Genetic variability in indigenous lowland rice under stagnant flooding

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CERTIFICATE- I

This is to certify that the thesis entitled **"GENETIC VARIABILITY IN INDIGENOUS LOWLAND RICE UNDER STAGNANT FLOODING"** submitted by **SOUMYA BISWAL, Adm. No. 07 PBG/14** to the Orissa University of Agriculture and Technology, Bhubaneswar in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **PLANT BREEDING AND GENETICS** is a faithful record of *bona fide* research work carried out by her under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma or published in any other form. 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 the thesis entitled **"GENETIC VARIABILITY IN INDIGENOUS LOWLAND RICE UNDER STAGNANT FLOODING"** submitted by **SOUMYA BISWAL** Adm. No.07 PBG/14 to the Orissa University of Agriculture and Technology, Bhubaneswar in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING AND GENETICS)** has been approved by the students' Advisory committee and the External Examiner.

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ABBREVIATION

DF-Days to 50% flowering

PHBF-Plant height before flooding

PHAF-Plant height after flooding

FPH-Final plant height

TBF-Tillers per plant before flooding

TAF- Tillers per plant after flooding

EBT-Ear bearing tiller per plant /Effective tiller per plant

PL-Panicle length

FGP-Fertile grains per panicle

GF%-Grain fertility %

GW-100 grain weight

HI-Harvest index

CHOBF-Carbohydrate content of plant before flooding

CHOAF- Carbohydrate content of plant after flooding

GY- Grain yield per plant

ha-hectare

NB-The characters are mentioned in abbreviated form in tables, as written above.

Abstract

The present investigation on “Genetic Variability in Indigenous Lowland Rice under Stagnant Flooding” aimed at evaluating 50 local landraces collected from 14 districts of Odisha alongwith 3 improved and 3 high yielding genotypes under stagnant flooding situation of 30cm-60cm for more than 30 days. Studies on genetic variability, character association, path coefficient analysis, genetic diversity and selection indices were carried out. Variability of the promising rice genotypes at physiological level was also done to study the diversity.The field experiment was laid out in RBD in the Rice Research Station of the Department of Plant Breeding & Genetics, College of Agriculture, Bhubaneswar during kharif 2015. Analysis of variance revealed highly significant differences among the test genotypes in respect of all the 15 characters. Mean performance of 56 lowland rice genotypes indicated that Upahar and Mrunalini were promising with respect to grain yield performance. The landrace ‘Ganjamgedi’ was found to possess highest yield among the landraces indicating that it can be used as a donor for grain yield improvement. In general PCV was higher than GCV in all the characters. All characters except days to 50% flowering had moderate to high PCV as well as GCV. High heritability along with high genetic advance were noticed for the characters such as plant height after flooding, final plant height, fertile grains per panicle. These are stable characters and can be considered for selection. Correlation studies indicated significant and positive association of grain yield per plant with days to 50% flowering, number of effective tillers/plant, carbohydrate content before flooding, carbohydrate content after flooding, and negatively correlated with plant height. Path analysis revealed that carbohydrate content after flooding exhibited maximum positive direct effect on grain yield. Also number of effective tillers/panicle, carbohydrate content before flooding, days to 50% flowering, fertility% and harvest index were observed to be the major indirect contributors towards grain yield. D^2 analysis showed that considerable diversity is available in the materials tested. The 56 genotypes were classified into 7 clusters. Based on inter-cluster distance, genotypes namely T-141,T-1242, Mrunalini, Upahar and Swarna from cluster III were selected for use as parents in hybridization programme. Similarly, Budidhan from cluster V and T-90 from Cluster VI were also selected. In the present investigation, selection indices were constructed using 13 characters with grain yield per plant as the economic criterion. The promising genotypes occupying better ranking in the 13 characters index namely Upahar, Mrunalini, Swarna, T-1242, Ganjamgedi, T-141, Kadalipendi were selected for their future use in breeding programme.

