genetic variability, heritability and genetic advance for different traits in studied bread wheat (*Triticum aestivum* L.) genotypes under different environments**

Env	Statistic	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
E01	*Mean*	91.74	99.20	132.78	33.59	11.35	108.38	36.06	11.60	20.24	46.29	18.21	40.27	42.04	438.17
	σ^2_g	12.98	13.85	1.91	10.14	1.06	233.65	68.33	1.44	3.22	117.87	12.89	14.93	21.68	7202.85
	σ^2_e	5.48	7.10	1.23	8.52	0.56	45.45	12.24	0.85	1.75	58.76	9.30	32.54	9.65	6298.52
	σ^2_p	15.72	17.40	2.52	14.40	1.34	256.38	74.45	1.86	4.09	147.25	17.54	31.20	26.51	10352.11
	GCV	3.93	3.75	1.04	9.48	9.06	14.10	22.93	10.33	8.86	23.46	19.72	9.60	11.08	19.37
	PCV	4.32	4.21	1.20	11.30	10.19	14.77	23.93	11.76	10.00	26.22	23.00	13.87	12.25	23.22
	GA	6.74	6.84	2.47	5.50	1.88	30.06	16.31	2.17	3.28	20.01	6.34	5.50	8.68	145.83
	GAM	7.35	6.90	1.86	16.38	16.57	27.74	45.24	18.68	16.19	43.23	34.82	13.67	20.64	33.28
	h^2	82.57	79.61	75.66	70.41	78.94	91.14	91.78	77.10	78.63	80.05	73.49	47.84	81.80	69.58
	LSD	4.63	5.29	2.19	5.79	1.48	13.50	7.05	1.82	2.60	15.41	6.14	11.33	6.31	159.39
	CV	2.55	2.69	0.83	8.69	6.61	6.22	9.70	7.96	6.53	16.56	16.75	14.17	7.39	18.11
E02	*Mean*	77.54	83.44	112.62	29.20	7.64	85.09	26.40	8.74	18.91	23.90	8.29	35.95	35.24	240.07
	σ^2_g	5.78	5.49	9.20	8.81	0.24	130.86	31.08	0.73	3.16	22.18	1.08	12.03	11.31	667.98
	σ^2_e	4.21	4.53	7.56	13.32	0.19	88.89	13.77	0.66	2.66	11.97	0.66	31.99	9.36	1047.61
	σ^2_p	7.88	7.76	12.98	15.47	0.33	175.31	37.97	1.06	4.49	28.16	1.41	28.02	16.00	1191.79
	GCV	3.10	2.81	2.69	10.17	6.41	13.44	21.12	9.76	9.40	19.70	12.52	9.65	9.55	10.77
	PCV	3.62	3.34	3.20	13.47	7.56	15.56	23.34	11.78	11.21	22.20	14.31	14.73	11.35	14.38
	GA	4.24	4.06	5.26	4.61	0.85	20.36	10.39	1.46	3.07	8.61	1.87	4.68	5.83	39.86
	GAM	5.47	4.87	4.67	15.80	11.18	23.93	39.36	16.67	16.24	36.02	22.57	13.02	16.54	16.60
	h^2	73.28	70.79	70.86	56.94	71.71	74.65	81.86	68.68	70.35	78.75	76.57	42.93	70.73	56.05
	LSD	4.20	4.35	5.41	7.25	0.86	18.56	7.44	1.62	3.23	6.87	1.60	11.19	6.02	63.97
	CV	2.65	2.55	2.44	12.50	5.69	11.08	14.06	9.32	8.63	14.48	9.79	15.73	8.68	13.48

$\boldsymbol{\sigma^2_g}$: genotypic variance; $\boldsymbol{\sigma^2_e}$**:** residual variance; σ^2_p: phenotypic variance; **GCV**: genotypic coefficient variance; **PCV**: phenotypic coefficient of variance; **GA**: genetic advance; **GAM**: genetic advance over mean (%); $\boldsymbol{h^2}$: broad sense heritability (%); **LSD**: least significant difference; **CV**: coefficient of variation (%)

Env	Statistic	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
E03	*Mean*	87.93	95.38	135.65	40.26	10.65	109.05	34.86	12.10	20.85	42.49	17.09	40.51	42.07	408.50
	σ^2_g	23.68	24.32	6.94	17.30	2.63	215.74	34.92	2.08	2.24	59.13	13.50	22.39	14.01	7012.79
	σ^2_e	5.85	7.37	4.22	11.20	1.24	41.44	8.17	0.41	1.48	59.98	8.13	29.71	9.44	5024.26
	σ^2_p	26.61	28.01	9.05	22.90	3.25	236.46	39.01	2.28	2.98	89.12	17.57	37.25	18.73	9524.92
	GCV	5.53	5.17	1.94	10.33	15.24	13.47	16.95	11.91	7.18	18.10	21.50	11.68	8.90	20.50
	PCV	5.87	5.55	2.22	11.88	16.94	14.10	17.92	12.48	8.28	22.22	24.53	15.07	10.29	23.89
	GA	9.46	9.47	4.75	7.45	3.01	28.90	11.52	2.83	2.67	12.90	6.64	7.56	6.67	148.02
	GAM	10.76	9.93	3.50	18.49	28.25	26.50	33.05	23.42	12.82	30.37	38.83	18.66	15.85	36.24
	h^2	89.01	86.84	76.67	75.55	80.98	91.24	89.53	91.11	75.15	66.35	76.85	60.12	74.79	73.63
	LSD	4.76	5.34	4.05	6.60	2.19	12.67	5.63	1.25	2.39	15.29	5.62	10.85	6.09	139.54
	CV	2.75	2.85	1.51	8.31	10.45	5.90	8.20	5.26	5.84	18.23	16.69	13.46	7.30	17.35
E04	*Mean*	62.89	69.90	99.77	29.86	6.80	74.50	14.08	7.14	13.88	24.16	7.40	31.25	35.13	216.34
	σ^2_g	20.13	19.29	16.25	4.53	0.30	86.88	14.75	0.69	1.32	26.75	1.29	10.47	13.19	1121.58
	σ^2_e	6.44	7.66	6.05	1.19	0.22	35.23	6.78	0.33	0.77	13.53	0.90	7.70	6.19	1145.80
	σ^2_p	23.35	23.12	19.27	5.12	0.41	104.50	18.13	0.86	1.71	33.51	1.74	14.32	16.29	1694.49
	GCV	7.13	6.28	4.04	7.12	8.06	12.51	27.27	11.66	8.29	21.41	15.38	10.35	10.34	15.48
	PCV	7.68	6.88	4.40	7.58	9.39	13.72	30.24	12.96	9.42	23.96	17.84	12.11	11.49	19.03
	GA	8.58	8.26	7.62	4.12	0.97	17.51	7.13	1.54	2.09	9.52	2.02	5.70	6.73	56.13
	GAM	13.65	11.82	7.64	13.80	14.24	23.50	50.66	21.62	15.03	39.40	27.30	18.24	19.16	25.94
	h^2	86.21	83.43	84.30	88.39	73.57	83.14	81.31	80.95	77.46	79.81	74.29	73.10	80.99	66.19
	LSD	5.01	5.45	4.84	2.17	0.93	11.81	5.17	1.13	1.73	7.24	1.86	5.49	4.90	67.33
	CV	4.04	3.96	2.47	3.65	6.83	7.97	18.49	8.00	6.33	15.23	12.79	8.88	7.08	15.65

σ^2_g: genotypic variance; **σ^2_e:** residual variance; σ^2_p: phenotypic variance; **GCV**: genotypic coefficient variance; **PCV**: phenotypic coefficient of variance; **GA**: genetic advance; **GAM**: genetic advance over mean (%); **h^2**: broad sense heritability (%); **LSD**: least significant difference; **CV**: coefficient of variation (%)

Env	Statistic	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
E05	*Mean*	99.52	106.81	140.79	33.72	10.55	108.32	37.04	12.08	21.47	42.25	16.08	38.68	42.93	378.33
	σ^2_g	3.59	4.33	6.99	6.09	1.52	210.92	28.66	1.82	2.73	57.37	6.54	8.39	18.66	2638.98
	σ^2_e	1.18	1.74	4.81	8.50	1.04	36.40	11.76	0.72	1.75	34.35	2.38	23.71	13.33	2525.53
	σ^2_p	4.18	5.20	9.39	10.34	2.04	229.12	34.54	2.18	3.61	74.55	7.73	20.24	25.33	3901.75
	GCV	1.90	1.95	1.88	7.32	11.71	13.41	14.45	11.16	7.70	17.93	15.91	7.49	10.06	13.58
	PCV	2.05	2.13	2.18	9.54	13.56	13.97	15.87	12.21	8.85	20.43	17.30	11.63	11.72	16.51
	GA	3.62	3.91	4.70	3.90	2.20	28.71	10.05	2.54	2.97	13.69	4.85	3.84	7.64	87.03
	GAM	3.63	3.66	3.34	11.58	20.82	26.50	27.12	21.02	13.81	32.39	30.15	9.93	17.80	23.00
	h^2	85.93	83.26	74.43	58.93	74.54	92.06	82.98	83.52	75.79	76.96	84.61	41.44	73.68	67.64
	LSD	2.13	2.60	4.39	5.85	2.01	12.06	6.84	1.68	2.61	11.54	3.10	9.65	7.30	101.42
	CV	1.09	1.24	1.56	8.64	9.67	5.57	9.26	7.01	6.15	13.87	9.60	12.59	8.51	13.28
E06	*Mean*	81.97	89.88	118.34	28.46	7.74	96.82	30.48	11.00	19.72	28.70	9.96	35.63	39.21	255.74
	σ^2_g	14.41	14.13	4.05	9.79	1.68	126.84	14.42	1.27	2.61	17.94	2.29	29.43	12.66	1166.69
	σ^2_e	7.70	9.00	3.51	8.84	1.43	96.26	8.13	0.66	2.31	28.86	1.80	21.57	10.42	1581.56
	σ^2_p	18.26	18.63	5.81	14.21	2.39	174.97	18.49	1.61	3.76	32.37	3.19	40.21	17.87	1957.47
	GCV	4.63	4.18	1.70	11.00	16.72	11.63	12.46	10.27	8.19	14.76	15.20	15.23	9.07	13.36
	PCV	5.21	4.80	2.04	13.25	19.97	13.66	14.11	11.52	9.84	19.82	17.94	17.80	10.78	17.30
	GA	6.95	6.75	3.46	5.35	2.23	19.75	6.91	2.07	2.77	6.50	2.64	9.56	6.17	54.32
	GAM	8.47	7.50	2.93	18.80	28.84	20.40	22.67	18.84	14.05	22.63	26.53	26.83	15.73	21.24
	h^2	78.92	75.85	69.77	68.91	70.11	72.49	78.00	79.36	69.30	55.42	71.77	73.18	70.83	59.60
	LSD	5.60	6.06	3.84	5.81	2.35	19.72	5.74	1.60	2.99	10.58	2.64	9.13	6.42	78.29
	CV	3.38	3.34	1.58	10.45	15.44	10.13	9.36	7.40	7.71	18.72	13.48	13.03	8.23	15.55

$\boldsymbol{\sigma^2_g}$: genotypic variance; $\boldsymbol{\sigma^2_e}$**:** residual variance; σ^2_p: phenotypic variance; **GCV**: genotypic coefficient variance; **PCV**: phenotypic coefficient of variance; **GA**: genetic advance; **GAM**: genetic advance over mean (%); $\boldsymbol{h^2}$: broad sense heritability (%); **LSD**: least significant difference; **CV**: coefficient of variation (%)

Env	**Statistic**	**DTH**	**DTA**	**DTM**	**GFD**	**NOT**	**PH**	**PL**	**SL**	**SPS**	**BY**	**GY**	**HI**	**TKW**	**TNG**
E07	*Mean*	90.44	97.85	139.18	41.32	10.57	104.71	36.24	9.80	20.92	41.23	16.07	39.13	40.99	401.54
	σ^2_g	24.23	23.61	2.90	17.62	2.38	192.61	29.67	1.36	3.27	155.20	29.84	15.73	18.09	21692.67
	σ^2_e	6.71	8.06	1.89	9.91	1.30	58.15	7.28	0.47	1.99	67.10	7.20	22.83	8.87	5266.29
	σ^2_p	27.58	27.63	3.84	22.58	3.03	221.69	33.31	1.59	4.26	188.74	33.44	27.15	22.53	24325.82
	GCV	5.44	4.97	1.22	10.16	14.59	13.25	15.03	11.88	8.64	30.21	33.98	10.14	10.38	36.68
	PCV	5.81	5.37	1.41	11.50	16.46	14.22	15.93	12.87	9.86	33.32	35.97	13.32	11.58	38.84
	GA	9.50	9.25	3.05	7.64	2.81	26.65	10.59	2.21	3.26	23.27	10.63	6.22	7.85	286.51
	GAM	10.51	9.45	2.19	18.49	26.63	25.45	29.22	22.59	15.58	56.44	66.13	15.90	19.16	71.35
	h^2	87.84	85.42	75.44	78.05	78.52	86.88	89.07	85.19	76.67	82.23	89.24	57.95	80.31	89.18
	LSD	5.10	5.59	2.71	6.19	2.27	15.01	5.36	1.35	2.81	16.16	5.28	9.42	5.99	142.87
	CV	2.86	2.90	0.99	7.62	10.79	7.28	7.45	7.01	6.74	19.87	16.69	12.21	7.27	18.07
E08	*Mean*	66.02	71.94	103.21	31.27	7.31	61.11	10.14	6.66	14.26	22.54	7.14	33.00	34.65	212.41
	σ^2_g	12.77	10.95	10.71	4.16	0.48	96.10	5.55	0.56	1.46	32.44	2.04	11.61	13.29	2090.00
	σ^2_e	4.45	8.91	6.16	3.35	0.26	64.05	4.43	0.50	1.12	23.75	1.07	13.75	4.71	1318.85
	σ^2_p	14.99	15.41	13.79	5.84	0.61	128.12	7.77	0.81	2.02	44.32	2.57	18.49	15.64	2749.42
	GCV	5.41	4.60	3.17	6.53	9.49	16.04	23.23	11.23	8.46	25.27	19.98	10.33	10.52	21.52
	PCV	5.86	5.46	3.60	7.73	10.71	18.52	27.48	13.52	9.95	29.54	22.46	13.03	11.41	24.69
	GA	6.79	5.75	5.94	3.55	1.27	17.49	4.10	1.28	2.11	10.04	2.62	5.56	6.92	82.11
	GAM	10.29	7.99	5.76	11.35	17.32	28.62	40.44	19.22	14.82	44.54	36.61	16.86	19.97	38.66
	h^2	85.17	71.08	77.67	71.33	78.49	75.01	71.45	69.02	72.26	73.20	79.15	62.82	84.94	76.02
	LSD	3.84	4.99	4.32	3.04	0.90	13.85	3.51	1.16	1.78	8.24	1.83	5.79	3.94	62.33
	CV	3.19	4.15	2.40	5.85	7.03	13.10	20.76	10.64	7.41	21.62	14.50	11.24	6.26	17.10

$\boldsymbol{\sigma^2_g}$: genotypic variance; $\boldsymbol{\sigma^2_e}$: residual variance; $\boldsymbol{\sigma^2_p}$: phenotypic variance; **GCV**: genotypic coefficient variance; **PCV**: phenotypic coefficient of variance; **GA**: genetic advance; **GAM**: genetic advance over mean(%); $\boldsymbol{h^2}$: broad sense heritability(%); **LSD**: least significant difference; **CV**: coefficient of variation(%)

Env	Statistic	DTH	DTA	DTM	GFD	NOT	PH	PL	SL	SPS	BY	GY	HI	TKW	TNG
E09	*Mean*	87.69	95.21	133.03	37.83	10.84	99.37	34.28	-	-	42.71	15.72	37.38	40.48	391.92
	σ^2_g	34.66	34.68	36.84	10.29	1.77	89.02	14.94	-	-	45.57	4.70	6.71	19.08	3108.15
	σ^2_e	7.90	9.77	11.52	7.52	0.74	32.14	8.02	-	-	24.85	1.73	14.45	7.73	1600.49
	σ^2_p	38.61	39.57	42.60	14.05	2.14	105.09	18.94	-	-	58.00	5.57	13.93	22.95	3908.39
	GCV	6.71	6.19	4.56	8.48	12.27	9.50	11.27	-	-	15.81	13.79	6.93	10.79	14.23
	PCV	7.09	6.61	4.91	9.91	13.48	10.32	12.70	-	-	17.83	15.01	9.98	11.84	15.95
	GA	11.49	11.36	11.63	5.66	2.49	17.89	7.07	-	-	12.33	4.11	3.70	8.21	102.42
	GAM	13.10	11.93	8.74	14.95	23.00	18.00	20.62	-	-	28.86	26.12	9.90	20.28	26.13
	h^2	89.77	87.65	86.48	73.23	82.81	84.71	78.84	-	-	78.58	84.47	48.15	83.16	79.52
	LSD	5.53	6.15	6.76	5.50	1.72	11.28	5.63	-	-	9.89	2.61	7.48	5.47	78.81
	CV	3.20	3.28	2.55	7.25	7.91	5.71	8.26	-	-	11.67	8.37	10.17	6.87	10.21
E10	*Mean*	76.26	82.73	112.50	29.78	7.87	92.22	27.69	-	-	32.40	10.58	32.88	32.36	328.32
	σ^2_g	25.53	21.30	21.90	10.08	0.67	57.67	12.90	-	-	23.58	3.16	10.21	12.99	2143.89
	σ^2_e	9.59	19.26	13.04	5.48	0.43	47.27	7.24	-	-	31.05	2.30	10.18	9.44	3096.69
	σ^2_p	30.32	30.94	28.43	12.83	0.88	81.31	16.52	-	-	39.11	4.31	15.30	17.71	3692.23
	GCV	6.63	5.58	4.16	10.67	10.36	8.23	12.97	-	-	14.99	16.79	9.72	11.14	14.10
	PCV	7.22	6.72	4.74	12.03	11.92	9.78	14.68	-	-	19.30	19.62	11.90	13.00	18.51
	GA	9.55	7.89	8.46	5.80	1.46	13.18	6.54	-	-	7.77	3.13	5.38	6.36	72.68
	GAM	12.52	9.54	7.52	19.48	18.54	14.29	23.61	-	-	23.98	29.61	16.35	19.65	22.14
	h^2	84.19	68.86	77.06	78.63	75.51	70.93	78.08	-	-	60.30	73.26	66.72	73.35	58.06
	LSD	6.09	8.64	7.11	4.61	1.30	13.69	5.33	-	-	11.10	3.06	6.44	6.11	110.14
	CV	4.06	5.31	3.21	7.86	8.34	7.45	9.72	-	-	17.20	14.35	9.71	9.49	16.95

$\boldsymbol{\sigma^2_g}$: genotypic variance; $\boldsymbol{\sigma^2_e}$: residual variance; $\boldsymbol{\sigma^2_p}$: phenotypic variance; **GCV**: genotypic coefficient variance; **PCV**: phenotypic coefficient of variance; **GA**: genetic advance; **GAM**: genetic advance over mean(%); $\boldsymbol{h^2}$: broad sense heritability(%); **LSD**: least significant difference; **CV**: coefficient of variation(%), “-“: trait not observed

Annexure 5: Summary statistics of observed clusters extracted from hierarchical clustering analysis on bread wheat data set pooled over different water regimes

Traits	Cluster	IR				RF				DT			
		Min	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**
DTH	I	87.33	98.50	92.28	3.26	71.50	86.00	78.99	3.45	57.00	69.00	64.18	3.30
	II	89.83	95.72	92.44	2.19	71.17	85.17	77.92	3.30	59.00	75.50	66.18	4.12
	II	81.42	102.00	90.05	4.27	73.33	85.17	79.57	3.66	54.25	70.50	63.10	3.66
	IV	80.08	99.67	90.51	4.39	72.50	84.17	79.14	3.18	55.00	69.75	62.70	3.57
	V	83.08	100.25	90.39	3.67	70.83	86.50	79.15	3.96	55.50	74.25	64.23	3.94
	VI	83.17	97.99	91.06	3.53	70.67	83.17	77.98	3.57	55.25	71.75	65.04	3.58
	VII	83.00	99.08	90.71	4.03	69.57	85.17	77.25	3.44	57.00	71.00	65.87	3.39
	VIII	84.42	99.25	91.29	4.19	73.33	85.33	80.06	3.25	59.25	73.00	65.97	3.96
DTA	I	94.67	106.75	99.75	3.32	78.50	92.83	85.83	3.52	64.00	75.50	70.86	3.37
	II	97.42	103.30	99.79	2.31	78.33	92.33	84.66	3.23	66.50	81.00	72.67	3.80
	II	88.25	109.50	97.46	4.28	79.67	92.33	86.48	3.88	60.25	77.50	69.39	3.64
	IV	88.33	107.08	97.95	4.34	78.67	91.17	85.86	3.27	60.50	76.50	69.09	3.66
	V	90.67	107.03	97.83	3.72	77.67	93.50	85.91	3.93	61.75	79.50	70.69	3.86
	VI	90.67	104.61	98.35	3.45	78.00	90.17	84.72	3.47	62.25	79.00	71.58	3.50
	VII	89.75	107.42	98.30	4.14	75.67	91.33	83.98	3.39	63.25	77.75	72.38	3.47
	VIII	92.67	107.17	98.73	4.04	80.00	91.83	86.76	3.26	66.50	79.75	72.50	3.90
DTM	I	131.83	144.13	136.96	3.09	109.67	120.50	114.79	2.55	95.50	111.00	101.27	3.64
	II	132.92	141.25	136.78	3.24	109.67	123.50	114.13	2.75	96.50	112.00	103.07	4.12
	II	130.50	142.42	135.43	3.20	109.67	123.83	114.58	3.14	92.25	107.00	100.54	3.44
	IV	130.00	142.33	135.76	2.74	110.17	119.50	114.41	2.05	93.00	108.50	100.28	3.27
	V	130.42	141.92	135.10	2.72	109.33	123.17	115.20	3.29	94.00	110.50	101.29	3.45
	VI	131.00	140.50	135.65	2.70	110.33	118.33	113.84	2.22	93.75	107.00	101.07	3.63
	VII	128.92	141.25	135.45	2.58	109.00	120.83	114.11	2.67	95.75	108.00	102.51	3.40
	VIII	132.08	140.75	136.69	2.55	111.50	123.83	115.90	3.24	97.50	110.13	103.24	3.53
GFD	I	33.17	43.42	37.16	2.48	24.83	35.67	28.97	2.83	28.25	38.50	30.41	2.36
	II	33.83	39.17	36.89	2.17	25.00	36.33	29.46	2.55	24.75	33.75	30.40	1.96
	II	32.92	43.17	37.91	2.38	22.33	33.83	28.03	3.07	28.50	34.50	31.15	1.29
	IV	32.42	43.67	37.73	2.80	24.67	35.00	28.61	2.69	24.50	38.75	31.19	2.70
	V	32.92	41.92	37.25	2.46	24.58	34.67	29.29	2.56	27.00	35.75	30.60	1.51
	VI	33.25	43.08	37.25	2.32	22.50	36.83	29.15	3.19	23.63	31.75	29.49	2.02
	VII	30.25	45.42	37.14	2.91	24.67	39.67	30.13	3.47	23.00	33.75	30.13	1.78
	VIII	33.58	42.17	37.90	2.81	25.33	31.67	29.05	2.12	26.25	34.75	30.74	2.16
NOT	I	9.11	12.34	10.75	0.77	6.94	9.68	8.09	0.64	6.83	8.90	7.80	0.53
	II	10.12	12.57	10.97	0.97	6.87	9.11	7.87	0.53	6.28	8.96	7.31	0.64
	II	9.01	12.42	10.98	0.80	6.54	9.06	7.61	0.61	5.81	9.52	7.18	0.68
	IV	9.64	12.16	10.86	0.62	6.49	9.52	7.87	0.63	5.80	8.83	6.85	0.55
	V	9.50	13.27	10.93	0.78	6.31	9.52	7.70	0.68	6.15	8.50	7.07	0.50
	VI	8.89	12.25	10.45	0.90	6.51	8.97	7.66	0.68	6.15	8.20	7.13	0.57
	VII	9.43	12.86	10.72	0.79	5.83	9.02	7.63	0.61	5.75	8.08	6.75	0.47
	VIII	9.54	12.45	10.85	0.79	6.39	8.42	7.21	0.59	6.06	7.72	6.67	0.42

DTH: days to heading; **DTA:** days to anthesis; **DTM:** days to maturity; **GFD:** grain filling duration; **Min:** minimum; **Max:** maximum; **σ**: standard deviation

Traits	Cluster	IR				RF				DT			
		Min	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**
PH	I	88.26	136.22	109.23	13.47	76.08	116.44	93.38	11.14	55.07	112.62	73.86	14.40
	II	93.88	125.74	107.67	12.58	73.39	118.66	91.95	10.45	49.56	85.60	66.79	10.13
	II	84.59	132.67	101.92	9.96	76.56	99.15	85.79	5.93	52.73	85.01	66.98	6.86
	IV	88.36	133.84	101.79	10.39	79.83	120.24	94.88	11.71	51.59	85.14	66.25	7.76
	V	77.56	143.04	107.58	13.82	74.95	115.28	89.45	10.70	52.30	103.83	70.82	11.28
	VI	91.55	129.61	105.14	10.61	64.53	106.33	85.52	7.18	54.14	75.39	64.69	7.05
	VII	84.53	122.28	99.74	8.01	73.46	117.57	91.58	11.40	49.32	78.11	63.82	6.44
	VIII	88.40	139.80	112.13	14.28	76.24	110.69	95.59	12.63	52.53	104.01	67.35	12.13
PL	I	27.99	48.35	36.68	5.44	20.06	35.94	27.68	3.66	7.95	17.91	12.33	2.50
	II	30.28	40.54	34.98	3.92	23.85	37.92	28.01	2.84	5.03	19.60	12.03	3.24
	II	27.93	41.45	34.79	3.23	20.83	31.53	26.65	3.06	6.45	18.79	12.96	3.02
	IV	26.72	47.30	35.15	4.40	22.25	38.89	28.85	4.23	6.19	19.40	12.52	2.80
	V	26.37	47.30	35.62	4.56	18.21	40.55	28.56	4.44	5.61	21.68	12.46	3.54
	VI	27.93	50.82	35.90	5.18	22.41	36.65	26.65	2.60	6.87	15.01	10.98	2.33
	VII	25.40	43.24	33.55	3.56	21.30	42.06	29.36	4.51	7.30	17.21	11.03	2.39
	VIII	30.65	48.59	38.70	5.27	20.95	39.47	28.62	4.26	8.13	16.84	11.43	2.51
SL	I	8.79	13.38	11.19	1.04	8.08	11.94	9.88	0.94	5.63	8.15	7.17	0.67
	II	9.40	11.20	10.16	0.87	7.18	13.74	9.89	1.05	5.18	8.45	6.92	0.79
	II	9.31	14.10	11.44	0.98	7.82	14.87	9.98	1.40	4.30	8.67	6.71	0.94
	IV	9.23	13.51	11.59	1.00	7.70	12.99	9.87	0.98	5.57	8.68	6.66	0.61
	V	9.48	17.60	11.46	1.21	8.41	11.60	9.67	0.85	5.27	9.43	7.14	0.88
	VI	9.04	15.54	11.32	1.24	8.19	11.60	9.99	0.82	5.17	8.34	6.80	0.76
	VII	9.11	13.44	11.48	1.04	7.81	13.16	9.91	1.00	5.50	8.95	6.73	0.74
	VIII	8.41	13.83	11.41	1.35	5.84	11.45	9.61	1.29	5.56	8.26	6.94	0.82
SPS	I	18.25	25.13	21.32	1.56	17.33	22.44	19.86	1.52	12.43	17.73	14.90	1.54
	II	19.75	22.31	20.75	1.08	15.67	22.67	19.73	1.55	12.27	17.82	14.73	1.27
	II	17.62	24.23	21.01	1.57	16.50	22.08	19.07	1.79	11.68	16.19	13.87	1.35
	IV	18.38	23.65	21.08	1.54	16.50	22.17	19.34	1.42	10.83	17.10	13.47	1.05
	V	17.96	25.63	20.57	1.59	15.00	21.83	19.29	1.66	12.34	16.85	14.24	1.03
	VI	15.80	24.35	20.93	1.91	15.17	22.33	19.49	1.83	12.32	16.41	14.01	1.14
	VII	17.65	23.16	20.58	1.50	14.33	23.17	18.73	1.81	10.83	17.79	13.78	1.36
	VIII	17.42	23.71	20.69	1.86	13.50	22.33	18.73	1.99	11.33	16.25	13.82	1.51
BY	I	34.67	53.75	42.72	4.65	23.80	42.30	31.89	4.23	22.10	36.86	30.03	4.01
	II	47.11	53.06	49.26	2.27	22.07	34.87	29.17	3.14	16.76	35.91	26.93	4.65
	II	38.94	54.34	46.62	3.56	20.51	32.00	25.45	2.59	18.82	31.89	25.17	3.37
	IV	36.11	59.77	45.13	5.61	21.95	38.81	28.97	3.97	12.39	26.92	20.25	3.29
	V	35.81	56.36	43.16	4.15	21.68	38.17	28.83	3.67	14.71	34.73	23.19	3.54
	VI	33.55	50.66	39.16	3.86	22.45	35.11	27.71	2.66	14.75	29.72	23.04	3.63
	VII	34.97	49.67	41.39	3.32	16.45	33.23	26.78	3.67	14.32	32.45	21.20	3.83
	VIII	29.18	47.33	38.71	5.15	19.47	36.70	25.84	3.79	15.05	29.03	20.31	3.91

PH: plant height (cm); **PL:** peduncle length (cm); **SL:** spike length; **SPS:** spikelet per spike; **BY:** biological yield per plant (gm); **Min:** minimum; **Max:** maximum; **σ**: standard deviation

Traits	Cluster	IR				RF				DT			
		Min	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**
GY	I	12.90	19.93	16.18	1.49	9.38	12.86	10.66	0.72	6.69	10.97	8.90	1.16
	II	17.95	20.72	19.59	1.10	7.62	11.92	10.05	0.92	6.10	9.71	8.13	1.07
	II	16.03	20.95	18.35	1.24	7.27	10.09	8.58	0.74	6.47	9.53	7.91	0.87
	IV	13.93	21.11	17.41	1.66	7.66	11.85	9.69	0.94	5.01	7.99	6.46	0.74
	V	12.66	19.02	16.33	1.44	8.20	12.47	9.90	0.91	5.43	8.73	7.21	0.74
	VI	12.40	17.10	14.93	1.15	8.19	11.57	9.79	0.87	5.60	8.52	7.26	0.79
	VII	14.64	19.01	16.29	1.00	6.27	10.70	9.02	0.99	4.97	8.00	6.85	0.79
	VIII	8.98	16.27	13.62	1.62	7.39	9.64	8.45	0.72	4.80	7.72	6.16	0.97
HI	I	31.35	43.14	38.47	3.09	27.15	41.38	34.36	3.82	26.21	36.97	30.28	3.14
	II	38.44	42.49	40.38	2.00	27.72	41.35	35.22	3.31	26.90	38.75	30.78	2.90
	II	33.84	43.75	39.88	2.37	29.63	41.43	34.96	2.92	25.33	38.43	32.15	3.03
	IV	35.76	45.09	39.22	2.20	25.46	45.53	34.40	4.01	24.35	41.61	33.19	3.04
	V	32.78	44.86	38.47	2.81	29.77	41.79	35.12	3.23	24.02	39.63	32.00	3.27
	VI	31.92	44.45	38.49	2.75	30.02	40.20	36.00	2.52	27.83	39.07	32.26	2.99
	VII	34.97	44.10	39.88	2.23	25.68	41.96	34.64	3.71	22.26	41.32	33.23	3.57
	VIII	29.87	43.75	35.73	3.17	26.71	39.93	33.79	4.17	25.20	40.70	31.84	4.10
TKW	I	31.20	49.87	41.53	3.47	28.66	38.90	33.33	2.46	25.15	37.71	31.09	3.42
	II	34.19	38.58	35.80	1.70	26.69	41.43	35.05	3.23	24.49	39.97	31.98	4.14
	II	33.20	45.84	39.81	2.77	30.67	41.07	35.71	2.84	28.51	39.22	34.87	2.86
	IV	31.28	48.97	40.27	3.93	29.99	42.16	36.49	3.04	29.11	45.34	36.90	3.63
	V	34.10	50.02	41.71	3.62	29.87	42.51	35.65	3.21	26.32	43.00	34.88	3.46
	VI	38.29	49.99	43.55	3.15	27.80	41.70	33.86	3.09	29.67	41.86	34.76	3.48
	VII	37.32	48.01	42.02	2.49	32.33	44.40	37.61	3.18	31.16	43.16	35.80	3.06
	VIII	29.59	49.02	43.58	4.75	31.20	40.97	36.00	3.07	29.17	43.08	37.23	3.76
TNG	I	349.13	447.61	391.57	23.86	302.78	353.17	325.42	11.17	266.84	336.37	291.32	17.62
	II	539.39	568.89	552.62	10.54	271.35	315.39	291.15	11.36	227.40	336.51	260.88	26.15
	II	438.48	504.64	465.19	16.54	221.91	266.74	244.79	12.40	208.38	259.91	232.87	14.43
	IV	413.11	468.43	435.85	10.73	249.21	308.85	269.85	12.54	156.36	205.16	178.10	13.32
	V	360.95	425.17	393.99	17.31	266.66	299.82	281.46	9.07	183.11	242.12	211.32	13.94
	VI	316.54	366.68	345.24	12.12	271.84	314.69	292.49	11.44	173.54	251.83	212.94	18.19
	VII	360.59	421.02	390.98	12.92	192.22	272.07	242.14	17.69	150.77	229.60	195.22	19.91
	VIII	284.45	338.50	315.03	16.11	214.69	261.69	237.98	13.58	130.79	198.27	168.07	20.25
TNSC	I	143.87	181.97	162.70	9.63	147.07	205.23	166.47	13.14	146.27	218.23	183.55	16.33
	II	131.54	156.66	139.32	10.28	110.51	175.40	146.02	13.56	188.57	268.32	213.77	19.43
	II	116.10	177.91	145.48	15.02	143.27	187.33	166.83	12.69	130.99	185.15	163.85	11.55
	IV	103.98	145.08	127.87	11.15	140.00	174.92	156.26	8.14	128.83	201.96	175.60	16.04
	V	102.92	140.48	124.24	8.19	160.74	199.68	180.17	9.52	156.33	222.81	191.36	11.43
	VI	109.02	160.93	133.85	12.55	145.88	164.56	154.63	5.47	225.03	304.42	255.54	22.07
	VII	124.58	161.53	140.96	8.04	112.69	155.33	140.79	8.82	206.55	248.95	224.75	10.99
	VIII	115.95	171.56	149.11	13.93	157.25	195.08	171.46	10.84	188.28	215.58	202.41	7.72

GY: grain yield per plant (gm), **HI:** harvest index (%); **TKW:** thousand kernel weight (gm); **TNG:** total number of grains per plant; **TNSC:** total non-structural carbohydrates (mg/g); **Min:** minimum; **Max:** maximum; **σ**: standard deviation

Traits	Cluster	IR				RF				DT			
		Min	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**	**Min**	**Max**	*Mean*	**σ**
Fructans	I	91.29	125.40	108.60	9.28	83.86	136.74	102.74	12.57	82.88	152.45	119.92	15.73
	II	76.77	104.12	85.75	11.00	48.62	104.56	83.53	12.49	122.37	200.01	149.08	18.59
	II	64.17	123.09	91.88	14.17	80.28	118.63	103.43	11.41	70.33	121.73	101.45	10.23
	IV	50.22	91.13	75.48	10.62	79.43	108.18	93.86	7.13	65.82	134.82	112.07	15.24
	V	50.49	88.06	71.87	7.84	96.16	132.83	114.85	8.61	96.00	157.44	127.56	11.12
	VI	60.05	109.06	81.28	12.04	83.70	99.85	92.33	4.88	159.42	236.05	187.87	20.53
	VII	73.37	107.55	88.00	7.60	51.65	92.26	79.09	8.48	142.84	182.50	159.38	10.03
	VIII	63.71	116.43	95.09	13.20	94.88	128.60	106.28	9.80	123.00	149.84	138.55	7.31
Fructose	I	9.07	12.42	10.41	0.82	9.94	13.72	12.23	0.85	10.12	14.37	11.95	1.18
	II	9.80	10.98	10.41	0.47	10.23	13.74	12.09	0.75	9.21	16.28	12.11	1.36
	II	8.72	12.73	10.49	0.88	9.85	13.50	11.73	0.94	9.58	14.64	11.70	1.40
	IV	8.98	12.40	10.12	1.00	9.11	13.68	11.51	0.82	9.68	15.54	11.83	1.29
	V	8.48	12.54	10.07	0.77	10.53	13.70	11.95	0.79	9.68	16.86	12.28	1.39
	VI	8.03	12.03	9.95	0.89	9.99	13.29	11.84	0.72	10.58	15.99	13.28	1.39
	VII	8.69	12.48	9.90	0.73	9.76	13.44	11.80	0.78	10.20	15.31	12.63	1.20
	VIII	9.14	12.38	10.56	0.91	10.16	13.67	12.21	0.83	9.52	15.38	12.31	1.52
Glucose	I	11.01	13.25	11.87	0.50	13.03	15.75	14.09	0.71	12.90	15.55	13.85	0.62
	II	11.34	12.11	11.68	0.36	11.61	16.64	13.61	0.76	9.11	16.51	14.17	1.28
	II	10.51	13.62	11.65	0.59	12.48	17.63	14.21	0.99	8.60	15.39	13.44	1.20
	IV	10.30	12.02	11.31	0.45	12.03	15.59	13.86	0.68	12.36	15.89	13.87	0.80
	V	10.39	12.49	11.34	0.43	13.05	16.87	14.89	0.99	11.44	16.35	13.75	0.91
	VI	8.91	12.15	11.47	0.54	12.64	14.94	13.67	0.55	13.39	16.77	14.85	0.91
	VII	10.92	12.75	11.65	0.43	12.26	14.92	13.42	0.62	12.63	16.96	14.21	1.05
	VIII	11.07	12.47	11.80	0.40	12.75	16.64	14.66	0.93	12.34	15.12	13.72	0.73
Sucrose	I	30.72	33.80	31.82	0.69	35.87	39.61	37.41	0.98	36.57	39.99	37.84	0.83
	II	31.05	32.09	31.48	0.45	34.06	40.94	36.79	1.06	31.43	41.52	38.42	1.77
	II	29.91	34.29	31.47	0.83	35.16	42.11	37.46	1.36	30.36	40.03	37.26	1.68
	IV	29.58	31.85	30.96	0.61	34.69	39.39	37.04	0.94	35.74	40.45	37.83	1.08
	V	29.62	32.62	30.97	0.60	35.99	41.50	38.47	1.42	34.59	41.32	37.76	1.24
	VI	27.52	32.17	31.15	0.76	35.44	38.56	36.79	0.74	37.53	42.13	39.54	1.26
	VII	30.38	32.85	31.42	0.59	34.99	38.67	36.49	0.87	36.36	42.47	38.54	1.44
	VIII	30.66	32.51	31.67	0.57	35.63	41.09	38.30	1.31	36.03	39.76	37.83	0.97
WSC	I	120.63	194.96	153.62	14.40	124.27	188.62	153.80	21.41	165.57	211.94	195.56	13.38
	II	144.53	174.67	156.27	11.65	84.76	148.61	125.72	12.05	122.96	224.10	174.29	20.89
	II	125.27	188.34	152.75	14.52	153.51	214.91	176.27	13.06	146.71	220.36	179.08	17.64
	IV	112.73	165.28	148.09	12.00	134.76	182.07	157.35	10.84	150.05	214.94	190.61	15.47
	V	122.61	176.91	148.83	13.56	135.34	200.49	171.34	18.64	137.89	219.97	182.89	17.81
	VI	129.99	184.62	161.31	11.99	141.95	178.92	154.41	8.57	118.77	219.58	149.54	24.13
	VII	137.13	187.57	164.20	12.40	90.45	168.29	128.96	18.34	147.80	211.16	175.75	13.10
	VIII	124.26	175.81	149.26	12.90	104.11	165.77	135.25	16.18	144.71	198.21	164.69	14.04

Fructans (mg/g); **Fructose (mg/g)**; **Glucose (mg/g); Sucrose (mg/g)**; **WSC:** water-soluble carbohydrates (mg/g); **Min:** minimum; **Max:** maximum; **σ**: standard deviation

Annexure 6: Cluster membership of 302 bread wheat genotypes under irrigated, rainfed and drought condition