CHAPTER-1

INTRODUCTION

INTRODUCTION

Rice is the seed of the grass species *Oryza sativa* (Asian rice) or *Oryza glaberrima* (African rice). As a cereal grain, it is the most widely consumed staple food for a large part of the world's human population, especially in Asia. It is the agricultural commodity worldwide with 3rd highest production after Sugarcane and maize. (FAOSTAT data,2012)

It is a good example of crop domestication; it has maturity duration varying from 80 to 180 days and adaptability to a wide range of land and water. It can grow in flooded condition, where no other crop could possibly be grown. Before 3000 B.C. domestication of rice might have started and centre of origin is mostly in South and South-East Asia. South Odisha(Jeypore) has been identified as a secondary center of origin of cultivated rice (Ramiah and Ghose,1951; Ramiha and Rao, 1953).

India accounts for the one fourth of the rice production of the world with the first place occupied by china. India has an are of 45.16 million hectares under rice cultivation with an output of 104.10 million tones which average to 2.3 tonnes per hectares(Gangashetty , 2013).

The traditional method for cultivating rice is flooding the fields while, or after, setting the young seedlings. This simple method requires sound planning and servicing of the water damming and channeling, but reduces the growth of less robust weed and pest plants that have no submerged growth state. While flooding is not mandatory for the cultivation of rice, all other methods of irrigation require higher effort in weed and pest control during growth periods and a different approach for fertilizing the soil.

Rice cultivated with a total harvested area of about 153 million hectares and producing more than 600 million tons annually. About 90% of the rice in the world is grown in South Asia (58 million hectares), Southeast Asia (43 million hectares) and East Asia (31.5 million hectares). In Asia and sub-Saharan Africa (8 million hectares), almost all rice is grown on small farms of 0.5-3 ha. Yields range from less than 1 ton/ha under very poor rainfed conditions to 10 tons/ha in intensive temperate irrigated systems. Total rice area in many countries is shrinking and prime rice land has been diverted for urbanization, industrialization and infrastructure developments (Zeigler and Barclay,2008)

It is staple food for more than 70% Indians and source of livelihood for 120-150 millions rural households. It is the cheapest source of food, energy and protein for developing countries. It contributes to 43% of total food grain production and 53% of cereal production. It is grown in about 44.6 million hectares in India, which is about 36.58% of net cropped area and 44.5% of area under cereals.(Agricultural Statistics-Ministry of statistics and programme implementation-2014)

Flooding is a serious , naturally occurring problem for rice production in the rainfed lowlands of South and South east Asia during the monsoon season.50% of the rice growing area in the ecosystem is affected by flash-flooding at various stages of growth. Flash-flooding and submergence adversely affect at least 16% of the rice lands of the world (~22 m ha). In eastern India, ~13 m ha of rice lands are unfavourably affected by excess water and periodically suffer from flash-floods and complete submergence. Improvement of germplasm is likely the best option to withstand submergence and stabilize productivity in these environments.(Dey and Upadhyaya, 1996)

Deepwater varieties of rice (*Oryza sativa*) are grown in flooded conditions with water more than 50 cm deep for at least a month. More than 100 million people in South and Southeast Asia rely on deepwater rice for their sustenance. There are two adaptations which permit the rice to thrive in deeper water, floating rice and traditional talls. Traditional talls are varieties that are grown at water depths of between 50 cm and 100 cm and have developed to be taller and have longer leaves than standard rice. Floating rice grows in water deeper than 100 cm through advanced elongation ability. This means when a field where rice is grown under flooded condition, it accelerates the growth in the internodal region of the stem which allows the plant to keep some of its foliage on top of the water. The Indica cultivar is the main type of deepwater rice, although varieties of Japonica have been found in Burma, Bangladesh and India (Das *et al.*2009).

Rainfed lowland deepwater rice together account for approximately 33% of global rice farm lands (IRRI Social Statistics Database,2014;Huke and Huke 1997).

Thailand, Bangladesh, India, Nepal, Myanmar, Laos and Cambodia have high % of rainfed lowland rice farms.(Serres and Fukao *et al.*,2010). One million ha of rice are lost every year due to submergence stress(Settler *et al.* 1989) and total economic loss of $600 millon per year (Herdt 1991).Of the lowland rice farms, 22 million ha are vulnerable to flash flooding.(Khush 1984).