Genotype	IR	RF	DT	Genotype	IR	RF	DT	Genotype	IR	RF	DT
Agralocal	1	1	1	HD2285	5	6	3	HTW-11	7	3	4
AKAW3717	2	2	2	HD2329	1	2	3	HTW-6	1	8	5
AKAW4627	3	2	3	HD2385	3	5	5	HUW12	5	2	3
AKW1071(purana)	4	3	4	HD2402	3	7	5	HUW206	4	2	6
AKW2862-1	4	4	4	HD2687	2	4	7	HUW234	7	2	5
Bacanora88	5	1	3	HD2733	5	5	4	HUW468	6	7	4
bageshwarlocal	1	4	2	HD2781	1	2	1	HUW598	5	7	1
Birsa Gehun	2	1	2	HD2824	7	6	5	HUW616	1	2	4
BRW3723	5	3	5	HD2888	7	4	6	HUW661	6	7	4
BWL9022	1	5	3	HD2932	7	4	3	HUW675	1	2	8
C306	6	4	2	HD2985	1	7	5	HUW677	5	4	4
CBW38	4	6	2	HD2987	7	7	1	HUW679	1	7	4
Chirya-3	4	6	5	HD2997	6	4	5	HW2004	1	5	3
D134	6	2	5	HD30	3	5	5	HW5205	5	4	4
DBW107	5	2	4	HD3016	6	8	8	HW5216	7	6	4
DBW110	1	7	6	HD3043	4	3	5	IC212140	3	6	1
DBW128	3	2	4	HD3045	4	5	4	IC212145	6	2	7
DBW129	1	1	5	HD3055	1	8	6	IC212151	1	7	5
DBW155	7	6	5	HD3059	5	5	8	IC212161	3	3	2
DBW16	7	5	4	HD3071	1	7	8	IC212182	1	4	1
DBW17	5	1	7	HD3086	7	4	6	IC212190	5	4	5
DBW31	6	3	7	HD3118	7	2	5	IC296432	5	7	8
DBW39	7	3	3	HD3127	7	6	6	IC321856	5	1	7
DBW46	3	4	3	HD3128	1	4	2	IC321866	5	7	5
DBW51	5	1	2	HD3132	4	8	5	IC321879	1	7	3
DBW52	7	3	3	HD3139	6	8	6	IC321886	1	4	3
DBW-71	8	4	4	HD3146	1	2	4	IC321888	5	4	5
DBW88	3	2	7	HD4730	6	3	5	IC321898	5	8	5
DBW90	5	7	2	HI1500	6	4	4	IC321899	6	8	1
DBW98	6	7	2	HI1531	3	1	5	IC321905A	1	2	3
Dharwad Dry	4	2	2	HI1544	5	1	2	IC321913	2	1	5
DL1266-5	3	4	7	HI1563	3	6	7	IC321931	7	4	4
DL788-2	6	3	5	HI1579	7	1	4	IC321946	5	4	5
DPW621-50	5	2	7	HI1580	3	5	4	IC321950	6	4	5
FKW1	3	5	7	HI1581	6	6	8	IC321951	3	7	7
FLW-11	4	1	2	Hindi62	1	5	6	IC321958	1	2	2
FLW29	3	5	5	HPW147	6	4	5	IC321988	8	8	5
FLW3	4	6	8	HPW251	5	7	8	IC322011A	5	1	2
FLW5	7	3	5	HPW266	5	4	7	IC322016	6	7	8
GL11	5	1	5	HPW347	7	1	7	K0617	3	5	5
GL27	1	7	3	HPW348	1	4	6	K1114	7	3	6
GL6	5	4	1	HPW349	1	5	2	K1204	5	7	5
GW173	3	2	6	HPW371	5	6	4	K307	7	1	5
GW2002-18	7	1	5	HPW400	7	2	4	K68	8	7	4
GW273	1	3	3	HS295	3	5	5	K8020	5	3	6
GW322	1	7	8	HS365	7	7	4	K8027	7	6	4
GW366	5	2	5	HS490	6	4	2	K8962	4	5	5
GW391	5	3	7	HS542	6	8	5	K9107	3	6	3
GW451	3	5	3	HS547	3	1	2	K9351	1	4	5
GW455	7	6	5	HS562	4	1	2	KB2012-03	6	1	7
GW496	3	3	6	HS577	6	7	5	KHARCHIA65	6	7	7
Halna	3	1	4	HS590	7	3	5	Kharchialocal	3	2	1
HD1981(PRATAP)	4	3	8	HS592	4	1	5	KRL19	4	1	5
HD2009	4	5	5	HS593	6	2	2	KRL35	5	4	5
HD2189	5	7	4	HS594	7	6	7	L2(Ad)	3	2	2
HD2270	4	2	5	HS595	1	7	5	PBW660	6	4	1
L5(AL)	5	1	1	PBW681	3	2	5	L25(AMB)	7	3	5

Genotype	IR	RF	DT	Genotype	IR	RF	DT	Genotype	IR	RF	DT
LALBAHADUR	5	6	5	PBW689	8	8	7	PBW674	3	5	7
LBRL4	5	7	4	PBW692	3	5	2	WH1126	5	3	4
LGM110	5	5	5	PBW697	6	6	3	WH1129	7	2	7
LGM130	5	1	2	PBW698	4	3	5	WH1132	7	4	7
LGM133	8	7	4	PBW702	4	3	2	WH1138	5	7	7
LGM134-B	6	7	5	PBW703	4	7	4	WH1142	1	6	5
LGM135	5	4	4	PBW704	6	5	4	WH1154	5	4	2
LGM162	4	1	5	PBW706	3	1	5	WH1156	3	5	8
LGM191	8	8	5	PBW722	3	6	6	WH1157	4	2	6
LGM205	6	4	5	PBW723	7	1	7	WH1164	8	2	6
LGM225-1	1	7	1	Pusa2019A	1	6	2	WH147	3	6	5
LGM225-R	5	4	1	PWR4099	7	4	3	WH423	5	7	4
LGM238	3	4	1	RAJ3765	4	6	3	WH542	7	7	7
LGM245	8	2	1	RAJ4037	6	7	5	WH595	3	5	5
LOK-1	5	8	3	RAJ4083	6	7	3	WH730	8	4	7
lok41	8	7	8	RAJ4124	3	2	4	WL3526	5	7	1
Lok44	5	7	5	RAJ4356	4	4	7	WL711	5	8	7
Lok54	1	5	5	RD20	8	8	4	WH1124	5	4	7
MACS6145	8	4	5	RSP561	7	4	3	WH1105	7	2	5
MACs62222	7	6	1	Safedlerma	4	6	5				
MACS6273	2	6	1	SKW441	6	3	8				
MACS6354	4	7	5	Sonalika	7	7	4				
MACS6507	6	2	5	Sonora64	5	1	5				
ML1194	5	8	8	T808	1	8	6				
MP1201	4	2	5	UAS304	8	1	2				
MP1202	8	7	5	UAS305	3	5	3				
MP1279	5	1	5	UAS316	6	7	4				
MP3211	3	6	2	UAS320	4	7	4				
MP3288	3	4	5	UP115	3	6	5				
MP4010	7	8	3	UP2338	3	3	7				
MP4106	1	4	5	UP2425	7	4	7				
NARMADA4	1	4	4	UP262	3	2	4				
NB29-13-5-9	3	4	2	UP2691	6	4	7				
NB29-6-2-12	5	2	1	UP2855	6	6	4				
NI5439	8	1	3	UP2864	8	5	2				
NIAW34	5	7	8	UP2890	5	2	8				
NIAW917	7	4	4	UP2891	6	7	7				
NP846	5	4	7	VL1004	7	3	2				
NP852	5	2	6	VL3004	6	4	6				
NW2036	4	1	6	VL639	8	2	3				
NW4035	1	2	5	VL738	5	6	2				
PBW138	5	4	3	VL798	3	2	4				
PBW175	7	4	7	VL802	4	6	6				
PBW343	4	4	2	VL804	3	2	5				
PBW373	3	6	2	VL892	3	1	5				
PBW396	3	3	3	VL900	3	2	6				
PBW502	6	3	4	VL907	6	1	6				
PBW550	7	6	3	VL946	3	4	8				
PBW579	4	4	7	VL967	7	7	6				
PBW590	3	4	5	WBM1587	1	5	2				
PBW596	7	5	4	WBM1591	7	8	7				
PBW610	6	7	3	WH1046	3	2	4				
PBW621	4	4	7	WH1061	1	4	6				
PBW644	8	5	6	WH1080	5	7	5				
PBW65	4	1	6	WH1097	7	4	5				
PBW658	1	1	7	WH1100	4	7	4				

Annexure 7: Distribution of significant MTAs for studied traits for each data set on different linkage groups of *Triticum aestivum* genome

DS	**MTAs**	**MTAs**
	DTH	**DTA**
E01	7B(1); 5B(2); 5A(5); 2B(2); 2A(1)	7B(1); 5A(5); 3A(1); 2A(3)
E02	7B(1); 7A(1); 6B(1); 5A(6); 3B(2); 2B(1); 2A(1)	6B(2); 5A(4); 3B(2); 2B(1)
E03	7B(2); 7A(2); 6B(2); 5A(9); 3B(3); 3A(1); 2B(1); 1D(1); 1B(1)	7B(1); 7A(2); 6B(1); 5A(6); 3B(1); 2B(2); 1D(3)
E04	7A(2); 5B(1); 4A(5); 3A(2); 1A(1)	7A(1); 5B(1); 4A(5); 3B(1); 3A(2); 1A(2)
E05	7B(2); 6B(3); 5D(1); 5A(2); 3D(1); 3B(2); 3A(1); 2B(1); 1B(1)	7A(1); 6B(1); 3D(1); 3B(2); 3A(1); 1B(1); 1A(1)
E06	6B(6); 3B(2); 2B(4); 1B(1)	6B(6); 5A(1); 3B(2); 2B(4); 1B(2)
E07	7A(3); 6B(1); 5B(1); 5A(2); 4A(4); 1A(1)	7A(1); 6B(4); 5B(1); 5A(5); 4A(4); 2B(1)
E08	7D(1); 7B(1); 5A(1); 3A(1); 2B(1)	7D(1); 5A(1)
E09	6A(3); 5A(11); 4A(1); 3B(1); 3A(3); 2D(1); 1D(2); 1B(1); 1A(2)	6D(1); 6A(1); 5A(11); 3B(1); 3A(3); 2D(1); 1D(1); 1B(1); 1A(2)
E10	6B(4); 6A(1); 5B(1); 5A(13); 4B(1); 4A(1); 3A(2); 2A(1); 1D(2); 1B(3); 1A(1)	7A(1); 6B(3); 6A(1); 5B(1); 5A(9); 4B(1); 3A(2); 2A(1); 1D(1); 1B(1); 1A(1)
IR	7B(1); 7A(2); 6B(3); 6A(1); 5A(8); 3A(2); 2B(3); 1D(2); 1B(1); 1A(1)	7B(1); 6B(1); 6A(1); 5A(9); 3A(2); 2B(3); 1D(2); 1B(1); 1A(1)
RF	6B(7); 6A(2); 5A(8); 3B(1); 2B(4); 1B(2); 1A(1)	7A(1); 6B(6); 6A(1); 5A(7); 3B(1); 2B(4); 1B(2)
DT	7D(1); 5B(1)	7D(1); 6B(1); 5D(1); 5B(1)
	DTM	GFD
E01	7D(1); 7B(1); 7A(1); 6B(1); 4A(2); 2A(1)	7B(1); 6B(1); 5B(1); 5A(6); 3B(1)
E02	6B(1); 6A(1); 3B(2)	7A(1); 6B(4); 5A(6)
E03	7B(4); 6B(1); 2B(2)	7B(1); 7A(1); 6B(3); 5A(3); 3D(1); 3B(1); 2B(1); 1D(1); 1A(3)
E04	7D(1); 7A(2); 6B(1); 5B(2); 5A(2); 4A(4); 3A(2); 2B(6); 1A(1)	5B(1); 1A(1)
E05	7B(2); 7A(2); 6B(2); 3B(1)	5D(1); 3D(11); 1A(1)
E06	7D(3); 7A(7); 6B(2); 6A(1); 2A(2); 1B(1); 1A(5)	6B(1); 5A(2); 3B(3); 3A(1)
E07	7D(3); 5D(1); 5A(1); 2B(9); 1A(1)	7B(1); 7A(1); 6B(3); 5B(4); 5A(3); 4B(2); 4A(5); 2A(1); 1D(1); 1A(1)
E08	7D(1); 6B(2); 5A(5); 3A(1); 1A(5)	7A(1); 6B(6); 2D(1); 1D(3); 1B(1)
E09	6D(1); 6B(4); 3B(7); 2D(1); 2A(2); 1A(1)	7B(1); 7A(1); 6B(7); 6A(2); 5A(1); 4B(3); 4A(3); 3B(10); 2D(1); 2A(2)
E10	6B(2); 5A(17); 3A(4); 2A(1)	7A(2); 5B(1); 5A(4); 4B(4); 4A(2); 3D(1); 3B(1); 1D(6); 1A(2)
IR	3A(1); 2A(2)	7B(1); 6A(26); 5A(5); 4B(1); 3D(1); 3B(4); 2B(3); 1D(1); 1A(4)
RF	7A(2); 5A(1); 3A(1); 2D(1); 2A(29)	6B(1); 6A(1); 5B(1); 5A(1); 1B(2); 1A(2)
DT	7D(1); 7A(1); 5A(5); 2B(9); 2A(1); 1A(1)	7A(1); 5B(1); 1B(1)

DS	MTAs	MTAs
	NOT	**PH**
E01	7A(1); 6D(4); 5B(1); 3A(1)	7D(1); 7B(5); 6B(1); 4B(9); 2D(1); 1A(7)
E02	6D(1); 3B(1); 3A(2); 2B(2)	6D(4); 4B(2); 4A(1); 3D(4); 3A(2); 2D(2); 1B(2); 1A(8)
E03	7A(2); 6B(1); 5D(1); 5A(2); 4B(1); 2D(2); 2B(3); 2A(22); 1B(1)	5B(1); 4B(1); 3D(1); 3A(3); 2B(1); 1A(7)
E04	7A(1); 6A(1); 5B(7); 1B(1); 1A(2)	7B(2); 6B(2); 5D(2); 5B(19); 4B(2); 3B(2); 1B(1)
E05	4B(1); 4A(1); 2D(1); 2B(2); 2A(1)	7A(1); 6D(1); 5D(2); 3D(1); 3B(1); 3A(5); 2D(1); 1A(1)
E06	7B(1); 6B(1); 1A(2)	6D(5); 4A(1); 3D(5); 3A(8); 1B(1); 1A(2)
E07	7A(2); 6B(2); 5B(1); 4B(3)	7D(1); 6B(1); 5B(2); 3D(6); 3B(1); 2D(2); 1B(1); 1A(3)
E08	7D(2); 7B(4); 7A(5); 6B(3); 6A(4); 5B(7); 5A(1); 4D(1); 4B(5); 4A(3); 3D(1); 3B(10); 2D(3); 2B(11); 2A(4); 1D(1); 1B(6); 1A(4)	7A(3); 6B(1); 5B(10); 4B(1); 3D(1); 3A(2); 2D(1)
E09	7B(2); 4B(1); 3B(2)	7A(1); 4A(2); 2B(1); 1B(2)
E10	3B(1)	7A(1); 4A(2); 2B(1); 1B(2); 1A(10)
IR	7A(2); 5B(1); 4B(1); 4A(1); 2A(46)	7D(1); 7A(1); 5B(1); 5A(1); 4B(2); 3D(1); 3A(3); 1B(1); 1A(8)
RF	5B(2); 2B(2); 1A(2)	6D(4); 5B(1); 4A(1); 3D(2); 3A(3); 2B(2); 1B(1); 1A(8)
DT	6A(1); 5B(5); 4A(2); 3B(3); 2B(2); 1D(1)	7A(2); 6B(2); 5D(1); 5B(27); 4B(3); 3D(1); 3A(2); 2D(1); 1B(3)
	PL	**SL**
E01	7B(4); 7A(1); 6B(1); 5B(3); 5A(1); 4A(1); 3B(1); 3A(1); 2A(1); 1A(2)	6B(7); 5A(1); 3A(1); 2A(2)
E02	7A(1); 5B(3); 5A(3); 4B(7); 3D(3); 3B(2); 2B(1); 1B(3); 1A(17)	6B(1); 5A(1); 4A(1); 3D(2); 3B(3); 3A(1); 1B(1); 1A(1)
E03	7D(1); 7A(1); 4B(2); 3A(2); 1B(1); 1A(2)	7B(1); 7A(2); 4A(2); 3B(2); 1D(1); 1B(3); 1A(3)
E04	7A(1); 6B(1); 5B(4); 5A(1); 4A(1); 2D(2)	7B(1); 5B(1); 3A(1); 2A(3)
E05	5A(2); 4B(2); 4A(2); 3D(1); 3B(18)	7B(1); 7A(3); 6A(1); 5D(2); 5B(1); 5A(4); 3B(3); 2A(1); 1D(3); 1B(1); 1A(9)
E06	7A(1); 4A(1); 3D(4); 3B(3); 3A(2)	7B(1); 6B(1); 5B(1); 3B(2); 2A(1); 1D(1); 1B(1); 1A(3)
E07	6B(3); 4A(1); 3D(2); 2B(1); 2A(4)	7B(1); 7A(10); 4B(1); 2B(1); 2A(1); 1D(3)
E08	7B(2); 7A(1); 6A(1); 5B(3); 5A(2); 4B(3); 3B(3); 3A(3); 2D(5); 1B(1)	2B(1)
E09	5B(1); 4B(13); 2B(1); 1A(6)	
E10	6B(1); 5A(4); 4B(3); 3B(1); 2B(1); 1A(1)	
IR	7B(1); 7A(1); 4B(2); 3D(2); 1A(9)	4A(2); 3B(3); 2B(7); 2A(1); 1D(3); 1B(2); 1A(2)
RF	7A(2); 5B(1); 5A(4); 4B(9); 3D(3); 3B(2); 1B(1); 1A(8)	7D(1); 7A(1); 6B(1); 6A(1); 5D(4); 5A(1); 4A(1); 3D(4); 3B(2); 3A(1); 1D(1); 1B(1); 1A(1)
DT	7B(1); 7A(4); 5B(4); 5A(2); 4B(3); 3B(1); 3A(1); 2D(4); 2A(2)	5A(1); 2B(1); 2A(1)

DS	MTAs	MTAs
	SPS	**BY**
E01	6B(3); 5B(1); 5A(1); 3D(3); 2B(5); 2A(1); 1A(1)	7B(2); 6D(1); 6B(4); 5B(1); 3B(3); 1B(1)
E02	6B(1); 2B(2)	7A(4); 6B(6); 6A(1); 5B(1); 3B(5); 2D(1); 1A(1)
E03	7B(1); 7A(5); 6B(2); 6A(3); 3D(1); 3A(1)	7B(1); 6B(2); 6A(1); 5A(2); 3B(1); 2B(4); 2A(17); 1B(3)
E04	6B(1); 5B(7); 3B(1); 1D(1)	7A(2); 4A(1); 3D(9); 3B(1); 2B(1)
E05	7B(2); 7A(7); 6A(8); 5B(1); 2B(1); 1B(1); 1A(1)	7B(1); 6B(4); 6A(1); 5D(1); 5B(1); 3B(1); 2A(1); 1B(2)
E06	7B(1); 7A(9); 3A(1); 2D(1); 2A(1)	6D(4); 6B(4); 6A(3); 4D(1); 1A(1)
E07	7A(1); 6B(3); 2B(1); 1D(1); 1A(1)	7B(1); 5B(3); 5A(2); 4A(1); 3D(5); 2B(4); 2A(1); 1B(5); 1A(1)
E08	7A(8); 5A(1); 2A(1); 1D(1); 1B(1); 1A(1)	3B(1); 2B(3)
E09		7B(3); 3A(1); 2A(1); 1B(1)
E10		7A(1); 6A(3); 5B(2)
IR	7A(5); 6B(3); 6A(4); 3D(1); 2B(1); 1A(2)	7A(1); 5D(1); 5A(1); 4A(1); 3D(2); 3B(1); 2D(1); 2B(1); 1D(1); 1B(3)
RF	7A(5); 6B(3); 2B(7); 2A(1)	7A(3); 6A(5); 5B(2); 2B(14); 2A(1); 1B(4)
DT	7A(6); 3B(2); 2A(1); 1D(3)	2A(2); 3B(1); 3D(1); 4A(1); 6A(1); 7A(1); 7D(1)
	GY	**HI**
E01	7B(10); 6D(1); 6B(9); 5A(2)	6B(2); 5A(2); 3D(12); 3B(7); 2B(1); 1B(1)
E02	7B(1); 7A(7); 6B(4); 5B(3); 4A(1); 3B(2); 2B(3)	7A(6)
E03	6B(1); 3B(2); 3A(2); 2A(5); 1B(1)	7A(1); 6B(3); 5A(4); 3B(2); 3A(3); 2B(1)
E04	7B(1); 4A(2); 3A(4)	5B(15); 4A(3); 3A(1); 2B(1); 2A(1)
E05	7B(1); 7A(1); 6B(2); 6A(1); 3A(2); 2A(1); 1D(1); 1A(1)	7B(2); 6D(2); 5B(1); 5A(2); 4B(1); 3B(2); 3A(4); 2B(2); 2A(1); 1B(1)
E06	7B(5); 7A(2); 6B(2); 6A(1); 5D(1); 5B(3); 4A(1); 3A(1); 1D(4)	4A(1); 3D(6); 2B(2)
E07	7B(1); 7A(2); 6A(4); 5D(1); 5B(5); 5A(1); 4D(1); 4B(1); 4A(1); 3D(2); 3B(2); 2D(2); 2B(5); 2A(3); 1B(5); 1A(2)	7B(1); 7A(1); 6B(2); 2B(1); 1A(2)
E08	5B(2); 3B(2); 2B(2); 1B(1); 1A(1)	7D(2); 7B(1); 7A(3); 6D(1); 2A(1)
E09	7B(5); 6B(1); 3B(1); 1A(1)	6D(1); 6B(1); 6A(1); 5B(1); 3A(2); 1A(1)
E10	-	6A(1); 5A(1); 2B(4); 2A(1); 1B(4)
IR	5D(1); 5A(1); 3D(7); 3B(1); 3A(3); 2B(1); 1A(1)	6B(1); 5B(1); 3B(2); 3A(4)
RF	7B(3); 7A(1); 6B(1); 6A(6); 5D(1); 5B(6); 4A(1); 1B(1)	7A(2); 5B(1); 4A(1); 3D(6); 3B(1); 2B(2)
DT	7A(2); 6A(2); 5B(1); 4A(1); 3D(1); 3A(1); 1B(1)	5B(17); 4A(3); 2B(1)

DS	**MTAs**	**MTAs**
	TNSC	**WSC**
E01	5B(3);5A(2);3B(1)	-
E02	7B(1);6B(2);5B(1);5A(2);3A(11);1B(5)	3A(2);2A(1)
E03	5B(8);3B(2);3A(1);1A(2)	6B(1);4B(5);3A(1);2A(1)
E04	6A(3);4B(1);3B(1);3A(2);1B(1)	5B(1);4B(1);3D(1);2D(7)
E05	3B(1);2D(1);1B(3);1A(3)	7B(2);7A(2)
E06	7B(3);7A(10);5D(3);1A(1)	7A(3);6D(6);6B(1);3B(11);3A(3);1A(7)
E07	3B(7);2A(1)	7A(4);5B(1);3D(5);3A(1);2B(2)
E08	7B(5);6B(1);6A(1);5B(2);3D(1); 3A(3);2D(2);1A(6)	7B(2);5A(2);3B(1);3A(2);2B(1)
IR	2B(1);1A(1)	7A(1);6D(1);4B(8);3A(1);2B(10);1B(5)
RF	6D(3);2B(1)	7A(1);6D(4);6B(1);6A(1);3D(1);3A(1)
DT	7A(1);6B(1);6A(1);3A(13);2B(1);1B(12)	4A(1);3D(2);3B(1);2B(6)
	Glucose	**Fructose**
E01	6B(1);3B(5)	7A(1);5B(6);5A(4);3B(2);3A(1);1B(2)
E02	7B(7);1B(1);1A(2)	5B(8);2B(3);1B(2);1A(3)
E03	7B(1);6B(2);5B(1);1B(2)	7A(1);5B(5);3B(1);3A(1);2B(1)
E04	6A(1);5B(19);5A(1);2A(6);1B(4);1A(1)	5B(1);3B(19);2B(1)
E05	7B(9);6B(1);4A(1);3B(2)	6B(2);5A(1);2D(1);1A(7)
E06	7B(1);7A(2);6D(1);5D(1);5A(1);4A(1);2A(5)	7A(5);3B(2);2B(1);1B(1)
E07	5B(4);5A(1);3A(1);2B(2);2A(2)	1B(2);1A(3)
E08	7D(1);6A(2);3D(1);1D(1)	7B(1);3B(2);3A(1);2B(10);1A(3)
IR	7B(1);6B(3);6A(4);5B(2);3B(3);3A(2);2A(1);1B(1)	5B(2);3A(1);2A(5);1A(8)
RF	6D(3);6B(1);5A(1);1B(2)	7B(1);7A(1);2D(1);1B(2);1A(6)
DT	7A(1);6A(3);2A(5);1B(1)	7D(1);7A(8);2B(1);1B(5)
	Sucrose	**Fructans**
E01	6B(1);3B(5)	5B(2);5A(3);3B(2)
E02	7B(9);1B(1);1A(4)	7B(2);7A(1);6B(1);5B(1);5A(5); 3B(1);3A(11);1D(1);1B(4)
E03	6B(1);5B(1);1B(2)	5B(8);3A(1);2A(1);1A(2)
E04	6A(1);5B(1);5A(1);2A(6);1B(4);1A(1)	6A(4);4B(1);3B(1);3A(3);1B(1)
E05	7B(8);6B(2);4A(1);3B(2)	2D(1);1B(2);1A(3)
E06	7B(1);7A(2);6D(1);5D(2);5A(1);4A(1);2A(6)	7B(3);7A(8);5D(3);3A(1);1B(1)
E07	5B(4);5A(1);3B(2);3A(3);2B(1);2A(2)	3B(7);1B(1)
E08	7D(1);6A(2);3D(1);1D(1)	7B(5);6B(1);6A(1);5B(2);3A(3);2D(2); 1A(8)
IR	7B(1);6B(3);6A(3);5B(3);3B(2);2A(1)	1A(1)
RF	6D(3);5A(1);1B(2)	6D(2);2B(1)
DT	7A(1);6B(1);6A(3);2A(5);1B(1)	7A(1);6A(1);3A(11);2B(1);1B(9)

Annexure 8: List of stable MTAs and associated IWGSC Ref Seq1.0 genes

Trait	SNP	LG	Position	MAF	FDR	SNP effect	$-\log_{10}P$	PEV	Gene
DTH; GFD	AX-94501008	7B	1.72	0.158	0.34-0.96	-1.68-2.00	2.92-3.55	5.65-25.38	TraesCS7D02G543400
TKW; TNG	AX-94404953	7B	7.73	0.344	0.92-0.99	-6.46-0.98	2.93-4.20	8.83-11.11	TraesCS7D02G539500
PL	AX-94722223	5A	70.36	0.341	0.56-0.65	0.70-0.76	3.29-3.37	8.95-16.63	TraesCS7D02G509500
SPS; TKW	AX-94440790	7A	111.03	0.435	0.07-0.99	-0.61-1.42	3.31-4.87	7.46-17.16	TraesCS7D02G467700
DTH	AX-94583229	7A	37.77	0.09	0.71-1.00	1.44-2.04	2.90-2.94	14.26-22.87	TraesCS7D02G433100
DTA; DTM	AX-94508292	7D	127.78	0.191	0.74-1.00	1.14-1.36	2.98-3.15	11.66-22.02	TraesCS7D02G397800
DTM	AX-95070617	7A	30.66	0.135	0.76-0.99	-1.20--1.03	3.11-3.32	7.73-13.44	TraesCS7D02G188300
BY	AX-94503932	7A	30.66	0.246	0.47-0.58	1.00-1.54	3.21-4.01	18.74-23.17	TraesCS7D02G183600
TKW	AX-94883629	7A	29.9	0.252	0.80-1.00	1.20-1.23	3.22-3.55	7.53-8.24	TraesCS7D02G142800
TKW	AX-95022590	7B	1.72	0.468	0.59-1.00	0.96-1.10	3.02-3.27	7.95-11.92	TraesCS7B02G492700
TKW	AX-94767893	7B	2.5	0.442	0.71-0.80	0.94-1.02	2.91-3.03	6.60-11.60	TraesCS7B02G484300
TKW	AX-94848105	7B	18.98	0.163	0.97-0.97	-1.17--1.15	3.01-3.02	11.16-11.17	TraesCS7B02G471600
TNG	AX-94960851	7B	35.91	0.249	0.99-1.00	-8.12--5.52	3.07-3.21	5.12-8.26	TraesCS7B02G430700
TKW	AX-95157119	7B	92.74	0.478	0.59-1.00	0.90-1.50	3.17-3.77	9.81-14.23	TraesCS7B02G387200
SL	AX-94754235	7B	104.44	0.493	0.60-0.86	0.30-0.34	2.95-3.00	16.45-17.61	TraesCS7B02G363700
SPS	AX-95176438	7B	106	0.07	0.59-0.99	-0.96--0.80	2.90-3.24	11.88-13.14	TraesCS7B02G362200
TKW	AX-94684001	7D	154.24	0.294	0.99-1.00	-1.45--1.13	2.95-3.17	8.95-10.24	TraesCS7B02G318000
PH	AX-94749857	7A	29.9	0.422	0.77-0.87	-3.69--2.58	2.99-3.50	42.22-51.47	TraesCS7B02G299700
TKW	AX-95170264	7A	29.9	0.271	0.80-1.00	1.10-1.22	3.27-3.36	7.13-8.44	TraesCS7B02G044200
DTM	AX-95071279	7A	142.16	0.075	0.47-0.76	-2.15--1.07	3.19-4.27	13.27-22.55	TraesCS7A02G501500
SPS; TKW	AX-94512826	7A	109.61	0.439	0.07-1.00	-1.54-0.62	2.91-4.95	7.65-17.31	TraesCS7A02G482200
SPS; TKW	AX-94514616	7A	108.01	0.437	0.07-0.99	-1.43-0.63	3.40-4.99	7.51-17.28	TraesCS7A02G482000
SPS; TKW	AX-94430071	7A	110.66	0.435	0.07-0.99	-1.38-0.59	3.20-4.74	7.29-17.10	TraesCS7A02G481400
PH	AX-95186177	7D	154.24	0.284	0.55-0.86	-3.35--2.77	2.96-3.45	41.68-51.82	TraesCS7A02G417900
PL	AX-94458183	7A	29.9	0.224	0.09-0.65	1.49-1.56	3.82-4.77	11.00-17.34	TraesCS7A02G351900
BY	AX-95256072	7A	29.86	0.287	0.58-0.97	0.71-1.02	2.94-3.24	5.12-18.78	TraesCS7A02G348800
DTH; DTA	AX-94856882	7A	37.77	0.083	0.64-1.00	1.37-2.22	2.93-3.32	13.54-27.87	TraesCS7A02G285100
BY	AX-94827150	7A	30.66	0.254	0.42-0.58	-1.61--0.96	3.13-4.54	18.63-23.83	TraesCS7A02G183100
GY	AX-94671981	7A	29.9	0.066	0.45-0.84	0.34-0.42	3.38-4.03	7.18-10.36	TraesCS7A02G145100
SPS	AX-95203408	7A	29.86	0.206	0.75-0.96	0.52-0.64	2.94-3.44	5.83-8.07	TraesCS7A02G131200

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	-log$_{10}$P	PEV	Gene
SPS	AX-94805980	7A	29.86	0.068	0.59-1.00	-0.80--0.80	2.90-3.16	11.77-15.01	TraesCS7A02G123900
SL	AX-94616385	7A	24.94	0.233	0.60-0.95	-0.42--0.41	3.12-3.25	17.83-23.73	TraesCS7A02G087900
SPS	AX-94547961	6B	160.1	0.083	0.66-0.98	0.79-0.93	3.11-3.38	9.27-12.70	TraesCS6D02G399000
PH	AX-94387694	6D	15.08	0.188	0.44-0.67	-3.91--2.82	3.01-3.82	37.18-44.03	TraesCS6D02G397500
WSC	AX-94413225	6D	17.65	0.151	0.53-0.95	-13.35--8.68	3.13-3.29	5.47-5.58	TraesCS6D02G392900
WSC	AX-94921095	6D	17.65	0.153	0.53-0.95	-13.37--8.45	3.02-3.34	5.32-5.64	TraesCS6D02G391300
WSC	AX-95120751	6D	17.65	0.179	0.53-0.95	-12.94--7.98	3.06-3.50	5.37-5.88	TraesCS6D02G391200
SPS	AX-94611674	6A	221.75	0.307	0.93-0.99	0.53-0.58	2.96-3.10	13.41-16.71	TraesCS6D02G389200
SPS	AX-95124661	6A	218.41	0.2	0.59-0.99	0.52-0.60	3.16-3.44	11.81-17.34	TraesCS6D02G383700
PL	AX-94993577	2D	43.61	0.248	0.65-0.84	-1.13--0.93	3.20-4.14	16.78-17.76	TraesCS6D02G140200
PH	AX-94603303	6B	62.83	0.264	0.35-0.42	-3.63--3.48	2.93-3.22	14.16-16.97	TraesCS6D02G087600
TKW	AX-94624949	6A	0	0.234	0.55-1.00	-1.42--1.22	3.29-3.68	7.15-12.51	TraesCS6D02G011700
DTA; DTH	AX-95069379	6B	2.48	0.085	0.65-0.94	-1.74--1.27	2.94-3.43	15.24-27.88	TraesCS6D02G008200
SPS	AX-94740659	6B	147.99	0.133	0.88-1.00	-0.74--0.55	3.08-3.59	10.23-17.18	TraesCS6B02G459700
SPS; SL	AX-94857834	6A	221.75	0.215	0.59-0.99	0.28-0.63	2.89-3.73	12.27-18.99	TraesCS6B02G449900
TNG	AX-94588720	6A	100.72	0.14	0.23-0.96	7.83-9.10	3.11-4.54	4.24-6.72	TraesCS6B02G265600
TNG	AX-95013272	6A	100.72	0.131	0.23-0.96	7.91-9.97	3.55-4.50	4.90-6.66	TraesCS6B02G265300
TNG	AX-94820327	6B	61.24	0.183	0.99-1.00	-17.07--12.97	2.92-3.36	4.68-8.67	TraesCS6B02G121300
DTM	AX-94614727	6B	2.48	0.063	0.76-0.99	1.19-1.41	3.06-3.07	7.66-13.10	TraesCS6B02G010000
DTH; DTA	AX-94932242	6B	1.69	0.065	0.65-0.99	-2.31--1.48	2.95-3.22	13.03-27.89	TraesCS6B02G007400
DTA; DTM	AX-94704418	6B	1.69	0.379	0.18-0.88	-1.65--0.97	2.89-3.86	17.84-31.01	TraesCS6B02G006400
DTH	AX-94990291	6B	2.48	0.056	0.94-0.96	0.91-1.99	3.02-3.07	5.65-15.43	TraesCS6B02G000300
TKW	AX-95147877	6A	221.75	0.168	0.69-0.99	-1.36--1.05	2.89-3.00	10.32-13.48	TraesCS6A02G416500
SPS	AX-94433019	6B	147.99	0.136	0.89-1.00	0.55-0.69	3.14-3.24	15.32-17.07	TraesCS6A02G411900
GY	AX-95125171	6A	217.8	0.083	0.84-0.88	-0.50--0.30	2.89-3.03	3.98-6.67	TraesCS6A02G404800
TNG; TNG	AX-94471685	6A	100.72	0.135	0.36-0.96	7.44-9.21	3.06-4.01	4.16-5.90	TraesCS6A02G236800
Glucose; Sucrose	AX-94916179	6D	83.87	0.449	0.91-0.99	-0.40--0.20	2.99-3.49	3.48-5.76	TraesCS6A02G235200
TKW	AX-94478216	6A	0	0.238	0.55-1.00	-1.28--1.18	2.97-3.44	6.74-12.17	TraesCS6A02G007800
PH	AX-95166955	5D	1.58	0.1	0.20-0.42	-4.63--3.90	2.94-3.84	14.18-17.79	TraesCS5D02G557600
GY	AX-94524442	4A	98.78	0.45	0.68-0.84	0.19-0.32	3.27-3.36	4.54-7.16	TraesCS5D02G549600
GY	AX-94724895	5D	4.8	0.424	0.36-0.79	0.20-0.39	3.76-4.48	6.38-7.75	
TKW	AX-94597114	5B	254.02	0.068	0.79-0.99	1.66-2.03	2.96-2.98	6.80-11.50	TraesCS5D02G520800

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	-log$_{10}$P	PEV	Gene
PL	AX-94497850	5A	15.76	0.206	0.65-0.84	-2.19--1.53	3.83-3.95	17.35-17.78	TraesCS5D02G448900
DTH; GFD	AX-95002541	5A	10.64	0.314	0.22-0.98	-1.02-1.80	2.92-3.65	21.15-30.78	TraesCS5D02G402900
DTA; DTH	AX-95110067	5A	10.64	0.306	0.22-0.69	1.46-1.75	3.12-3.64	26.35-30.76	TraesCS5D02G402100
TKW	AX-94776701	5A	80.92	0.071	0.97-0.98	1.69-1.90	3.07-3.21	9.40-11.24	TraesCS5D02G272600
Glucose; Sucrose	AX-94419960	5B	55.29	0.228	0.71-0.96	-0.87--0.26	3.20-4.07	4.75-6.69	TraesCS5D02G218400
HI	AX-95187318	5B	55.29	0.133	0.50-0.56	1.64-1.88	3.37-3.40	4.69-5.66	TraesCS5D02G205100
PH	AX-94713994	5B	55.29	0.13	0.31-0.69	3.31-3.81	2.97-3.60	9.54-17.06	TraesCS5D02G202100
PH	AX-94586152	5B	54.23	0.071	0.31-0.69	4.19-4.72	2.90-3.68	9.44-16.96	TraesCS5D02G110400
PH	AX-94412625	5B	53.86	0.322	0.55-0.97	3.19-4.04	2.97-3.90	44.27-51.92	TraesCS5D02G101600
PH	AX-94483424	5B	52.43	0.458	0.16-0.31	3.10-3.44	3.39-4.25	14.78-18.35	TraesCS5D02G074500
PH	AX-94877950	5B	52.43	0.457	0.16-0.31	-3.49--3.15	3.52-4.38	14.95-18.52	TraesCS5D02G070900
GFD	AX-94931820	5B	16.31	0.181	0.98-0.99	-0.63--0.63	3.00-3.77	6.63-7.67	TraesCS5D02G017600
DTH	AX-94948453	4A	98.78	0.169	0.48-0.69	-1.78--1.53	3.10-3.11	26.28-30.19	TraesCS5B02G563900
PL	AX-94878590	5B	233.87	0.151	0.09-0.65	1.60-1.69	3.48-4.53	10.64-16.88	TraesCS5B02G500200
PL	AX-95255236	5B	233.87	0.153	0.09-0.65	1.60-1.70	3.48-4.62	10.78-16.89	
PL	AX-94924231	5A	13.46	0.323	0.52-0.94	-1.04--0.96	3.16-3.24	18.42-34.98	TraesCS5B02G428300
DTA; GFD	AX-94926419	5A	10.64	0.342	0.12-1.00	-1.90-1.33	2.91-4.35	13.58-31.39	TraesCS5B02G397900
DTH	AX-94395124	5A	10.64	0.42	0.36-0.65	0.89-1.47	3.01-3.38	27.93-30.48	TraesCS5B02G394800
PH	AX-94640891	5B	161.85	0.163	0.20-0.31	-3.84--3.61	3.49-3.84	14.92-17.79	TraesCS5B02G373100
PH	AX-94987852	5B	161.85	0.085	0.40-0.69	3.85-4.58	2.98-2.99	9.56-14.23	TraesCS5B02G372300
GY	AX-94421372	5B	161.41	0.08	0.42-0.88	-0.51-2.48	2.89-3.02	3.97-6.15	TraesCS5B02G371800
NOT	AX-94742429	5B	94.49	0.173	0.25-0.98	0.21-0.27	2.91-3.40	10.63-22.73	TraesCS5B02G236400
Sucrose	AX-94490070	5B	55.29	0.233	0.75-0.96	-0.80--0.35	3.01-3.60	4.38-5.94	TraesCS5B02G210800
Glucose; Sucrose	AX-95105243	5B	55.29	0.224	0.71-0.96	-0.76--0.25	3.25-3.73	4.85-6.18	TraesCS5B02G210100
HI	AX-95249855	5B	55.29	0.143	0.50-0.56	-1.79--1.58	3.34-3.42	4.72-5.61	TraesCS5B02G201700
HI	AX-94473314	5B	55.29	0.138	0.50-0.56	1.60-1.81	3.30-3.41	4.72-5.54	TraesCS5B02G198300
HI	AX-94410728	5B	55.29	0.145	0.50-0.56	1.58-1.81	3.42-3.45	4.77-5.72	TraesCS5B02G197300
HI	AX-94721904	5B	55.29	0.141	0.50-0.56	1.55-1.75	3.21-3.32	4.58-5.42	TraesCS5B02G195700
PH	AX-95158231	5B	55.29	0.362	0.20-0.44	2.75-3.10	2.89-3.74	14.12-17.65	TraesCS5B02G179300
PH	AX-94461509	5B	55.15	0.07	0.20-0.63	-5.49--4.71	3.75-4.64	10.64-17.93	TraesCS5B02G131500
PH	AX-94919062	5B	52.43	0.458	0.16-0.31	-3.47--3.08	3.40-4.36	14.79-18.49	TraesCS5B02G065200
PL	AX-94494739	5B	0	0.088	0.58-0.85	-1.86--1.51	2.91-3.00	10.44-34.74	TraesCS5B02G001300