Farmers usually cultivate the land races in floodprone lowlands that can tolerate more than 10 days of complete submergence and accelerate growth upon desubmergence..But these submergence tolerant land races yield less than 2 ton/ha as compared to the 6-8 tons of grain per hectare produced by semidwarf HYV.

50% of the rice-growing area in this ecosystem is affected by flash flooding at various stages of growth (Dey and Upadhyaya,1996). Also the intensively farmed irrigated areas has become increasingly vulnerable to flooding because of the popularity of semi-dwarf cultivars. As a consequence, there is also a need for irrigated rice cultivars that can survive a medium depth of water. For these reasons, importance is given to breeding of submergence tolerance rice in the tropics utilizing the inherent variability in tolerance present in the available landraces (Mackill *et al.,1993*)

The rainfed lowland rice area in the state comprised of 1.5 million hectares which is nearly 35% of the total rice area; have shallow, semi-deep and deep water situations. Shallow lowlands occupy a major area (1.0 m ha) followed by semi-deep water (0.35 m ha) and deep water with 0.15 m ha. Erratic rainfall and uncontrolled water situations are the major constraints in these rainfed ecosystems. Some of the other adverse factors like impeded drainage and water logging, flash floods and terminal drought leading to poor crop stand and sub-optimal plant population and continued use of traditional low input responsive and low yielding varieties restrict rice production in the state.

In semi deep-water lands the crop is generally direct seeded in May-June with or without beushaning depending upon water depth. In deepwater lands direct seeding in May is rather mandatory. Severe yield loss occurs due to stem-borer and bacterial leaf blight. Lack of suitable rice varieties with high yield and resistance to stem borer, bacterial leaf blight and submergence tolerance and tolerance to stagnant flooding are the major constraints to high productivity in these ecologically handicapped semi-deep and deep-water lands of the state.

Suitable plant type for rainfed lowlands can be suggested considering morpho-physiological traits like semi-dwarf to intermediate stature, late maturity duration (150-155 days),lodging resistance, moderate tillering habit, desirable canopy structure with dark green erect leaves, larger panicles, high grain number (more than 200 grains per panicle) with improved fertility, photo-period sensitivity and thermo-insensitivity, improved harvest index of 0.5, tolerance to early drought and flash flood submergence, disease and insect resistance and superior grain quality for genetic enhancement of yield in low land rice. Prolonged water logging during rainy season for the most part of the crop growth reduces tillering and growth of the normal rice crop.(Gautam *et al.*2015)

Realizing the importance of high yield and greater stability of production of lowland rice and in the light of above discussions, the present investigation on genetic basis of yield variation in lowland rice with special reference to stagnant flooding was undertaken involving 50 local land races of rice and 6 check varieties with the following objectives:

- To compare rice plant characterstics before and after stagnant flooding.
- To study the biochemical changes before and after stagnant flooding.
- To select rice genotype with improved agro-economic and morpho-physiological traits.
- To select suitable rice genotypes with tolerance to stagnant flooding.

CHAPTER-2

REVIEW OF LITERATURES

REVIEW OF LITERATURES

Sharma (1995) suggested that in some flood prone areas,vegetative propagation using tall and vigorous tillers uprooted from established direct seeded crops gives higher productivity.

Mishra .(1996) found submergengence tolerance is governed by single dominant gene.

Sarkar *et al*,.(1996) studied submergence tolerance mechanism in respect to seedling height, carbohydrate, chlorophyll and specific leaf weight (SLW) on 5 rice cultivars and concluded submergence tolerant cultivars maintain more carbohydrates more chlorophyll and SLW as compared with susceptible cultivars during submergence.

Setter *et al*.(1996) concluded that environments where elongation ability is not required, there is a potential to increase submergence tolerance of agriculturally important cultivars by selecting for least elongation, at least during periods of complete submergence and this trade-off between stimulated elongation growth and submergence tolerance will have important ecological consequences for the distribution of plant species in different flood-prone environments.

Setter *et al*.(1997) experimented effects of elongation growth on tolerance to complete submergence for up to 14 days and showed negative correlation between per cent survival and elongation growth of genotypes during complete submergence.He suggested that a common factor related to tolerance of limited gas diffusion, (e.g. one of the enzymes of alcoholic fermentation) may be responsible for genotypic differences in submergence tolerance of rice. An alternative possibility is that a gene for a transcription factor is involved in the expression of a multiple gene cascade that confers submergence tolerance.

Straeten *et al*.(1997) observed, ethylene plays a key role in the rapid elongation of deepwater rice and the mRNA levels were suppressed by ACC, GA, submergence and wounding.

Sharma and Ghosh (1999) concluded that grain yield of flood-prone lowland rice can be increased by establishing the crop early through direct seeding using high-density seed and basal N fertilization.

Das *et al* .(2000),studied effect of submergence on the activity of starch phosphorylase in 25-day-old seedlings of four rice cultlvars, and concluded that rice plants with higher pre-submergence starch content had a better survivability under submergence.

Quimio *et al.*(2000),suggested that ethanol production of tillers of To transgenic plants was positively correlated with survival after submergence.

Zhou *et al.*(2001) observed, gene family *OS-ACS5* may play a fundamental role in the growth-promoting increase in ethylene biosynthesis during the first hours of submergence in deepwater rice.

Kawano *et al.*(2002) found the tolerant cultivar showed a rapid recovery of total ascorbate and ascorbic acid and strong negative correlations were observed between malondialdehyde formation with ascorbate concentration (r=−0.93) and with percentage of survival (r=−0.98); concluded that accumulation of ethylene during submergence adversely affected antioxidant mechanism in intolerant rice cultivars after desubmergence, and ascorbic acid was an important antioxidant in vivo for the recovery of submerged rice seedlings.

Jackson and Ram (2003) observed that oxygen shortage and imbalance in production and consumption of assimilates is involved in submergence injury and DNA marker for major QTL is helpful for breeding programme in submergence.

Toojinda *et al.*(2003) found several major QTL determining plant survival, height, shoot elongation identified to be located on chromosome 9 and some secondary QTL on chromosome 1,2,5,7,10,11 and these identified QTL contributed to increased submergence tolerance.

Tsuji *et al.*(2003) found post-hypoxic injuries in plants are primarily caused by bursts of reactive oxygen species and acetaldehyde and accumulations of acetaldehyde in rice during re-aeration following submergence then during re-aeration, acetaldehyde-oxidizing aldehyde dehydrogenase (ALDH) activity increased, thereby causing the acetaldehyde content to decrease in rice.

Singh *et al.*(2004) found out the most remunerative, high energy output and water-use efficient cropping sequence for semi-deep water and flood-prone situation and concluded that total energy output and energy-use efficiency were highest with rice-mustard &-maize + cowpea sequence in both situations.

Das *et al.*(2005) observed seedling survival showed a stronger association with Non Structural Carbohydrate maintained after submergence than with NSC before submergence and suggested that carbohydrates maintained after submergence, being the result of both initial level, and the level used during submergence is more important for survival.

Fukao *et al.*(2006) demonstrated that the Sub1 region haplotype determine ethylene- and GA-mediated metabolic and developmental responses to submergence through differential expression of Sub1A and Sub1C. Submergence tolerance in lowland rice is conferred by a specific allele variant of Sub1A that dampens ethylene production and GA responsiveness, causing quiescence in growth that correlates with the capacity for regrowth upon desubmergence.

Patra *et al.*(2006) evaluated the difference in respect of apiculus and stigma colour, leaf length and breadth, plant height, awning characteristics of submergence tolerant cultivars namely 'Kalaputia', 'Kusuma' and 'FR 13A' and the mean quantitative characters of both the genotypes also showed that they were different.

Sarkar *et al.*(2006) focused on current physiological understanding of tolerance to submergence in rice with greater emphasis on floodwater environments, new genetic resources and potential of DNA marker technology for incorporating multiple traits associated with tolerance, to enhance and speed progress through breeding.