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	$-\log_{10}P$	PEV	Gene
GY	AX-95224829	5D	219.57	0.154	0.42-0.59	0.69-1.72	3.03-4.09	6.15-8.76	TraesCS5B02G001300
HI	AX-94405899	5A	58.38	0.47	0.90-0.93	1.38-1.40	3.15-3.25	6.14-32.02	TraesCS5A02G529200
DTM; DTA	AX-95115670	5A	13.46	0.324	0.52-0.99	0.75-1.37	3.07-3.53	8.26-20.71	TraesCS5A02G435300
DTM; DTA	AX-94441589	5A	13.46	0.324	0.47-0.99	0.76-1.42	3.12-3.50	8.21-20.69	TraesCS5A02G432100
PL	AX-94835026	5A	13.46	0.337	0.42-0.50	1.00-1.51	3.14-3.51	30.95-35.26	TraesCS5A02G427100
PL	AX-94413482	5A	13.46	0.322	0.46-0.94	-1.47--0.98	2.93-3.28	18.17-35.02	TraesCS5A02G426800
DTA; GFD	AX-94395687	5A	10.64	0.346	0.12-1.00	-1.32-1.91	2.91-4.53	13.80-31.50	TraesCS5A02G393000
DTA; GFD	AX-94654737	5A	10.64	0.331	0.17-1.00	-1.26-1.70	2.91-4.28	13.80-31.11	TraesCS5A02G392700
DTA; DTH	AX-94445381	5A	10.64	0.291	0.48-0.88	-1.65--0.96	2.89-3.10	22.27-30.18	TraesCS5A02G392500
DTH; DTM	AX-94796479	5A	11.38	0.379	0.12-0.80	1.12-2.34	2.97-4.52	14.30-31.75	TraesCS5A02G392000
DTA; DTM	AX-94699167	5A	11.38	0.385	0.11-1.00	0.75-2.41	2.91-5.13	12.72-32.45	TraesCS5A02G391400
DTH	AX-94543559	5A	10.64	0.291	0.43-0.69	-1.68--1.50	3.03-3.25	26.19-30.34	TraesCS5A02G391200
DTH	AX-95257620	5A	89.02	0.053	0.76-0.96	-2.51--0.94	3.16-3.25	5.78-14.68	TraesCS5A02G320300
DTH	AX-94456473	5A	89.02	0.053	0.76-0.96	0.94-2.51	3.16-3.25	5.78-14.68	TraesCS5A02G320100
HI	AX-94389848	5B	55.29	0.141	0.50-0.56	1.55-1.75	3.21-3.32	4.58-5.42	TraesCS5A02G199700
NOT; PH	AX-94600532	5B	45.36	0.437	0.16-0.91	0.13-3.17	2.89-4.47	14.27-24.95	TraesCS5A02G041600
Glucose; Sucrose	AX-94560557	2A	179.61	0.264	0.52-0.99	0.25-0.55	3.22-3.86	4.09-5.78	TraesCS4D02G271400
PL; PH	AX-94807852	4B	94.44	0.08	0.10-1.00	1.64-5.88	3.01-4.31	30.65-51.48	TraesCS4D02G041500
TKW	AX-94904565	4D	0	0.372	0.29-0.95	0.86-1.33	3.48-4.70	7.64-14.32	TraesCS4D02G006200
TKW	AX-94546744	4B	146.87	0.058	0.97-0.98	-2.02--1.97	2.95-3.10	9.03-11.28	TraesCS4D02G003600
SPS; TKW	AX-95173991	7A	109.61	0.427	0.10-0.99	-0.58-1.32	3.06-4.48	6.91-17.01	TraesCS4B02G358900
PL	AX-94438800	4B	86.54	0.179	0.11-1.00	1.29-1.97	2.93-4.90	19.07-36.72	TraesCS4B02G264100
PL; GFD	AX-94502357	4B	86.54	0.196	0.58-0.94	-1.30--1.03	2.90-3.64	5.82-34.82	TraesCS4B02G260800
GFD; GFD	AX-94623317	4B	86.54	0.198	0.59-0.71	-1.09--1.07	2.98-3.45	5.93-9.72	TraesCS4B02G260200
PL; PH	AX-95238241	4B	89.57	0.221	0.10-0.72	-3.20--1.24	3.93-5.02	11.87-36.63	TraesCS4B02G207600
PH; PL	AX-94938436	4B	89.57	0.252	0.20-0.72	-2.74--1.20	3.15-3.75	11.03-30.95	TraesCS4B02G206900
TNG	AX-95222171	3B	85.27	0.407	0.99-1.00	-9.20--5.90	2.90-3.48	5.52-8.01	TraesCS4B02G201100
PH	AX-94785791	4B	89.71	0.186	0.31-0.69	2.81-3.15	3.02-3.34	9.60-14.72	TraesCS4B02G155800
PL	AX-94695861	4B	90.35	0.071	0.56-0.65	1.21-1.41	3.23-3.55	8.74-16.98	TraesCS4B02G084400
PH	AX-94629926	4B	111.19	0.314	0.55-0.67	-3.25--2.38	3.54-3.66	42.32-51.88	TraesCS4B02G019400
PH; HI	AX-94871084	4A	87.58	0.12	0.78-1.00	-3.88-2.03	2.97-3.32	11.82-41.78	TraesCS4B02G016000
PH	AX-94907472	4A	192.3	0.321	0.61-0.96	-2.43--2.32	3.44-4.38	26.94-28.52	TraesCS4A02G444800

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	**SNP**	**LG**	**Position**	**MAF**	**FDR**	**SNP effect**	**-log$_{10}$P**	**PEV**	**Gene**
BY	AX-95257049	4A	90.98	0.355	0.50-0.76	1.22-3.73	2.90-2.99	7.62-9.13	TraesCS4A02G305300
PL	AX-94594579	4B	90.35	0.078	0.56-0.65	-1.28--1.16	3.19-3.21	8.69-16.53	TraesCS4A02G230200
NOT	AX-95245753	4A	77.63	0.462	0.21-0.98	0.13-0.19	3.08-3.25	11.11-22.35	TraesCS4A02G223300
HI	AX-94432115	2B	126.67	0.251	0.50-0.56	1.31-1.53	3.49-3.50	4.84-5.84	TraesCS4A02G135300
BY	AX-94392971	3D	194.75	0.292	0.50-0.76	-4.39--1.41	3.00-3.01	7.76-9.16	TraesCS3D02G543800
SL	AX-94880594	3D	178.6	0.073	0.82-0.98	0.56-0.60	3.00-3.33	15.29-19.11	TraesCS3D02G529200
PH; HI	AX-94934210	3D	174.67	0.213	0.19-1.00	-3.97-2.01	2.93-4.39	11.62-44.60	TraesCS3D02G524000
PL; PH	AX-94731719	3D	175.42	0.216	0.15-1.00	-3.66-1.96	2.91-4.42	11.48-44.17	TraesCS3D02G523200
HI	AX-94541936	3D	174.29	0.203	0.25-1.00	1.26-2.03	3.04-4.25	11.66-26.36	TraesCS3D02G521900
HI; PH	AX-95111016	3D	174.29	0.194	0.07-1.00	-2.29-3.88	3.13-5.30	12.65-44.50	TraesCS3D02G521300
SL	AX-94978418	3B	204.37	0.128	0.82-0.98	-0.33--0.32	2.98-3.24	14.83-19.41	TraesCS3D02G516800
SL	AX-94915269	3B	204.37	0.116	0.68-0.98	-0.38--0.36	3.45-3.85	15.46-20.20	TraesCS3D02G514000
PH; SPS	AX-94544285	3D	153.17	0.203	0.31-0.99	-3.77--0.47	3.03-3.70	10.48-16.80	TraesCS3D02G508100
PH	AX-95087614	3A	170.08	0.065	0.89-0.95	5.36-6.94	2.93-3.28	49.00-51.43	TraesCS3D02G460600
SPS	AX-94518159	3B	126.94	0.291	0.75-0.96	-0.34--0.33	3.00-3.12	4.77-6.09	TraesCS3D02G454800
SL	AX-94934740	3B	102.29	0.146	0.60-0.80	0.38-0.53	3.14-3.29	18.04-23.59	TraesCS3D02G437200
SL	AX-95004760	3B	102.29	0.146	0.60-0.80	0.36-0.51	2.98-3.16	17.88-23.39	TraesCS3D02G434700
Fructans	AX-95225454	3A	77.94	0.115	0.24-0.94	-13.66--12.80	3.02-4.65	9.40-10.09	TraesCS3D02G258300
PL	AX-95181743	3B	83.69	0.38	0.43-0.58	1.05-1.73	3.00-3.01	30.80-34.73	TraesCS3D02G124300
NOT	AX-94888872	3B	9.82	0.427	0.21-0.98	0.11-0.17	3.02-3.21	11.05-22.27	TraesCS3D02G006900
SL	AX-94883935	3A	250.41	0.118	0.82-0.98	-0.35--0.32	2.89-3.34	14.71-19.55	TraesCS3B02G592000
PH	AX-95222491	3A	186.94	0.126	0.26-0.60	-4.34--3.72	3.99-4.14	10.98-15.80	TraesCS3B02G525700
DTA; DTH	AX-94712794	3A	127.87	0.206	0.26-0.68	1.05-1.86	3.21-3.94	22.83-30.36	TraesCS3B02G448900
PL	AX-94461356	3B	85.27	0.282	0.68-0.96	1.70-2.14	2.91-2.95	32.30-35.07	TraesCS3B02G302100
PL	AX-94485572	3B	85.27	0.282	0.68-0.96	1.70-2.14	2.91-2.95	32.30-35.07	
PL	AX-94448198	3B	85.27	0.282	0.68-0.96	1.70-2.14	2.91-2.95	32.30-35.07	TraesCS3B02G301800
WSC	AX-95111986	7A	113.4	0.209	0.53-0.95	7.07-10.80	3.22-3.26	5.53-5.61	TraesCS3B02G244700
PL	AX-94567252	3B	83.69	0.38	0.43-0.58	1.05-1.73	3.00-3.01	30.80-34.73	TraesCS3B02G142100
DTA; DTH	AX-95144587	3B	83.69	0.252	0.61-0.94	-1.14--0.94	3.00-3.43	14.69-28.43	TraesCS3B02G100700
BY	AX-95240885	3B	61.77	0.199	0.66-0.78	-3.51--0.77	3.25-3.70	13.79-22.22	TraesCS3B02G067600
BY	AX-94486759	3B	61.01	0.392	0.66-0.78	0.71-2.96	3.04-3.10	12.88-22.04	TraesCS3B02G064500
NOT	AX-95152594	3B	13.6	0.088	0.21-0.98	0.21-0.30	3.24-3.38	11.29-22.54	TraesCS3B02G038400

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	$-\log_{10}$P	PEV	Gene
SL	AX-94809409	3B	8.28	0.116	0.20-0.95	-0.52--0.44	3.15-4.38	16.64-25.09	TraesCS3B02G026700
PL	AX-94598770	3D	194.61	0.286	0.97-1.00	-1.50--1.25	2.99-3.16	24.28-36.36	TraesCS3A02G538500
BY	AX-95255318	3D	194.75	0.289	0.50-0.76	-4.49--1.40	2.93-3.08	7.88-9.06	TraesCS3A02G538200
SL	AX-94681641	3D	175.97	0.133	0.82-0.98	0.32-0.33	3.09-3.34	14.97-19.55	TraesCS3A02G526100
HI	AX-94777654	3D	176.17	0.201	0.83-1.00	1.04-1.96	2.97-3.20	11.57-25.09	TraesCS3A02G519800
PH; HI	AX-94722325	3D	176.91	0.208	0.27-1.00	-2.00-4.46	3.01-4.26	11.61-51.49	TraesCS3A02G518500
PH	AX-94511558	3A	222.38	0.246	0.39-0.69	-3.11--2.44	3.00-3.36	10.08-14.26	TraesCS3A02G505000
NOT	AX-94646681	3B	186.73	0.261	0.21-0.91	-0.29--0.17	3.57-4.84	13.38-22.94	TraesCS3A02G489900
DTA; DTM	AX-95218695	3A	127.87	0.109	0.61-0.99	-2.17--1.64	3.02-3.44	17.41-26.56	TraesCS3A02G413700
PH	AX-94522663	3A	84.43	0.241	0.30-0.80	-6.37--3.67	2.95-4.26	41.75-42.93	TraesCS3A02G305600
SPS	AX-94686023	6B	105	0.433	0.89-0.99	-0.44--0.44	2.91-3.31	13.15-17.17	
Fructans; TNSC	AX-94472299	3A	77.94	0.116	0.23-0.95	-13.98--12.36	2.90-4.40	8.62-9.72	TraesCS3A02G258500
Fructans; TNSC	AX-95204178	3A	77.94	0.14	0.23-0.95	11.15-13.20	3.09-4.33	8.89-9.74	TraesCS3A02G258100
PH; HI	AX-94407346	3A	74.06	0.176	0.08-0.97	-9.80-4.43	3.01-5.28	7.29-52.71	TraesCS3A02G244700
PH	AX-94473921	3A	73.31	0.181	0.30-0.97	5.93-9.14	2.98-4.13	37.02-51.80	TraesCS3A02G233300
NOT	AX-94461492	2B	104.59	0.07	0.21-0.98	0.22-0.34	3.00-3.37	11.28-22.25	TraesCS2D02G502600
TKW	AX-94551988	2A	130.2	0.357	0.97-0.98	-1.06--0.99	3.15-3.72	9.31-12.14	TraesCS2D02G478700
SL	AX-94679692	4A	214.31	0.434	0.80-0.95	0.27-0.36	3.01-3.02	23.42-23.45	TraesCS2D02G464300
DTM	AX-94933613	2B	103.81	0.12	0.74-0.74	-1.73--1.48	3.33-3.58	16.96-21.35	TraesCS2D02G408300
DTM	AX-94836925	2B	103.81	0.116	0.74-0.74	-1.66--1.39	3.25-3.39	16.71-21.26	TraesCS2D02G405000
NOT	AX-95128830	2A	1.59	0.369	0.32-0.53	-0.60--0.23	3.00-3.13	12.31-15.79	TraesCS2D02G050300
NOT	AX-94849785	2A	1.59	0.37	0.32-0.53	-0.58--0.23	2.92-2.98	12.10-15.68	TraesCS2D02G049500
NOT	AX-95188846	2A	1.59	0.364	0.32-0.53	0.23-0.57	2.93-2.99	12.11-15.69	TraesCS2D02G048800
NOT	AX-94946002	2A	1.59	0.35	0.32-0.53	0.23-0.67	2.93-3.86	13.32-15.69	TraesCS2D02G047900
DTH; DTA	AX-95005889	2B	27.22	0.331	0.43-1.00	-1.47--1.08	2.96-3.57	12.18-28.04	TraesCS2D02G039500
PL	AX-95256064	2D	17.23	0.058	0.09-0.65	-1.60--1.43	3.45-4.75	10.97-16.84	TraesCS2D02G004000
PL	AX-94554516	2D	17.23	0.058	0.13-0.65	1.40-1.52	3.21-4.27	10.25-16.53	TraesCS2D02G003700
PL	AX-95174821	2D	17.23	0.061	0.09-0.65	1.43-1.57	3.38-4.57	10.70-16.75	
HI; TKW	AX-94406983	2B	104.59	0.098	0.71-0.96	-2.53--1.36	2.91-4.31	7.25-25.31	TraesCS2B02G558300
NOT	AX-94577588	2B	104.59	0.444	0.53-1.00	0.13-0.40	2.89-2.98	6.88-11.97	TraesCS2B02G543700
NOT	AX-95256964	2B	104.59	0.485	0.53-1.00	0.14-0.46	3.50-3.54	7.65-12.88	TraesCS2B02G541200
SL	AX-95168949	2B	103.81	0.284	0.56-0.90	0.38-0.39	2.90-3.57	14.46-24.10	TraesCS2B02G448400

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	-$\log_{10}$P	PEV	Gene
DTM	AX-94520095	2B	103.81	0.118	0.74-0.79	-1.59--1.34	2.99-3.15	16.39-20.93	TraesCS2B02G431400
DTM	AX-94508388	2B	103.81	0.131	0.74-0.74	-1.65--1.38	3.39-3.52	16.88-21.43	TraesCS2B02G430300
NOT;	AX-94670661	2B	103.81	0.103	0.21-0.98	0.18-0.28	3.14-3.26	11.12-22.42	TraesCS2B02G425800
SL	AX-95158415	2B	96.73	0.41	1.00-1.00	0.19-0.21	3.00-3.04	5.31-5.41	TraesCS2B02G371100
DTH; DTA	AX-95130954	1B	147.26	0.493	0.56-0.94	0.95-1.67	3.00-3.48	15.07-30.06	TraesCS2B02G172300
SPS	AX-94614804	2B	77.03	0.133	0.67-0.98	-0.64--0.53	2.95-3.19	9.04-12.43	TraesCS2B02G111000
DTM	AX-94594842	2A	24.5	0.322	0.44-0.92	-0.73--0.67	2.95-3.11	12.67-12.93	TraesCS2B02G094700
DTM	AX-94717360	2A	22.81	0.336	0.44-0.92	-0.83--0.72	3.63-3.81	13.65-13.84	TraesCS2B02G094100
NOT	AX-95162683	2A	1.59	0.375	0.32-0.53	0.25-0.65	3.53-3.66	13.04-16.49	TraesCS2B02G065300
NOT	AX-94652823	2A	1.59	0.355	0.32-0.53	0.23-0.55	2.98-3.04	12.10-15.84	TraesCS2B02G058500
NOT	AX-94454353	2A	1.59	0.355	0.32-0.53	0.23-0.58	3.00-3.02	12.15-15.78	TraesCS2B02G056800
DTH; DTA	AX-94870786	2B	27.22	0.339	0.34-1.00	1.13-1.71	3.04-3.87	15.49-28.18	TraesCS2B02G053600
Glucose; Sucrose	AX-95135556	2A	178.03	0.264	0.52-0.99	-0.52--0.25	3.08-3.52	3.88-5.26	TraesCS2A02G564900
HI	AX-94961148	2B	104.59	0.101	0.83-0.96	1.38-2.39	3.17-3.63	12.63-25.06	TraesCS2A02G527600
SL	AX-94874921	2A	124.18	0.173	0.96-1.00	0.21-0.27	2.89-3.11	4.35-5.09	TraesCS2A02G460800
DTA; DTH	AX-95229999	2B	103.81	0.096	0.61-0.94	1.30-1.61	2.92-3.53	14.95-28.55	TraesCS2A02G442500
DTM	AX-94772101	2B	103.81	0.126	0.74-0.74	-1.61--1.36	3.24-3.42	16.74-21.24	TraesCS2A02G411200
PH	AX-94570302	2D	216.14	0.218	0.27-0.86	-3.96--3.44	3.45-4.36	42.75-45.23	TraesCS2A02G344200
SPS	AX-95138084	2B	77.03	0.121	0.66-0.98	0.61-0.69	3.09-3.70	9.25-13.14	TraesCS2A02G095600
DTM	AX-94639372	2A	21.23	0.249	0.44-0.76	0.67-0.83	2.92-4.48	12.90-14.78	TraesCS2A02G069500
NOT	AX-95120279	2A	1.59	0.367	0.32-0.53	0.24-0.63	3.16-3.40	12.69-15.99	TraesCS2A02G050600
NOT	AX-94700495	2A	1.59	0.367	0.32-0.53	0.23-0.60	2.92-3.08	12.25-15.67	TraesCS2A02G050400
DTM	AX-94726853	2A	1.59	0.091	0.44-0.46	-2.63--1.38	3.38-3.73	13.74-17.81	TraesCS2A02G049500
NOT	AX-95177447	2A	1.59	0.364	0.32-0.53	-0.59--0.22	3.06-3.33	12.58-15.87	TraesCS2A02G046500
DTA; DTH	AX-95153371	2B	27.22	0.332	0.34-0.94	1.16-1.47	2.98-3.77	14.64-28.32	TraesCS2A02G041100
PL	AX-94817725	1B	92.71	0.282	0.21-0.61	1.25-2.37	2.90-3.69	31.54-34.64	TraesCS1D02G406600
PH	AX-94502320	1B	47.46	0.404	0.50-0.96	2.02-2.78	3.39-3.63	26.04-42.19	TraesCS1D02G378100
PL	AX-94414079	1A	74.11	0.198	0.21-1.00	2.17-3.91	3.07-3.74	31.59-36.43	TraesCS1D02G269200
PL	AX-94924436	1A	74.86	0.191	0.10-0.93	-4.82--3.56	3.49-4.16	31.07-37.37	TraesCS1D02G250700
SL	AX-94797689	1A	74.86	0.201	0.60-0.86	0.78-0.88	2.92-2.97	16.41-17.57	TraesCS1D02G249200
PL	AX-94728505	1A	74.11	0.186	0.10-0.58	-5.04--2.37	2.97-4.60	32.56-34.71	TraesCS1D02G208600
PH	AX-94755693	1A	74.11	0.159	0.50-0.96	2.51-4.32	2.92-3.63	25.21-51.89	TraesCS1D02G195500

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	-log$_{10}$P	PEV	Gene
BY	AX-94851536	1B	24.64	0.07	0.50-0.76	-7.57--2.31	3.23-3.35	8.26-9.47	TraesCS1D02G191100
PL	AX-95233406	1A	74.11	0.138	0.10-0.94	-4.21--1.87	3.14-4.25	12.03-37.30	TraesCS1D02G178000
BY	AX-94428251	1B	25.42	0.068	0.50-0.76	-7.68--2.32	3.14-3.29	8.17-9.35	TraesCS1D02G168800
SL; DTH	AX-95216172	1D	95.7	0.125	0.41-0.80	-1.90--0.41	3.00-3.95	13.72-24.56	TraesCS1D02G147600
TKW	AX-94531706	1D	67.44	0.281	0.62-1.00	-1.46--1.11	3.11-3.29	8.33-11.71	TraesCS1D02G038000
DTH	AX-94769111	1B	8.24	0.125	0.64-0.76	1.21-1.71	3.06-3.10	14.43-23.07	TraesCS1D02G013800
DTH	AX-94541931	1D	3.38	0.246	0.61-0.69	-1.70--1.36	2.92-3.28	26.49-29.98	TraesCS1D02G002000
DTA; DTH	AX-95080354	1B	147.26	0.453	0.19-0.63	0.94-1.59	3.22-3.81	28.16-30.95	TraesCS1B02G469500
GFD	AX-94429181	1B	76.83	0.397	0.94-0.98	0.45-0.55	2.96-2.99	5.08-6.53	TraesCS1B02G420100
BY	AX-94827580	1B	36.42	0.09	0.04-0.76	2.40-7.69	3.97-5.10	6.47-10.54	TraesCS1B02G335400
PH	AX-95152246	1B	35.34	0.125	0.20-0.31	-3.86--3.63	3.39-3.72	14.79-17.62	TraesCS1B02G333100
Glucose; Sucrose	AX-94384779	1B	26.22	0.12	0.94-1.00	0.30-0.51	2.91-3.63	5.42-5.96	TraesCS1B02G279100
PL;	AX-94823818	1A	74.86	0.186	0.10-0.81	-4.85--2.55	3.43-4.37	32.29-37.14	TraesCS1B02G264900
Fructans; TNSC	AX-94923277	1B	24.64	0.344	0.35-0.95	-10.68--8.77	2.89-3.85	8.61-9.33	TraesCS1B02G109400
PH	AX-94925165	1B	115.93	0.472	0.46-0.87	-3.14--2.48	3.04-3.65	44.59-51.50	TraesCS1A02G416200
GFD	AX-94736642	1A	88.71	0.473	0.30-0.49	-1.39--0.64	3.25-4.47	19.85-25.49	TraesCS1A02G374300
SPS	AX-94407377	1A	88.71	0.226	0.93-1.00	-0.59--0.46	2.99-3.16	15.35-16.75	TraesCS1A02G369900
GFD	AX-94964398	1A	88.71	0.191	0.71-0.74	0.81-1.04	3.04-3.18	9.14-19.51	TraesCS1A02G366600
GFD; DTH	AX-95146857	1A	84.76	0.203	0.25-1.00	-2.42-2.63	2.95-4.37	16.77-26.83	TraesCS1A02G353200
Fructose	AX-94583506	1A	81.31	0.42	1.00-1.00	0.21-0.59	2.90-3.37	3.68-4.61	TraesCS1A02G340000
Fructose	AX-94960090	1A	81.31	0.42	1.00-1.00	0.21-0.59	2.90-3.37	3.68-4.61	TraesCS1A02G339600
DTM	AX-94694621	1A	74.11	0.261	0.95-0.99	-1.21--1.04	2.89-3.63	8.41-16.05	TraesCS1A02G295100
SL	AX-95213368	1A	74.86	0.204	0.60-0.86	0.65-0.96	2.94-3.33	16.41-23.34	TraesCS1A02G249700
PL	AX-95164417	1A	74.86	0.193	0.10-1.00	-4.45--2.90	3.29-4.27	32.19-36.65	TraesCS1A02G247500
PL	AX-94749944	1A	74.11	0.186	0.10-0.58	-5.04--2.37	2.97-4.60	32.56-34.71	TraesCS1A02G201600
PH	AX-94623356	1A	74.11	0.14	0.63-0.95	2.89-3.79	2.93-3.34	25.70-51.43	TraesCS1A02G200600
PH	AX-95195514	1A	74.11	0.135	0.67-0.96	2.72-3.88	3.02-3.13	25.35-51.57	TraesCS1A02G196800
PH	AX-94399186	1A	74.11	0.178	0.66-0.95	2.78-3.91	3.04-3.37	41.79-51.70	TraesCS1A02G193400
SL; DTA	AX-94629635	1D	95.7	0.113	0.07-0.86	-1.92--0.36	3.05-5.34	13.47-25.71	TraesCS1A02G110400
SL	AX-95259891	1A	58.79	0.075	0.17-0.68	-0.67--0.51	3.26-4.64	18.00-20.82	TraesCS1A02G025900
SL	AX-94405726	1A	54.04	0.196	0.80-0.95	-0.44--0.32	3.18-3.25	23.63-23.73	TraesCS1A02G009900
PH; PL	AX-95082367	1A	74.11	0.171	0.44-0.96	1.20-4.47	2.92-4.20	25.89-52.40	-

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	-log$_{10}$P	PEV	Gene
DTA; GFD	AX-94404219	5A	10.64	0.326	0.12-1.00	-1.99-1.36	3.01-4.40	13.28-31.40	-
PH; PL	AX-94500378	1A	74.11	0.168	0.44-0.96	-4.39--1.15	2.90-4.01	25.33-52.18	-
PH	AX-94912730	1A	74.11	0.156	0.47-0.96	2.63-4.68	3.10-3.69	25.41-51.99	-
PH	AX-94875204	1A	74.11	0.145	0.48-0.95	2.99-4.64	3.20-3.56	25.76-51.84	-
TKW	AX-94506140	1A	50.59	0.125	0.55-0.99	1.34-1.79	2.91-3.54	6.81-13.98	-
DTH; DTA	AX-94532701	5A	10.64	0.302	0.12-0.81	0.91-1.91	2.96-4.27	14.36-31.47	-
TKW	AX-94410073	4D	0	0.385	0.31-0.95	-1.28--0.80	3.26-4.37	8.17-13.99	-
DTA; DTH	AX-94805904	3A	127.08	0.208	0.26-0.99	-1.86--1.02	2.90-3.80	20.42-30.22	-
DTA; DTH	AX-95136668	6A	43.06	0.075	0.35-0.81	1.45-2.83	2.91-3.42	22.38-30.52	-
DTH; DTA	AX-94523287	6B	10.65	0.083	0.32-0.64	1.38-2.05	2.89-4.43	16.60-29.95	-
DTH; DTA	AX-94563582	6B	1.69	0.271	0.12-0.93	1.28-2.28	3.12-4.84	15.63-31.64	-
PH	AX-94574625	6D	17.65	0.196	0.34-0.96	-4.00--2.89	2.89-4.03	37.39-44.30	-
PL	AX-94536132	1A	74.86	0.188	0.10-0.93	-5.65--3.39	2.90-4.34	22.50-36.90	-
SL; SPS	AX-94425541	1D	95.7	0.121	0.16-0.95	0.42-0.53	2.89-4.66	5.03-25.37	-
SPS	AX-94560056	2A	22.81	0.369	0.66-1.00	0.31-0.46	2.97-3.55	6.21-12.93	-
BY; GY	AX-95108394	2B	76.24	0.063	0.37-0.76	-7.03--1.01	2.98-4.09	3.84-10.03	-
DTA; DTH	AX-94679841	1A	58.79	0.331	0.17-0.99	-2.02--1.03	2.97-3.99	24.12-31.15	-
DTA; DTH	AX-95243523	6B	1.69	0.061	0.48-1.00	0.90-2.37	2.97-4.16	3.97-28.09	-
DTM	AX-94581141	5A	13.83	0.337	0.60-0.95	-1.34--1.03	3.11-3.40	8.07-17.45	-
GFD	AX-94610810	5A	13.46	0.43	0.74-0.97	-0.83--0.62	3.03-3.08	15.48-19.78	-
GFD	AX-95124645	3D	110.02	0.103	0.36-0.78	1.10-2.16	2.92-4.31	11.63-25.11	-
GFD	AX-94404055	6A	33.79	0.061	0.30-0.74	1.27-1.87	2.98-3.31	5.94-25.56	-
PH	AX-95659028	6B	45.96	0.236	0.20-0.63	3.78-4.31	3.59-4.16	10.41-17.76	-
PH	AX-94821409	6D	14.34	0.189	0.31-0.47	-4.17--3.06	3.54-4.29	37.65-44.50	-
PL	AX-94407277	7A	115.7	0.09	0.15-1.00	-2.39--1.69	3.15-4.37	31.24-36.51	-
PL	AX-94511420	1A	74.11	0.143	0.43-0.72	1.53-2.56	2.97-3.40	11.12-34.71	-
SL	AX-95222141	1B	0.79	0.447	0.04-0.68	0.28-0.43	3.19-5.53	17.92-20.30	-
TKW	AX-94388425	7A	29.9	0.236	0.45-0.74	1.07-1.43	3.51-4.51	8.98-12.26	-
TKW	AX-94449286	6A	0	0.223	0.57-1.00	-1.31--1.17	2.96-3.33	6.74-12.01	-
DTA; DTH	AX-94916741	5B	98.7	0.36	0.98-1.00	1.07-1.41	2.89-3.22	21.87-24.54	-
DTA; DTH	AX-95223292	6B	10.65	0.468	0.59-0.98	-0.82--0.66	3.13-3.68	19.32-28.43	-
DTH	AX-94600879	7B	98.96	0.36	0.98-0.98	-1.03--0.75	3.02-3.41	19.18-22.74	-

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Trait	SNP	LG	Position	MAF	FDR	SNP effect	$-log_{10}P$	PEV	Gene
DTH	AX-94581354	1D	3.38	0.475	0.12-0.69	1.49-1.54	3.06-4.21	26.23-31.41	-
DTM	AX-94662661	2B	103.81	0.121	0.74-0.74	1.39-1.59	3.02-3.39	16.71-20.96	-
Fructose	AX-94504454	1A	81.31	0.42	1.00-1.00	0.21-0.59	2.90-3.37	3.68-4.61	-
GFD	AX-94413265	7A	24.94	0.364	0.94-0.98	-0.72--0.57	3.05-3.17	5.38-6.60	-
GFD	AX-95652956	4B	86.54	0.206	0.58-0.71	-1.07--0.96	2.92-3.08	6.07-8.97	-
Glucose; Sucrose	AX-95685387	6A	0	0.06	0.52-0.99	0.51-0.97	3.43-3.95	4.97-5.20	-
Glucose; Sucrose	AX-94865722	2A	179.61	0.261	0.52-0.99	0.24-0.56	3.02-3.91	3.80-5.85	-
GY	AX-94668872	5B	219.91	0.176	0.68-0.79	-0.33--0.32	3.20-3.70	7.67-9.16	-
GY	AX-94640914	1A	74.11	0.08	0.42-0.86	-2.52--0.80	3.06-3.24	6.47-7.25	-
HI	AX-94791648	5B	55.29	0.14	0.50-0.56	1.60-1.80	3.31-3.46	4.78-5.57	-
HI	AX-94794189	5B	55.29	0.14	0.50-0.56	1.60-1.80	3.31-3.46	4.78-5.57	-
HI	AX-95629874	5B	55.29	0.14	0.50-0.56	1.57-1.78	3.27-3.37	4.65-5.50	-
HI	AX-95187081	5B	55.29	0.141	0.50-0.56	1.55-1.75	3.21-3.32	4.58-5.42	-
HI	AX-95629919	5B	55.29	0.141	0.50-0.56	1.55-1.75	3.21-3.32	4.58-5.42	-
HI; PH	AX-95652182	5B	55.29	0.136	0.31-0.69	-1.74-3.69	2.90-3.23	4.44-14.53	-
HI	AX-95684694	5B	55.29	0.143	0.55-0.59	1.52-1.74	3.15-3.18	4.37-5.33	-
HI; PH	AX-95631141	5B	55.29	0.14	0.31-0.69	-3.78-1.72	2.93-3.31	4.35-14.67	-
HI; PH	AX-95653566	5B	55.29	0.143	0.31-0.66	-3.30-1.69	2.91-3.22	4.29-16.57	-
HI	AX-95173977	4A	214.31	0.287	0.50-0.56	-1.90--1.56	3.68-4.04	5.12-6.67	-
HI	AX-95242416	4A	214.31	0.281	0.50-0.56	-1.89--1.54	3.29-3.66	4.54-6.09	-
HI	AX-94521055	3B	9.82	0.111	0.93-0.97	0.89-1.93	3.07-3.48	28.45-32.26	-
HI	AX-94382065	3B	8.28	0.118	0.76-0.93	1.05-1.90	3.55-4.28	29.83-32.34	-
NOT	AX-94457687	5B	52.43	0.424	0.83-0.91	-0.16--0.15	3.12-3.51	22.87-25.21	-
NOT	AX-95232609	2A	1.59	0.367	0.32-0.53	-0.62--0.24	3.06-3.31	12.56-15.87	-
NOT	AX-94794106	2A	1.59	0.372	0.32-0.53	0.24-0.62	3.04-3.31	12.55-15.83	-
NOT	AX-94985425	2A	1.59	0.369	0.32-0.53	0.24-0.61	3.07-3.19	12.40-15.87	-
NOT	AX-95096301	2A	1.59	0.364	0.32-0.53	0.24-0.58	3.10-3.12	12.27-15.94	-
NOT	AX-94863436	7A	33.72	0.058	0.32-0.93	0.34-0.78	3.01-3.12	12.55-15.80	-
PH	AX-94411211	7A	100.09	0.156	0.31-0.60	4.04-5.04	3.60-3.91	10.87-15.06	-
PH	AX-94412521	7A	29.9	0.191	0.26-0.60	4.69-5.65	4.08-4.17	11.25-15.72	-
PH	AX-95125039	2D	291.68	0.301	0.34-0.69	2.82-3.53	3.11-3.39	10.13-14.41	-
PH; PL	AX-95215762	4B	94.44	0.081	0.39-0.75	1.44-5.79	2.89-3.61	31.03-43.93	-
LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation									

Trait	**SNP**	**LG**	**Position**	**MAF**	**FDR**	**SNP effect**	**-log$_{10}$P**	**PEV**	**Gene**
PH	AX-94454802	6D	17.65	0.164	0.71-0.78	3.01-4.11	3.06-3.30	36.65-41.85	-
PL	AX-94588976	7A	121.66	0.457	0.65-0.84	-1.02--0.75	3.04-3.20	16.51-16.58	-
PL	AX-95103864	4B	90.35	0.076	0.56-0.65	-1.34--1.17	3.11-3.35	8.57-16.71	-
PL	AX-94874038	5A	13.46	0.324	0.46-0.52	0.98-1.46	2.90-3.29	30.68-35.03	-
PL	AX-94876965	1A	74.86	0.189	0.13-1.00	-4.87--3.17	3.11-4.00	31.88-36.47	-
PL	AX-94674955	4A	77.63	0.193	0.67-0.96	-1.58--1.25	3.01-3.08	32.40-35.20	-
PL	AX-94584538	4A	74.86	0.204	0.71-0.97	-1.66--1.62	2.91-3.28	24.42-35.03	-
PL	AX-95230878	4B	86.54	0.239	0.20-0.72	-1.21--1.15	3.26-4.01	10.92-35.78	-
SL	AX-94664966	5A	43	0.141	0.82-0.96	-0.33--0.28	3.05-3.88	16.03-19.18	-
SL	AX-94600501	7B	236.73	0.291	0.95-0.96	0.23-0.41	2.90-3.75	4.03-24.33	-
SPS	AX-95630100	6A	218.41	0.206	0.59-0.93	0.47-0.61	2.89-3.31	11.97-16.61	-
TKW	AX-95078056	2A	0	0.495	0.69-0.95	-1.05--0.93	2.98-3.38	12.08-14.07	-
TKW	AX-94490431	7A	29.9	0.269	0.80-1.00	1.13-1.23	3.38-3.41	7.29-8.50	-
TKW	AX-95238603	6A	183.23	0.475	0.95-0.98	0.71-0.92	2.93-3.13	9.29-13.47	-
TKW	AX-94804372	7B	1.72	0.41	0.55-0.99	-0.99--0.96	3.07-3.42	10.42-12.14	-
TKW	AX-94848356	7B	1.72	0.467	0.55-1.00	-1.09--0.96	3.05-3.38	7.99-12.09	-
TNG	AX-94567094	7B	2.09	0.304	0.99-1.00	-8.30--5.91	3.18-3.20	5.08-8.45	-
TNG	AX-94538262	7A	141.38	0.073	0.92-1.00	9.24-17.40	3.06-3.10	4.46-5.91	-
WSC	AX-94426796	6D	17.65	0.179	0.53-0.95	-12.94--7.98	3.06-3.50	5.37-5.88	-

LG: linkage group; FDR: false discovery rate; MAF: Minor allele frequency; PEV: explained phenotypic variation

Annexure 9: InterPro and GoSlim descriptions of identified putative genes associated with significant and stable MTAs

Gene stable ID	InterPro Short Description	GOSlim Description
TraesCS1A02G009900	NB-ARC; P-loop_NTPase; LRR_dom_sf; WH-like_DNA-bd_sf; RX-like_CC; Rx_N	molecular_function; nucleotide binding; binding; biological_process; response to stress
TraesCS1A02G025900	Prot_kinase_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf; Kinase_OSR1/WNK_CCT	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS1A02G110400	bHLH_dom; HLH_DNA-bd_sf	molecular_function; binding; protein binding
TraesCS1A02G193400	Homeobox_dom; START_lipid-bd_dom; Homeobox-like_sf; Homeobox_CS; GLABRA2/ANL2/PDF2/ATML1-like	molecular_function; binding; DNA binding; nucleic acid binding; lipid binding; biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process
TraesCS1A02G196800	RSN1_7TM; PHM7_cyt; Csc1_N	cellular_component; membrane; plasma membrane; intracellular; cytoplasm; Golgi apparatus; transport; biological_process; transporter activity; molecular_function
TraesCS1A02G201600	Sugar/inositol_transpt; MFS_sugar_transport-like; Sugar_transporter_CS; MFS_dom; MFS_trans_sf	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function
TraesCS1A02G249700	Dienelactn_hydro; AB_hydrolase	molecular_function; catalytic activity; hydrolase activity
TraesCS1A02G339600	Prot_kinase_dom; Ser-Thr/Tyr_kinase_cat_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS1A02G340000	WD40_repeat; SSU_processome_Utp12; WD40/YVTN_repeat-like_dom_sf; WD40_repeat_dom; WD40_repeat_CS; G-protein_beta_WD-40_rep; PWP2; WD40_repeat_dom_sf	molecular_function; binding; protein binding
TraesCS1A02G353200	PLC-like_Pdiesterase_TIM-brl; GP_PDE_dom	biological_process; metabolic process; lipid metabolic process; molecular_function; catalytic activity; hydrolase activity
TraesCS1A02G366600	Pectinesterase_inhib_dom; Invertase/methylesterase_inhib	molecular_function; enzyme regulator activity; biological_process; regulation of molecular function
TraesCS1A02G369900	SF3b5/RDS3-10; Splicing_factor_3B_subunit_5	biological_process; cellular process; metabolic process; nucleobase-containing compound metabolic process; cellular_component; intracellular; nucleus
TraesCS1A02G374300	Bifunc_inhib/LTP/seed_store; nsLTP2; Bifun_inhib/LTP/seed_sf	transport; biological_process
TraesCS1A02G416200	Prot_kinase_dom; Ser-Thr/Tyr_kinase_cat_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS1B02G109400	Prot_kinase_dom; Ser-Thr/Tyr_kinase_cat_dom; Kinase-like_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS1B02G264900	PEP_util_C; PPDK_PEP-bd; PEP-util_enz_mobile_dom;	molecular_function; binding; cellular_component; intracellular; nucleus; nucleotide binding; catalytic