Das and Ramakrishnaya (2007) observed the oxidizing activity of roots, starch and total sugar content decreased in all genotypes under submergence, the tolerant cultivar FR13A had the highest root oxidase activity, starch and total sugar content compared to the other two cultivars and each of these factors is expected to have contributed to the ability of the plants to survive the stress.

Perata and Voesenek (2007) saw transcription factor belonging to the B-2 subgroup of the ethylene response factors (ERFs)/ethylene-responsive element binding proteins (EREBPs)/apetala 2-like proteins (AP2) within theSub1 locus determines submergence tolerance in rice and these genes control highly conserved hormonal, physiological and developmental processes that determine the rate of elongation when submerged.

Srivastava *et al.* (2007) concluded that under water low shoot elongation, high shoot carbohydrate and higher post submergence SOD activity are possible physiological markers for submergence tolerance.

Fukao and Bailey-Serres (2008) observed that submergence-tolerant lowland rice restricts carbohydrate consumption used for cell division and cell elongation that promotes underwater elongation. This tolerance is the result of limited ethylene production and sensitivity.

Kawano *et al.*(2008) observed that physiological response of Saligbeli was different to other *O. glaberrima* genotypes in terms of FFR,it exhibited enhanced shoot elongation with the increase in DMA during submergence. These features seemed to be a unique way to cope with submergence ,the vigorous growth of Saligbeli and IHP underwater should be further investigated for improving FFR in rice.

Das *et al.*(2009) observed rate of decreasing levels of total sugar and starch content in rice plants during complete submergence could be considered as an indicator of submergence tolerance as revealed through repeated experiments with two submergence tolerant and two susceptible varieties. Younger the seedlings (7 days), quicker are depletion than in older seedlings of 10 and 15 days. Drastic reduction is thus prominent under prolonged submergence period (15 days) than 7 or 10 days of complete submergence. Susceptible varieties show maximum decrease in starch and sugar content than resistant varieties.

They also observed lower intensity of light and warmer temperatures seem to reduce biomass and increase mortality under flooding; an increase in the concentrations of O_2 and CO_2 and a decrease in water pH did not improve survival in clear unshaded water;turbid floodwaterwas more damaging to rice as plant mortality increased as the percentage of silt increased, and the effects ofwater turbidity cannot be explained by the reduction in light penetration alone;most tolerant rice cultivar, FR13A, experienced higher mortality when flooded with turbid floodwater. Correlation studies revealed that cultivars with the capacity to maintain higher biomass, higher chlorophyll, and non-structural carbohydrate concentrations after submergence had higher survival.

Hattori *et al.*(2009) discovered genes SNORKEL1 and SNORKEL2, which trigger deepwater response by encoding ethylene response factors involved in ethylene signaling; under deepwater conditions, ethylene accumulates in the plant and induces expression of these two genes and the products of SNORKEL1 and SNORKEL2 then trigger remarkable internode elongation via gibberellin.

Septiningsih *et al.*(2009), developed tolerant varieties by marker-assisted backcrossing through two or three backcrosses, and evaluated their performance to determine the effect of Sub1 in different genetic backgrounds and concluded that Sub1A is the primary contributor to tolerance, while Sub1C alleles do not seem important. Lack of dominance of Sub1 suggests that the Sub1A-1 allele should be carried by both parents for developing tolerant rice hybrids.

Singh *et al.*(2009) concluded the introgression of Sub1 into popular varieties did not have any negative impact on their performance under control conditions but considerably enhanced their yield and grain quality following short-term submergence.

Bailey-Serres *et al.*(2010) observed at the molecular level, Sub1 is a variable polygenic locus encoding two or three ethylene responsive factor (ERF) DNA binding proteins and induction of Sub1A expression by ethylene during submergence disrupts the elongation escape strategy typical of lowland and deepwater rice, by limiting ethylene-induced gibberellic acid-promoted elongation and due to the conditional activity of Sub1A,and the new "Sub1" mega-varieties effectively provide submergence tolerance without apparent ill effect on development, productivity, or grain quality.