Gene stable ID	InterPro Short Description	GOSlim Description
	Pyruvate_phosphate_dikinase; ATP_grasp_subdomain_1; Pyrv/PenolPyrv_Kinase-like_dom; PEP_util_AS; PEP_util_CS; Phosphohistidine_dom_sf; Pyrv_Kinase-like_dom_sf	activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cytoplasm; cytosol; chloroplast; plastid
TraesCS1B02G333100	Actin; Arp6	cellular_component; intracellular; nucleus; biological_process; cellular process; cellular component organization
TraesCS1B02G420100	PSI_PsaH	biological_process; cellular process; metabolic process; photosynthesis; cellular_component; intracellular; membrane; thylakoid
TraesCS1B02G469500	Leu-rich_rpt; Leu-rich_rpt_typical-subtyp; Leu-rich_rpt_Cys-con_subtyp; LRR_dom_sf; NB-ARC; P-loop_NTPase; Rx_N	molecular_function; binding; protein binding; nucleotide binding
TraesCS1D02G013800	Prot_kinase_dom; S_locus_glycoprot_dom; Bulb-type_lectin_dom; Pan_app; Ser/Thr_kinase_AS; Kinase-like_dom_sf; Protein_kinase_ATP_BS; SRK-like_kinase; Bulb-type_lectin_dom_sf	cellular_component; membrane; molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; cell communication; reproduction; pollination
TraesCS1D02G038000	Galectin_CRD; Glyco_trans_31; ConA-like_dom_sf; Nucleotide-diphossugar_trans	cellular_component; membrane; molecular_function; binding; carbohydrate binding; biological_process; cellular process; metabolic process; biosynthetic process; cellular protein modification process; protein metabolic process; intracellular; cytoplasm; Golgi apparatus; catalytic activity; transferase activity
TraesCS1D02G147600	RRM_dom; Nucleotide-bd_a/b_plait_sf; DAZAP1_RRM2; RBD_domain_sf	molecular_function; binding; nucleic acid binding; RNA binding
TraesCS1D02G178000	DNA_mismatch_repair_MutS_C; MutS2; DNA_mismatch_repair_MutS_core; P-loop_NTPase; DNA_mismatch_repair_MutS_sf	molecular_function; nucleotide binding; binding; catalytic activity; hydrolase activity; nuclease activity; DNA binding; nucleic acid binding; biological_process; cellular process; metabolic process; response to stress; DNA metabolic process; nucleobase-containing compound metabolic process
TraesCS1D02G191100	Glutathione_S-Trfase_N; Glutathione-S-Trfase_C-like; Thioredoxin-like_sf; Glutathione-S-Trfase_C_sf; Glutathione_S-Trfase	molecular_function; catalytic activity; transferase activity; biological_process; cellular process; metabolic process; cellular_component; intracellular; cytoplasm; binding; protein binding
TraesCS1D02G195500	Mitochondrial_sb/sol_carrier; Mt_carrier_dom_sf	cellular_component; membrane
TraesCS1D02G208600	PP2C_BS; PPM-type_phosphatase_dom; PP2C; PPM-type_dom_sf	molecular_function; binding; catalytic activity; hydrolase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS1D02G249200	Dienelactn_hydro; AB_hydrolase	molecular_function; catalytic activity; hydrolase activity
TraesCS1D02G250700	GDSL; SGNH_plant_lipase-like; SGNH_hydro_sf	molecular_function; catalytic activity; hydrolase activity
TraesCS1D02G378100		cellular_component; membrane
TraesCS1D02G406600	F-box_dom; DUF295; F-box-like_dom_sf	molecular_function; binding; protein binding
TraesCS2A02G041100	Biotin_lipoyl; 2-oxoacid_DH_actylTfrase; 2-oxoA_DH_lipoyl-BS; SucB; Single_hybrid_motif; CAT-like_dom_sf	molecular_function; catalytic activity; transferase activity; biological_process; cellular process; metabolic process; generation of precursor metabolites and energy; cellular_component; intracellular; cytoplasm
TraesCS2A02G046500	Peptidase_S10; AB_hydrolase	molecular_function; catalytic activity; hydrolase activity; biological_process; metabolic process; protein metabolic process
TraesCS2A02G049500	Terpene_synth_N; Terpene_synthase_metal-bd;	molecular_function; catalytic activity; binding

Gene stable ID	InterPro Short Description	GOSlim Description
	Terpenoid_cyclase/PrenylTrfase; Isoprenoid_synthase_dom_sf; Terpene_cyclase-like_1_C; Terpene_synth_N_sf	
TraesCS2A02G050400		cellular_component; membrane
TraesCS2A02G050600	PPIase_FKBP_dom; TPR_1; TPR-like_helical_dom_sf; TPR-contain_dom; TPR_repeat; PPIase_FKBP	molecular_function; catalytic activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; binding; protein binding; cellular_component; membrane
TraesCS2A02G069500	Pept_M24; PH-like_dom_sf; DUF1747; FACT_Spt16; FACT-Spt16_Nlobe; Creatin/AminoP/Spt16_NTD; Spt16_M24; Creatinase/aminopeptidase-like; Spt16	cellular_component; intracellular; nucleus; nucleoplasm
TraesCS2A02G095600	Peptidase_S9; 6-blade_b-propeller_TolB-like; AB_hydrolase	molecular_function; catalytic activity; hydrolase activity; biological_process; metabolic process; protein metabolic process
TraesCS2A02G344200	Pectinesterase_cat; Pectinesterase_inhib_dom; Pectin_lyase_fold/virulence; Pectin_lyas_fold; Pectinesterase_Asp_AS; Invertase/methylesterase_inhib	cellular_component; membrane; cell wall; external encapsulating structure; molecular_function; enzyme regulator activity; biological_process; regulation of molecular function; cellular process; cellular component organization; catalytic activity; hydrolase activity; metabolic process; carbohydrate metabolic process; catabolic process
TraesCS2A02G411200	Sugar_P_transporter; MFS; MFS_dom; MFS_trans_sf	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function
TraesCS2A02G442500	bHLH_dom; HLH_DNA-bd_sf	molecular_function; binding; protein binding
TraesCS2A02G527600	Glyco_trans_8; Nucleotide-diphossugar_trans; GAUT	molecular_function; catalytic activity; transferase activity; cellular_component; intracellular; cytoplasm; membrane; Golgi apparatus; endosome; biological_process; cellular process; cellular component organization; metabolic process; biosynthetic process; carbohydrate metabolic process
TraesCS2B02G053600	Biotin_lipoyl; 2-oxoacid_DH_actylTfrase; 2-oxoA_DH_lipoyl-BS; SucB; Single_hybrid_motif; CAT-like_dom_sf	molecular_function; catalytic activity; transferase activity; biological_process; cellular process; metabolic process; generation of precursor metabolites and energy; cellular_component; intracellular; cytoplasm
TraesCS2B02G058500	Sugar/inositol_transpt; MFS_sugar_transport-like; Sugar_transporter_CS; MFS_dom; MFS_trans_sf	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function
TraesCS2B02G065300	Pumilio_RNA-bd_rpt; ARM-like; ARM-type_fold; PUM-HD; Pumilio_RNA-bd	molecular_function; binding; nucleic acid binding; RNA binding
TraesCS2B02G094100	Prot_kinase_dom; Ser-Thr/Tyr_kinase_cat_dom; Ubox_domain; Kinase-like_dom_sf; Znf_RING/FYVE/PHD; UspA; Rossmann-like_a/b/a_fold	molecular_function; catalytic activity; transferase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; nucleotide binding; binding; kinase activity
TraesCS2B02G111000	Peptidase_S9; AB_hydrolase	molecular_function; catalytic activity; hydrolase activity; biological_process; metabolic process; protein metabolic process
TraesCS2B02G172300	Oxid_FAD_bind_N; BBE; FAD-bd_PCMH; FAD-bd_PCMH_sub1; FAD-bd_PCMH-like_sf	molecular_function; catalytic activity; biological_process; metabolic process; nucleotide binding; binding
TraesCS2B02G431400	WD40_repeat; WD40/YVTN_repeat-like_dom_sf; WD40_repeat_dom; WD40_repeat_CS; WD40_repeat_dom_sf	molecular_function; binding; protein binding; biological_process; cellular process; response to stress

Gene stable ID	**InterPro Short Description**	**GOSlim Description**
TraesCS2B02G543700	bHLH_dom; MASH1/Ascl1a-like; HLH_DNA-bd_sf	molecular_function; binding; DNA binding; nucleic acid binding; protein binding; biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process
TraesCS2B02G558300	Glyco_trans_8; Nucleotide-diphossugar_trans; GAUT	cellular_component; membrane; molecular_function; catalytic activity; transferase activity; intracellular; cytoplasm; Golgi apparatus; biological_process; cellular process; cellular component organization; metabolic process; biosynthetic process; carbohydrate metabolic process; endosome
TraesCS2D02G004000	TRM6	cellular_component; intracellular; nucleus; biological_process; cellular process; metabolic process; nucleobase-containing compound metabolic process
TraesCS2D02G039500	Biotin_lipoyl; 2-oxoacid_DH_actylTfrase; 2-oxoA_DH_lipoyl-BS; SucB; Single_hybrid_motif; CAT-like_dom_sf	molecular_function; catalytic activity; transferase activity; biological_process; cellular process; metabolic process; generation of precursor metabolites and energy; cellular_component; intracellular; cytoplasm
TraesCS2D02G047900	Scorpion_toxin-like; Defensin_plant; Scorpion_toxin-like_sf	biological_process; response to stress
TraesCS2D02G048800	ABC_transporter-like; AAA+_ATPase; ABC_transporter_CS; P-loop_NTPase	molecular_function; nucleotide binding; binding; catalytic activity; hydrolase activity; cellular_component; membrane
TraesCS2D02G049500	Chaprnin_Cpn60; Cpn60/TCP-1; Chaperonin_Cpn60_CS; GroEL-like_apical_dom_sf; TCP-1-like_intermed_sf; GROEL-like_equatorial_sf	cellular_component; intracellular; cytoplasm; molecular_function; nucleotide binding; binding; biological_process; cellular process; chloroplast; plastid; cytosol; protein binding; transport; cellular component organization
TraesCS2D02G050300	PPIase_FKBP_dom; TPR_1; TPR-like_helical_dom_sf; TPR-contain_dom; TPR_repeat; PPIase_FKBP	cellular_component; membrane; molecular_function; catalytic activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; binding; protein binding
TraesCS2D02G464300	WD40_repeat; WD40/YVTN_repeat-like_dom_sf; WD40_repeat_dom; WD40_repeat_CS; WD40_repeat_dom_sf	transport; biological_process; cellular_component; intracellular; cytoplasm; membrane; Golgi apparatus; molecular_function; binding; protein binding
TraesCS2D02G478700	SET_dom; Znf_MYND	molecular_function; binding; protein binding
TraesCS2D02G502600	Peroxidase_pln; Haem_peroxidase; Haem_peroxidase_sf; Peroxidases_heam-ligand_BS; Peroxidases_AS; Secretory_peroxidase	molecular_function; binding; catalytic activity; biological_process; response to stress; cellular_component; extracellular region; cellular process; metabolic process; catabolic process
TraesCS3A02G233300	ADP_ATP_car	cellular_component; membrane; transporter activity; molecular_function; transport; biological_process
TraesCS3A02G244700	Alliinase_C; PyrdxlP-dep_Trfase_major; PyrdxlP-dep_Trfase_dom1; PyrdxlP-dep_Trfase	molecular_function; catalytic activity
TraesCS3A02G258100	GDSL; SGNH_plant_lipase-like; SGNH_hydro_sf	molecular_function; catalytic activity; hydrolase activity
TraesCS3A02G305600	Dynein_light_chain_typ-1/2; DLC_sf	cellular_component; intracellular; cytoplasm; cytoskeleton; molecular_function; catalytic activity; hydrolase activity; motor activity; biological_process; cellular process
TraesCS3A02G413700	Znf_TAZ; BTB/POZ_dom; SKP1/BTB/POZ_sf; TAZ_dom_sf	cellular_component; intracellular; nucleus; molecular_function; binding; biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process; catalytic activity; transferase activity; cellular component organization; cellular protein modification process; protein metabolic process; transcription regulator activity; protein binding

Gene stable ID	InterPro Short Description	GOSlim Description
TraesCS3A02G489900	Small_GTPase; Small_GTP-bd_dom; P-loop_NTPase	molecular_function; nucleotide binding; binding; catalytic activity; hydrolase activity
TraesCS3A02G505000	Cyt_P450; Cyt_P450_E_grp-I; Cyt_P450_CS; Cyt_P450_sf	molecular_function; binding; catalytic activity; biological_process; metabolic process
TraesCS3A02G518500	TPR-like_helical_dom_sf; PRORP_C; PPR_long	molecular_function; binding; protein binding
TraesCS3A02G519800	NB-ARC; P-loop_NTPase; LRR_dom_sf; Rx_N	molecular_function; nucleotide binding; binding
TraesCS3A02G538500	PP2C_BS; PPM-type_phosphatase_dom; PP2C; PPM-type_dom_sf	molecular_function; binding; catalytic activity; hydrolase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS3B02G026700	EamA_dom; WAT1-related	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function; plasma membrane
TraesCS3B02G038400	Prot_inh_BBI; Bowman-Birk_prot_inh	cellular_component; extracellular region; molecular_function; enzyme regulator activity; biological_process; cellular process; metabolic process; regulation of molecular function; protein metabolic process
TraesCS3B02G064500	EF_hand_dom; EF-hand-dom_pair; EF_Hand_1_Ca_BS	molecular_function; binding
TraesCS3B02G100700	DUF1664	cellular_component; membrane
TraesCS3B02G142100	Peptidase_C19_UCH; Znf_UBP; UBA-like_sf; Znf_RING/FYVE/PHD; UBA; Ubiquitinyl_hydrolase; USP_CS; USP_dom; Papain-like_cys_pep_sf; UBP13_Znf-UBP_var	cellular_component; intracellular; nucleus; molecular_function; binding; biological_process; cellular process; metabolic process; catabolic process; protein metabolic process; multicellular organism development; anatomical structure development; post-embryonic development; reproduction; embryo development; catalytic activity; hydrolase activity; cellular protein modification process; cytoplasm; cytosol; cell differentiation; growth; cell growth; protein binding
TraesCS3B02G244700	Pentatricopeptide_repeat; TPR-like_helical_dom_sf	molecular_function; binding; protein binding
TraesCS3B02G448900	SANT/Myb; Homeobox-like_sf; Myb_dom	molecular_function; binding; DNA binding; nucleic acid binding
TraesCS3B02G525700	BTB/POZ_dom; FA58C; Galactose-bd-like_sf; SKP1/BTB/POZ_sf; BACK; Methyltransf_FA	molecular_function; binding; protein binding
TraesCS3B02G592000	Oxoglu/Fe-dep_dioxygenase; DIOX_N; IPNS-like	molecular_function; catalytic activity; biological_process; metabolic process; binding
TraesCS3D02G006900	Glyco_hydro_1; Glycoside_hydrolase_SF	molecular_function; catalytic activity; hydrolase activity; biological_process; metabolic process; carbohydrate metabolic process; cellular_component; membrane
TraesCS3D02G124300	NHTrfase_class1_PyrdxlP-BS; Aminotransferase_I/II; PyrdxlP-dep_Trfase_major; PyrdxlP-dep_Trfase_dom1; PyrdxlP-dep_Trfase	molecular_function; binding; catalytic activity; biological_process; metabolic process; biosynthetic process; cellular process; cellular_component; intracellular; cytoplasm; cytosol; response to abiotic stimulus; response to light stimulus; transferase activity; catabolic process; secondary metabolic process
TraesCS3D02G258300	ABC_transporter-like; AAA+_ATPase; ABC1_TM_dom; ABC_transporter_CS; P-loop_NTPase; ABC1_TM_sf; Type_I_exporter	cellular_component; membrane; molecular_function; nucleotide binding; binding; transporter activity; transport; biological_process; catalytic activity; hydrolase activity
TraesCS3D02G434700	PB1_dom; B3_DNA-bd; Auxin_resp; DNA-bd_pseudobarrel_sf; AUX/IAA_dom	biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process; cellular_component; intracellular; nucleus; molecular_function; binding; DNA binding; nucleic acid binding; response to chemical; response to endogenous stimulus; cell communication; signal transduction; protein binding

Gene stable ID	InterPro Short Description	GOSlim Description
TraesCS3D02G437200	Jacalin-like_lectin_dom; Dirigent; Jacalin-like_lectin_dom_plant; Jacalin-like_lectin_dom_sf	molecular_function; binding; carbohydrate binding; cellular_component; extracellular region
TraesCS3D02G454800		cellular_component; intracellular; membrane
TraesCS3D02G514000		cellular_component; membrane
TraesCS3D02G516800	Thioredoxin; Thioredoxin_domain; Thioredoxin_CS; Thioredoxin-like_sf	molecular_function; catalytic activity; biological_process; cellular process; cellular homeostasis; metabolic process; cellular_component; cell
TraesCS3D02G521300	Cyt_P450; Cyt_P450_E_grp-I; Cyt_P450_sf	molecular_function; binding; catalytic activity; biological_process; metabolic process
TraesCS3D02G521900	SET_dom; Znf_PHD; Znf_FYVE_PHD; Znf_RING/FYVE/PHD; Znf_PHD-finger	molecular_function; binding; protein binding
TraesCS3D02G523200	PyrdxlP-dep_de-COase; Glutamate_decarboxylase; PyrdxlP-dep_Trfase_major; PyrdxlP-dep_Trfase	molecular_function; binding; catalytic activity; biological_process; cellular process; metabolic process
TraesCS3D02G529200	Pentatricopeptide_repeat; TPR-like_helical_dom_sf	molecular_function; binding; protein binding
TraesCS3D02G543800	PWWP_dom; RBD_domain_sf	molecular_function; binding; nucleic acid binding
TraesCS4A02G135300	Malic_N_dom; Malic_N_dom_sf	molecular_function; catalytic activity; biological_process; metabolic process
TraesCS4A02G223300	NB-ARC; P-loop_NTPase; LRR_dom_sf; RX-like_CC; Rx_N	molecular_function; nucleotide binding; binding
TraesCS4A02G230200	Pentatricopeptide_repeat; TPR-like_helical_dom_sf	molecular_function; binding; protein binding
TraesCS4A02G305300	Ribosomal_L1; Ribosomal_L1_3-a/b-sand; Ribosomal_L1_CS; Ribosomal_L1-like; Ribosomal_L1/biogenesis	molecular_function; binding; nucleic acid binding; RNA binding; structural molecule activity; biological_process; cellular process; metabolic process; biosynthetic process; protein metabolic process; translation; cellular_component; intracellular; ribosome
TraesCS4B02G016000	Znf_CCHC; Znf_RING/FYVE/PHD; DWNN_domain; Zn_knuckle_CX2CX3GHX4C; RBBP6; Znf_CCHC_sf	cellular_component; intracellular; nucleus; molecular_function; binding; nucleic acid binding; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; catalytic activity; transferase activity; nucleobase-containing compound metabolic process
TraesCS4B02G155800	Znf_B-box; CCT_domain	molecular_function; binding; protein binding; cellular_component; intracellular; nucleus
TraesCS4B02G206900	Armadillo; Ubox_domain; Neurochondrin; ARM-like; Znf_RING/FYVE/PHD; ARM-type_fold; Adaptor_Cbl_N_dom_sf	molecular_function; catalytic activity; transferase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; cell communication; signal transduction; binding; protein binding
TraesCS4B02G260200		cellular_component; membrane
TraesCS4B02G264100	SLC26A/SulP_fam; STAS_dom; SLC26A/SulP_dom; S04_transporter_CS; STAS_dom_sf	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function
TraesCS4B02G358900	CASP_dom	cellular_component; membrane; plasma membrane
TraesCS4D02G003600	PsbP_C; Mog1/PsbP_a/b/a-sand	molecular_function; binding; biological_process; cellular process; metabolic process; photosynthesis; cellular_component; intracellular; membrane; thylakoid

Gene stable ID	**InterPro Short Description**	**GOSlim Description**
TraesCS4D02G006200	HAD-SF_hydro_IA; PGP-like_dom2; HAD_sf; HAD-like_sf; HAD_2	molecular_function; catalytic activity; hydrolase activity; biological_process; cellular process; metabolic process; biosynthetic process; cellular protein modification process; protein metabolic process; binding; protein binding
TraesCS4D02G041500	GTD-bd; MYOB	cellular_component; membrane; molecular_function; binding; protein binding
TraesCS5A02G041600	Pentatricopeptide_repeat; TPR-like_helical_dom_sf	molecular_function; binding; protein binding
TraesCS5A02G199700	AMP-dep_Synth/Lig; AMP-binding_CS; ACAS_N; AMP-dep_Synthh-like_sf	cellular_component; membrane; molecular_function; catalytic activity
TraesCS5A02G320100	Ribosomal_L44e; Ribosomal_zn-bd	molecular_function; structural molecule activity; biological_process; cellular process; metabolic process; biosynthetic process; protein metabolic process; translation; cellular_component; intracellular; ribosome; cytoplasm; cytosol
TraesCS5A02G320300	Sig_transdc_resp-reg_receiver; CCT_domain; CheY-like_superfamily	cellular_component; intracellular; nucleus; biological_process; cell communication; cellular process; signal transduction; molecular_function; binding; protein binding
TraesCS5A02G391200	HMA_dom_sf	molecular_function; binding; transport; biological_process
TraesCS5A02G391400	Spo11/TopoVI_A; Meiotic_Spo11; Spo11/TopoVI_A_N; TOPRIM_Topo6A/Spo11; Spo11/TopoVI_A_sf; WH-like_DNA-bd_sf	molecular_function; nucleotide binding; binding; DNA binding; nucleic acid binding; catalytic activity; cellular_component; intracellular; biological_process; cellular process; metabolic process; catabolic process; DNA metabolic process; nucleobase-containing compound metabolic process; nuclease activity; hydrolase activity
TraesCS5A02G392000	COBRA_pln	biological_process; cellular process; cellular component organization; cellular_component; membrane
TraesCS5A02G392500	Prot_kinase_dom; Kinase-like_dom_sf; Protein_kinase_ATP_BS	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS5A02G392700	ABC_transporter-like; AAA+_ATPase; ABC1_TM_dom; ABC_transporter_CS; P-loop_NTPase; ABC1_TM_sf; Type_I_exporter	cellular_component; membrane; molecular_function; nucleotide binding; binding; transporter activity; transport; biological_process; catalytic activity; hydrolase activity
TraesCS5A02G393000	Prot_kinase_dom; Leu-rich_rpt; Leu-rich_rpt_typical-subtyp; Ser/Thr_kinase_AS; Kinase-like_dom_sf; LRR_N_plant-typ; Protein_kinase_ATP_BS; LRR_dom_sf	cellular_component; membrane; molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; protein binding
TraesCS5A02G426800	Prot_kinase_dom; EF_hand_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf; EF-hand-dom_pair; Protein_kinase_ATP_BS; EF_Hand_1_Ca_BS	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS5A02G432100	Cupin_1; RmlC_Cupin_sf; RmlC-like_jellyroll	molecular_function; binding
TraesCS5A02G435300	BTB/POZ_dom; MATH/TRAF_dom; TRAF-like; SKP1/BTB/POZ_sf; BPM_C	molecular_function; binding; protein binding
TraesCS5B02G131500	DUF3700; Ntn_hydrolases_N	cellular_component; membrane; plasma membrane
TraesCS5B02G179300	PPM-type_phosphatase_dom; PP2C; PPM-type_dom_sf	molecular_function; catalytic activity; hydrolase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process

Gene stable ID	InterPro Short Description	GOSlim Description
TraesCS5B02G193600	JAMM/MPN+_dom; RNaseH-like_sf; PRO8NT; PROCN; PROCT; Prp8_U6-snRNA-bd; Prp8_U5-snRNA-bd; RRM_spliceosomal_PrP8; PRP8_domainIV; PRP8; MPN; Prp8_U5-snRNA-bd_sf	molecular_function; binding; nucleic acid binding; RNA binding; biological_process; cellular process; metabolic process; nucleobase-containing compound metabolic process; cellular_component; intracellular; nucleus; protein binding
TraesCS5B02G195700	Pentatricopeptide_repeat; TPR-like_helical_dom_sf	molecular_function; binding; protein binding
TraesCS5B02G196700	Hypoxia_induced_domain	cellular_component; membrane
TraesCS5B02G197300	K+_transporter	cellular_component; membrane; transporter activity; molecular_function; transport; biological_process
TraesCS5B02G197900	RRM_dom; PWI_dom; Nucleotide-bd_a/b_plait_sf; RBM25_RRM; RBD_domain_sf	molecular_function; binding; nucleic acid binding; biological_process; cellular process; metabolic process; nucleobase-containing compound metabolic process
TraesCS5B02G198000	AMP-dep_Synth/Lig; AMP-binding_CS; ACAS_N; AMP-dep_Synthh-like_sf	molecular_function; catalytic activity; cellular_component; membrane
TraesCS5B02G198300	Xant/urac/vitC	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function
TraesCS5B02G201700	Annexin; Annexin_repeat; Annexin_sf; Annexin_repeat_CS	molecular_function; binding; lipid binding
TraesCS5B02G210100	Aldehyde_DH_dom; Ald_DH/histidinol_DH; Ald_DH_N; Ald_DH_C; Ald_DH_CS_GLU	molecular_function; catalytic activity; biological_process; metabolic process
TraesCS5B02G210800	Chloro_AB-bd_pln; Chloroa_b-bind; Chlorophyll_a/b-bd_dom_sf	cellular_component; membrane; biological_process; cellular process; metabolic process; generation of precursor metabolites and energy; photosynthesis
TraesCS5B02G236400	HSF_DNA-bd; HSF_fam; WH-like_DNA-bd_sf; WH_DNA-bd_sf	molecular_function; biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process; transcription regulator activity; DNA-binding transcription factor activity; binding; DNA binding; nucleic acid binding; cellular_component; intracellular; nucleus; response to stress; response to abiotic stimulus
TraesCS5B02G371800	Prot_kinase_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS5B02G372300	TPR-like_helical_dom_sf	cellular_component; membrane; molecular_function; binding; protein binding
TraesCS5B02G394800	TPR-like_helical_dom_sf; TPR-contain_dom; TPR_repeat	molecular_function; binding; protein binding
TraesCS5B02G397900	Prot_kinase_dom; Leu-rich_rpt; Leu-rich_rpt_typical-subtyp; Ser/Thr_kinase_AS; Kinase-like_dom_sf; LRR_N_plant-typ; Protein_kinase_ATP_BS; LRR_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; protein binding; cellular_component; membrane
TraesCS5B02G500200	DNA_methylase_N6_adenine_CS; PrmC-related; Small_mtfrase_dom; SAM-dependent_MTases	molecular_function; binding; nucleic acid binding; catalytic activity; transferase activity; biological_process; metabolic process
TraesCS5B02G563900	Chaprnin_Cpn60; Cpn60/TCP-1; Chaperonin_Cpn60_CS; GroEL-like_apical_dom_sf; TCP-1-like_intermed_sf; GROEL-like_equatorial_sf	molecular_function; nucleotide binding; binding; biological_process; cellular process; multicellular organism development; anatomical structure development; post-embryonic development; reproduction; embryo development; cellular_component; membrane; extracellular region; intracellular; cytoplasm; mitochondrion; thylakoid; cellular component organization; chloroplast; plastid; cytosol; ribosome
TraesCS5D02G017600	Modifying_wall_lignin1/2	cellular_component; membrane

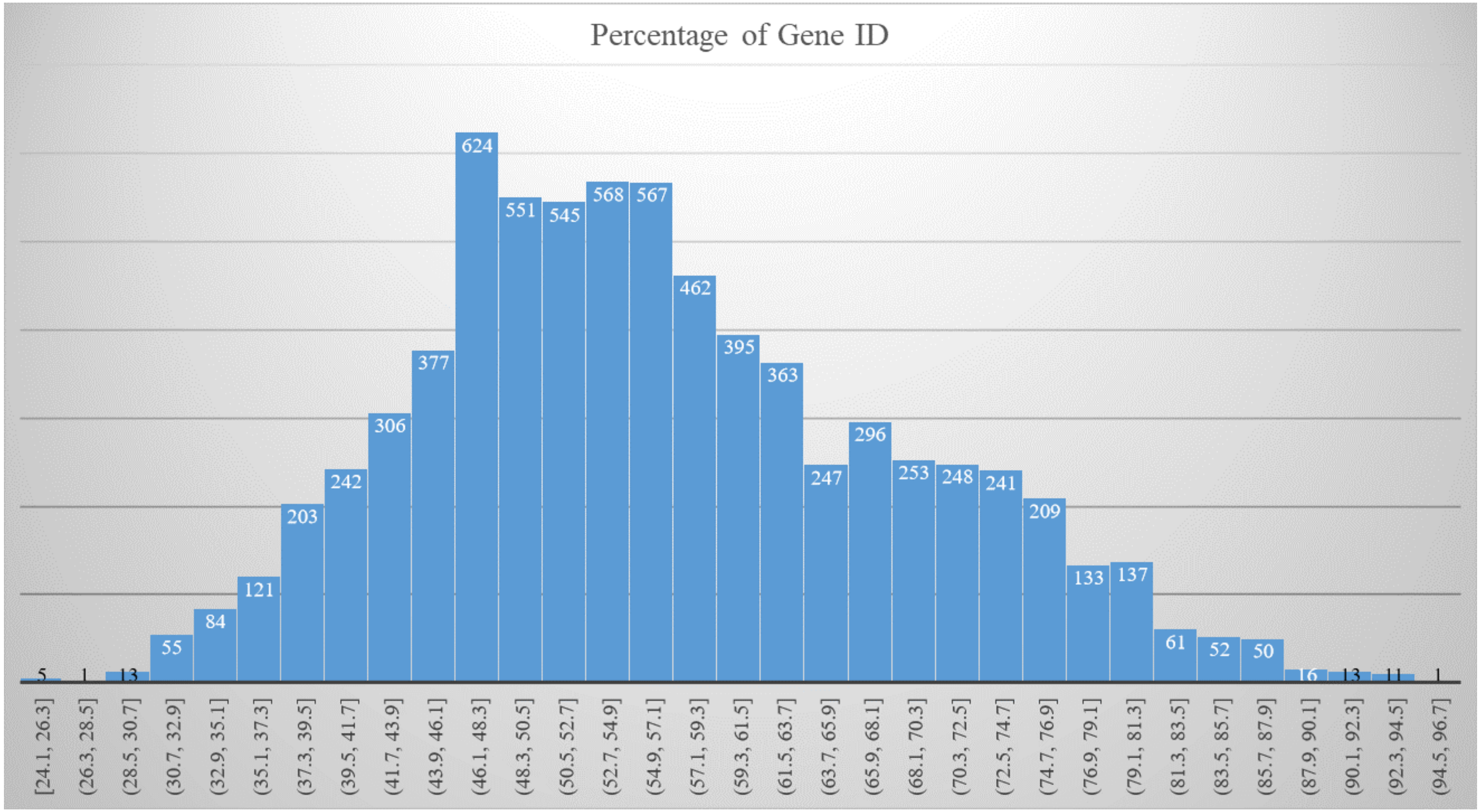
Gene stable ID	InterPro Short Description	GOSlim Description
TraesCS5D02G070900	MoaA_NifB_PqqE_Fe-S-bd_CS; Elp3/MiaB/NifB; rSAM; Mob_synth_C; MoaA; Aldolase_TIM	molecular_function; binding; catalytic activity; biological_process; cellular process; metabolic process; biosynthetic process; protein metabolic process; cellular_component
TraesCS5D02G101600	DUF4149	cellular_component; membrane
TraesCS5D02G202100	Pumilio_RNA-bd_rpt; ARM-like; ARM-type_fold; PUM-HD	molecular_function; binding; nucleic acid binding; RNA binding
TraesCS5D02G205100	Endo-beta-glucanase; GH81_N; GH81_C	molecular_function; catalytic activity; hydrolase activity
TraesCS5D02G218400	Aldehyde_DH_dom; Ald_DH/histidinol_DH; Ald_DH_N; Ald_DH_C; Ald_DH_CS_GLU	molecular_function; catalytic activity; biological_process; metabolic process
TraesCS5D02G402100	Mit_carrier; Mitochondrial_sb/sol_carrier; Mt_carrier_dom_sf	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function; intracellular; cytoplasm; mitochondrion
TraesCS5D02G402900	Prot_kinase_dom; Leu-rich_rpt; Leu-rich_rpt_typical-subtyp; Ser/Thr_kinase_AS; Kinase-like_dom_sf; LRR_N_plant-typ; Protein_kinase_ATP_BS; LRR_dom_sf	cellular_component; membrane; molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; protein binding
TraesCS5D02G520800	Prot_kinase_dom; EGF-like_dom; EGF-like_Ca-bd_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf; Protein_kinase_ATP_BS; EGF_Ca-bd_CS; WAK_GUB	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; carbohydrate binding
TraesCS5D02G549600	Prot_kinase_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf; Protein_kinase_ATP_BS; Nuclear_transport_factor_2_euk; NTF2-like_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS5D02G557600	Leu-rich_rpt; NB-ARC; P-loop_NTPase; LRR_dom_sf; RX-like_CC; Rx_N	molecular_function; nucleotide binding; binding; protein binding
TraesCS6A02G235200	WD40_repeat; WD40_repeat_dom; WD40_repeat_CS; G-protein_beta_WD-40_rep; WD40_repeat_dom_sf; WDR44/Dgr2	molecular_function; binding; protein binding
TraesCS6A02G236800	RNA-helicase_DEAD-box_CS; Helicase_C; DEAD/DEAH_box_helicase_dom; Helicase_ATP-bd; RNA_helicase_DEAD_Q_motif; P-loop_NTPase	molecular_function; binding; nucleic acid binding; nucleotide binding; catalytic activity; hydrolase activity
TraesCS6A02G399400	Sig_transdc_resp-reg_receiver; GAF; HisK_dim/P; CheY-like_superfamily; ETR; GAF-like_dom_sf; HisK_dim/P_sf; HATPase_C_sf	cellular_component; membrane; molecular_function; binding; nucleotide binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; cell communication; signal transduction; signaling receptor activity; response to chemical; response to endogenous stimulus; protein binding
TraesCS6A02G404800	Smg8/Smg9; SMG8	biological_process; cellular process; metabolic process; catabolic process; nucleobase-containing compound metabolic process
TraesCS6A02G411900	Prot_kinase_dom; EGF-like_dom; EGF-like_Ca-bd_dom; Ser/Thr_kinase_AS; Growth_fac_rcpt_cys_sf; Kinase-like_dom_sf; Protein_kinase_ATP_BS; EGF_Ca-bd_CS; WAK_GUB	cellular_component; membrane; molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; carbohydrate binding
TraesCS6A02G416500	Lnp	cellular_component; membrane; biological_process; cellular process; cellular component organization
TraesCS6B02G000300	Armadillo; HECT_dom; ARM-like; ARM-type_fold;	molecular_function; catalytic activity; transferase activity; biological_process; cellular process;

Gene stable ID	InterPro Short Description	GOSlim Description
	Hect_E3_ubiquitin_ligase	metabolic process; cellular protein modification process; protein metabolic process; binding; protein binding
TraesCS6B02G006400		cellular_component; membrane
TraesCS6B02G007400	AA_transpt_TM	cellular_component; membrane
TraesCS6B02G010000	MORF/ORRM1/DAG-like	biological_process; cellular process; metabolic process; nucleobase-containing compound metabolic process
TraesCS6B02G060700	bHLH_dom; HLH_DNA-bd_sf	molecular_function; binding; protein binding
TraesCS6B02G121300		cellular_component; membrane
TraesCS6B02G265300	RNA-helicase_DEAD-box_CS; Helicase_C; DEAD/DEAH_box_helicase_dom; Helicase_ATP-bd; RNA_helicase_DEAD_Q_motif; P-loop_NTPase	molecular_function; binding; nucleic acid binding; nucleotide binding; catalytic activity; hydrolase activity
TraesCS6B02G265600	SAM-dependent_MTases; SAM_MPBQ_MSBQ_MT; Methyltransf_25	cellular_component; membrane; molecular_function; catalytic activity; transferase activity; biological_process; metabolic process
TraesCS6B02G449900	Amino_oxidase; SWIRM; Homeobox-like_sf; TFIIS/LEDGF_dom_sf; FAD/NAD-bd_sf; WH-like_DNA-bd_sf	molecular_function; catalytic activity; biological_process; metabolic process; binding; DNA binding; nucleic acid binding; protein binding
TraesCS6D02G008200	O_MeTrfase_dom; Plant_MeTrfase_dimerisation; O-MeTrfase_COMT; SAM-dependent_MTases; WH-like_DNA-bd_sf; WH_DNA-bd_sf	molecular_function; binding; protein binding; catalytic activity; transferase activity; biological_process; metabolic process; cellular process; biosynthetic process
TraesCS6D02G011700	Gprotein_alpha_su; GproteinA_insert; P-loop_NTPase	molecular_function; nucleotide binding; binding; catalytic activity; hydrolase activity; biological_process; cell communication; cellular process; signal transduction
TraesCS6D02G087600	Pentatricopeptide_repeat; TPR-like_helical_dom_sf	molecular_function; binding; protein binding
TraesCS6D02G140200	NAC-dom; NAC_dom_sf	molecular_function; binding; DNA binding; nucleic acid binding; biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process; cellular_component; intracellular; nucleus
TraesCS6D02G383700	Prot_kinase_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf; Protein_kinase_ATP_BS	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS6D02G389200	Amino_oxidase; SWIRM; Homeobox-like_sf; TFIIS/LEDGF_dom_sf; FAD/NAD-bd_sf; WH-like_DNA-bd_sf	molecular_function; catalytic activity; biological_process; metabolic process; binding; DNA binding; nucleic acid binding; protein binding
TraesCS6D02G391300	F-box_dom; LRR_dom_sf; F-box-like_dom_sf	molecular_function; binding; protein binding
TraesCS6D02G392900	RRM_dom; Nucleotide-bd_a/b_plait_sf; RBD_domain_sf	molecular_function; binding; nucleic acid binding
TraesCS6D02G399000	NB-ARC; P-loop_NTPase; LRR_dom_sf	molecular_function; nucleotide binding; binding
TraesCS7A02G087900	B3_DNA-bd; DNA-bd_pseudobarrel_sf	molecular_function; binding; DNA binding; nucleic acid binding
TraesCS7A02G123900	Thioredoxin_domain; Thioredoxin-like_sf	biological_process; cellular process; cellular homeostasis; molecular_function; catalytic activity; cellular_component; cell

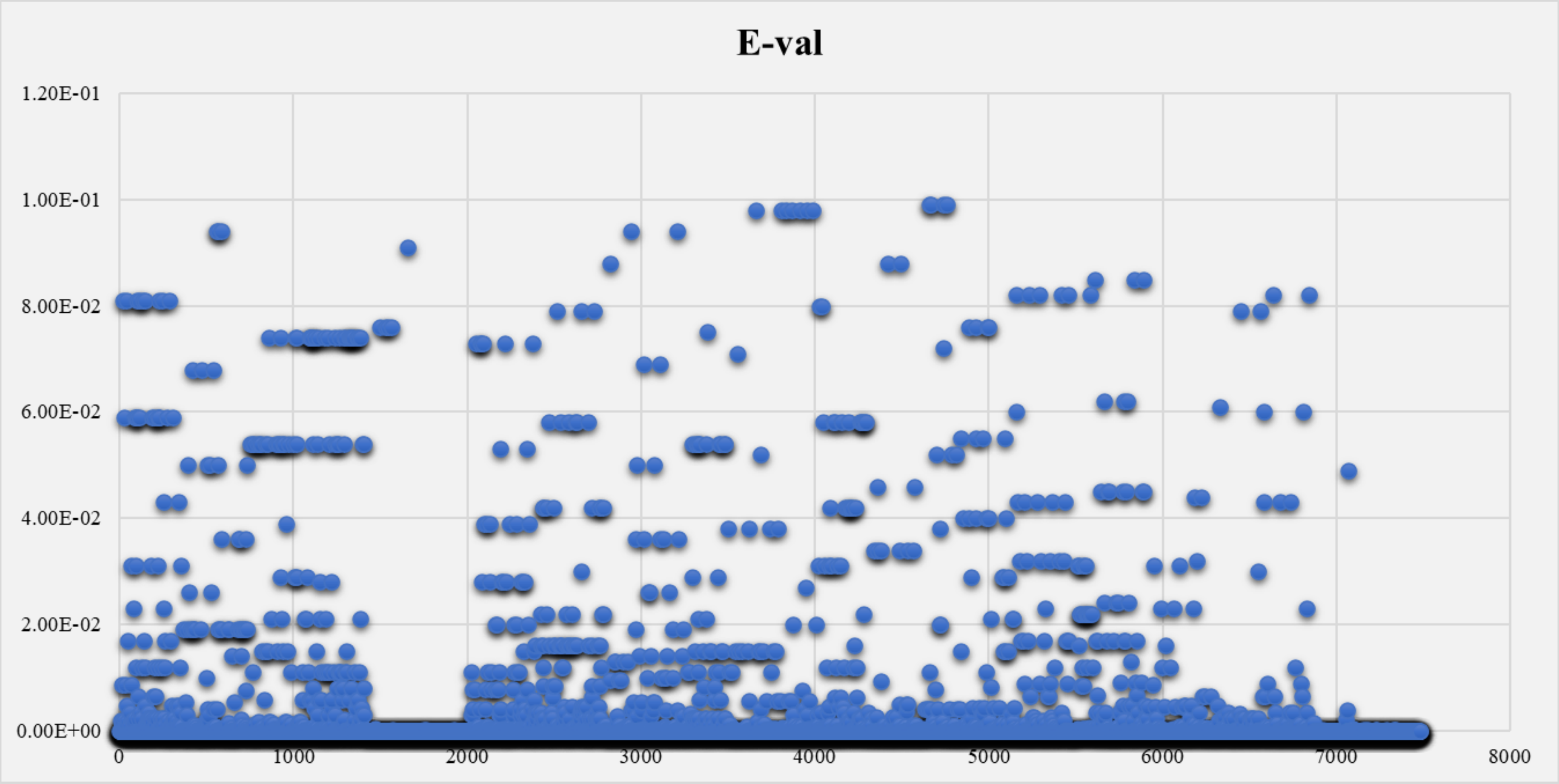
Gene stable ID	InterPro Short Description	GOSlim Description
TraesCS7A02G131200	RNR_lg_C; ATP-cone_dom; RNR_R1-su_N; NrdE_NrdA; RNR_lsu_N; Rrm1	molecular_function; nucleotide binding; binding; biological_process; metabolic process; cellular process; biosynthetic process; catalytic activity
TraesCS7A02G145100	PB1_dom; Prot_kinase_dom; Ser-Thr/Tyr_kinase_cat_dom; Ser/Thr_kinase_AS; Kinase-like_dom_sf; Protein_kinase_ATP_BS	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process; protein binding
TraesCS7A02G183100	EF_hand_dom; NaCa_Exmemb; EF-hand-dom_pair; EF_Hand_1_Ca_BS	cellular_component; membrane; molecular_function; binding; transport; biological_process
TraesCS7A02G481400	Cyt_c_oxidase_su6a; Cyt_c_oxidase_su6a_sf	cellular_component; intracellular; cytoplasm; membrane; mitochondrion; transporter activity; molecular_function; catalytic activity
TraesCS7A02G482000	HAD-SF_hydro_IA; HAD-SF_hydro_IA_REG-2-like; HAD_sf; HAD-like_sf	molecular_function; catalytic activity; hydrolase activity
TraesCS7A02G482200	CDC50/LEM3_fam	cellular_component; membrane
TraesCS7B02G044200	Acyl-CoA_oxidase_C; Acyl-CoA_Oxase/DH_cen-dom; AcylCo_DH/oxidase_C; AcylCoA_DH/oxidase_NM_dom; Acyl-CoA_oxidase; AcylCo_DH-like_C	molecular_function; nucleotide binding; binding; biological_process; metabolic process; cellular process; lipid metabolic process; catalytic activity; cellular_component; intracellular; cytoplasm; peroxisome; catabolic process
TraesCS7B02G299700	Expansin; Expansin/allergen_DPBB_dom; Expansin_CBD; Expan_Lol_pI; RlpA-like_DPBB; Expansin_CBD_sf; RlpA-like_sf	cellular_component; membrane; extracellular region; cell wall; external encapsulating structure; biological_process; cellular process; cellular component organization; response to abiotic stimulus; anatomical structure development
TraesCS7B02G362200	Prot_kinase_dom; Ser-Thr/Tyr_kinase_cat_dom; Kinase-like_dom_sf	molecular_function; nucleotide binding; binding; catalytic activity; transferase activity; kinase activity; biological_process; cellular process; metabolic process; cellular protein modification process; protein metabolic process
TraesCS7B02G363700	6PGDH_NADP-bd; 6-PGluconate_DH-like_C_sf; HIBADH; 6PGD_dom2; HIBADH-related; NADP-bd; NAD(P)-bd_dom_sf; 3-OH-isobutyrate_DH-rel_CS	molecular_function; catalytic activity; biological_process; metabolic process; nucleotide binding; binding; protein binding; cellular process; catabolic process
TraesCS7B02G387200	Aspartic_peptidase_A1; Peptidase_aspartic_dom_sf; TAXi_C; TAXi_N; PEPTIDASE_A1; Pepsin-like_plant	molecular_function; catalytic activity; hydrolase activity; biological_process; metabolic process; protein metabolic process
TraesCS7B02G430700	ENTH_VHS; ANTH_dom	cellular_component; membrane; molecular_function; binding; lipid binding
TraesCS7B02G471600	Peptidase_M41; AAA+_ATPase; ATPase_AAA_core; ATPase_AAA_CS; FtsH; P-loop_NTPase; Peptidase_M41-like; AAA_lid_3	cellular_component; membrane; molecular_function; nucleotide binding; binding; catalytic activity; hydrolase activity; biological_process; metabolic process; protein metabolic process
TraesCS7D02G142800	Nodulin-like; MFS_trans_sf	cellular_component; membrane
TraesCS7D02G183600	C2_dom; Armadillo; ARM-like; ARM-type_fold; C2_domain_sf	molecular_function; binding; protein binding
TraesCS7D02G188300	Glyco_trans_8; Nucleotide-diphossugar_trans; GAUT	molecular_function; catalytic activity; transferase activity; cellular_component; intracellular; cytoplasm; membrane; Golgi apparatus; biological_process; cellular process; cellular component organization; metabolic process; biosynthetic process; carbohydrate metabolic process
TraesCS7D02G397800	Znf_C2H2_type; Znf_C2H2_sf	molecular_function; binding; nucleic acid binding
TraesCS7D02G433100	GDP-Fuc_O-FucTrfase; FucosylTrfase_pln	molecular_function; catalytic activity; transferase activity; biological_process; metabolic process;

Gene stable ID	InterPro Short Description	GOSlim Description
		carbohydrate metabolic process
TraesCS7D02G467700	F-box_dom; F-box-assoc_interact_dom; F-box-like_dom_sf	molecular_function; binding; protein binding
TraesCS7D02G509500	ARPC3; ARPC3_sf	cellular_component; intracellular; cytoskeleton; biological_process; cellular process; cellular component organization; cytoplasm; molecular_function; binding; protein binding
TraesCS7D02G539500	MIP; MIP_CS; Aquaporin-like; Aquaporin_transptr	cellular_component; membrane; transport; biological_process; transporter activity; molecular_function
TraesCS7D02G543400	NAC-dom; NAC_dom_sf	cellular_component; intracellular; nucleus; molecular_function; binding; DNA binding; nucleic acid binding; biological_process; cellular process; metabolic process; biosynthetic process; nucleobase-containing compound metabolic process

Annexure 10: Similarity distribution in BLASTP results reported against query sequences in *T. aestivum*



Annexure 11: Distribution of E-value in BLAST results



Annexure 12: Details of identified *TaFrcu* genes

Nomenclature	Transcript ID	Gene ID	Chr	Gene start (bp)	Gene end (bp)	TL	TC	GC (%)
TaFruc1A.1	*TraesCS1A02G394000.1*	*TraesCS1A02G394000*	1A	560260083	560263148	1844	1	45.24
TaFruc1B.1	*TraesCS1B02G422700.1*	*TraesCS1B02G422700*	1B	645548098	645552814	1937	1	49.97
TaFruc1D.1	*TraesCS1D02G402500.1*	*TraesCS1D02G402500*	1D	467650627	467654301	1928	1	44.03
TaFruc2A.1	*TraesCS2A02G295400.1*	*TraesCS2A02G295400*	2A	508030243	508034286	2322	1	53.68
TaFruc2A.2	*TraesCS2A02G488500.2*	*TraesCS2A02G488500*	2A	722754578	722756932	1891	2	61.61
TaFruc2A.3	*TraesCS2A02G488900.2*	*TraesCS2A02G488900*	2A	722830825	722842044	2389	2	51.69
TaFruc2A.4	*TraesCS2A02G489000.1*	*TraesCS2A02G489000*	2A	723060949	723063405	2019	1	62.03
TaFruc2A.5	*TraesCS2A02G588300.1*	*TraesCS2A02G588300*	2A	777622662	777627335	2131	1	48.4
TaFruc2A.6	*TraesCS2A02G588700.1*	*TraesCS2A02G588700*	2A	777807113	777812845	2566	1	46.24
TaFruc2A.7	*TraesCS2A02G590900.1*	*TraesCS2A02G590900*	2A	778797752	778807122	2462	1	45.81
TaFruc2B.1	*TraesCS2B02G311900.1*	*TraesCS2B02G311900*	2B	446080168	446084251	2370	1	53.06
TaFruc2B.2	*TraesCS2B02G516300.1*	*TraesCS2B02G516300*	2B	711319189	711321656	1879	1	60.17
TaFruc2B.3	*TraesCS2B02G516700.2*	*TraesCS2B02G516700*	2B	711723785	711727892	1785	2	55.26
TaFruc2B.4	*TraesCS2B02G516800.1*	*TraesCS2B02G516800*	2B	711866805	711869464	2138	1	59.25
TaFruc2B.5	*TraesCS2B02G594600.1*	*TraesCS2B02G594600*	2B	779149373	779149759	300	1	48.32
TaFruc2B.6	*TraesCS2B02G594900.1*	*TraesCS2B02G594900*	2B	779251292	779256095	2135	1	47.21
TaFruc2B.7	*TraesCS2B02G595000.1*	*TraesCS2B02G595000*	2B	779260732	779262711	1706	1	54.04
TaFruc2D.1	*TraesCS2D02G293200.1*	*TraesCS2D02G293200*	2D	375592753	375596635	2197	1	53.62
TaFruc2D.2	*TraesCS2D02G489200.2*	*TraesCS2D02G489200*	2D	588245673	588250234	1773	2	53.55
TaFruc2D.3	*TraesCS2D02G489400.1*	*TraesCS2D02G489400*	2D	588452741	588455049	1870	1	59.68
TaFruc2D.4	*TraesCS2D02G564900.1*	*TraesCS2D02G564900*	2D	635161247	635166604	2216	1	50.02
TaFruc2D.5	*TraesCS2D02G565000.1*	*TraesCS2D02G565000*	2D	635203984	635207763	1962	1	51.4
TaFruc3A.1	*TraesCS3A02G029700.1*	*TraesCS3A02G029700*	3A	15617949	15619294	999	1	53.05

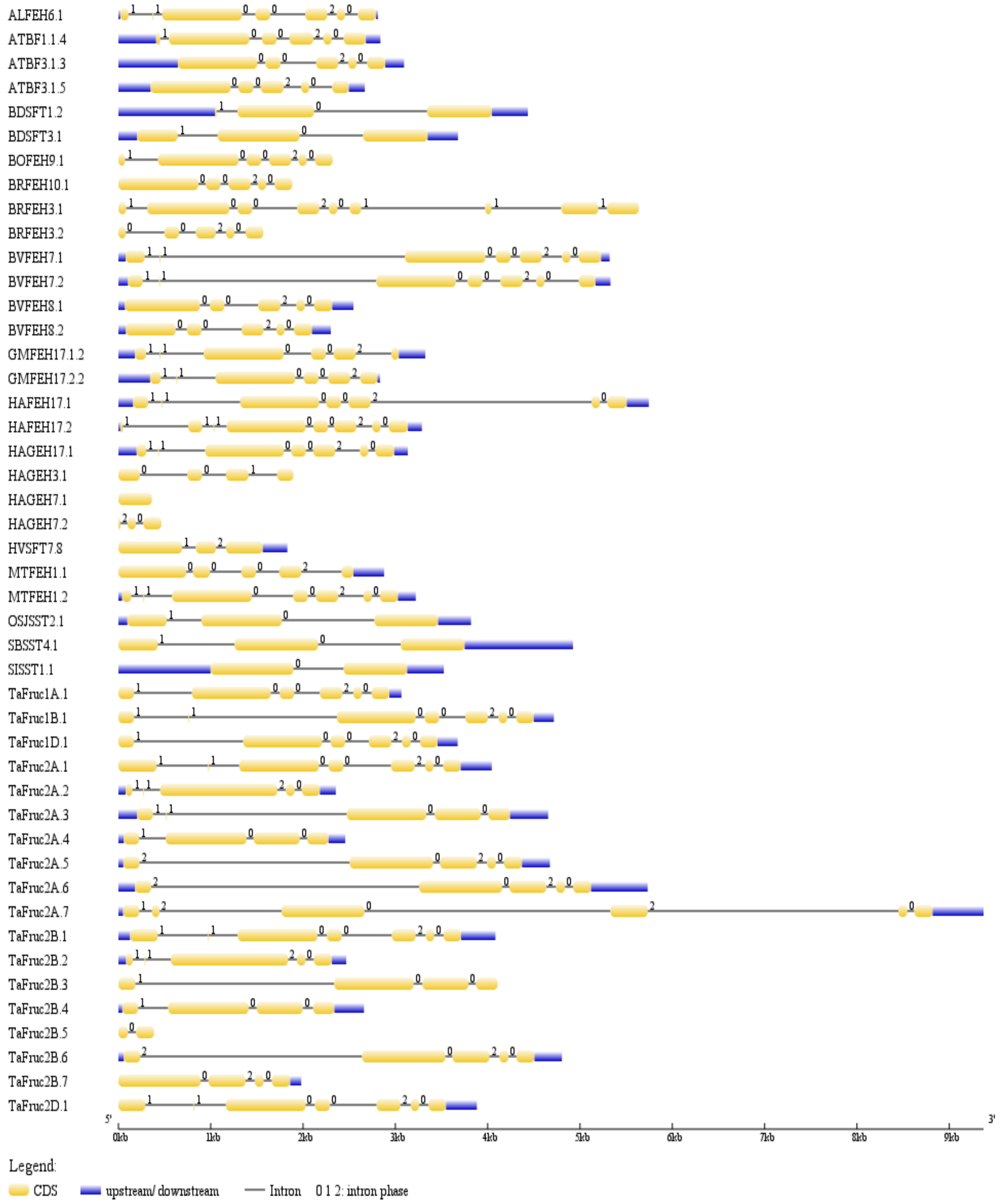
Nomenclature	**Transcript ID**	**Gene ID**	**Chr**	**Gene start (bp)**	**Gene end (bp)**	**TL**	**TC**	**GC (%)**
TaFruc3A.2	*TraesCS3A02G516900.1*	*TraesCS3A02G516900*	3A	734127800	734131501	2364	1	46
TaFruc3B.1	*TraesCS3B02G028200.1*	*TraesCS3B02G028200*	3B	12142281	12142813	309	1	47.28
TaFruc3B.2	*TraesCS3B02G028500.1*	*TraesCS3B02G028500*	3B	12302917	12305457	1752	1	53.72
TaFruc3B.3	*TraesCS3B02G584500.1*	*TraesCS3B02G584500*	3B	811445015	811448708	2305	1	46.4
TaFruc3D.1	*TraesCS3D02G015900.1*	*TraesCS3D02G015900*	3D	5649356	5651648	1802	1	55.26
TaFruc3D.2	*TraesCS3D02G524600.1*	*TraesCS3D02G524600*	3D	604397506	604401112	2207	1	45.61
TaFruc4A.1	*TraesCS4A02G248700.1*	*TraesCS4A02G248700*	4A	559494033	559496353	1989	1	58.77
TaFruc4A.2	*TraesCS4A02G321400.2*	*TraesCS4A02G321400*	4A	609813224	609823675	4022	2	44.32
TaFruc4A.3	*TraesCS4A02G321500.1*	*TraesCS4A02G321500*	4A	609917276	609922935	2584	2	40.25
TaFruc4A.4	*TraesCS4A02G321600.2*	*TraesCS4A02G321600*	4A	609925870	609929741	2239	2	44.4
TaFruc4A.5	*TraesCS4A02G321700.1*	*TraesCS4A02G321700*	4A	610034075	610036709	1752	1	52.41
TaFruc4A.6	*TraesCS4A02G484800.1*	*TraesCS4A02G484800*	4A	738886426	738890686	2457	1	55.08
TaFruc4A.7	*TraesCS4A02G485000.3*	*TraesCS4A02G485000*	4A	738960730	738964876	1433	3	49.77
TaFruc4A.8	*TraesCS4A02G485400.2*	*TraesCS4A02G485400*	4A	739064735	739068557	2547	2	51.43
TaFruc4A.9	*TraesCS4A02G485500.1*	*TraesCS4A02G485500*	4A	739079337	739081425	1688	1	52.61
TaFruc4A.10	*TraesCS4A02G485600.1*	*TraesCS4A02G485600*	4A	739129344	739132353	1953	1	51.23
TaFruc4A.11	*TraesCS4A02G485700.2*	*TraesCS4A02G485700*	4A	739151566	739154805	2348	2	51.42
TaFruc4A.12	*TraesCS4A02G485800.1*	*TraesCS4A02G485800*	4A	739272852	739276534	2385	1	52.19
TaFruc4A.13	*TraesCS4A02G485900.1*	*TraesCS4A02G485900*	4A	739310199	739314035	2447	1	52.78
TaFruc4A.14	*TraesCS4A02G486000.1*	*TraesCS4A02G486000*	4A	739415334	739419007	2351	1	55.93
TaFruc4B.1	*TraesCS4B02G066000.1*	*TraesCS4B02G066000*	4B	58925787	58928009	1944	1	60.55
TaFruc4B.2	*TraesCS4B02G356800.1*	*TraesCS4B02G356800*	4B	647622640	647626484	2003	1	53.5
TaFruc4D.1	*TraesCS4D02G065000.1*	*TraesCS4D02G065000*	4D	40396352	40398476	1903	1	60.71
TaFruc4D.2	*TraesCS4D02G350500.1*	*TraesCS4D02G350500*	4D	502708408	502712304	2127	1	52.17

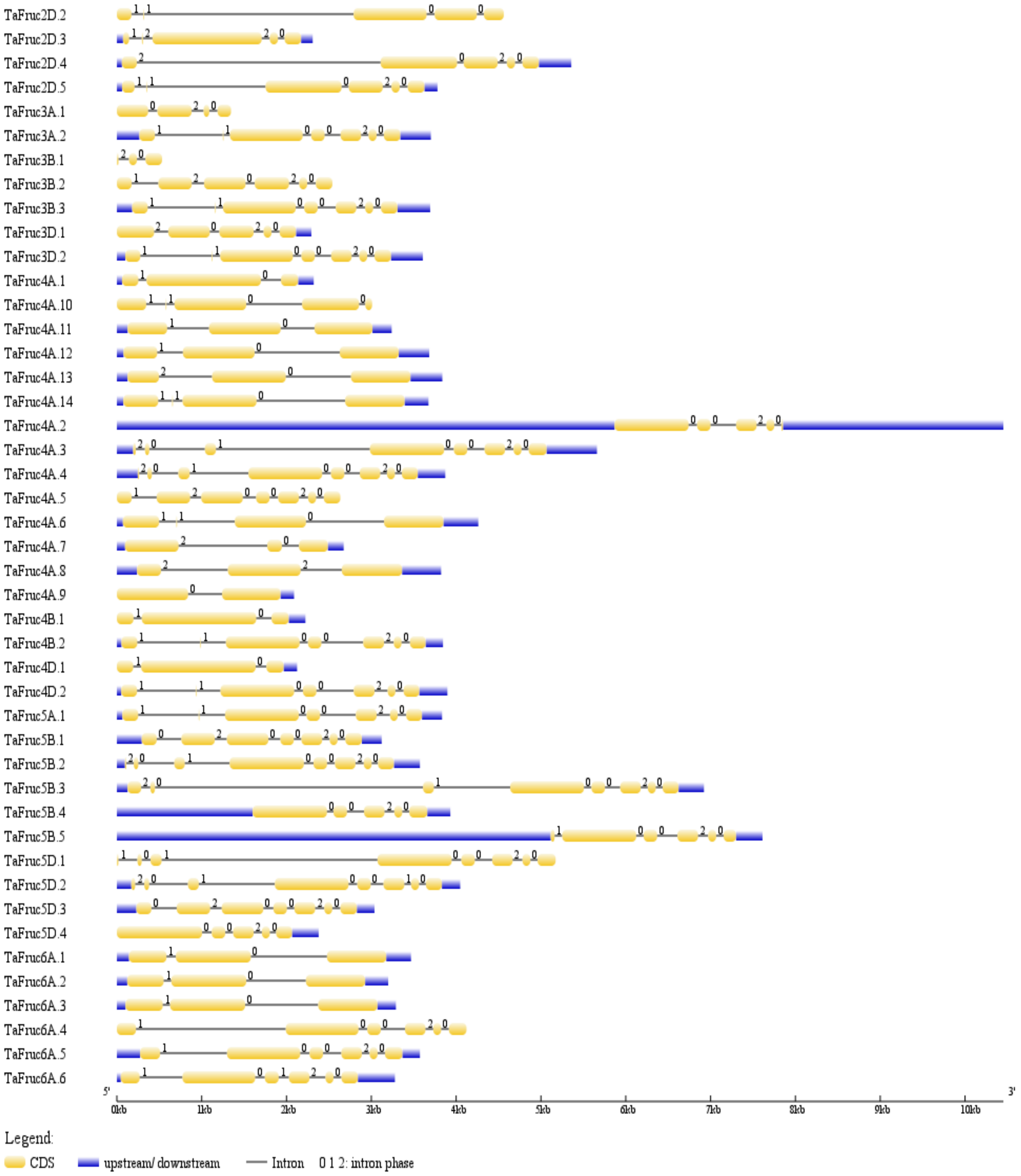
Nomenclature	**Transcript ID**	**Gene ID**	**Chr**	**Gene start (bp)**	**Gene end (bp)**	**TL**	**TC**	**GC (%)**
TaFruc5A.1	*TraesCS5A02G526200.1*	*TraesCS5A02G526200*	5A	687148842	687152675	2047	1	51.85
TaFruc5B.1	*TraesCS5B02G556600.1*	*TraesCS5B02G556600*	5B	705052959	705056080	2145	1	52.08
TaFruc5B.2	*TraesCS5B02G556700.2*	*TraesCS5B02G556700*	5B	705064023	705068035	2155	2	39.17
TaFruc5B.3	*TraesCS5B02G557100.1*	*TraesCS5B02G557100*	5B	705133150	705140071	2326	1	43.08
TaFruc5B.4	*TraesCS5B02G557300.2*	*TraesCS5B02G557300*	5B	705256012	705260890	1861	2	41.57
TaFruc5B.5	*TraesCS5B02G557400.1*	*TraesCS5B02G557400*	5B	705266461	705274072	2037	1	43.56
TaFruc5D.1	*TraesCS5D02G551900.1*	*TraesCS5D02G551900*	5D	557536230	557541402	1788	1	40.67
TaFruc5D.2	*TraesCS5D02G552000.1*	*TraesCS5D02G552000*	5D	557543729	557547776	2176	1	43.45
TaFruc5D.3	*TraesCS5D02G552900.1*	*TraesCS5D02G552900*	5D	557945818	557948854	2045	1	51.79
TaFruc5D.4	*TraesCS5D02G553000.2*	*TraesCS5D02G553000*	5D	558030214	558035197	2001	2	38.52
TaFruc6A.1	*TraesCS6A02G023100.1*	*TraesCS6A02G023100*	6A	11554651	11558118	2459	1	52.74
TaFruc6A.2	*TraesCS6A02G023200.1*	*TraesCS6A02G023200*	6A	11568527	11571725	2406	1	53.86
TaFruc6A.3	*TraesCS6A02G023300.2*	*TraesCS6A02G023300*	6A	11587722	11591011	2341	2	53.34
TaFruc6A.4	*TraesCS6A02G060700.2*	*TraesCS6A02G060700*	6A	32658028	32662149	1785	2	44.83
TaFruc6A.5	*TraesCS6A02G060800.1*	*TraesCS6A02G060800*	6A	32667678	32671250	2285	1	44.58
TaFruc6A.6	*TraesCS6A02G069000.1*	*TraesCS6A02G069000*	6A	37413578	37416855	2260	1	48.23
TaFruc6B.1	*TraesCS6B02G031300.1*	*TraesCS6B02G031300*	6B	18593033	18596332	2314	1	53.12
TaFruc6B.2	*TraesCS6B02G031500.1*	*TraesCS6B02G031500*	6B	18645460	18648979	2647	1	54.4
TaFruc6B.3	*TraesCS6B02G031600.2*	*TraesCS6B02G031600*	6B	18655748	18659002	2396	2	53.21
TaFruc6B.4	*TraesCS6B02G031700.1*	*TraesCS6B02G031700*	6B	18729867	18734470	2323	1	55.13
TaFruc6B.5	*TraesCS6B02G080700.3*	*TraesCS6B02G080700*	6B	57283367	57288151	2560	3	44.89
TaFruc6B.6	*TraesCS6B02G080800.1*	*TraesCS6B02G080800*	6B	57320500	57325258	4008	1	46.1
TaFruc6D.1	*TraesCS6D02G026300.2*	*TraesCS6D02G026300*	6D	10042972	10046264	2376	2	53.66
TaFruc6D.2	*TraesCS6D02G026400.1*	*TraesCS6D02G026400*	6D	10066078	10069418	2532	1	53.97

Nomenclature	Transcript ID	Gene ID	Chr	Gene start (bp)	Gene end (bp)	TL	TC	GC (%)
TaFruc6D.3	*TraesCS6D02G026500.2*	*TraesCS6D02G026500*	6D	10101171	10104340	2273	2	54.51
TaFruc6D.4	*TraesCS6D02G026600.2*	*TraesCS6D02G026600*	6D	10118909	10122447	2420	2	51.23
TaFruc6D.5	*TraesCS6D02G064100.1*	*TraesCS6D02G064100*	6D	30212081	30228039	1371	1	44.86
TaFruc6D.6	*TraesCS6D02G064200.2*	*TraesCS6D02G064200*	6D	30236386	30239754	2057	2	43.69
TaFruc6D.7	*TraesCS6D02G064300.1*	*TraesCS6D02G064300*	6D	30245066	30248568	2210	1	43.85
TaFruc6D.8	*TraesCS6D02G064400.1*	*TraesCS6D02G064400*	6D	30281142	30285808	2463	1	44.98
TaFruc6D.9	*TraesCS6D02G066800.1*	*TraesCS6D02G066800*	6D	32858418	32861502	2085	1	48.23
TaFruc7A.1	*TraesCS7A02G009100.1*	*TraesCS7A02G009100*	7A	3982822	3986635	2383	1	53.64
TaFruc7A.2	*TraesCS7A02G009200.2*	*TraesCS7A02G009200*	7A	4014507	4017160	1947	2	57.69
TaFruc7A.3	*TraesCS7A02G009400.1*	*TraesCS7A02G009400*	7A	4067455	4072522	2456	1	50.3
TaFruc7A.4	*TraesCS7A02G009500.3*	*TraesCS7A02G009500*	7A	4206019	4209108	2353	3	52.3
TaFruc7A.5	*TraesCS7A02G009600.3*	*TraesCS7A02G009600*	7A	4251676	4255084	2404	3	50.51
TaFruc7A.6	*TraesCS7A02G009700.1*	*TraesCS7A02G009700*	7A	4327689	4330356	2015	1	52.51
TaFruc7A.7	*TraesCS7A02G009800.2*	*TraesCS7A02G009800*	7A	4429532	4435570	2722	2	48.03
TaFruc7A.8	*TraesCS7A02G010200.1*	*TraesCS7A02G010200*	7A	4625252	4629547	2508	1	54.66
TaFruc7A.9	*TraesCS7A02G060300.3*	*TraesCS7A02G060300*	7A	29661723	29665450	2321	3	51.23
TaFruc7A.10	*TraesCS7A02G060400.1*	*TraesCS7A02G060400*	7A	29784035	29787043	2323	1	54.6
TaFruc7D.1	*TraesCS7D02G008700.1*	*TraesCS7D02G008700*	7D	4198465	4202181	2380	1	54.78
TaFruc7D.2	*TraesCS7D02G008800.2*	*TraesCS7D02G008800*	7D	4267640	4270860	2499	2	55.17
TaFruc7D.3	*TraesCS7D02G008900.1*	*TraesCS7D02G008900*	7D	4288688	4293044	2355	1	50.72
TaFruc7D.4	*TraesCS7D02G009100.2*	*TraesCS7D02G009100*	7D	4411975	4415156	2477	2	52.36
TaFruc7D.5	*TraesCS7D02G009200.2*	*TraesCS7D02G009200*	7D	4423362	4426567	2456	2	51.31
TaFruc7D.6	*TraesCS7D02G009300.1*	*TraesCS7D02G009300*	7D	4501472	4503395	1530	1	53.53
TaFruc7D.7	*TraesCS7D02G009400.2*	*TraesCS7D02G009400*	7D	4515237	4518875	2346	2	51.31

Nomenclature	Transcript ID	Gene ID	Chr	Gene start (bp)	Gene end (bp)	TL	TC	GC (%)
TaFruc7D.8	*TraesCS7D02G009700.1*	*TraesCS7D02G009700*	7D	4647462	4654744	2154	1	56.01
TaFruc7D.9	*TraesCS7D02G010000.2*	*TraesCS7D02G010000*	7D	4792710	4797318	2510	2	54.8
TaFruc7D.10	*TraesCS7D02G054800.3*	*TraesCS7D02G054800*	7D	29402451	29405760	2543	3	51.09
TaFruc7D.11	*TraesCS7D02G055000.1*	*TraesCS7D02G055000*	7D	29549953	29552899	2277	1	55.31
TaFrucUn.1	*TraesCSU02G080200.1*	*TraesCSU02G080200*	Un	71717793	71721140	2055	1	43.4
TaFrucUn.2	*TraesCSU02G173900.1*	*TraesCSU02G173900*	Un	260888579	260890930	1862	1	53.66
TaFrucUn.3	*TraesCSU02G175300.1*	*TraesCSU02G175300*	Un	263767835	263770186	1862	1	53.66
TaFrucUn.4	*TraesCSU02G216800.1*	*TraesCSU02G216800*	Un	319810948	319812455	1191	1	54.24
TaFrucUn.5	*TraesCSU02G250400.1*	*TraesCSU02G250400*	Un	382718415	382719038	400	1	48.08

Annexure 13: Comparison between gene structures of fructans genes belonging to different plant species as predicted from GSDS v2.0 server:




TaFruc2D.2
TaFruc2D.3
TaFruc2D.4
TaFruc2D.5
TaFruc3A.1
TaFruc3A.2
TaFruc3B.1
TaFruc3B.2
TaFruc3B.3
TaFruc3D.1
TaFruc3D.2
TaFruc4A.1
TaFruc4A.10
TaFruc4A.11
TaFruc4A.12
TaFruc4A.13
TaFruc4A.14
TaFruc4A.2
TaFruc4A.3
TaFruc4A.4
TaFruc4A.5
TaFruc4A.6
TaFruc4A.7
TaFruc4A.8
TaFruc4A.9
TaFruc4B.1
TaFruc4B.2
TaFruc4D.1
TaFruc4D.2
TaFruc5A.1
TaFruc5B.1
TaFruc5B.2
TaFruc5B.3
TaFruc5B.4
TaFruc5B.5
TaFruc5D.1
TaFruc5D.2
TaFruc5D.3
TaFruc5D.4
TaFruc6A.1
TaFruc6A.2
TaFruc6A.3
TaFruc6A.4
TaFruc6A.5
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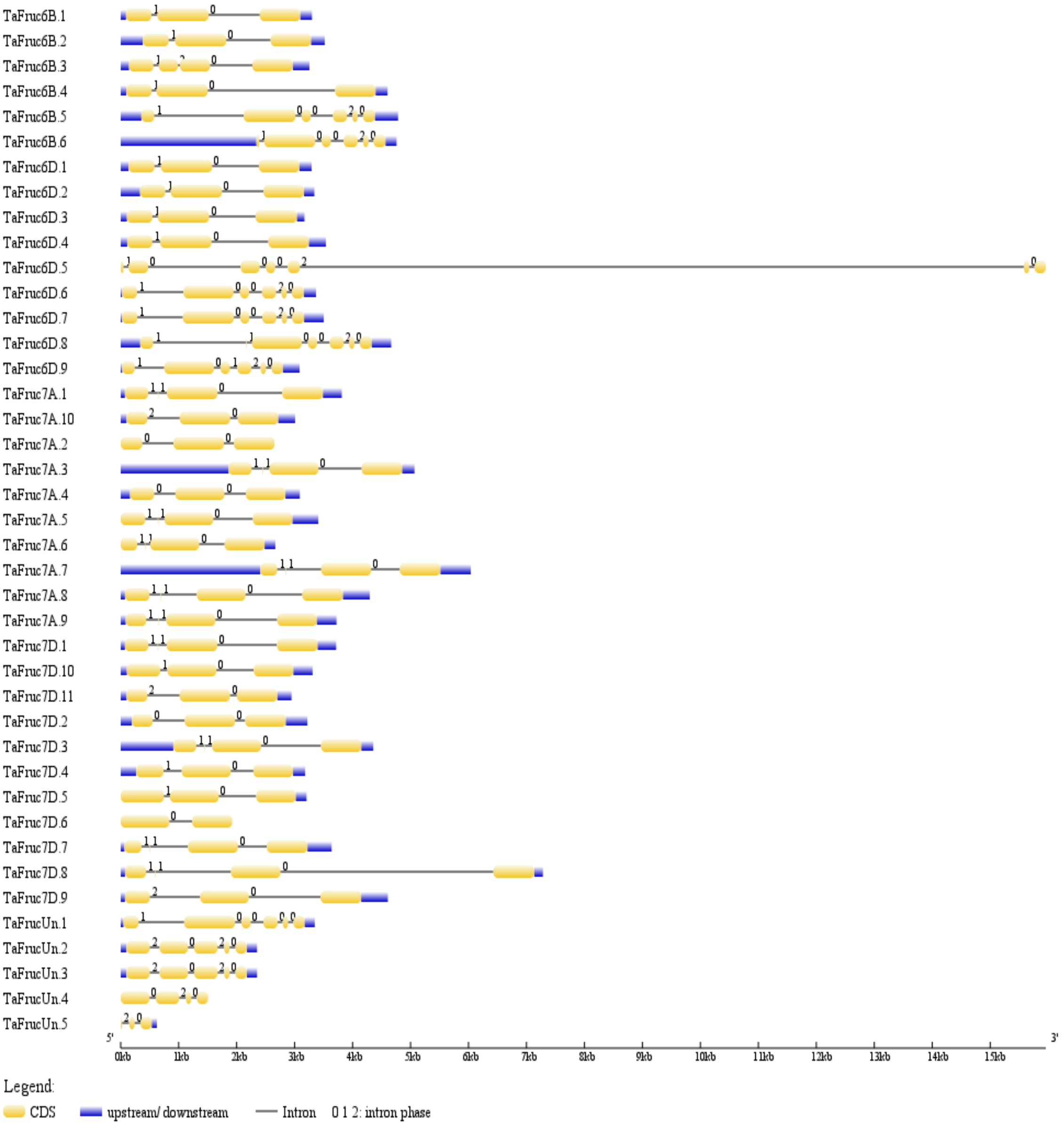
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TaFruc6B.3
TaFruc6B.4
TaFruc6B.5
TaFruc6B.6
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TaFruc6D.4
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TaFruc6D.6
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Legend:
CDS
upstream/ downstream
Intron
0 1 2: intron phase

Annexure 14: Summary statistics of *TaFruc* duplicate gene pairs

Sequence names	**Sd**	**Sn**	**S**	**N**	**ps**	**pn**	**ds**	**dn**	**ds/dn**	**ps/pn**	**dN/dS**	**Td**	**GD**	**Selection**
TaFruc1A.1 TaFruc1B.1	20.50	18.50	369.83	1256.17	0.06	0.01	0.06	0.01	3.87	3.76	0.26	4.43	SD	Purifying
TaFruc1A.1 TaFruc1D.1	17.50	18.50	369.50	1256.50	0.05	0.01	0.05	0.01	3.29	3.22	0.30	3.76	SD	Purifying
TaFruc2A.2 TaFruc2B.2	38.00	19.00	376.00	1184.00	0.10	0.02	0.11	0.02	6.69	6.30	0.15	8.35	SD	Purifying
TaFruc2A.4 TaFruc2B.4	36.00	30.00	414.50	1283.50	0.09	0.02	0.09	0.02	3.89	3.72	0.26	7.10	SD	Purifying
TaFruc2A.5 TaFruc2D.4	33.00	20.00	407.00	1309.00	0.08	0.02	0.09	0.02	5.56	5.31	0.18	6.60	SD	Purifying
TaFruc2A.6 TaFruc2B.6	124.83	106.17	405.50	1304.50	0.31	0.08	0.40	0.09	4.60	3.78	0.22	30.48	SD	Purifying
TaFruc2A.6 TaFruc2D.4	115.67	96.33	406.00	1304.00	0.28	0.07	0.36	0.08	4.61	3.86	0.22	27.57	SD	Purifying
TaFruc2B.5 TaFruc2D.4	4.00	6.00	67.17	220.83	0.06	0.03	0.06	0.03	2.24	2.19	0.45	4.78	SD	Purifying
TaFruc2B.6 TaFruc2D.4	34.00	23.00	406.83	1309.17	0.08	0.02	0.09	0.02	4.98	4.76	0.20	6.82	SD	Purifying
TaFruc3A.1 TaFruc3B.2	45.00	37.00	218.17	747.83	0.21	0.05	0.24	0.05	4.71	4.17	0.21	18.55	SD	Purifying
TaFruc3A.1 TaFruc3D.1	28.00	22.00	220.00	746.00	0.13	0.03	0.14	0.03	4.64	4.32	0.22	10.73	SD	Purifying
TaFruc3A.1 TaFruc4A.5	98.33	61.67	216.83	749.17	0.45	0.08	0.70	0.09	7.98	5.51	0.13	53.54	SD	Purifying
TaFruc3A.1 TaFruc5B.1	99.00	58.00	216.00	750.00	0.46	0.08	0.71	0.08	8.68	5.93	0.12	54.48	SD	Purifying
TaFruc3A.1 TaFruc5D.3	91.33	59.67	216.50	749.50	0.42	0.08	0.62	0.08	7.37	5.30	0.14	47.69	SD	Purifying
TaFruc3A.1 TaFrucUn.4	28.00	25.00	220.00	746.00	0.13	0.03	0.14	0.03	4.07	3.80	0.25	10.73	SD	Purifying
TaFruc3A.2 TaFruc3D.2	47.00	17.00	382.00	1277.00	0.12	0.01	0.13	0.01	10.01	9.24	0.10	10.34	SD	Purifying
TaFruc3B.1 TaFruc3B.2	6.00	10.00	66.50	236.50	0.09	0.04	0.10	0.04	2.21	2.13	0.45	7.39	TD	Purifying
TaFruc3B.1 TaFruc5B.1	23.00	17.00	67.83	235.17	0.34	0.07	0.45	0.08	5.94	4.69	0.17	34.71	SD	Purifying
TaFruc3B.1 TaFruc5D.3	22.00	16.00	67.17	235.83	0.33	0.07	0.43	0.07	6.05	4.83	0.17	33.12	SD	Purifying
TaFruc3B.1 TaFrucUn.2	9.00	9.00	66.50	236.50	0.14	0.04	0.15	0.04	3.82	3.56	0.26	11.48	SD	Purifying
TaFruc3B.1 TaFrucUn.3	9.00	9.00	66.50	236.50	0.14	0.04	0.15	0.04	3.82	3.56	0.26	11.48	SD	Purifying
TaFruc3B.1 TaFrucUn.4	16.00	9.00	66.50	236.50	0.24	0.04	0.29	0.04	7.43	6.32	0.13	22.32	SD	Purifying
TaFruc3B.1 TaFrucUn.5	0.00	1.00	66.33	236.67	NA	0.00	NA	0.00	NA	NA	NA	NA	NA	NA
TaFruc3B.2 TaFruc4A.5	143.00	119.00	390.83	1301.17	0.37	0.09	0.50	0.10	5.15	4.00	0.19	38.60	SD	Purifying
TaFruc3B.2 TaFruc5B.1	143.00	121.00	389.50	1296.50	0.37	0.09	0.50	0.10	5.06	3.93	0.20	38.79	SD	Purifying
TaFruc3B.2 TaFruc5D.3	145.00	117.00	388.33	1297.67	0.37	0.09	0.52	0.10	5.38	4.14	0.19	39.74	SD	Purifying
TaFruc3B.2 TaFrucUn.2	45.83	45.17	342.50	1184.50	0.13	0.04	0.15	0.04	3.77	3.51	0.27	11.34	SD	Purifying
TaFruc3B.2 TaFrucUn.3	45.83	45.17	342.50	1184.50	0.13	0.04	0.15	0.04	3.77	3.51	0.27	11.34	SD	Purifying
TaFruc3B.2 TaFrucUn.4	56.67	34.33	258.00	894.00	0.22	0.04	0.26	0.04	6.59	5.72	0.15	19.99	SD	Purifying
TaFruc3B.2 TaFrucUn.5	6.00	9.00	66.50	236.50	0.09	0.04	0.10	0.04	2.46	2.37	0.41	7.39	SD	Purifying
TaFruc3B.3 TaFruc3D.2	50.50	21.50	384.00	1275.00	0.13	0.02	0.14	0.02	8.48	7.80	0.12	11.12	SD	Purifying