Dubois *et al.* (2011) concluded that submergence elongation enhancement of lowland rice is due to alteration of gibberellins (GA) metabolism leading to an increase in active GA (GA1) content.

Jantaboon *et al.*(2011) developed through the single seed descent (SSD) method, a large population of recombinant inbred lines (RILs) and demonstrated the potential of using marker-assisted selection (MAS) in the identification of the ideotype from the offspring and found all of the ID1 lines exhibited submergence tolerance and jasmine-like cooking quality and displayed a low amylose content, a fragrance and a high alkali spreading value.

Manzanilla *et al.*(2011) studied the performance in farmers' fields of lines with the Sub1 gene that confers tolerance of submergence for up to two weeks by incorporating the Sub1 gene by MABC, and concluded that depending on the timing of flood with respect to growth stage, shorter duration and shallow flashfloods can result in less than 10% production losses while deeper and stagnant water with two weeks' duration and >100 cm depth can cause damage ranging from 40% to 77%.The analysis indicated that farmers prefer rice cultivars that are tolerant of submergence, have early to medium maturity relative to their commonly grown varieties, are resistant to pests and diseases, and are resistant to lodging, among other traits.

Sarkar and Bhattacharjee (2011) observed Sub1, SC3, ART5 genotypes possess one or more of the adaptive traits required for the flood-prone ecosystem, which range from temporary submergence of 1–2 weeks to long period of stagnant water tolerance.

Singh *et al.*(2011) observed varieties combining tolerance of prolonged stagnant flooding with Sub1 will have broader adaptation in flood-prone areas and greater impacts on yield stability.

Hendawy *et al.*(2012) the contrasting rice genotypes expressed differential growth responses in genotypes with lower shoot elongation ratio using different quiescence strategies during submergence period.

Sakagami (2012) found cultivars of *O. glaberrima* adapt to long-term complete submergence apparently because of their greater photosynthetic capacity developed by leaves that have newly emerged above floodwaters through rapid shoot elongation and the Saligbeli cultivar of *O. glaberrima*, with its unique physiological mechanisms, is apparently well-adapted to both conditions for short and prolonged submergence and concluded that it, therefore, holds promise as a selective and breeding rice genotype for use in different floodprone regions in Africa.

Nguyen *et al.*(2013) found maintenance of standing water after heading, larger input of N fertilizer, and appropriate weed management were found to contribute to higher yields for both lowland rice(LR) and floating rice(FR).

Pucciariello and Perata (2013) observed that submergence-tolerant traits have also been shown to be present in some diploid CC type wild rice accessions, Sub1C-like genes ; therefore, it is possible that they harbor a distinctive molecular mechanism of submergence tolerance,can be achieved in intergenomic crosses.

Sakagami *et al.*(2013) analyzed physiological mechanisms of escape from complete submergence by evaluating photosynthesis, photochemical reaction, and plant behavior during and after submergence in *Oryza glaberrima* and found, it that submergence escape strategy effectively uses stored carbohydrates for shoot elongation and leaf extension in a severely photosynthesis-limited environment under complete submergence more than *Oryza sativa*.

Gautam *et al.*(2014) concluded post-submergence N and basal P application increased the concentration of NSC, enhanced survival percentage and reduced shoot elongation and pre-submergence N application enhanced under-water shoot elongation, which leads to reduced survival, depletion of chlorophyll and NSC;and soluble carbohydrates after submergence are more important for survival than at the initial level.

Hirano *et al.*(2014), compared growth responses of floating rice (FR) and deepwater rice (DWR) to severe flooding conditions,by taking 2 FR varieties, and 2 DWR varieties and suggested that FR can regulate internode elongation in response to rising water level so as to keep the top of the uppermost leaf sheath above the water surface.

Lakshmi *et al.,*(2014) studied on biochemical changes in submerged rice soil amended with different vermicomposts under integrated nutrient management and concluded that Conjunctive application of organics along with inorganics exhibited higher grain yields over application of inorganics only .