Sd: The number of observed synonymous substitutions; Sn: The number of observed non-synonymous substitutions; S: The number of potential synonymous substitutions (the average for the two compared sequences); N: The number of potential non-synonymous substitutions (the average for the two compared sequences); ps: The proportion of observed synonymous substitutions: Sd/S; pn: The proportion of observed non-synonymous substitutions: Sn/N; ds: The Jukes-Cantor correction for multiple hits of ps; dn: The Jukes-Cantor correction for multiple hits of pn; ds/dn: The ratio of synonymous to non-synonymous substitutions

Sequence names	**Sd**	**Sn**	**S**	**N**	**ps**	**pn**	**ds**	**dn**	**ds/dn**	**ps/pn**	**dN/dS**	**Td**	**GD**	**Selection**
TaFruc4A.2 TaFruc5D.2	55.67	81.33	295.17	1042.83	0.19	0.08	0.22	0.08	2.64	2.42	0.38	16.71	SD	Purifying
TaFruc4A.3 TaFruc5B.4	26.17	24.83	334.83	1198.17	0.08	0.02	0.08	0.02	3.93	3.77	0.25	6.35	SD	Purifying
TaFruc4A.4 TaFruc5B.3	45.50	46.50	374.67	1305.33	0.12	0.04	0.13	0.04	3.63	3.41	0.28	10.19	SD	Purifying
TaFruc4A.4 TaFruc5D.2	56.50	44.50	374.83	1305.17	0.15	0.03	0.17	0.03	4.82	4.42	0.21	12.95	SD	Purifying
TaFruc4A.5 TaFruc5B.1	48.00	30.00	388.00	1298.00	0.12	0.02	0.14	0.02	5.76	5.35	0.17	10.40	SD	Purifying
TaFruc4A.5 TaFruc5D.3	40.00	18.00	386.83	1299.17	0.10	0.01	0.11	0.01	7.96	7.46	0.13	8.56	SD	Purifying
TaFruc4A.5 TaFrucUn.2	123.33	90.67	341.33	1185.67	0.36	0.08	0.49	0.08	6.11	4.73	0.16	37.92	SD	Purifying
TaFruc4A.5 TaFrucUn.3	123.33	90.67	341.33	1185.67	0.36	0.08	0.49	0.08	6.11	4.73	0.16	37.92	SD	Purifying
TaFruc4A.5 TaFrucUn.4	103.83	64.17	257.83	894.17	0.40	0.07	0.58	0.08	7.66	5.61	0.13	44.42	SD	Purifying
TaFruc4A.6 TaFruc7A.8	47.50	16.50	478.83	1423.17	0.10	0.01	0.11	0.01	9.11	8.56	0.11	8.18	SD	Purifying
TaFruc4A.6 TaFruc7D.9	45.00	14.00	482.67	1425.33	0.09	0.01	0.10	0.01	10.07	9.49	0.10	7.66	SD	Purifying
TaFruc4A.7 TaFruc7D.8	28.00	18.00	250.33	856.67	0.11	0.02	0.12	0.02	5.68	5.32	0.18	9.32	SD	Purifying
TaFruc4A.8 TaFruc7A.7	51.00	23.00	421.00	1349.00	0.12	0.02	0.13	0.02	7.66	7.11	0.13	10.16	SD	Purifying
TaFruc4A.8 TaFruc7D.7	54.50	20.50	422.00	1348.00	0.13	0.02	0.14	0.02	9.23	8.49	0.11	10.90	SD	Purifying
TaFruc4A.9 TaFruc7A.6	50.00	31.00	339.33	1133.67	0.15	0.03	0.16	0.03	5.89	5.39	0.17	12.62	SD	Purifying
TaFruc4A.9 TaFruc7D.6	52.33	25.67	340.17	1132.83	0.15	0.02	0.17	0.02	7.48	6.79	0.13	13.25	SD	Purifying
TaFruc4B.1 TaFruc4D.1	60.00	28.00	408.50	1277.50	0.15	0.02	0.16	0.02	7.35	6.70	0.14	12.58	SD	Purifying
TaFruc4B.2 TaFruc4D.2	45.00	25.00	394.17	1279.83	0.11	0.02	0.12	0.02	6.26	5.84	0.16	9.53	SD	Purifying
TaFruc4B.2 TaFruc5A.1	50.00	24.00	395.00	1279.00	0.13	0.02	0.14	0.02	7.30	6.75	0.14	10.66	SD	Purifying
TaFruc5B.1 TaFruc5D.3	39.00	19.00	388.50	1306.50	0.10	0.01	0.11	0.01	7.34	6.90	0.14	8.29	SD	Purifying
TaFruc5B.1 TaFrucUn.2	128.83	92.17	341.83	1185.17	0.38	0.08	0.52	0.08	6.38	4.85	0.16	40.28	SD	Purifying
TaFruc5B.1 TaFrucUn.3	128.83	92.17	341.83	1185.17	0.38	0.08	0.52	0.08	6.38	4.85	0.16	40.28	SD	Purifying
TaFruc5B.1 TaFrucUn.5	23.00	16.00	67.83	235.17	0.34	0.07	0.45	0.07	6.33	4.98	0.16	34.71	SD	Purifying
TaFruc5B.2 TaFruc5D.2	85.50	100.50	367.00	1310.00	0.23	0.08	0.28	0.08	3.45	3.04	0.29	21.46	SD	Purifying
TaFruc5B.3 TaFruc5D.2	38.00	23.00	380.17	1332.83	0.10	0.02	0.11	0.02	6.14	5.79	0.16	8.25	SD	Purifying
TaFruc5D.3 TaFrucUn.2	124.33	87.67	341.33	1185.67	0.36	0.07	0.50	0.08	6.41	4.93	0.16	38.36	SD	Purifying
TaFruc5D.3 TaFrucUn.3	124.33	87.67	341.33	1185.67	0.36	0.07	0.50	0.08	6.41	4.93	0.16	38.36	SD	Purifying
TaFruc5D.3 TaFrucUn.5	22.00	15.00	67.17	235.83	0.33	0.06	0.43	0.07	6.48	5.15	0.15	33.12	SD	Purifying
TaFruc6A.1 TaFruc6B.1	182.67	107.33	479.50	1476.50	0.38	0.07	0.53	0.08	6.96	5.24	0.14	40.92	SD	Purifying
TaFruc6A.1 TaFruc6B.2	117.00	51.00	483.67	1481.33	0.24	0.03	0.29	0.04	8.29	7.03	0.12	22.46	SD	Purifying
TaFruc6A.1 TaFruc6B.3	174.67	84.33	471.50	1439.50	0.37	0.06	0.51	0.06	8.37	6.32	0.12	39.29	SD	Purifying
TaFruc6A.1 TaFruc6B.4	180.17	107.83	478.50	1477.50	0.38	0.07	0.52	0.08	6.81	5.16	0.15	40.22	SD	Purifying
TaFruc6A.1 TaFruc6D.1	63.50	30.50	482.67	1482.33	0.13	0.02	0.14	0.02	6.93	6.39	0.14	11.13	SD	Purifying

Sd: number of observed synonymous substitutions; Sn: number of observed non-synonymous substitutions; S: number of potential synonymous substitutions (average for two compared sequences); N: number of potential non-synonymous substitutions (average for two compared sequences); ps: proportion of observed synonymous substitutions: Sd/S; pn: proportion of observed non-synonymous substitutions: Sn/N; ds: Jukes-Cantor correction for multiple hits of ps; dn: Jukes-Cantor correction for multiple hits of pn; ds/dn: ratio of synonymous to non-synonymous substitutions

Sequence names	**Sd**	**Sn**	**S**	**N**	**ps**	**pn**	**ds**	**dn**	**ds/dn**	**ps/pn**	**dN/dS**	**Td**	**GD**	**Selection**
TaFruc6A.1 TaFruc6D.2	166.83	87.17	477.00	1467.00	0.35	0.06	0.47	0.06	7.61	5.89	0.13	36.23	SD	Purifying
TaFruc6A.1 TaFruc6D.3	187.17	103.83	483.50	1472.50	0.39	0.07	0.54	0.07	7.35	5.49	0.14	41.88	SD	Purifying
TaFruc6A.1 TaFruc6D.4	189.17	100.83	479.33	1473.67	0.39	0.07	0.56	0.07	7.81	5.77	0.13	43.09	SD	Purifying
TaFruc6A.2 TaFruc6B.1	178.50	112.50	475.33	1468.67	0.38	0.08	0.52	0.08	6.45	4.90	0.16	40.07	SD	Purifying
TaFruc6A.2 TaFruc6B.2	187.17	97.83	477.00	1467.00	0.39	0.07	0.56	0.07	7.95	5.88	0.13	42.73	SD	Purifying
TaFruc6A.2 TaFruc6B.3	94.00	59.00	470.33	1440.67	0.20	0.04	0.23	0.04	5.52	4.88	0.18	17.88	SD	Purifying
TaFruc6A.2 TaFruc6B.4	173.00	115.00	474.33	1469.67	0.36	0.08	0.50	0.08	6.05	4.66	0.17	38.43	SD	Purifying
TaFruc6A.2 TaFruc6D.1	168.17	93.83	476.00	1468.00	0.35	0.06	0.48	0.07	7.15	5.53	0.14	36.75	SD	Purifying
TaFruc6A.2 TaFruc6D.2	74.50	51.50	478.33	1474.67	0.16	0.03	0.17	0.04	4.88	4.46	0.21	13.43	SD	Purifying
TaFruc6A.2 TaFruc6D.3	168.17	109.83	479.33	1464.67	0.35	0.08	0.47	0.08	5.99	4.68	0.17	36.38	SD	Purifying
TaFruc6A.2 TaFruc6D.4	175.00	108.00	474.83	1466.17	0.37	0.07	0.51	0.08	6.54	5.00	0.15	39.01	SD	Purifying
TaFruc6A.3 TaFruc6B.1	95.50	54.50	481.33	1486.67	0.20	0.04	0.23	0.04	6.13	5.41	0.16	17.72	SD	Purifying
TaFruc6A.3 TaFruc6B.2	174.83	106.17	479.17	1476.83	0.36	0.07	0.50	0.08	6.61	5.08	0.15	38.45	SD	Purifying
TaFruc6A.3 TaFruc6B.4	91.83	50.17	480.33	1487.67	0.19	0.03	0.22	0.03	6.40	5.67	0.16	16.98	SD	Purifying
TaFruc6A.3 TaFruc6D.1	173.83	112.17	478.17	1477.83	0.36	0.08	0.50	0.08	6.21	4.79	0.16	38.25	SD	Purifying
TaFruc6A.3 TaFruc6D.2	170.83	106.17	475.00	1469.00	0.36	0.07	0.49	0.08	6.44	4.98	0.16	37.68	SD	Purifying
TaFruc6A.3 TaFruc6D.3	77.83	52.17	485.33	1482.67	0.16	0.04	0.18	0.04	5.01	4.56	0.20	13.88	SD	Purifying
TaFruc6A.3 TaFruc6D.4	119.33	59.67	479.17	1479.83	0.25	0.04	0.30	0.04	7.30	6.18	0.14	23.28	SD	Purifying
TaFruc6A.4 TaFruc6D.8	24.00	11.00	390.33	1319.67	0.06	0.01	0.06	0.01	7.65	7.38	0.13	4.94	SD	Purifying
TaFruc6A.5 TaFruc6D.6	29.00	26.00	385.83	1342.17	0.08	0.02	0.08	0.02	4.04	3.88	0.25	6.09	SD	Purifying
TaFruc6A.5 TaFruc6D.7	37.83	40.17	387.00	1350.00	0.10	0.03	0.10	0.03	3.45	3.29	0.29	8.05	SD	Purifying
TaFruc6A.6 TaFruc6D.9	49.00	32.00	382.33	1324.67	0.13	0.02	0.14	0.02	5.72	5.31	0.18	10.81	SD	Purifying
TaFruc6B.1 TaFruc6B.2	185.50	109.50	480.17	1475.83	0.39	0.07	0.54	0.08	6.95	5.21	0.14	41.76	TD	Purifying
TaFruc6B.1 TaFruc6D.4	125.33	53.67	480.17	1478.83	0.26	0.04	0.32	0.04	8.62	7.19	0.12	24.68	SD	Purifying
TaFruc6B.2 TaFruc6D.4	197.17	105.83	480.00	1473.00	0.41	0.07	0.60	0.08	7.88	5.72	0.13	45.77	SD	Purifying
TaFruc6B.3 TaFruc6D.4	191.17	93.83	470.17	1437.83	0.41	0.07	0.59	0.07	8.58	6.23	0.12	45.07	SD	Purifying
TaFruc6B.4 TaFruc6D.3	62.00	31.00	485.33	1482.67	0.13	0.02	0.14	0.02	6.60	6.11	0.15	10.77	SD	Purifying
TaFruc6B.4 TaFruc6D.4	112.00	50.00	479.17	1479.83	0.23	0.03	0.28	0.03	8.10	6.92	0.12	21.55	SD	Purifying
TaFruc6B.5 TaFruc6D.8	22.00	12.00	393.67	1322.33	0.06	0.01	0.06	0.01	6.36	6.16	0.16	4.47	SD	Purifying
TaFruc6D.1 TaFruc6D.2	170.33	89.67	477.67	1472.33	0.36	0.06	0.48	0.06	7.62	5.86	0.13	37.22	TD	Purifying
TaFruc6D.1 TaFruc6D.4	190.00	103.00	479.00	1474.00	0.40	0.07	0.56	0.07	7.70	5.68	0.13	43.42	TD	Purifying
TaFruc6D.2 TaFruc6D.3	179.33	107.67	480.00	1464.00	0.37	0.07	0.52	0.08	6.68	5.08	0.15	39.78	TD	Purifying
TaFruc6D.2 TaFruc6D.4	193.33	103.67	475.50	1465.50	0.41	0.07	0.59	0.07	7.89	5.75	0.13	45.07	TD	Purifying

Sd: number of observed synonymous substitutions; Sn: number of observed non-synonymous substitutions; S: number of potential synonymous substitutions (average for two compared sequences); N: number of potential non-synonymous substitutions (average for two compared sequences); ps: proportion of observed synonymous substitutions: Sd/S; pn: proportion of observed non-synonymous substitutions: Sn/N; ds: Jukes-Cantor correction for multiple hits of ps; dn: Jukes-Cantor correction for multiple hits of pn; ds/dn: ratio of synonymous to non-synonymous substitutions

Sequence names	Sd	Sn	S	N	ps	pn	ds	dn	ds/dn	ps/pn	dN/dS	Td	GD	Selection
TaFruc6D.3 TaFruc6D.4	107.50	47.50	484.17	1474.83	0.22	0.03	0.26	0.03	8.00	6.89	0.12	20.25	TD	Purifying
TaFruc6D.7 TaFrucUn.1	57.00	68.00	389.33	1377.67	0.15	0.05	0.16	0.05	3.19	2.97	0.31	12.53	SD	Purifying
TaFruc7A.1 TaFruc7D.1	49.50	23.50	470.00	1447.00	0.11	0.02	0.11	0.02	6.91	6.49	0.14	8.73	SD	Purifying
TaFruc7A.2 TaFruc7D.2	61.00	34.00	455.00	1402.00	0.13	0.02	0.15	0.02	5.99	5.53	0.17	11.36	SD	Purifying
TaFruc7A.4 TaFruc7D.4	47.00	23.00	441.33	1403.67	0.11	0.02	0.11	0.02	6.93	6.50	0.14	8.84	SD	Purifying
TaFruc7A.8 TaFruc7D.9	48.50	15.50	479.17	1422.83	0.10	0.01	0.11	0.01	9.91	9.29	0.10	8.36	SD	Purifying
TaFrucUn.2 TaFrucUn.5	9.00	8.00	66.50	236.50	0.14	0.03	0.15	0.03	4.31	4.00	0.23	11.48	TD	Purifying
TaFrucUn.3 TaFrucUn.5	9.00	8.00	66.50	236.50	0.14	0.03	0.15	0.03	4.31	4.00	0.23	11.48	TD	Purifying
TaFrucUn.4 TaFrucUn.5	16.00	8.00	66.50	236.50	0.24	0.03	0.29	0.03	8.38	7.11	0.12	22.32	TD	Purifying

Sd: number of observed synonymous substitutions; Sn: number of observed non-synonymous substitutions; S: number of potential synonymous substitutions (average for two compared sequences); N: number of potential non-synonymous substitutions (average for two compared sequences); ps: proportion of observed synonymous substitutions: Sd/S; pn: proportion of observed non-synonymous substitutions: Sn/N; ds: Jukes-Cantor correction for multiple hits of ps; dn: Jukes-Cantor correction for multiple hits of pn; ds/dn: ratio of synonymous to non-synonymous substitutions

Annexure 15: Composition of polypeptide chains translated by *TaFruc* genes

Gene	Ala	Cys	Asp	Glu	Phe	Gly	His	Ile	Lys	Leu	Met	Asn	Pro	Gln	Arg	Ser	Thr	Val	Trp	Tyr	Total
TaFruc1A.1	5.61	0.70	6.67	4.04	3.68	8.07	2.98	4.21	5.79	8.60	1.58	4.91	6.32	2.98	5.09	7.72	4.21	8.77	3.51	4.56	570.00
TaFruc1B.1	5.77	0.70	6.29	4.02	3.67	8.04	2.80	4.72	6.12	8.57	1.40	5.07	6.29	3.15	5.07	7.52	4.02	8.57	3.67	4.55	572.00
TaFruc1D.1	5.62	0.70	5.98	4.04	3.69	7.73	2.81	4.57	6.15	8.61	1.41	4.92	6.68	2.99	5.27	8.26	4.04	8.44	3.51	4.57	569.00
TaFruc2A.1	8.77	1.36	5.60	4.24	3.63	6.66	2.57	4.08	5.60	8.77	1.51	4.08	6.51	2.57	6.20	8.02	4.99	7.87	3.03	3.93	661.00
TaFruc2A.2	10.44	0.92	7.14	6.04	4.21	10.99	2.93	2.01	3.85	8.06	1.65	4.03	5.86	2.01	6.41	5.13	3.85	8.42	3.30	2.75	546.00
TaFruc2A.3	9.49	1.36	8.14	3.90	3.39	8.64	2.54	2.71	2.88	7.97	2.03	4.24	5.93	2.54	5.42	7.80	3.39	11.02	3.05	3.56	590.00
TaFruc2A.4	9.97	1.18	6.59	5.41	4.05	9.63	2.87	3.04	3.21	8.28	1.35	4.05	5.57	2.87	5.91	7.09	4.90	8.11	2.70	3.21	592.00
TaFruc2A.5	8.97	1.35	6.09	4.74	3.72	8.46	2.54	3.38	3.72	7.78	1.69	5.25	6.26	3.05	6.60	6.26	4.40	9.48	2.88	3.38	591.00
TaFruc2A.6	9.32	1.53	6.10	4.92	3.73	8.64	3.05	3.73	3.22	8.14	1.86	4.41	5.76	2.37	7.29	6.10	5.08	8.31	2.88	3.56	590.00
TaFruc2A.7	8.89	1.45	6.14	4.85	3.88	9.21	2.75	2.42	3.23	7.59	2.10	4.20	5.49	3.07	7.27	6.14	5.82	9.21	2.91	3.39	619.00
TaFruc2B.1	8.51	1.28	5.62	4.17	3.05	7.06	2.57	4.01	5.62	8.83	1.61	4.17	6.58	1.93	6.74	6.90	5.30	8.83	3.21	4.01	623.00
TaFruc2B.2	10.44	0.92	7.14	6.41	3.85	10.62	2.93	2.01	3.66	7.88	1.83	4.21	6.04	2.01	6.41	4.95	4.03	8.24	3.30	3.11	546.00
TaFruc2B.3	9.26	1.35	8.08	4.04	3.37	8.59	2.86	3.20	2.86	8.42	1.85	4.21	5.56	2.53	5.39	7.91	3.70	10.44	3.03	3.37	594.00
TaFruc2B.4	9.81	1.18	6.43	5.08	4.23	9.81	2.71	2.71	3.21	8.29	1.69	4.23	5.92	3.05	5.41	7.45	4.23	8.63	2.71	3.21	591.00
TaFruc2B.5	4.04	1.01	4.04	5.05	4.04	12.12	4.04	6.06	3.03	5.05	2.02	6.06	2.02	2.02	8.08	10.10	5.05	12.12	1.01	3.03	99.00
TaFruc2B.6	8.95	1.35	6.08	4.90	3.72	8.11	2.36	3.38	3.72	8.45	1.69	5.24	5.91	3.04	6.76	7.09	3.55	9.46	2.87	3.38	592.00
TaFruc2B.7	8.52	1.14	6.82	4.36	3.41	9.09	2.27	4.92	4.17	7.01	2.65	3.98	5.30	2.65	6.44	6.63	5.30	8.33	3.03	3.98	528.00
TaFruc2D.1	8.55	1.29	5.65	4.19	2.90	6.94	2.58	4.19	5.32	8.71	1.61	4.19	6.45	1.94	6.77	7.74	5.16	8.55	3.23	4.03	620.00
TaFruc2D.2	8.98	1.36	8.14	3.90	3.56	8.64	2.54	2.88	2.88	8.14	2.03	4.24	5.59	2.54	5.59	7.80	3.90	10.85	3.05	3.39	590.00
TaFruc2D.3	10.49	1.27	7.78	5.61	3.62	10.49	2.71	1.81	4.88	7.96	2.35	3.44	5.79	1.99	5.97	5.24	4.52	7.78	3.25	3.07	553.00
TaFruc2D.4	8.63	1.35	5.92	4.57	3.72	8.80	2.54	3.21	3.55	7.95	1.69	5.25	6.09	3.21	6.60	6.77	4.06	9.81	2.88	3.38	591.00
TaFruc2D.5	9.62	1.55	6.19	4.12	3.44	8.08	2.58	3.61	4.30	8.08	2.23	3.95	6.01	2.58	6.19	6.87	5.15	8.76	2.92	3.78	582.00
TaFruc3A.1	7.23	1.51	8.43	4.82	6.33	6.63	3.31	4.22	7.83	6.93	0.60	4.52	3.01	1.81	6.33	5.42	6.02	9.04	2.11	3.92	332.00
TaFruc3A.2	6.22	1.73	6.74	4.49	4.15	8.46	2.07	5.70	4.66	7.94	2.25	5.18	5.35	2.94	5.01	8.81	3.63	7.43	3.28	3.97	579.00
TaFruc3B.1	7.84	1.96	5.88	4.90	4.90	4.90	1.96	8.82	7.84	6.86	2.94	5.88	3.92	2.94	5.88	5.88	7.84	4.90	0.98	2.94	102.00
TaFruc3B.2	7.72	1.03	6.00	4.46	4.46	7.03	3.77	4.12	6.86	7.20	1.54	4.80	5.66	2.40	4.63	6.00	5.66	8.75	3.09	4.80	583.00
TaFruc3B.3	6.04	1.55	6.74	4.66	4.32	8.64	2.25	6.04	4.49	8.12	2.07	5.35	5.18	2.76	5.01	9.15	3.45	6.91	3.28	3.97	579.00
TaFruc3D.1	7.22	1.11	7.04	4.26	4.81	7.22	3.33	4.07	6.85	6.48	1.67	4.44	5.74	2.22	5.37	5.74	5.93	8.52	2.96	5.00	540.00
TaFruc3D.2	6.07	1.21	6.59	4.68	3.99	8.84	2.08	5.55	4.68	8.32	2.08	5.20	5.37	2.95	5.03	9.19	3.81	7.11	3.29	3.99	577.00
TaFruc4A.1	9.12	0.69	8.61	2.93	3.96	8.78	3.27	4.30	4.30	7.40	1.89	3.44	6.20	2.24	5.85	5.34	4.99	8.95	3.27	4.48	581.00
TaFruc4A.10	7.85	0.92	6.00	4.31	3.08	8.00	3.69	3.23	3.38	9.08	2.62	4.46	5.23	2.31	6.31	6.31	8.00	8.62	2.62	4.00	650.00
TaFruc4A.11	10.54	0.90	6.17	4.37	3.01	8.58	3.16	4.52	3.77	6.78	2.56	3.46	6.17	3.16	5.42	7.23	5.57	8.58	2.56	3.46	664.00
TaFruc4A.12	9.10	0.77	6.48	4.48	3.70	8.18	2.78	4.17	2.31	8.64	2.47	4.01	5.56	2.62	6.02	6.17	7.56	8.33	2.47	4.17	648.00
TaFruc4A.13	9.72	0.62	7.25	4.63	3.40	8.02	2.62	4.32	2.47	7.10	2.16	4.01	5.25	2.01	5.56	7.41	7.25	8.80	2.62	4.78	648.00
TaFruc4A.14	9.64	0.75	7.23	4.67	3.31	9.04	2.56	3.31	3.61	7.23	1.36	3.01	5.42	2.86	4.82	7.68	6.78	8.89	2.56	5.27	664.00

Gene	**Ala**	**Cys**	**Asp**	**Glu**	**Phe**	**Gly**	**His**	**Ile**	**Lys**	**Leu**	**Met**	**Asn**	**Pro**	**Gln**	**Arg**	**Ser**	**Thr**	**Val**	**Trp**	**Tyr**	**Total**
TaFruc4A.2	4.71	1.07	8.78	5.35	3.85	7.49	1.93	7.07	4.28	9.21	2.36	4.93	5.78	2.78	4.50	8.78	4.28	5.35	3.21	4.28	467.00
TaFruc4A.3	6.34	2.00	7.01	4.84	4.17	7.85	2.17	7.51	3.67	7.35	2.84	5.01	5.84	2.84	5.34	7.85	4.17	6.34	3.01	3.84	599.00
TaFruc4A.4	5.63	1.54	7.85	4.61	4.95	8.19	2.39	6.31	3.41	8.02	1.88	4.78	5.63	2.90	5.12	8.70	5.12	6.48	2.73	3.75	586.00
TaFruc4A.5	7.72	1.03	6.52	3.77	4.63	7.38	3.09	4.80	6.69	7.20	1.72	5.15	5.66	2.23	5.66	6.35	4.46	8.06	3.09	4.80	583.00
TaFruc4A.6	10.49	0.76	7.90	4.86	2.74	10.03	1.98	3.80	2.74	7.90	1.98	3.50	5.02	2.28	5.32	6.53	6.23	8.81	3.04	4.10	658.00
TaFruc4A.7	7.31	1.04	8.88	5.74	2.61	6.01	3.39	3.66	2.87	7.83	2.61	3.66	4.70	2.35	6.01	8.09	6.79	9.66	2.35	4.44	383.00
TaFruc4A.8	8.60	0.97	7.63	4.71	2.76	8.44	2.76	3.25	2.92	8.12	3.57	3.73	4.71	2.76	6.01	6.82	6.66	8.28	2.76	4.55	616.00
TaFruc4A.9	8.06	0.98	6.29	5.11	3.73	8.25	3.34	3.14	3.93	8.25	2.16	4.72	5.50	1.57	5.70	7.27	6.48	8.45	2.75	4.32	509.00
TaFruc4B.1	8.76	0.69	8.59	2.92	3.95	8.59	3.09	3.78	4.30	8.08	2.06	3.44	6.19	2.41	6.01	5.50	4.98	8.93	3.26	4.47	582.00
TaFruc4B.2	8.09	0.69	6.37	3.10	3.79	8.78	2.93	4.13	5.68	9.12	2.41	4.30	7.75	2.75	4.48	6.54	4.65	6.88	3.10	4.48	581.00
TaFruc4D.1	9.47	0.69	8.78	2.93	3.96	8.26	2.93	4.30	4.13	7.57	2.07	3.27	5.68	2.75	6.02	5.34	5.16	8.95	3.27	4.48	581.00
TaFruc4D.2	7.92	0.69	6.54	3.10	3.61	8.78	2.24	3.96	6.20	9.29	2.24	4.30	7.57	2.75	4.48	6.54	4.99	6.88	3.10	4.82	581.00
TaFruc5A.1	7.57	0.69	6.20	3.27	3.79	8.78	2.41	3.96	6.02	9.12	2.24	4.48	7.75	2.75	4.30	6.71	5.16	7.06	3.10	4.65	581.00
TaFruc5B.1	7.53	1.20	6.85	3.94	4.11	7.19	3.25	4.79	6.85	7.36	1.37	4.79	5.65	2.05	5.65	5.99	4.97	8.22	3.08	5.14	584.00
TaFruc5B.2	6.16	1.88	6.68	4.62	4.79	7.19	2.74	6.85	3.60	7.71	2.05	5.31	5.65	3.08	4.97	9.25	3.77	6.51	3.08	4.11	584.00
TaFruc5B.3	5.85	2.05	7.42	4.11	5.21	8.21	2.53	6.00	3.79	8.53	2.21	4.90	6.16	2.84	4.27	8.85	4.90	6.16	2.69	3.32	633.00
TaFruc5B.4	6.05	1.32	7.94	4.91	4.16	8.32	2.46	7.56	3.97	7.18	2.65	5.67	5.29	2.65	5.29	7.18	4.54	6.05	3.02	3.78	529.00
TaFruc5B.5	4.42	1.54	9.23	4.81	3.46	8.08	2.50	6.73	4.04	8.65	2.88	4.81	5.96	2.69	4.62	8.85	4.04	5.38	2.88	4.42	520.00
TaFruc5D.1	6.39	1.68	7.23	5.04	4.20	7.90	2.18	7.56	3.70	7.06	2.69	4.87	5.71	2.86	5.55	8.07	4.20	6.22	3.03	3.87	595.00
TaFruc5D.2	5.54	1.85	7.55	4.36	5.20	8.05	2.35	6.71	3.52	8.05	2.35	5.37	5.87	2.85	4.70	8.56	4.70	5.87	2.85	3.69	596.00
TaFruc5D.3	7.36	1.03	6.68	3.77	4.45	7.53	3.25	4.97	6.85	7.19	1.71	4.97	5.65	2.23	5.48	5.99	4.79	8.05	3.08	4.97	584.00
TaFruc5D.4	5.87	1.78	7.12	5.34	3.91	7.65	3.20	7.65	4.27	7.47	2.49	4.98	4.98	3.02	4.45	9.25	3.56	5.69	3.02	4.27	562.00
TaFruc6A.1	9.94	0.89	8.16	3.86	2.67	9.94	2.82	2.97	2.97	7.86	3.12	3.41	5.49	2.23	5.49	6.97	6.38	8.01	2.82	4.01	674.00
TaFruc6A.2	9.85	1.19	8.21	3.58	2.54	10.15	2.69	2.84	2.69	8.21	2.99	3.58	5.22	2.09	5.22	6.87	7.01	8.21	2.84	4.03	670.00
TaFruc6A.3	9.66	0.89	7.58	3.71	2.67	9.96	2.97	2.53	2.82	7.88	2.97	4.31	5.20	2.08	5.50	6.69	6.84	8.92	2.82	4.01	673.00
TaFruc6A.4	7.24	1.18	7.74	5.05	5.22	9.09	2.02	5.39	4.38	8.25	2.19	4.55	6.23	2.86	4.71	7.24	3.54	6.23	3.20	3.70	594.00
TaFruc6A.5	6.32	2.66	6.16	3.83	4.49	7.99	2.50	5.82	3.00	8.99	1.83	5.32	6.32	2.66	4.99	8.65	3.83	6.66	3.49	4.49	601.00
TaFruc6A.6	7.94	1.35	7.77	5.07	4.56	8.11	2.70	3.89	4.56	9.12	2.20	3.55	5.57	2.03	5.91	8.78	4.22	5.91	3.04	3.72	592.00
TaFruc6B.1	10.25	0.89	7.43	4.01	2.82	10.10	2.67	2.82	2.82	7.88	2.97	3.86	5.50	1.78	6.09	6.69	6.69	7.88	2.82	4.01	673.00
TaFruc6B.2	9.76	0.89	7.54	3.85	2.51	9.76	2.66	3.11	2.81	7.99	3.25	4.14	5.33	2.07	5.62	7.40	6.51	7.99	2.81	3.99	676.00
TaFruc6B.3	10.38	0.92	7.79	3.82	2.44	9.62	3.21	2.75	2.60	8.55	2.75	3.82	4.73	1.98	5.50	6.72	7.33	8.24	2.90	3.97	655.00
TaFruc6B.4	9.81	0.89	7.58	4.01	2.67	9.96	2.97	2.53	2.82	8.17	3.27	3.86	5.20	1.93	5.35	6.98	6.69	8.47	2.82	4.01	673.00
TaFruc6B.5	7.15	1.16	7.99	4.83	4.66	9.32	2.00	5.82	4.16	8.65	2.33	4.83	6.32	2.66	4.49	7.15	3.83	5.82	3.16	3.66	601.00
TaFruc6B.6	5.89	2.39	7.18	4.79	3.87	8.29	2.39	6.45	4.24	8.29	2.21	4.79	4.97	3.13	5.34	7.00	4.42	6.08	3.68	4.60	543.00
TaFruc6D.1	10.21	0.89	8.28	3.55	2.66	9.62	2.96	2.66	2.66	7.84	3.11	3.40	5.33	2.51	5.33	7.54	6.21	8.14	2.81	4.29	676.00
TaFruc6D.2	9.38	0.89	7.89	3.72	2.53	9.97	2.68	2.98	2.68	8.63	2.68	3.87	5.36	1.79	5.65	6.70	7.44	8.33	2.83	4.02	672.00
TaFruc6D.3	9.73	0.88	7.52	3.69	2.65	10.32	2.80	2.51	2.65	8.70	2.80	3.98	5.16	2.06	5.75	6.49	6.49	9.00	2.80	3.98	678.00

Gene	**Ala**	**Cys**	**Asp**	**Glu**	**Phe**	**Gly**	**His**	**Ile**	**Lys**	**Leu**	**Met**	**Asn**	**Pro**	**Gln**	**Arg**	**Ser**	**Thr**	**Val**	**Trp**	**Tyr**	**Total**
TaFruc6D.4	10.13	0.89	7.15	3.87	2.83	10.13	2.83	2.98	2.83	7.90	2.68	4.47	5.51	1.79	5.37	6.41	7.30	8.05	2.83	4.02	671.00
TaFruc6D.5	5.26	2.63	8.77	4.61	4.39	8.77	2.41	6.14	5.04	7.89	2.19	4.61	5.04	2.63	4.61	7.02	4.39	6.36	3.29	3.95	456.00
TaFruc6D.6	6.10	2.64	6.10	3.95	4.61	7.58	2.47	5.60	3.13	8.40	1.81	5.44	6.43	2.97	5.27	9.23	3.95	6.75	3.29	4.28	607.00
TaFruc6D.7	5.69	2.76	5.85	4.23	4.39	7.64	2.28	5.85	4.07	8.46	1.79	5.20	6.50	3.09	5.04	8.62	4.39	6.67	3.41	4.07	615.00
TaFruc6D.8	7.05	1.17	8.05	5.03	4.87	8.72	2.01	5.87	4.19	8.39	2.18	4.53	6.54	2.85	4.70	7.38	3.52	6.04	3.19	3.69	596.00
TaFruc6D.9	8.14	1.36	7.80	4.58	4.24	7.63	2.71	3.22	5.08	9.49	2.20	3.73	5.42	2.54	5.59	8.98	4.07	6.27	3.05	3.90	590.00
TaFruc7A.1	9.53	0.76	6.96	4.99	3.33	8.77	2.57	3.93	3.78	7.26	1.36	3.03	5.75	2.27	4.84	7.72	6.81	8.47	2.57	5.30	661.00
TaFruc7A.10	8.55	0.78	7.47	4.04	3.42	8.40	2.95	4.20	2.80	6.84	2.02	3.73	4.82	1.87	5.29	8.09	7.78	9.49	2.49	4.98	643.00
TaFruc7A.2	9.88	0.62	7.10	4.94	3.09	8.64	2.47	4.32	2.47	7.41	1.70	3.70	5.25	2.31	5.25	7.25	7.10	8.64	2.62	5.25	648.00
TaFruc7A.3	9.71	0.77	6.47	4.16	3.70	7.70	2.77	4.16	2.47	8.78	2.47	4.16	5.39	2.77	6.16	6.78	6.78	8.32	2.47	4.01	649.00
TaFruc7A.4	10.05	0.93	6.96	4.48	3.40	8.81	3.09	4.33	3.71	7.11	2.63	3.71	5.41	3.09	5.26	6.80	5.56	8.66	2.63	3.40	647.00
TaFruc7A.5	7.98	1.07	6.13	4.75	3.22	7.98	3.07	2.76	3.68	8.59	3.07	3.68	5.37	2.61	6.90	6.29	7.36	8.74	2.61	4.14	652.00
TaFruc7A.6	8.70	0.99	5.58	4.93	3.61	8.21	3.45	2.79	3.78	8.05	2.30	4.76	5.42	1.97	5.75	7.39	6.73	8.54	2.96	4.11	609.00
TaFruc7A.7	8.71	0.81	7.74	4.52	2.90	8.39	3.06	3.55	2.90	7.90	3.71	3.87	4.68	2.74	5.48	6.77	6.77	8.06	2.90	4.52	620.00
TaFruc7A.8	10.35	0.76	7.91	4.87	2.74	9.74	1.98	3.65	2.74	7.91	2.13	3.50	5.02	2.28	5.33	6.70	6.39	8.83	3.04	4.11	657.00
TaFruc7A.9	8.24	0.95	6.34	4.91	3.33	8.08	3.49	3.33	3.33	8.72	3.33	4.44	5.39	2.54	5.55	6.18	7.13	7.77	2.69	4.28	631.00
TaFruc7D.1	9.97	0.76	7.40	5.14	3.32	8.61	2.42	3.63	3.78	7.40	1.36	2.87	5.59	2.27	4.68	7.70	6.50	8.61	2.72	5.29	662.00
TaFruc7D.10	8.56	1.43	6.56	4.99	3.71	7.42	3.42	3.14	3.14	8.84	3.42	4.14	5.14	2.43	6.13	6.56	6.70	7.56	2.71	3.99	701.00
TaFruc7D.11	8.86	0.78	7.78	3.89	3.42	7.78	2.80	3.89	3.11	7.00	2.33	3.27	4.35	2.02	5.75	8.40	7.62	9.49	2.64	4.82	643.00
TaFruc7D.2	9.32	0.62	7.30	4.50	3.11	8.23	2.64	4.35	2.64	6.99	1.86	3.73	4.97	1.86	5.43	7.76	7.45	9.32	2.64	5.28	644.00
TaFruc7D.3	8.95	1.08	6.33	4.48	3.70	8.18	2.78	3.86	2.47	8.49	2.62	3.86	5.40	2.93	6.02	6.48	7.56	8.33	2.47	4.01	648.00
TaFruc7D.4	10.21	1.05	6.76	4.65	3.15	8.26	3.15	4.50	3.60	6.91	2.70	3.30	5.71	3.00	5.71	7.66	5.41	8.26	2.55	3.45	666.00
TaFruc7D.5	8.07	1.32	6.08	4.76	3.70	7.54	3.04	3.04	3.84	9.66	3.17	3.44	4.76	2.91	6.75	6.88	6.61	7.80	2.65	3.97	756.00
TaFruc7D.6	7.47	0.79	5.89	4.72	3.34	8.25	3.14	3.34	4.13	8.64	2.36	5.30	5.50	1.77	5.70	7.27	6.68	8.45	2.75	4.52	509.00
TaFruc7D.7	8.86	0.81	7.89	4.51	2.90	8.53	2.58	3.54	2.90	7.73	3.86	3.54	4.67	2.74	5.80	6.92	6.76	7.89	2.90	4.67	621.00
TaFruc7D.8	9.49	1.71	6.84	5.13	3.58	7.78	2.80	3.73	2.49	7.93	2.33	4.35	5.13	2.95	4.82	7.78	5.75	8.40	2.64	4.35	643.00
TaFruc7D.9	10.18	0.76	7.90	4.86	2.74	10.03	1.98	3.50	2.74	7.90	1.98	3.50	5.17	2.28	5.32	6.38	6.53	9.12	3.04	4.10	658.00
TaFrucUn.1	5.08	3.11	6.72	4.59	4.92	8.20	2.13	5.25	4.26	8.36	2.30	4.92	6.56	2.79	4.92	8.36	3.93	6.56	3.44	3.61	610.00
TaFrucUn.2	7.20	0.95	7.39	4.17	4.92	7.20	3.22	4.55	6.44	6.82	1.52	4.73	5.49	2.27	5.87	5.68	5.68	7.95	3.03	4.92	528.00
TaFrucUn.3	7.20	0.95	7.39	4.17	4.92	7.20	3.22	4.55	6.44	6.82	1.52	4.73	5.49	2.27	5.87	5.68	5.68	7.95	3.03	4.92	528.00
TaFrucUn.4	7.07	1.26	7.32	4.80	5.30	7.07	3.28	3.28	8.59	6.82	1.52	3.54	3.28	2.02	6.82	5.81	6.31	9.09	2.53	4.29	396.00
TaFrucUn.5	7.84	1.96	5.88	4.90	4.90	4.90	2.94	8.82	7.84	6.86	2.94	5.88	3.92	1.96	5.88	5.88	7.84	4.90	0.98	2.94	102.00
Average	**8.18**	**1.21**	**7.06**	**4.46**	**3.76**	**8.43**	**2.75**	**4.29**	**4.07**	**7.97**	**2.24**	**4.33**	**5.54**	**2.50**	**5.59**	**7.17**	**5.48**	**8.00**	**2.89**	**4.10**	**586.23**
Minimum	**4.04**	**0.62**	**4.04**	**2.92**	**2.44**	**4.90**	**1.93**	**1.81**	**2.31**	**5.05**	**0.60**	**2.87**	**2.02**	**1.57**	**4.27**	**4.95**	**3.39**	**4.90**	**0.98**	**2.75**	**99.00**
Maximum	**10.54**	**3.11**	**9.23**	**6.41**	**6.33**	**12.12**	**4.04**	**8.82**	**8.59**	**9.66**	**3.86**	**6.06**	**7.75**	**3.21**	**8.08**	**10.10**	**8.00**	**12.12**	**3.68**	**5.30**	**756.00**