Ranawake *et al.*(2014) observed all the survived rice cultivars were elongated (100%) under 14-day submergence stress at both seedling and vegetative stages compared to that of control plants. Some survived rice cultivars reduced the plant height at 5-day and 9-day complete submergence stresses at both seedling and vegetative stages compared to that of control plants but none of the cultivars reduced the plant height at 14-day complete submergence stress compared to that of control plants was able to survive.

Sarkar *et al.*(2014) identified "Kalaketaki" which can withstand up to 20-days of complete submergence and also has good regeneration capacity. This genotype would be of immense use as a valuable gene source in breeding new cultivars tolerant to complete submergence for longer duration.

Singh et al. (2014) observed that during submergence, FR13A showed not only slower leaf elongation but also accumulated extra biomass and was able to recover faster than Sub1 lines. This suggests the possibility of further improvements in submergence tolerance by incorporating additional traits present in FR13A or other similar landraces.

Anandan *et al.*(2015),suggested that breeders who involved in breeding rice cultivars for pro-longed flooding situation should emphasize on parameters leaf blade length, sheath length and area to breed genotype suitable for prolonged flooding condition.

Gautam *et al.*(2015), observed urea foliar spray after desubmergence significantly enhanced the photosynthesis and narrowed down the flowering time which led to higher grain yield and productivity and suggested that a simple alteration in the time and method of N application with basal P can significantly contribute to higher rice yield in flash-flood prone areas.

Haque *et al.*(2015),observed that lower number of plants per hill is more suitable in submerged condition and Field water use efficiency was significantly higher at continuous saturated condition and lower at submerged condition.

Iftekharuddaula *et al.* (2015) reported submergence tolerant high yielding rice variety was developed using BR11 as a recipient parent applying foreground, phenotypic and background selection approaches and the study demonstrated the efficiency of recombinant selection and better adaptability of the newly released submergence tolerant high yielding variety in flash flood prone different areas of the country with respect to submergence tolerance and yield potential.

Okishio *et al.*(2015) observed the Amazonian wild rice Oryza grandiglumis has two contrasting adaptation mechanisms to flooding sub-mergence: a quiescence response to complete submergence at the seedling stage and an escape response based on internodal elongation to partial submergence at the mature stage and said that enhanced internodal elongation of submerged O. grandiglumis plants is not triggered by ethylene accumulated during submergence but by the moist surroundings provided by submergence.

Sarangi *et al.*(2015) suggested water depth becomes less significant when a tolerant variety and good management were combined by taking rice varieties in variable stagnant flooding stress of 38–62 cm during 2013 and 28–47 cm during 2014.

Septiningsih et al. (2015); suggested that using marker assisted backcrossing (MABC) strategy, new submergence tolerant varieties Ciherang-Sub1 and PSB Rc18-Sub1 were developed in less than 2 years, presenting a promising approach to convert additional popular varieties in the future.

Zhang *et al.*(2015) evaluated a significant positive correlation between the panicle number and nitrogen content; however, no significant correlation was found for phosphorus content; observed with decrease in rice yield of less than 10%, half, 2/3, and complete submergence of the plants can be performed at the tillering stage for 1-3 days; this treatment will increase the space available for rice field water management/control and will improve rainfall resource utilization.

Gautam *et al.*(2016) observed the impact of submergence on survival, chlorophyll, photosynthesis, post-recovery growth and anti-oxidant capacities in four rice cultivars namely IR 64, IR 64-Sub1, Swarna and Swarna-Sub1 having differential response to potassium application, and concluded that Potassium at higher levels was more beneficial in terms of improving survival, photosynthesis and growth after recovery. Potassium at higher levels was more beneficial in terms of improving survival, photosynthesis and growth after recovery between elongation ability of rice cultivars under control condition and under stress condition was also depends on the growth stage and the submergence period.