Annexure 16: Detailed results from KEGG annotation of 104 *TaFruc* gene

***TaFruc* gene**	**KEGG term**	**Enzyme code**	**Process/Function/Site of action**											
TaFruc1A.1	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc1B.1	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc1D.1	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2A.1	K01193	EC:3.2.1.26	P	DRB	P	DRF	P	CS	-	-	-	-	-	-
TaFruc2A.2	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2A.3	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2A.4	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2A.5	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2A.6	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2A.7	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2B.1	K01193	EC:3.2.1.26	P	DRB	P	DRF	P	CS	-	-	-	-	-	-
TaFruc2B.2	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2B.3	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2B.4	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2B.5	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2B.6	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2B.7	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2D.1	K01193	EC:3.2.1.26	P	DRB	P	DRF	P	CS	-	-	-	-	-	-
TaFruc2D.2	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2D.3	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2D.4	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc2D.5	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc3A.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc3A.2	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc3B.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc3B.2	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc3B.3	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc3D.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc3D.2	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc4A.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc4A.10	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.11	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.12	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.13	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.14	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-

TaFruc gene	KEGG term	Enzyme code	Process/Function/Site of action											
TaFruc4A.2	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc4A.3	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc4A.4	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc4A.5	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc4A.6	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.7	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.8	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4A.9	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc4B.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc4B.2	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc4D.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc4D.2	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc5A.1	K01193	EC:3.2.1.26	-	-	-	-	-	-	-	-	-	-	-	-
TaFruc5B.1	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc5B.2	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc5B.3	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc5B.4	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc5B.5	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc5D.1	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc5D.2	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc5D.3	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFruc5D.4	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6A.1	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6A.2	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6A.3	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6A.4	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6A.5	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6A.6	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6B.1	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6B.2	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6B.3	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6B.4	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6B.5	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6B.6	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6D.1	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6D.2	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6D.3	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-

***TaFruc* gene**	**KEGG term**	**Enzyme code**	**Process/Function/Site of action**									
TaFruc6D.4	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc6D.5	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6D.6	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6D.7	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6D.8	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc6D.9	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFruc7A.1	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.10	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.2	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.3	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.4	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.5	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.6	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.7	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.8	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7A.9	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.1	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.10	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.11	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.2	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.3	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.4	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.5	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.6	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.7	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.8	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFruc7D.9	K21351	EC:2.4.1.99	P	DRB	P	CRGS	C	CW	C	Vac	P	PRD	-	-
TaFrucUn.1	K20848	EC:3.2.1.153	P	RW	C	CW	F	BFA	P	DRF	P	RKa	C	PM
TaFrucUn.2	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFrucUn.3	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFrucUn.4	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-
TaFrucUn.5	K01193	EC:3.2.1.26	P	SM	P	SuCa	C	CW	P	NS	F	SAGA	-	-

P: process; **C:** site of action: **F:** function; **BFA:** beta-fructofuranosidase activity; **CS:** carbohydrate storage; **CW:** cell wall; **CRGS:** cellular response to gibberellin stimulus; **DRB:** defense response to bacteria; **DRF:** defense response to fungi; **NS:** nectar secretion**; PM:** plasma membrane; **PRD:** primary root development; **RW:** response to wounding; **SAGA:** sucrose alpha-glucosidase activity; **SM:** starch metabolism; **SuCa:** Sucrose catabolic activity; **RKa:** response to karrikin; **V:** vacuoles; **EC:2.4.1.99:** sucrose:sucrose fructosyltransferase; **EC:3.2.1.26:** beta-fructofuranosidase; **EC:3.2.1.153:** fructan beta-(2,1)-fructosidase (inulinase)

Annexure 17: List of SSR molecular markers designed for *TaFruc* genes

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
TaFruc1B.1	1930	18	56.82	55.56	F-ATCGCCACCACCTACAAC	298	CCGCCGCCGCCG	12
	2227	21	56.06	42.86	R-AATACAAGATCAAGGGCAGAG			
TaFruc2A.1	210	21	55.04	42.86	F-TGTGAGAGCAATGGTAGTTCT	209	GGCGGCGGCGGC	12
	418	21	55	38.1	R-TACCGTTGATCCAGTTCTTTA			
	1104	21	55.58	42.86	F-GCCTTTTCGTCCTGATTATAC	168	GCATGCATGCATGCAT	16
	1271	21	55.16	38.1	R-CACATTCCCATGAAGAGATTA			
	2170	22	55.78	45.45	F-CAGGTAGCTGCCTAATCATATC	114	CATGCATGCATG	12
	2283	20	54.8	40	R-GAATCGCCTGAAAATATCAC			
	799	21	54.52	42.86	F-CTTTAGCTAGCTTGCACTTGT	152	TATTTTATTTTATTT	15
	950	21	54.29	33.33	R-CACCAACATGATGATGATAAA			
TaFruc2A.2	297	20	55.06	40	F-CGCATTTTATGTTCCTCTTC	145	GTTAGTTAGTTA	12
	441	21	55.03	38.1	R-AAGGAAAATTTCTGTCAGTCC			
TaFruc2A.3	4406	20	55.62	40	F-GATGCTGCAAAGGAGAAATA	149	TAGTAGTAGTAG	12
	4554	21	53.95	38.1	R-TTCACCTTGGAAATACACTCT			
	1050	20	54.97	50	F-GTTGTTCAGTCGTCACACAG	153	CAAACAAACAAA	12
	1202	20	55.48	45	R-GCTTGCTTGTGTTAGACCAT			
	1486	21	55.15	42.86	F-TGGAGATGTGTCTAGGCTTTA	151	GACCGACCGACC	12
	1636	21	54.83	38.1	R-TGAAGGATCTCTTCTTCCTTT			
	4236	20	54.35	45	F-CTATTAGGATTTCGGAGCTG	192	GGACGGACGGAC	12
	4427	21	55.73	33.33	R-AATATTTCTCCTTTGCAGCAT			
	4236	20	54.35	45	F-CTATTAGGATTTCGGAGCTG	192	GGATGGATGGAT	12
	4427	21	55.73	33.33	R-AATATTTCTCCTTTGCAGCAT			
TaFruc2A.4	59	18	54.73	55.56	F-CATGGCTGTGCTCTCTCT	179	CTCCTCCTCCTC	12
	237	20	55	45	R-GTTAATTCGTACCGTTCTGC			
TaFruc2A.5	281	21	54.83	42.86	F-TAGCTAATCTGATCCTTCGTG	149	CATGCATGCATG	12
	429	21	55.44	47.62	R-AGGAGAAACTGGAGACTGTGT			
	406	21	54.52	47.62	F-CGTACACAGTCTCCAGTTTCT	150	TGCTTGCTTGCTTGCT	16
	555	21	54.65	42.86	R-AGGAGGAAAGTCGAGTGTAAT			
TaFruc2A.6	419	20	54.66	40	F-ATCTGATCCTTCTTGCATGT	155	GATGGATGGATG	12
	573	21	54.96	47.62	R-GAAGACGTAGAAGAGCGTGTA			
	494	19	55.21	42.11	F-CATGCATTCATGGTGACTT	151	GTACGTACGTAC	12
	644	21	55.07	47.62	R-GTGAGCTCTCTCTAGCAAACA			
	553	21	54.96	47.62	F-TACACGCTCTTCTACGTCTTC	150	GCTTGCTTGCTT	12
	702	20	55.22	40	R-GACGGTAATCCAGTGAAAAA			
	1839	20	54.2	30	F-TTTGAAACTCCAAAATGTCA	172	CATGCATGCATG	12

TaFruc Genes	Start	Length	Tm (℃)	GC%	Sequence	Product size	SSR	SL
	2010	21	54.92	33.33	R-AGCAAAGCAATCATACAAAAG			
	1981	21	54.75	38.1	F-ACACGACGTCTTTTGTATGAT	133	TTGCTTGCTTGC	12
	2113	21	54.74	33.33	R-ACGGGAATCTAAAGGAAAATA			
	1981	21	54.75	38.1	F-ACACGACGTCTTTTGTATGAT	133	TGCTTGCTTGCT	12
	2113	21	54.74	33.33	R-ACGGGAATCTAAAGGAAAATA			
TaFruc2A.7	3354	19	55.29	52.63	F-GCGTACCTTTCTCCACACT	203	CCGCCGCCGCCG	12
	3556	19	55.8	52.63	R-GAGAAGAAGGCTGTGGATG			
	5822	21	54.8	33.33	F-TCTTCTTATCCATGATTCCAA	146	GGAGGAGGAGGA	12
	5967	21	54.95	47.62	R-CTCCTTTACCCACTATCCTGT			
	7170	21	55.18	38.1	F-TTCGTGCGTAATATTCTCTGT	149	CAGCAGCAGCAG	12
	7318	21	54.94	47.62	R-CACTCGTTGGGTAACTATCAG			
	8330	21	54.79	42.86	F-GCTTATCCATGTGAAGTTGTC	151	TCTGTCTGTCTG	12
	8480	21	55.12	47.62	R-CCAGCTTGTACACTTTGTCTC			
TaFruc2B.1	213	21	55.04	42.86	F-TGTGAGAGCAATGGTAGTTCT	218	TGCTGCTGCTGCTGC	15
	430	21	55	38.1	R-TACCGTTGATCCAGTTCTTTA			
	213	21	55.04	42.86	F-TGTGAGAGCAATGGTAGTTCT	218	GGCGGCGGCGGC	12
	430	21	55	38.1	R-TACCGTTGATCCAGTTCTTTA			
	2148	21	54.95	42.86	F-GGAATCCAGGTAGCTAATCAT	106	CATGCATGCATG	12
	2253	21	55.51	38.1	R-AATATCACGCAAACAACTGAG			
	2025	21	54.86	47.62	F-TACGACTACGGCAACTTCTAC	229	ATCATATCATATCAT	15
	2253	21	55.51	38.1	R-AATATCACGCAAACAACTGAG			
TaFruc2B.3	2971	20	55.14	55	F-GACACGGTCCAGGACTACTA	140	GACGACGACGAC	12
	3110	18	55.61	55.56	R-GGGTCGAAGAAGGACTTG			
	3823	21	54.41	38.1	F-CTGAATCTTTTGCTCTGTTTC	159	CGGCGGCGGCGG	12
	3981	21	54.27	42.86	R-AACACATATAGGTGGCTGTTC			
	893	20	55.71	45	F-GTCATCAGCCAGAAAAACAC	157	CAAACAAACAAA	12
	1049	21	55.03	42.86	R-ATCTAACTACCAATGGCTTCC			
	1109	21	54.43	42.86	F-TACCTTGGAGATGTGTTTAGG	149	GACCGACCGACC	12
	1257	21	54.92	38.1	R-TCTCTTCTTCCTTTTCCTGTT			
TaFruc2B.6	287	21	54.83	42.86	F-TAGCTAATCTGATCCTTCGTG	138	GATGGATGGATG	12
	424	22	54.83	45.45	R-GACTGTGTATACGTACCATTCG			
	287	21	54.83	42.86	F-TAGCTAATCTGATCCTTCGTG	138	CATGCATGCATG	12
	424	22	54.83	45.45	R-GACTGTGTATACGTACCATTCG			
TaFruc2D.1	47	21	55.47	47.62	F-CTACCTGTTCTTCTTCCCATC	148	TGCTGCTGCTGCTGC	15
	194	18	55.01	61.11	R-AGGAGGTGGGTCTCGTAG			
	177	18	55.01	61.11	F-CTACGAGACCCACCTCCT	155	GGCGGCGGCGGC	12
	331	21	55.95	47.62	R-TCTAGCTCGAACAGGAGAGAT			

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
	895	20	54.7	45	F-CTGCTAGAAGAATCCGTGTT	148	GCATGCATGCATGCAT	16
	1042	21	54.52	38.1	R-TATAATGGTTTCTGCATAGGG			
	2020	21	54.95	42.86	F-GGAATCCAGGTAGCTAATCAT	118	CATGCATGCATG	12
	2137	20	54.8	40	R-GAATCGCCTGAAAATATCAC			
	1897	21	54.8	42.86	F-TACGATTACGGCAACTTCTAC	175	ATCATATCATATCAT	15
	2071	21	54.39	47.62	R-GGTTACTACGTACACCAGCAT			
TaFruc2D.2	3425	20	55.14	55	F-GACACCGTCCAGGACTACTA	140	GACGACGACGAC	12
	3564	18	55.61	55.56	R-GGGTCGAAGAAGGACTTG			
	436	21	54.91	38.1	F-GCATGTTCAGAATTTGGATAG	141	TAGATAGATAGA	12
	576	19	56.05	47.37	R-ATGGATGGATAAGCACGAG			
	848	21	55.77	42.86	F-AGAGAGTTGAGCTTTGGTTGT	164	CAAACAAACAAA	12
	1011	21	55.33	42.86	R-ACCTAGTTTGATGGTCGAGAT			
	1321	21	53.9	38.1	F-GCAAGCAGGAGTATATTGTTT	164	CAAACAAACAAA	12
	1484	21	54.89	38.1	R-TGACCTCAAACGTCTTACATT			
	1688	21	54.5	42.86	F-TACCTTCGAGATGTGATTAGG	146	GACCGACCGACC	12
	1833	21	54.82	42.86	R-CTTCTTCCTTTTCCTGTTACC			
	1813	21	54.82	42.86	F-GGTAACAGGAAAAGGAAGAAG	150	CCACCCACCCAC	12
	1962	21	55.95	38.1	R-CAATTAATACACTTGCCAACG			
	1955	21	56.05	38.1	F-ATTAATTGTTTCTGCCTCCTG	151	TAAGATAAGATAAGA	15
	2105	20	55.39	30	R-CTCAAAATTGCCATGTTTTT			
TaFruc2D.4	294	21	54.85	47.62	F-GATCCTTCTTGTGTACTGTGC	145	CATGCATGCATG	12
	438	21	56.05	47.62	R-ACAAGGAGAAACTGGAGACTG			
	409	21	54.82	47.62	F-TGGTACGTACAGTCTCCAGTT	153	TGCTTGCTTGCTTGCT	16
	561	21	54.65	42.86	R-AGGAGGAAAGTCGAGTGTAAT			
	2934	21	55.15	47.62	F-CCCTTGTAGGTATAAGCCAGT	149	TTTGTTTGTTTG	12
	3082	21	55.11	38.1	R-TCAGTTAATTCACTCCGAGAA			
TaFruc2D.5	3081	21	55.06	38.1	F-GGGTGTTCAAATACAATCAGA	149	ATTTTATTTTATTTT	15
	3229	21	55.18	38.1	R-ATTTGTTGGAACACATACGAG			
TaFruc3B.3	3087	21	55.22	33.33	F-AACTGAAAATGAATGATGTGC	139	CGGCGGCGGCGG	12
	3225	19	54.76	47.37	R-GTTGAAGGCATACATGTGG			
	3487	21	55.12	42.86	F-TTTCCTTGACCTCTAGGATTC	144	AGTAGTAGTAGT	12
	3630	21	55.25	33.33	R-TAATACCGATGCTGAGAAAAA			
TaFruc3D.1	2125	21	54.89	52.38	F-GATCGAGGAGTAGAAGTAGCC	152	TAGCTAGCTAGC	12
	2276	21	54.9	42.86	R-GGACTCATCCACTAAAACCTT			
	2121	19	55.26	52.63	F-GGACGATCGAGGAGTAGAA	156	TAGCCTAGCCTAGCC	15
	2276	21	54.9	42.86	R-GGACTCATCCACTAAAACCTT			
TaFruc3D.2	281	21	55.56	42.86	F-TGTTCTTCATATGCCTCTCTG	147	CCTCCTCCTCCTCCTCCT	18

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
	427	21	55.05	33.33	R-TTTTTCAGTAACACCCAAGAA			
TaFruc4A.10	443	21	54.74	38.1	F-TTTGGAAGAAGAAACTGACTG	159	TTTGTTTGTTTG	12
	601	21	55.82	47.62	R-GATCCTACTCACTCACCGTTT			
	486	21	55.02	33.33	F-GATGTCTTTTTGTTTGTTTGC	155	CATGCATGCATG	12
	640	21	54.98	38.1	R-CAATGGATAGGCATAAAAGTG			
	1556	21	54.79	38.1	F-TTTACCACGTGTTTACCATCT	153	CATTCATTCATT	12
	1708	21	54.88	42.86	R-GAACGGAGGGACTATTTATGT			
TaFruc4A.11	164	20	54.98	50	F-AGAGACTCCCTTTCCAGTTC	295	GGCGGCGGCGGCGGC	15
	458	20	54.97	50	R-GAGTCTTCTTGGACAGAACG			
	22	21	55.17	42.86	F-ATACCTCACCAAGATCCACTT	149	TACATACATACA	12
	170	21	54.89	42.86	R-AGTCTCTTGATCGGCTTATCT			
	599	21	54.92	38.1	F-CAATCGATTAGTTCATTCCAG	165	TTTGTTTGTTTG	12
	763	21	54.92	42.86	R-GGAAAAGACAGTCAGTTTGTG			
	599	21	54.92	38.1	F-CAATCGATTAGTTCATTCCAG	165	TTGCTTGCTTGC	12
	763	21	54.92	42.86	R-GGAAAAGACAGTCAGTTTGTG			
	743	21	54.92	42.86	F-CACAAACTGACTGTCTTTTCC	157	CATGCATGCATG	12
	899	21	54.79	38.1	R-ATTTAGGAACGGAGGAAGTAA			
	965	21	54.54	33.33	F-AGATTCACTCATTTTGTTTCG	150	GTATGTATGTAT	12
	1114	21	55.05	47.62	R-GGTACAGTCCACGGTAATACA			
	1929	21	54.78	42.86	F-CCAGGTATGCTATTGTTCATC	138	ATGCATGCATGC	12
	2066	21	55.43	38.1	R-TGCATGCACTAACATACTCAA			
TaFruc4A.12	663	20	54.61	55	F-AGTACGTCCGTCACTAGCTC	167	GTCTGTCTGTCT	12
	829	21	55.83	47.62	R-GGGGTTGTACTGGTAGAAGAA			
TaFruc4A.14	3499	21	55.54	33.33	F-ATTTTTGTTCTTCGTTCTGGT	155	TGATGATGATGATGATGA	18
	3653	21	55.26	42.86	R-TCACTTATACTTGGTGGCATC			
TaFruc4A.2	444	21	54.85	42.86	F-TAGTTTCCAGATCTTCTGCTG	150	TCACTCACTCAC	12
	593	21	56.32	42.86	R-ATAAAGAAAGGAGGGGAGCTA			
	3489	21	55.13	38.1	F-TTCCCTATAATACGTCAAGCA	159	TGTTTGTTTGTT	12
	3647	21	54.98	38.1	R-TCATCAAATCTTGGTGTATCC			
	4650	21	55.16	52.38	F-AAGAGGTACAGGACTGCCTAC	144	TTTTCTTTTCTTTTC	15
	4793	21	54.8	38.1	R-TGATTGGTCACGAATAGAAGT			
TaFruc4A.3	132	21	54.85	47.62	F-GAAGGTGACTGACTTGTATGC	143	TGCTGCTGCTGC	12
	274	21	54.64	38.1	R-CTGGTTAACTGAACCTTTCAA			
	5347	21	55.01	33.33	F-AACAAATATGAGCTTGTGCAT	155	ATGTATGTATGTATGT	16
	5501	21	55.14	38.1	R-TGTTCAAACAGAGGAGAAAGA			
	2320	21	55.13	38.1	F-CCAAATGAACACTGAAGTCAT	157	TTATTTTATTTTATT	15
	2476	21	54.46	38.1	R-TTTTTGGTACATGGTTCTAGG			

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
TaFruc4A.4	102	21	54.71	42.86	F-AGGTGAGAAGAGGGATTCTTA	151	CTGCTGCTGCTGCTG	15
	252	21	54.54	42.86	R-CGACATCGATCAAGAGTAAGT			
	102	21	54.71	42.86	F-AGGTGAGAAGAGGGATTCTTA	151	CCCTCCCTCCCT	12
	252	21	54.54	42.86	R-CGACATCGATCAAGAGTAAGT			
	327	20	54.96	40	F-TCCAATTAACTGTTGCTCCT	152	TCACTCACTCAC	12
	478	21	54.89	38.1	R-GAAATGGGAGCTTATTTTAGG			
	3691	21	55	38.1	F-ATTCGGAATAAGAACAGAACC	177	TAATTAATTAAT	12
	3867	21	54.83	33.33	R-AACAAATGTTACAAGCAAAGC			
TaFruc4A.6	1179	21	54.54	38.1	F-GTTCAAAAACTCGATAGGTCA	161	ATATATATATAT	12
	1339	21	55.21	38.1	R-TTCGTTGATTAGGTGGATATG			
	76	18	59.89	61.11	F-AGTCCCGGGCCATTAGTC	294	GCGGCGGCGGCGGCGGCG	18
	369	18	59.9	61.11	R-CGGAGGTCTTCTCCGACA			
	1028	21	55.16	38.1	F-TAGCTACCAGATCCAAAACAA	169	TTGTTGTTGTTGTTG	15
	1196	21	55.48	38.1	R-CCTATCGAGTTTTTGAACACA			
	4089	21	54.66	42.86	F-TTACTGCCTTCCAAGTGTAAC	114	ATGATGATGATG	12
	4202	21	54.95	33.33	R-CTCTTTCCCCAATAATTTCAT			
	599	21	55.45	42.86	F-ATCGATGGAGAAGAACTGACT	140	ATGCATGCATGCATGC	16
	738	21	55.92	47.62	R-AGATCGGTTGATCAGGAGTAG			
	925	21	55.55	42.86	F-GCAAGTTAGTTGGTTGTCAGA	144	GATGGATGGATGGATG	16
	1068	21	54.49	38.1	R-GCCGGTTTTATTACTACCTTT			
	3877	21	54.39	38.1	F-CGGTAATGCATATTCACCTAT	146	ATGGATGGATGG	12
	4022	21	55.47	33.33	R-AAACAACAAACAAACGAACAG			
TaFruc4A.8	268	18	56.92	55.56	F-TACGCGTACAAGCCACTG	254	TGGTGGTGGTGGTGG	15
	521	21	55.09	47.62	R-GTACCGCTCATGTAGTTCTTG			
TaFruc4B.2	3081	21	55.48	42.86	F-CCGTGTTCTTCAGAGTATTCA	126	TCTCTCTCTCTCTCTC	16
	3206	20	55.58	45	R-GAAATAGATGGACGGGAGAT			
	31	19	55.08	52.63	F-GACCCTCTTAACTGCAAGC	218	GCTGCTGCTGCT	12
	248	21	55.74	42.86	R-ATCTTACCGTTGATCCAGTTC			
	25	18	55.08	55.56	F-TCCCTCGACCCTCTTAAC	224	GCAAGCAAGCAA	12
	248	21	55.74	42.86	R-ATCTTACCGTTGATCCAGTTC			
	2593	20	55	45	F-AAGTCATCGATCTTGTCCAC	161	CTTGCTTGCTTG	12
	2753	21	55.11	38.1	R-TTTTGCTACGTGATGTAGGTT			
TaFruc4D.2	2975	21	54.62	42.86	F-TCTTCAGAGTCTTCAAGGATG	162	TCTCTCTCTCTC	12
	3136	21	55.43	42.86	R-GCAATACTCCTTCCCATTTAC			
	5	18	54.91	50	F-ATCCATCCATCCCTGTCT	248	GCAAGCAAGCAA	12
	252	21	55.22	42.86	R-AGTGGGTATCTTACCGTTGAT			
TaFruc5A.1	2449	21	55.66	47.62	F-TCTAGGTAGCTTCTGGTCCAT	184	CTTGCTTGCTTG	12

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
	2632	21	54.95	47.62	R-AAGTAGTATGAGGGGAGGTTG			
TaFruc5B.1	2881	20	55.23	55	F-GGGCAGTAGTAGCAACAGAG	145	TAGCTAGCTAGC	12
	3025	21	54.7	38.1	R-TTCCTGCATTTCTAACAACTC			
TaFruc5B.3	361	21	55.22	47.62	F-GATTAATGTGTCCTCCTCTCC	161	TCACTCACTCAC	12
	521	21	55.13	42.86	R-AGTTCCTAGAGAAATGCTGCT			
	3166	23	53.82	34.78	F-CATATTCAAACATGAGAGAGAGA	128	GAGGGAGGGAGGGAGGGAGGGAGG	24
	3293	21	54.57	33.33	R-GTGTTCACACAAAACAAAACA			
	3172	21	54.17	47.62	F-CAAACATGAGAGAGAGAGAGG	175	GGAGGGAGGGAG	12
	3346	21	54.72	33.33	R-CATATTTATGTTGCCGCTTAT			
	6767	21	54.97	33.33	F-TTTGGAATAAGAACAGAACCA	155	TAATTAATTAAT	12
	6921	21	55.86	38.1	R-GGACCAAAAACACACTTTTCT			
	3234	21	55.47	38.1	F-GAAAGACGCCTTAGGATTAAA	152	TTTTGTTTTGTTTTG	15
	3385	21	55.58	47.62	R-GACCACAATAGGTCCATCTCT			
TaFruc5D.1	61	21	54.69	42.86	F-ATGGAAGGTGACTGACTTGTA	148	TGCTGCTGCTGCTGCTGCTGC	21
	208	21	54.84	38.1	R-GTGACAGAAAACGAAACAATC			
TaFruc5D.2	644	21	54.85	38.1	F-TTTCAAACTACGGTGTAAAGC	142	TAATAATAATAATAA	15
	785	21	55.2	38.1	R-AATTTGGTGAGAAGAAAGAGG			
TaFruc5D.3	2849	20	55.03	50	F-CGATCGAGGATTCAGAGTAG	144	TAGCTAGCTAGC	12
	2992	21	56.06	33.33	R-GGAAAAGGTTCTGAAACAAAA			
TaFruc5D.4	1013	21	54.69	33.33	F-AATTTACCCTTAATTGGCTGT	135	TTATTATTATTA	12
	1147	21	55.32	38.1	R-TGTCTAACCAAATTGTCCTTG			
TaFruc6A.5	32	21	54.8	38.1	F-TCATTCTCTACCACGACATTT	154	CCTCCTCCTCCTCCTCCT	18
	185	21	54.75	47.62	R-CTGCTTAGTTAGGTGCTTCTG			
	3089	21	55.32	38.1	F-CTCTGCCATTTCTCCTTTTAT	139	GGTGGTGGTGGT	12
	3227	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
	3089	21	55.32	38.1	F-CTCTGCCATTTCTCCTTTTAT	139	ATGGATGGATGG	12
	3227	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
TaFruc6A.6	17	21	55.9	42.86	F-CAATCAGCACTTTCATGTCTC	114	CTCCTCCTCCTCCTCCTCCTCCTC	24
	130	20	55.62	40	R-AGATTCATCAAAGGGGAAAC			
TaFruc6B.1	1596	21	55.07	33.33	F-TTAGCACAAACTTGAATGGTT	151	ATAGATAGATAG	12
	1746	21	55.5	42.86	R-ATGACAGCAACATCTCGTTAG			
TaFruc6B.2	76	21	54.47	38.1	F-CATAATCGAGCTGGATAACAT	212	TGGATGGATGGA	12
	287	21	55.19	38.1	R-TAAACTTGACAAGAACGAGGA			
TaFruc6B.4	1590	21	54.9	42.86	F-CTTGAATGGTTAGGAGTGTTG	153	ATAGATAGATAGATAG	16
	1742	21	55.01	42.86	R-GGGTACATCCTCCTTTTCTAA			
	3060	21	55.04	42.86	F-CTATTTTCCCCTACGAGATGT	157	ATAGATAGATAG	12
	3216	21	55.83	42.86	R-ATCAAGTTAGGTGGTTCTTGG			

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
TaFruc6B.5	13	21	54.99	38.1	F-CAGAAAAATAGCAATCCACAC	147	TCCTCCTCCTCC	12
	159	21	55.19	52.38	R-AGCTCTGGAGACTGTAGATCC			
	35	21	55.09	47.62	F-ATACATCCTATCGCTCTCCTC	171	GGAAGGAAGGAA	12
	205	21	55.01	42.86	R-AGTCATGGGTCTCTTTCTTTC			
	4115	21	54.79	33.33	F-ATTTCCCCTGTTATTCATTTC	133	ATGGATGGATGG	12
	4247	21	54.7	42.86	R-GATAAACTCTGGATGTGATGC			
TaFruc6B.6	1091	21	55.1	42.86	F-CATTTCCTTCATCTCCTCTCT	158	CCTCCTCCTCCT	12
	1248	19	55.51	47.37	R-AGGAATCTCCCTCTTTGCT			
	4281	21	55.23	47.62	F-CTAAGGAGGCTCTGCTATTTC	148	GGTGGTGGTGGT	12
	4428	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
	4281	21	55.23	47.62	F-CTAAGGAGGCTCTGCTATTTC	148	ATGGATGGATGG	12
	4428	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
TaFruc6D.1	1579	21	54.88	42.86	F-GTACTTGCCACTTTCAACATC	158	TTGTTGTTGTTG	12
	1736	21	54.72	33.33	R-CTCCTAACCATGCAAATTAAA			
TaFruc6D.3	2056	21	54.55	33.33	F-ACAGTTGCTAATGCCTTTTTA	158	TGTGTGTGTGTGTGTGTG	18
	2213	21	55.15	33.33	R-TCCCTTTTTCTTGTTTAATCC			
	1591	21	54.84	42.86	F-ACACTATCGCTTTGTTAGCAC	152	ATAGATAGATAG	12
	1742	21	55.5	42.86	R-ATGACAGCAACATCTCGTTAG			
TaFruc6D.4	2071	20	55.5	45	F-GTAACCAAAACCTTGGTGTG	147	CATACATACATA	12
	2217	21	55.04	47.62	R-GCTGGAACTGTACTCAATCTG			
	2390	21	55.07	33.33	F-TTACACAAGCAAAAGGAATGT	164	TAATTAATTAAT	12
	2553	21	54.62	42.86	R-ATCGACTGCAACAGTAAGAAC			
TaFruc6D.5	14293	21	54.57	33.33	F-CATCATTTGTGTTGAGTTTCA	149	ATATATATATATATATAT ATATATATATATATATAT ATATATATATATATAT	52
	14441	21	54.68	38.1	R-TGAAATGGTCGTAAGATTAGC			
	14693	21	54.49	42.86	F-AGAGGTGGGTGAAGAATAACT	161	ATATATATATATATATAT ATATATATATATATATAT ATATAT	42
	14853	21	55.53	47.62	R-ATACGATCTGGTGCTAGGAGT			
	4768	21	55.42	47.62	F-GAAGATCAAGAGGAACCAGAC	154	GATGATGATGAT	12
	4921	21	55.41	42.86	R-ACTTCAGCTTCTCCTTTTGAC			
	9652	21	54.58	38.1	F-GGAAGAAGAAGGAAGAAGAAA	242	GAAGAAGAAGAAGAAGAA	18
	9893	22	54.97	45.45	R-GGAATAGAGGAGAAGAAGAGGT			
	9753	21	54.86	33.33	F-AGAATGAGAGGAAAAAGGAAA	158	AAGAAGAAGAAG	12
	9910	21	54.17	38.1	R-AAGAGGAGAAGAAGAAAGGAA			
	15725	21	55.16	38.1	F-TACCAGAATTGAGAATGGATG	167	TGGTGGTGGTGG	12
	15891	21	55.74	38.1	R-TGGTACTTCCATTGTTGAAGA			
	9292	18	53.51	55.56	F-TCCTCCCTCTGTAAGCAC	172	TATGTATGTATG	12

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
	9463	23	50.56	30.43	R-CATACATATACGAACATACATCA			
	10209	21	55.07	42.86	F-TATGTCGTTGTCGATATACCC	155	ATGTATGTATGT	12
	10363	21	54.2	38.1	R-AAGTTATCACGGTCGAAGTTA			
	8266	21	55.12	33.33	F-CTGTTCAAAATCATTGAAAGC	196	AAAATAAAATAAAAT	15
	8461	20	55.18	30	R-TGCCTGTTTTTGTTTTCTTT			
TaFruc6D.6	2871	21	55.23	47.62	F-CTAAGGAGGCTCTGCTATTTC	148	GGTGGTGGTGGT	12
	3018	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
	2871	21	55.23	47.62	F-CTAAGGAGGCTCTGCTATTTC	148	ATGGATGGATGG	12
	3018	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
TaFruc6D.7	2876	21	55.23	47.62	F-CTAAGGAGGCTCTGCTATTTC	148	GGTGGTGGTGGT	12
	3023	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
	2876	21	55.23	47.62	F-CTAAGGAGGCTCTGCTATTTC	148	ATGGATGGATGG	12
	3023	20	55.23	45	R-ATAAACTCTGGACGTGATGC			
TaFruc6D.8	33	21	54.81	42.86	F-CTATACATCCAATCCCTCCTT	154	TCCTCCTCCTCCTCC	15
	186	21	55.18	42.86	R-CATCAGTCTCTTTCTTTCACG			
	277	20	55.33	50	F-CTTCTTATCGCCTCCTACCT	144	CCTCTCCTCTCCTCT	15
	420	21	55.06	42.86	R-GGATATATAGCTGGGGAAGAA			
TaFruc6D.9	5	18	56.4	55.56	F-CTTCCATGTCTCCCGTTC	152	CTCCTCCTCCTCCTCCTC	18
	156	21	54.85	47.62	R-TACAGGACGACCCTATGACTA			
	2493	21	54.55	38.1	F-TCTTTGAGAACATTGGTTAGG	170	TGGTGGTGGTGG	12
	2662	18	55	55.56	R-CTAGCCATGATGCAGACC			
TaFruc7A.1	3554	21	54.88	47.62	F-CAGTTGGAGATGGAGTACAAG	160	ATGATGATGATGATG	15
	3713	20	54.99	35	R-TCCCCAACAAATTGATTTAC			
	13	21	56.03	42.86	F-TCGGTCAGAAAAGAATCTACC	293	CGGCCGGCCGGC	12
	305	18	58.06	61.11	R-GAGGAGGCCACAGATTCC			
	13	21	56.03	42.86	F-TCGGTCAGAAAAGAATCTACC	294	GGCGGGGCGGGGCGG	15
	306	18	58.06	61.11	R-GGAGGAGGCCACAGATTC			
	454	20	55.33	50	F-CCGGACAAGTACTACCAGAA	150	TTTCTTTTTCTTTTTCTT	18
	603	20	54.75	40	R-AAACAAAACAGGAAGCAGAG			
TaFruc7A.10	2860	21	53.98	33.33	F-TGAATTAGATGATGTTGGTCA	150	TTATTTATTTAT	12
	3009	18	51.01	38.89	R-ACGAAATACAAAGGTTGC			
TaFruc7A.3	1670	21	54.32	38.1	F-CAACCGATAGATGTCTCAAAT	140	ATATATATATAT	12
	1809	21	54.9	42.86	R-ACCATTAAACTGGACACACAC			
	2263	21	55.52	33.33	F-TGTTACGGAATTCATTGTCAT	150	AGAAAGAAAGAA	12
	2412	21	55.59	47.62	R-GTAGCCATGTCAGTCATCAAC			
	2360	21	54.74	42.86	F-GGAGAAAGAAAGAAACTGACC	152	CACGCACGCACG	12
	2511	22	55.01	50	R-AGTACATAGAGACGGACAGACC			

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
TaFruc7A.4	120	21	54.82	38.1	F-TAAAGAAAGTCCCTTTCCAGT	204	GGCGGCGGCGGCGGCGGCGGCGGC	24
	323	18	54.77	61.11	R-GACGACTAGCACCACCAC			
	21	21	55.29	42.86	F-TTTCCTCTTGAGGATAGAAGG	120	TACATACATACA	12
	140	21	54.82	38.1	R-ACTGGAAAGGGACTTTCTTTA			
	587	21	55.05	38.1	F-CATCATTCCACTGACTGATTT	147	TTTGTTTGTTTG	12
	733	21	54.73	42.86	R-GACAGTCAGTTTGTGTTTTCC			
	587	21	55.05	38.1	F-CATCATTCCACTGACTGATTT	147	TTGCTTGCTTGC	12
	733	21	54.73	42.86	R-GACAGTCAGTTTGTGTTTTCC			
	663	21	54.45	38.1	F-TATCTTTCACACTTTCGCTCT	150	CATGCATGCATGCATG	16
	812	21	55.22	42.86	R-ACGTACTAACCATTGGGATCT			
	790	20	55.17	45	F-GCAGATCCCAATGGTTAGTA	155	TGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTA	52
	944	21	55.76	42.86	R-CTGCACATTATTGAGTTCCAC			
	836	21	54.81	42.86	F-ACCAGCTGTCTGTTTGTATGT	160	ATGCATGCATGC	12
	995	21	54.82	42.86	R-TGGGATTGTACTGGTAGAAGA			
TaFruc7A.5	1627	21	55.2	38.1	F-TTTTACCACGTGTTTACCATC	157	ATATATATATATATATATATATATATATATATATATATATATATAT	46
	1783	21	55.35	33.33	R-CATAATGAACGAATGCAAGAT			
	453	21	55.52	33.33	F-TTTTCAGATTCAAATCCTCCT	153	TTTGTTTGTTTG	12
	605	21	55.75	42.86	R-CACGTAAGCAAAAGGTAGTCA			
	585	21	55.75	42.86	F-TGACTACCTTTTGCTTACGTG	154	CATGCATGCATG	12
	738	21	55.65	33.33	R-AATTAATCAGCACGTTTCCTT			
TaFruc7A.6	158	18	55.24	55.56	F-TGGCAGAGACGGAGAGTA	130	GGCGGCGGCGGC	12
	287	21	54.78	42.86	R-CCATTCATGTAGTGCTTATCC			
TaFruc7A.7	2439	18	56.92	55.56	F-TACGCGTACAAGCCACTG	266	TGGTGGTGGTGGTGG	15
	2704	21	55.09	47.62	R-GTACCGCTCATGTAGTTCTTG			
TaFruc7A.8	4078	21	54.9	38.1	F-TAACTATTGGCAGGATGGATA	171	ATGATGATGATGATGATGATG	21
	4248	21	55.56	42.86	R-CGTACAAGTTGGAAGTCAGAA			
	568	21	54.82	33.33	F-CATTAATTTCTACGCGTTGTT	155	ATGCATGCATGC	12
	722	21	55.41	52.38	R-GGTTGACGAGGAGTACTAACC			
	3861	21	55.07	42.86	F-GGTAATGCATACTCACCCATA	135	ATGGATGGATGG	12
	3995	21	54.55	33.33	R-AAAACAACAAACAAACAGGAG			
	3941	21	55.41	52.38	F-GGATGGAGATGGAGTACTAGC	158	TGTTTGTTTGTT	12
	4098	21	54.9	38.1	R-TATCCATCCTGCCAATAGTTA			
TaFruc7A.9	461	21	54.86	33.33	F-CGATGATGGAATTTTTAGATG	151	TTTGTTTGTTTG	12
	611	21	55.09	42.86	R-AAGGTGGTCAGTTTCTTTCTC			
TaFruc7D.1	3540	21	53.98	33.33	F-TGAATTAGATGGTGTTGATGA	145	TGATGATGATGATGA	15

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
	3684	21	54.82	38.1	R-AAATTAGACAGCACGAACTTG			
TaFruc7D.10	540	21	55.09	42.86	F-GTTTGGAGGAAGAAACTGACT	160	TTTGTTTGTTTG	12
	699	21	55.82	47.62	R-GATCCTACTCACTCACCGTTT			
	1708	21	55	38.1	F-CAGTTCCATTCGTTCTTTATG	154	CATTCATTCATT	12
	1861	21	55.13	38.1	R-TCAATATACATCCGAATCAGG			
TaFruc7D.2	2102	21	54.96	38.1	F-CTATTCCGACCCGATATTATT	163	GTGTGTGTGTGT	12
	2264	20	55.21	50	R-GACAGTGATACCGCTGAGAT			
TaFruc7D.4	299	20	55.32	50	F-GATCAAGAGAGTCCCTTTCC	240	GGCGGCGGCGGCGGC	15
	538	18	58.11	55.56	R-CCACGTCGTTGAGATCGT			
	821	21	55.16	38.1	F-CATGGTTTGATCTATCTTCCA	155	TTTGTTTGTTTG	12
	975	21	55.22	42.86	R-ACGTACTAACCATTGGGATCT			
	821	21	55.16	38.1	F-CATGGTTTGATCTATCTTCCA	155	TTGCTTGCTTGC	12
	975	21	55.22	42.86	R-ACGTACTAACCATTGGGATCT			
	821	21	55.16	38.1	F-CATGGTTTGATCTATCTTCCA	155	CATGCATGCATG	12
	975	21	55.22	42.86	R-ACGTACTAACCATTGGGATCT			
TaFruc7D.5	5	21	54.89	33.33	F-GTCTAACTTCATTCGCAAAAA	160	AAGAAAGAAAGA	12
	164	21	53.99	42.86	R-GCTACAGAACTGAAGAGGAAA			
	552	21	55.52	33.33	F-TTTTCAGATTCAAATCCTCCT	153	TTTGTTTGTTTG	12
	704	21	55.75	42.86	R-CACGTAAGCAAAAGGTAGTCA			
	649	21	55.27	33.33	F-GTCTTTTTGTTTGTTTGCTTG	153	CATGCATGCATG	12
	801	21	55	52.38	R-GACATACAGAGAGACGACAGC			
TaFruc7D.7	19	21	55.25	42.86	F-ACCCACAATCTACCAAACTCT	288	CGCCGCCGCCGC	12
	306	18	57.36	55.56	R-AGCATCTCGTTGCTCCAC			
	19	21	55.25	42.86	F-ACCCACAATCTACCAAACTCT	288	TGGTGGTGGTGGTGG	15
	306	18	57.36	55.56	R-AGCATCTCGTTGCTCCAC			
TaFruc7D.8	3964	20	54.92	50	F-GTTGTCGGAGTAGATGAAGC	184	GCGGCGGCGGCG	12
	4147	18	56.02	61.11	R-CGCACTCCTAACCTAGCC			
	4024	18	55.14	55.56	F-CTGGACGAAGACGAAGTG	156	CGGCGGCGGCGGCGG	15
	4179	18	55.38	55.56	R-CAGGGTTCTTCGCCTACT			
	5097	18	56.78	61.11	F-GTAGGCGATGCAGGTCTC	210	CGGCGGCGGCGG	12
	5306	21	55.97	38.1	R-ATCTAATCTTGATCGGTTTGC			
	6361	21	54.54	38.1	F-TTCTTGATTGATGTCAGTGTG	126	TAACTAACTAACTAACTAACTAAC	24
	6486	21	56.41	47.62	R-CATAAGAGGAGGTTTGTCCTG			
TaFruc7D.9	78	18	59.89	61.11	F-AGTCCCGGGCCATTAGTC	294	GGCGGCGGCGGCGGC	15
	371	18	59.9	61.11	R-CGGAGGTCTTCTCCGACA			
	610	21	55.45	42.86	F-ATCGATGGAGAAGAACTGACT	139	ATGCATGCATGCATGC	16
	748	20	55.34	40	R-TATCCATGAGATCGGTTGAT			

***TaFruc* Genes**	**Start**	**Length**	**Tm (℃)**	**GC%**	**Sequence**	**Product size**	**SSR**	**SL**
	881	21	55.18	38.1	F-ATCTTTGGTTGGGTATTGACT	118	GTTGGTTGGTTGGTTG	16
	998	21	54.82	38.1	R-GATCCATCTACCGGTTTTATT			
	4174	21	54.39	38.1	F-CGGTAATGCATATTCACCTAT	137	ATGGATGGATGG	12
	4310	21	55.08	38.1	R-ACAGACAAACGAACAGAAAGA			
TaFrucUn.1	2940	21	55.16	38.1	F-TACCAGAATTGAGAATGGATG	167	TGGTGGTGGTGG	12
	3106	21	55.74	38.1	R-TGGTACTTCCATTGTTGAAGA			
TaFrucUn.2	2189	21	54.89	52.38	F-GGATCGAGGAGTAGAAGTAGC	143	TAGCTAGCTAGC	12
	2331	20	54.9	35	R-TTATTCATTCCCATGTTTCC			
TaFrucUn.3	2189	21	54.89	52.38	F-GGATCGAGGAGTAGAAGTAGC	143	TAGCTAGCTAGC	12
	2331	20	54.9	35	R-TTATTCATTCCCATGTTTCC			
TaFrucUn.5	467	19	55.2	47.37	F-ACATCAAGGTCACCAACCT	149	TAGCTAGCTAGC	12
	615	21	54.85	38.1	R-CCATCTCAGCGAAACTAATAA			
TaFrucUn.5	467	19	55.2	47.37	F-ACATCAAGGTCACCAACCT	149	TAGCCTAGCCTAGCC	15
	615	21	54.85	38.1	R-CCATCTCAGCGAAACTAATAA			

Annexure 18: List of miRNAs designed for targeting different *TaFruc* genes

***Ta* Genes**	**miRNA_Acc.**	**E**	**UPE**	**miRNA**		**Target**		**Fragments**		**I**	**M**
				Start	**End**	**Start**	**End**	**miRNA**	**Target**		
TaFrucUn.1	tae-miR1118	1.5	12.573	1	23	1985	2007	CACUACAUUAUGGAAUGGAGGGA	UGCCUCCGUUUUAUAAUGUAGUG	C	1
TaFruc6D.9	tae-miR1135	2	19.962	1	24	1903	1926	CUGCGACAAGUAAUUCCGAACGGA	UCUGUCCCGAAUUACUUGUCGCAG	C	1
TaFruc6D.2	tae-miR5049-3p	3	10.847	1	21	2507	2527	AAUAUGGAUCGGAGGGAGUAC	AUACUCCCUCCGUUCCAAAUU	C	1
TaFruc2D.4	tae-miR1120c-5p	3.5	18.365	1	21	2095	2114	UAAUAUAAGAACGUUUUUGAC	UGUAAAAACGU-CUUAUAUUA	T	1
TaFruc2A.5	tae-miR1120c-5p	3.5	16.817	1	21	2089	2108	UAAUAUAAGAACGUUUUUGAC	UGUAAAAACGU-CUUAUAUUA	T	1
TaFruc4A.8	tae-miR1127a	3.5	14.483	1	19	2435	2453	UCCUUCCGUUCGGAAUUAC	GUAGUUUUGCAUGGAAGGA	T	1
TaFruc6D.9	tae-miR1127b-3p	3.5	19.537	1	21	1901	1921	ACAAGUAUUUCUGGACGGAGG	CCUCUGUCCCGAAUUACUUGU	C	1
TaFruc5D.2	tae-miR6197-5p	3.5	23.743	1	21	2149	2169	UCUGUAAACAAAUGUAGGACG	UUUCAUAUGUAUGUUUACAGA	T	1
TaFruc4A.4	tae-miR6197-5p	3.5	13.088	1	21	2102	2122	UCUGUAAACAAAUGUAGGACG	UUUCAUAUGUAUGUUUACAGA	T	1
TaFruc5B.3	tae-miR6197-5p	3.5	17.161	1	21	2215	2235	UCUGUAAACAAAUGUAGGACG	UUUCAUAUGUAUGUUUACAGA	T	1
TaFruc4A.2	tae-miR1121	4	12.843	1	22	3540	3561	AGUAGUGAUCUAAACGCUCUUA	UAUGAGUGUUGAGAUGACUGCU	C	1
TaFruc7D.7	tae-miR1127a	4	13.994	1	19	2297	2315	UCCUUCCGUUCGGAAUUAC	GUAGUUUUGCAUGGGAGGA	T	1
TaFruc6D.4	tae-miR156	4	24.743	1	21	1807	1827	UGACAGAAGAGAGUGAGCACA	CCUGCGCACACACUUCUGUCA	T	1
TaFruc1B.1	tae-miR156	4	11.454	1	21	1891	1910	UGACAGAAGAGAGUGAGCACA	AUUGCU-ACUCUUUUUUGUUG	C	1
TaFruc1D.1	tae-miR156	4	12.856	1	21	1882	1901	UGACAGAAGAGAGUGAGCACA	AUUGCU-ACUCUUUUUUGUUG	C	1
TaFruc4A.4	tae-miR9667-5p	4	21.378	1	21	1972	1992	AAAUAUGGCAAACAAUGAAUG	CAUUUGUUGUUUUCAAUAUUU	C	1
TaFruc5D.2	tae-miR9667-5p	4	16.382	1	21	2017	2037	AAAUAUGGCAAACAAUGAAUG	CAUUUGUUGUUUUCAAUAUUU	C	1
TaFruc6B.2	tae-miR9674a-5p	4	20.819	1	21	98	118	GCAUCAUCCAUCCUACCAUUC	GCCUGGAUGGAUGGAUGAUGA	C	1
TaFruc7D.5	tae-miR9677a	4	24.725	1	22	1875	1895	UGGCCGUUGGUAGAGUAGGAGA	CCUCCUCCUC-ACCAACGGCCA	C	1
TaFruc4A.10	tae-miR9677a	4	24.215	1	22	1488	1508	UGGCCGUUGGUAGAGUAGGAGA	CCUCCUCCUC-ACCAACGGCCA	C	1
TaFruc7A.1	tae-miR9679-5p	4	15.39	1	21	2167	2187	CAGAACCAGAAUGAGUAGCUC	UUGUUCUUCGUUCUGGUUUUU	C	1
TaFruc4A.14	tae-miR9679-5p	4	13.132	1	21	2180	2200	CAGAACCAGAAUGAGUAGCUC	UUGUUCUUCGUUCUGGUUUUU	C	1
TaFruc7D.1	tae-miR9679-5p	4	12.704	1	21	2170	2190	CAGAACCAGAAUGAGUAGCUC	UUGUUCUUCGUUCUGGUUUUU	C	1
TaFruc6D.9	tae-miR1118	4.5	16.665	1	23	1856	1878	CACUACAUUAUGGAAUGGAGGGA	GACCUCUAGUCCAUACUGUUGUG	C	1
TaFruc2A.1	tae-miR1120b-3p	4.5	20.936	1	21	197	217	UUCUUAUAUUGUGGGACAGAG	CUCUGUGCCCCAGUGUGAGAG	C	1
TaFruc4A.3	tae-miR1136	4.5	18.98	1	24	1047	1070	UUGUCGCAGGUAUGGAUGUAUCUA	AGUGAGCAUCAAUUCCUGUGACAU	T	2
TaFruc5B.4	tae-miR1136	4.5	19.39	1	24	645	668	UUGUCGCAGGUAUGGAUGUAUCUA	AGUGAGCAUCAAUUCCUGUGACAU	T	1
TaFruc5D.1	tae-miR1136	4.5	18.208	1	24	843	866	UUGUCGCAGGUAUGGAUGUAUCUA	AGUGAGCAUCAAUUCCUGUGACAU	T	1
TaFruc6B.6	tae-miR1139	4.5	17.673	1	22	1612	1633	AGAGUAACAUACACUAGUAACA	AUCUGUUGGUGUAUGCCACUCU	C	1
TaFruc4D.1	tae-miR1847-5p	4.5	17.807	1	21	1833	1853	ACCUGCAGUUGGGCCAAUGAC	ACCAGAGGCUAGACUGCAGGU	T	1
TaFruc6D.9	tae-miR397-5p	4.5	18.693	1	21	2007	2027	UCACCGGCGCUGCACACAAUG	AAUGAUGUGAAGUGCUGGUGA	C	1
TaFruc2B.1	tae-miR408	4.5	19.433	1	21	1399	1419	CUGCACUGCCUCUUCCCUGGC	CUCAGGGACGGGGUGGUGAAG	C	1
TaFruc4A.2	tae-miR444a	4.5	15.83	1	21	2249	2269	UUGCUGCCUCAAGCUUGCUGC	GAAGCAGGCUGGAGGUGCCAA	T	1
TaFruc4A.2	tae-miR444b	4.5	15.83	1	21	2249	2269	UUGCUGCCUCAAGCUUGCUGC	GAAGCAGGCUGGAGGUGCCAA	T	1

Ta **Genes**	**miRNA_Acc.**	**E**	**UPE**	**miRNA**		**Target**		**Fragments**		**I**	**M**
				Start	**End**	**Start**	**End**	**miRNA**	**Target**		
TaFruc7A.1	tae-miR5086	4.5	19.397	1	21	508	528	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAAUAC	C	1
TaFruc5A.1	tae-miR5086	4.5	12.694	1	21	285	305	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAAUAC	C	1
TaFruc4A.14	tae-miR5086	4.5	24.542	1	21	521	541	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAAUAC	C	1
TaFruc2A.7	tae-miR531	4.5	21.066	1	21	598	617	CGCUCGCCGGAGCAGCGUGCA	GACCCGCUGCUCCG-CGAGUG	C	1
TaFruc2B.1	tae-miR531	4.5	22.763	1	21	721	740	CGCUCGCCGGAGCAGCGUGCA	GACCCGCUGCUCCG-CGAGUG	C	1
TaFruc2A.1	tae-miR531	4.5	23.098	1	21	709	728	CGCUCGCCGGAGCAGCGUGCA	GACCCGCUGCUCCG-CGAGUG	C	1
TaFruc6B.1	tae-miR5384-3p	4.5	23.111	1	21	1779	1799	UGAGCGCGCCGCCGUCGAAUG	GCCUCGACGGCGGCUUGCGCA	C	1
TaFruc6D.4	tae-miR5384-3p	4.5	21.469	1	21	1794	1814	UGAGCGCGCCGCCGUCGAAUG	GCCUCGACGGCGGCCUGCGCA	C	1
TaFruc6D.3	tae-miR5384-3p	4.5	24.921	1	21	1810	1830	UGAGCGCGCCGCCGUCGAAUG	GCCUCGACGGCGGCCUGCGCA	C	1
TaFruc6A.3	tae-miR5384-3p	4.5	20.062	1	21	1790	1810	UGAGCGCGCCGCCGUCGAAUG	GCCUCGACGGCGGCCUGCGCA	C	1
TaFruc7A.7	tae-miR6197-5p	4.5	15.688	1	21	2448	2468	UCUGUAAACAAAUGUAGGACG	GCUUAUGUGUUUGUUUACAAA	C	1
TaFruc7D.9	tae-miR9655-3p	4.5	11.479	1	21	2209	2229	CAAGGGAAGGAAGUAGCCAAC	UGUUGUUUUUUCUUUCUUUUG	C	1
TaFruc4A.4	tae-miR9660-5p	4.5	20.598	1	20	1968	1987	UUGCGAGCAACGGAUGAAUC	CAGUCAUUUGUUGUUUUCAA	C	1
TaFruc5D.2	tae-miR9660-5p	4.5	19.623	1	20	2013	2032	UUGCGAGCAACGGAUGAAUC	UAGUCAUUUGUUGUUUUCAA	C	1
TaFrucUn.3	tae-miR9669-5p	4.5	24.159	1	21	733	753	UACUGUGGGCACUUAUUUGAC	GUCAAAUACGUGCUCAAGGUG	C	1
TaFrucUn.2	tae-miR9669-5p	4.5	24.159	1	21	733	753	UACUGUGGGCACUUAUUUGAC	GUCAAAUACGUGCUCAAGGUG	C	1
TaFrucUn.2	tae-miR9676-5p	4.5	13.505	1	22	860	881	UGGAUGUCAUCGUGGCCGUACA	GCUACGACUAUGGUGACUUCUA	C	1
TaFrucUn.3	tae-miR9676-5p	4.5	13.505	1	22	860	881	UGGAUGUCAUCGUGGCCGUACA	GCUACGACUAUGGUGACUUCUA	C	1
TaFruc3B.2	tae-miR9676-5p	4.5	13.815	1	22	926	947	UGGAUGUCAUCGUGGCCGUACA	GCUACGACUAUGGUGACUUCUA	C	1
TaFrucUn.4	tae-miR9676-5p	4.5	14.998	1	22	365	386	UGGAUGUCAUCGUGGCCGUACA	GCUACGACUAUGGUGACUUCUA	C	1
TaFruc3A.1	tae-miR9676-5p	4.5	11.306	1	22	236	257	UGGAUGUCAUCGUGGCCGUACA	GCUACGACUAUGGUGACUUCUA	C	1
TaFruc6B.1	tae-miR9677a	4.5	5.774	1	22	2264	2286	UGGCCGUUGGUAGAGUA-GGAGA	UUUCUGUUUUCUACCAAUGGCCA	C	1
TaFruc7A.5	tae-miR9677a	4.5	24.301	1	22	1563	1583	UGGCCGUUGGUAGAGUAGGAGA	CCUCCUCCUC-ACCAACGGCCG	C	1
TaFruc7A.9	tae-miR9677a	4.5	22.689	1	22	1586	1606	UGGCCGUUGGUAGAGUAGGAGA	CCUCCUCCUC-ACCAACGGUCA	C	1
TaFruc7D.10	tae-miR9677a	4.5	22.689	1	22	1816	1836	UGGCCGUUGGUAGAGUAGGAGA	CCUCCUCCUC-ACCAACGGUCA	C	1
TaFruc7A.10	tae-miR9679-5p	4.5	17.323	1	21	2141	2161	CAGAACCAGAAUGAGUAGCUC	AUGUUCCUUGUUCUAGUUUUG	C	1
TaFruc7D.11	tae-miR9679-5p	4.5	17.436	1	21	2141	2161	CAGAACCAGAAUGAGUAGCUC	AUGUUCCUUGUUCUAGUUUUG	C	1
TaFruc6D.1	tae-miR9781	4.5	17.027	1	21	1204	1224	UUUUGUCACAUAUAAUACAUA	GAUGUUUUGCAUGUGAUGAAG	C	1
TaFruc6A.1	tae-miR9781	4.5	22.312	1	21	1206	1226	UUUUGUCACAUAUAAUACAUA	GAUGUUUUGCAUGUGAUGAAG	C	1
TaFruc1B.1	tae-miR1125	5	24.671	1	24	1304	1327	AACCAACGAGACCAACUGCGGCGG	AGGGCGGAGUAGGUCCCUUUGGUU	C	1
TaFruc1D.1	tae-miR1125	5	22.833	1	24	1295	1318	AACCAACGAGACCAACUGCGGCGG	AGGGCGGAGUAGGUCCCUUUGGUU	C	1
TaFruc1A.1	tae-miR1125	5	24.825	1	24	1295	1318	AACCAACGAGACCAACUGCGGCGG	AGGGCGGAGUAGGUCCCUUUGGUU	C	1
TaFruc2A.5	tae-miR1130a	5	16.238	1	23	2097	2119	CCUCCGUCUCGUAAUGUAAGACG	CGUCUUAUAUUAUUGUAUGGAGG	T	1
TaFruc2D.4	tae-miR1130a	5	19.144	1	23	2103	2125	CCUCCGUCUCGUAAUGUAAGACG	CGUCUUAUAUUAUUGUAUGGAGG	T	1
TaFrucUn.1	tae-miR1130b-3p	5	12.573	1	21	1987	2007	UCUUAUAUUAUGGGACGGAGG	CCUCCGUUUUAUAAUGUAGUG	C	1
TaFruc7A.9	tae-miR1130b-3p	5	24.343	1	21	2134	2154	UCUUAUAUUAUGGGACGGAGG	AGUCCAUCCCGUAGGGUGAGG	C	1

Ta **Genes**	**miRNA_Acc.**	**E**	**UPE**	**miRNA**		**Target**		**Fragments**		**I**	**M**
				Start	**End**	**Start**	**End**	**miRNA**	**Target**		
TaFruc4A.2	tae-miR1131	5	15.999	1	22	479	500	UAGUACCGGUUCGUGGCUAACC	GAUCGGUCUUGAACCCGUACUA	C	1
TaFruc5B.5	tae-miR1131	5	19.294	1	22	337	358	UAGUACCGGUUCGUGGCUAACC	GAUCGGUCUUGAACCCGUACUA	C	1
TaFruc5B.2	tae-miR1136	5	16.933	1	24	1757	1780	UUGUCGCAGGUAUGGAUGUAUCUA	UGCCCACAUGUAUGCCUUCAACAA	C	1
TaFruc5D.4	tae-miR1136	5	21.938	1	24	1596	1619	UUGUCGCAGGUAUGGAUGUAUCUA	UGCCCACAUGUAUGCCUUCAACAA	C	1
TaFruc4A.3	tae-miR1136	5	23.469	1	24	1872	1895	UUGUCGCAGGUAUGGAUGUAUCUA	CACCCACAUGUAUGCCUUCAACAA	C	2
TaFruc6D.6	tae-miR1136	5	14.673	1	24	561	584	UUGUCGCAGGUAUGGAUGUAUCUA	CCGUCUGACCCGUACCUGCGAGAA	C	2
TaFruc6D.6	tae-miR1136	5	22.785	1	24	1733	1756	UUGUCGCAGGUAUGGAUGUAUCUA	GGCCCACAUGUAUGCCUUCAACAA	C	2
TaFrucUn.2	tae-miR1136	5	21.701	1	24	1077	1100	UUGUCGCAGGUAUGGAUGUAUCUA	AAAACACAUCAAUGUCAGCAACAA	C	1
TaFrucUn.3	tae-miR1136	5	21.701	1	24	1077	1100	UUGUCGCAGGUAUGGAUGUAUCUA	AAAACACAUCAAUGUCAGCAACAA	C	1
TaFruc3A.2	tae-miR1136	5	23.97	1	24	1900	1923	UUGUCGCAGGUAUGGAUGUAUCUA	GGCCCACAUGUAUGCCUUCAACAA	C	1
TaFruc3B.3	tae-miR1136	5	22.009	1	24	1815	1838	UUGUCGCAGGUAUGGAUGUAUCUA	GGCCCACAUGUAUGCCUUCAACAA	C	1
TaFruc6A.5	tae-miR1136	5	19.464	1	24	1966	1989	UUGUCGCAGGUAUGGAUGUAUCUA	GGCCCACAUGUAUGCCUUCAACAA	C	1
TaFruc3D.2	tae-miR1136	5	22.446	1	24	1728	1751	UUGUCGCAGGUAUGGAUGUAUCUA	GGCCCACAUGUAUGCCUUCAACAA	C	1
TaFruc5B.5	tae-miR1136	5	18.704	1	24	172	195	UUGUCGCAGGUAUGGAUGUAUCUA	GCGACCCAUGGAAAUCUGCGACAA	C	1
TaFruc6D.9	tae-miR1138	5	16.907	1	23	1222	1244	GCUUAGAUGUGACAUCCUUAAAA	GAAAAAGGGUGACAUGUUUGAGA	C	1
TaFruc6A.3	tae-miR156	5	15.402	1	21	10	30	UGACAGAAGAGAGUGAGCACA	CAUCCUCUUCCUCUUUUGUUA	C	1
TaFruc6D.3	tae-miR156	5	18.84	1	21	6	26	UGACAGAAGAGAGUGAGCACA	CAUUCUCUUCCUCUUUUGUUA	C	1
TaFruc4D.1	tae-miR159a	5	14.889	1	21	1860	1880	UUUGGAUUGAAGGGAGCUCUG	CUGUGUGUCUUUUAGUUCAAA	C	1
TaFruc4D.1	tae-miR159b	5	14.889	1	21	1860	1880	UUUGGAUUGAAGGGAGCUCUG	CUGUGUGUCUUUUAGUUCAAA	C	1
TaFruc6D.2	tae-miR164	5	20.751	1	21	1773	1792	UGGAGAAGCAGGGCACGUGCA	ACCACG-GCUCUGUCUUUCCA	C	1
TaFruc3B.3	tae-miR164	5	23.225	1	21	209	229	UGGAGAAGCAGGGCACGUGCA	UCCUCGUCCUCUGCUUCUGCU	C	1
TaFruc3A.2	tae-miR167b	5	16.642	1	21	2292	2313	UGAAGCUGACAGCAUG-AUCUA	AUGAUGCGUGUUGUCAGCAUCG	C	1
TaFruc6B.5	tae-miR171a	5	21.283	1	21	766	786	UGAUUGAGCCGUGCCAAUAUC	GCUGCUGGACCGGCUCAGUCA	C	1
TaFruc6D.8	tae-miR171a	5	23.149	1	21	731	751	UGAUUGAGCCGUGCCAAUAUC	GUUGCUGGACCGGCUCAGUCA	C	1
TaFruc5B.4	tae-miR171b	5	23.422	1	21	182	202	UUGAGCCGUGCCAAUAUCACG	GCGGAUGUUGGACCGGCUCAG	T	1
TaFruc4A.12	tae-miR395b	5	16.325	1	20	1509	1528	UGAAGUGUUUGGGGGAACUC	CCUUUCGCCUAGACACUUCC	C	1
TaFruc4A.14	tae-miR396-5p	5	21.518	1	21	1466	1486	AACUGUGAACUCGCGGGGAUG	GAUCUCAGCGGCUUCACCGUU	T	1
TaFruc2D.3	tae-miR398	5	23.244	1	21	1350	1370	UGUGUUCUCAGGUCGCCCCCG	UUCCGGCGACCUGAGGGAGCA	C	1
TaFruc2D.4	tae-miR398	5	24.369	1	21	828	848	UGUGUUCUCAGGUCGCCCCCG	GAGGGGCGACUUGGCUACGCG	C	1
TaFruc4A.2	tae-miR408	5	21.886	1	21	2032	2053	CUGCACUGCCUC-UUCCCUGGC	GCCAGGGUGUGAGGCGGUGCAG	C	1
TaFruc5B.2	tae-miR444a	5	15.554	1	21	415	435	UUGCUGCCUCAAGCUUGCUGC	GGAUCAAUCUUGAGCCCGCAA	C	1
TaFruc5B.2	tae-miR444b	5	15.554	1	21	415	435	UUGCUGCCUCAAGCUUGCUGC	GGAUCAAUCUUGAGCCCGCAA	C	1
TaFruc7D.5	tae-miR5084	5	18.042	1	24	140	163	AUACAGUACUGCAGAGGAUCCUAA	AAACUUUCCUCUUCAGUUCUGUAG	C	1
TaFruc4A.10	tae-miR5086	5	17.715	1	21	379	399	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4B.2	tae-miR5086	5	15.129	1	21	274	294	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc7D.3	tae-miR5086	5	21.644	1	21	633	653	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1

***Ta* Genes**	**miRNA_Acc.**	**E**	**UPE**	**miRNA**		**Target**		**Fragments**		**I**	**M**
				Start	**End**	**Start**	**End**	**miRNA**	**Target**		
TaFruc7D.9	tae-miR5086	5	22.759	1	21	533	553	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc7A.6	tae-miR5086	5	22.959	1	21	319	339	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc7A.3	tae-miR5086	5	20.089	1	21	724	744	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc7D.5	tae-miR5086	5	20.607	1	21	769	789	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc7D.6	tae-miR5086	5	16.838	1	21	19	39	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4B.1	tae-miR5086	5	21.171	1	21	229	249	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc2D.3	tae-miR5086	5	16.978	1	21	178	198	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc2A.7	tae-miR5086	5	16.986	1	21	337	357	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc3B.2	tae-miR5086	5	17.59	1	21	199	219	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc7A.8	tae-miR5086	5	22.759	1	21	530	550	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc7D.4	tae-miR5086	5	17.378	1	21	763	783	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4A.9	tae-miR5086	5	19.089	1	21	19	39	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4D.1	tae-miR5086	5	21.395	1	21	226	246	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc2B.3	tae-miR5086	5	15.012	1	21	217	237	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4A.12	tae-miR5086	5	20.715	1	21	509	529	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc3D.1	tae-miR5086	5	18.91	1	21	70	90	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc7A.5	tae-miR5086	5	21.19	1	21	457	477	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc2A.6	tae-miR5086	5	16.312	1	21	385	405	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc2A.2	tae-miR5086	5	14.919	1	21	184	204	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc6B.2	tae-miR5086	5	21.827	1	21	853	873	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc4A.1	tae-miR5086	5	21.139	1	21	287	307	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc2B.2	tae-miR5086	5	17.331	1	21	189	209	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4A.11	tae-miR5086	5	16.007	1	21	617	637	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc2A.3	tae-miR5086	5	16.147	1	21	408	428	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc7D.1	tae-miR5086	5	19.583	1	21	511	531	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc4A.6	tae-miR5086	5	20.491	1	21	531	551	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFrucUn.2	tae-miR5086	5	21.68	1	21	133	153	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFrucUn.3	tae-miR5086	5	21.68	1	21	133	153	ACAUUGGUGGAAGGCGUGGUA	UACCACCUCUUCUACCAGUAC	C	1
TaFruc2D.2	tae-miR5086	5	16.147	1	21	205	225	ACAUUGGUGGAAGGCGUGGUA	UACCACUUCUUCUACCAGUAC	C	1
TaFruc6A.3	tae-miR5086	5	5.128	1	21	2276	2296	ACAUUGGUGGAAGGCGUGGUA	AGUUCUGUUUUCUACCAAUGA	C	2
TaFruc6A.3	tae-miR5086	5	23.92	1	21	1134	1154	ACAUUGGUGGAAGGCGUGGUA	GGCAGCGGCGUCCACCAAUGG	C	2
TaFruc5B.3	tae-miR5086	5	12.622	1	21	499	519	ACAUUGGUGGAAGGCGUGGUA	UACCAUGAAUUCUACCAAUAU	C	1
TaFruc5D.2	tae-miR5086	5	14.08	1	21	432	452	ACAUUGGUGGAAGGCGUGGUA	UACCAUGAAUUCUACCAAUAU	C	1
TaFruc3B.3	tae-miR5086	5	16.614	1	21	397	417	ACAUUGGUGGAAGGCGUGGUA	UACCACGAGUUCUACCAGUAU	C	1
TaFruc4A.4	tae-miR5086	5	13.833	1	21	387	407	ACAUUGGUGGAAGGCGUGGUA	UACCAUGAAUUCUACCAAUAU	C	1
TaFruc2D.5	tae-miR5086	5	10.392	1	21	89	109	ACAUUGGUGGAAGGCGUGGUA	GUCCUCGCCUUCCACCUCUGC	C	1

Ta Genes	miRNA_Acc.	E	UPE	miRNA		Target		Fragments		I	M
				Start	End	Start	End	miRNA	Target		
TaFruc6D.2	tae-miR5175-5p	5	16.962	1	21	2473	2493	UUCCAAAUUACUCGUCGUGGU	AUCAUCCCGACUAAUUUGGAU	T	1
TaFruc6A.1	tae-miR5384-3p	5	20.427	1	21	1834	1854	UGAGCGCGCCGCCGUCGAAUG	GCCUCGAUGGCGGCUUGCGCA	C	1
TaFruc7A.6	tae-miR9652-5p	5	10.639	1	22	1925	1946	CCUGUUUGUCAUUAAGUUUCUU	CUUGAGUUUAAUGUCAAAUAUG	C	1
TaFruc4A.7	tae-miR9653a-3p	5	19.11	1	21	147	167	UUUGAGACUUUGGCCAUGGCC	UGCCGUGCCCGAAGACCCAAA	C	1
TaFruc1A.1	tae-miR9654a-3p	5	23.602	1	22	1360	1381	UUCUGAAAGGCUUGAAGCGAAU	GUUUUCUUCAGGAUUUUCAGGG	T	1
TaFruc1B.1	tae-miR9654a-3p	5	20.897	1	22	1369	1390	UUCUGAAAGGCUUGAAGCGAAU	GUUUUCUUCAGGAUUUUCAGGG	T	1
TaFruc2B.7	tae-miR9656-3p	5	16.343	1	21	1400	1420	CUUCGAGACUCUGAACAGCGG	CGGUGGUAGAGAGUUUCGGAG	C	1
TaFruc2A.7	tae-miR9660-5p	5	22.458	1	20	2137	2156	UUGCGAGCAACGGAUGAAUC	AUUUCAUCAGUUGUUGGCAG	C	1
TaFruc7D.4	tae-miR9666b-3p	5	21.941	1	22	917	938	CGGUUGGGCUGUAUGAUGGCGA	CCGCCACCAUGCUGCCCAAUGG	T	1
TaFruc6B.2	tae-miR9667-5p	5	6.162	1	21	2490	2510	AAAUAUGGCAAACAAUGAAUG	GUUUUUUUGUUUUUCAUUUUU	C	1
TaFruc6B.6	tae-miR9667-5p	5	8.825	1	21	2024	2044	AAAUAUGGCAAACAAUGAAUG	ACUUCCAUAUUUUCCAUAUUU	C	1
TaFruc3A.1	tae-miR9669-5p	5	23.499	1	21	109	129	UACUGUGGGCACUUAUUUGAC	GUCAAGUACGUGCUCAAGGUG	C	1
TaFruc3D.1	tae-miR9669-5p	5	24.82	1	21	670	690	UACUGUGGGCACUUAUUUGAC	GUCAAGUACGUGCUCAAGGUG	C	1
TaFruc4D.2	tae-miR9674b-5p	5	15.646	1	21	2052	2072	AUAGCAUCAUCCAUCCUACCC	GGAUGAGAUCGAUGAUGCUAA	C	1
TaFruc5B.2	tae-miR9674b-5p	5	19.228	1	21	59	79	AUAGCAUCAUCCAUCCUACCC	UGCUUGGUUGGAUGCUGCUGU	C	1
TaFruc6B.4	tae-miR9676-5p	5	24.076	1	22	1141	1162	UGGAUGUCAUCGUGGCCGUACA	ACAACGGCGGCGGUGAUGUUUU	C	1
TaFruc6D.4	tae-miR9677a	5	17.432	1	22	2278	2300	UGGCCGUUGGUAGAGUA-GGAGA	UUUCUGUUUUUUACCAAUGGCCA	C	1
TaFruc6B.6	tae-miR9677b	5	18.222	1	21	801	821	CAGGGCGGGGAACAGGUGGCC	GACCAUUAGUUUCUCGCCUGG	C	1
TaFruc3B.3	tae-miR9677b	5	22.277	1	21	199	219	CAGGGCGGGGAACAGGUGGCC	UUCUUCCUGCUCCUCGUCCUC	C	1
TaFruc4A.2	tae-miR9678-3p	5	18.975	1	22	182	203	UCUGGCGAGGGACAUACACUGU	UGCGUGUAUGUUCUCCACCAGC	C	1
TaFruc5B.2	tae-miR9678-3p	5	20.813	1	22	128	149	UCUGGCGAGGGACAUACACUGU	UGCGUGUAUGUUCUCCACCAGC	C	1
TaFruc6B.2	tae-miR9773	5	19.386	1	24	2401	2424	UUUGUUUUUAUGUUAUUUUGUGAA	GCCUCAAUGUAAAAUGAAAAUGGA	C	1
TaFruc6D.1	tae-miR9773	5	18.247	1	24	2155	2178	UUUGUUUUUAUGUUAUUUUGUGAA	GCCUCAAUGUAAAAUGAAAAUGGA	C	1
TaFruc7D.2	tae-miR9775	5	17.791	1	22	2047	2068	UGUGCGCAAUAAGAUUUUGCUA	GCUGAGAAGCUCAUUGUGCACG	T	1
TaFruc4A.4	tae-miR9776	5	14.644	1	21	2139	2159	UUGGACGAGGAUGUGCAACUG	UGGUUUUACAUCUUCUGCCAA	C	1
TaFruc2B.2	tae-miR9778	5	21.796	1	21	1790	1810	UGCAUCAUCUCGAACUCGUCG	GCAUGCGAUUGAGCUGAUGUA	C	1
TaFruc2B.3	tae-miR9780	5	23.938	1	21	676	696	CGGGUCGGCGCUGCACGCGGC	UGGGAGCGCAACGCUGACCCG	T	1
TaFruc2B.2	tae-miR9780	5	24.567	1	21	870	890	CGGGUCGGCGCUGCACGCGGC	CCCGAGCGCGGCGACGACCCC	C	1
TaFruc6A.6	tae-miR9781	5	14.727	1	21	2164	2184	UUUUGUCACAUAUAAUACAUA	CUCAUAUUGUAUGCGACAAAC	C	1

C: Cleavage; E: Expectation; I: Inhibition; T: Translation : UPE: maximum energy to unpair target site

ABSTRACT

Title of Thesis : **Genome wide association mapping for water soluble carbohydrates in bread wheat (*Triticum aestivum* L.) under terminal water stress**
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Admission number : 2016A27D
Title of Degree : Doctor of Philosophy in Genetics and Plant Breeding
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Degree awarding University : Chaudhary Charan Singh Haryana Agricultural University, Hisar-125004, Haryana
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Genomic assisted breeding is one way to improve drought stress tolerance in wheat. To uncover the genomic regions for grain yield, its attributing traits, water soluble carbohydrates (WSCs) and its components mainly fructans, a comprehensive multidisciplinary study was conducted with a diverse set of 302 bread wheat genotypes. All the genotypes were evaluated under complete irrigation, rainfed and complete water stressed condition for two consecutive crop seasons at three locations (Hisar, Karnal and Baramati). The study indicated significant effect of different water regimes and locations on the expression of traits and as much as 80% of yield reduction was reported under DT. Seven promising drought tolerant verities were identified on the basis of drought susceptibility index. In this study, correlation between yield and studied traits largely varied with environmental and water conditions. However, shorter plant height, longer grain filling duration, days to heading, thousand kernel weight (35-40 g) is the most favorable trait combination for obtaining high grain yield under studied conditions. Positive correlation of WSCs with grain yield was reported only for drought tolerant genotypes. High values of all the genetic components were reported for all the traits within environments, however in pooled over management these values ranged between low to moderate for most of the studied traits due to genotype x environment. Traits like plant height, peduncle length, spikelet per spike and thousand kernel weight were least influenced with genotype x environment interaction thus found suitable for selection of grain yield. Substantial genetic diversity was reported in the studied material which was attributed by each of the studied trait equally. With 35K Axiom array and applying compressed mixed linear model, 431 stable SNPs were identified for 20 studied traits in 1288986.92 cM genomic region of bread wheat. These SNPs explained ca. 30-53% of phenotypic variations. Of 431 stable SNPs 77 were showing pleiotropy for various traits. Five SNPs (AX-94583229, AX-94879209, AX-94759517, AX-94887053 and AX-94964616) for fructans and total non-structural carbohydrates, three (AX-94508292, AX-95257620 and AX-94456473) for days to heading and one (AX-94412521) for plant height were most significant. In functional analysis of significant SNPs, 249 genes were identified which were mainly involved in carbohydrate metabolism and repair mechanism. Only few were reported with direct involvement in stress responses. In an *in silco* study 104 genes (*TaFruc*) transcribing into stable protein associated with fructans metabolism were identified. All of these were involved in either hydrolase or transferase activities of glycosyl groups of soluble sugars. These genes were found expressive under different stress conditions, mainly water stress. To facilitate the future breeding programs a total of 189 SSR molecular markers and 60 micro RNAs have been predicted successfully for *TaFruc* genes.

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- **Gaur, A.**, Parray, G. A., Shikari, A. B., and Najeeb, S. (2019) Capturing the genetic diversity for grain quality attributes in a set of Temperate Rice (*Oryza sativa* L.) germplasm by cluster analysis and the assessment of Wx gene polymorphism. *International Journal of Pure and Applied Biosciences*, **7(3)**, 67-73.
- Anu, Singh, V., Yashveer, S., Niwas, R., Malik, P., **Arpit**, Dey, S., and Ahlawat, U. (2019) Assessment of genetic variability, heritability and genetic advance for grain yield and its contributing traits in Wheat (*Triticum aestivum* L.). *International Journal of Current Microbiology and Applied Sciences*, **8(8)**, 1169-1174.
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- Sheoran, S., Pawar, S., **Gaur, A.**, Mishra, P. C., Tyagi, B.S., Singh, V., Sareen, S., Tiwari, R., Singh, G., and Singh, G. P. (2019) Identification of QTL regions and underlaying candidate genes for trait associated with drought tolerance in wheat. In: Golden Jubilee Conference on New Millennia agriculture novel trends and future scenario,CCS HAU, Hisar, Nov 2019.

Signature of student

UNDERTAKING OF COPYRIGHT

I, Arpit Gaur, Admission No. 2016A27D, undertake that I give copyright to the CCS HAU, Hisar of my thesis entitled **“Genome wide association mapping of stem water soluble carbohydrates in bread wheat (*Triticum aestivum* L)” under terminal water stress.**

I also undertake that patent, if any, arising out of the research work conducted during the program shall be filled by me only with due permission of the competent authority of CCS Haryana Agricultural University, Hisar.

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