CHAPTER-3

MATERIALS & METHODS

MATERIALS AND METHODS

The experiment was laid out at Rice Research Station, O.U.A.T., Bhubaneswar during 2015-16 kharif season. This station is located at 20^0 52 minutes north latitude and 82^0 52 minutes east longitude having an altitude 25.9 meter above the mean sea level and nearly 64 km to the west of Bay of Bengal. It falls in the humid and sub-tropical climatic zone of the state. The details of materials used, experimental methods followed and statistical techniques adopted during the course of investigation have been discussed below.

3.1 Experimental material

The experimental material for the present investigation consisted of 50 lowland rice landraces, 3 improved lowland varieties and 3 released high yielding varieties suitable for lowland ecology. The local landraces were collected from different parts of odisha state comprising of 14 districts spread over different agro-climatic zones of the state. These varieties are popular among the rice farmers in rainfed lowland areas. The list of all 56 rice genotypes used in this study are given in Table 1.

3.2 Experimental methods

The experimental material was sown in the mainfield on 6th July, 2015. The experiment was laid out in randomized block design with 56 entries and 2 replications. Each treatment consisted of 3 rows of 3 meter length with a row to row distance of 20 centimeter and plant to plant spacing of 15 centimeter. A fertilizer dose of 60 kg N, 30 kg P_2O_5 and 30 kg K_2O per hectares was applied as per the schedule management practices. The recommended package of practices were followed including need based plant protection measures to raise a normal crop.

Observations were recorded in respect of all metric characters on 5 competitive plants selected randomly from the middle row of each plot, whereas character like days to 50% flowering was recorded on plot basis.

Table 1. List of 56 lowland rice genotypes used in the study

Sl No.	Name of the Genotype	Remarks	Place of collection
1	**Mahipal**	Landrace	Nawapara
2	**Nadiarasi**	Landrace	Koraput
3	**Machakanta**	Landrace	Koraput
4	**Seulapana**	Landrace	Keonjhar
5	**Dhinkiasali**	Landrace	Keonjhar
6	**Kanthakamal**	Landrace	Keonjhar
7	**Ganjamgedi**	Landrace	Cuttack
8	**Dhulia**	Landrace	Balasore
9	**Julpaya**	Landrace	Malkangiri
10	**Nilarpati**	Landrace	Malkangiri
11	**Haladichudi**	Landrace	Kalahandi
12	**Ratanmali**	Landrace	Kalahandi
13	**Badashabhoga**	Landrace	Kalahandi
14	**Juiphoola**	Landrace	Jharsuguda
15	**Karpurakranti**	Landrace	Jharsuguda
16	**Ganjeijata**	Landrace	Angul
17	**Kalachampa**	Landrace	Angul
18	**Baudiachampa**	Landrace	Angul
19	**Ghumusara**	Landrace	Angul
20	**Bagudi**	Landrace	Angul
21	**Baiganmanji**	Landrace	Nayagarh
22	**Mayurakantha**	Landrace	Nayagarh
23	**Kadaliachampa**	Landrace	Nayagarh
24	**Champeisiali**	Landrace	Nayagarh
25	**Landi**	Landrace	Nayagarh
26	**Bhutia**	Landrace	Nayagarh
27	**Ranisaheba**	Landrace	Boud
28	**Kusuma**	Landrace	Boud
29	**Basabhoga**	Landrace	Sambalpur
30	**Jaladubi**	Landrace	Sambalpur
31	**Laxmi**	Landrace	Sambalpur

32	**Sunakathi**	Landrace	Sambalpur
33	**Khandasagar**	Landrace	Sambalpur
34	**Budidhan**	Landrace	Sambalpur
35	**Bagadachinamala**	Landrace	Sambalpur
36	**Ratnachudi**	Landrace	Sambalpur
37	**Jalagudi**	Landrace	Sambalpur
38	**Desijhilli**	Landrace	Sambalpur
39	**Kadalipendi**	Landrace	Sambalpur
40	**Champa**	Landrace	Puri
41	**Bankoi**	Landrace	Puri
42	**Biradiabankoi**	Landrace	Puri
43	**Habira**	Landrace	Puri
44	**Kakudimanji**	Landrace	Puri
45	**Jagabalia**	Landrace	Puri
46	**Dhoiabankoi**	Landrace	Puri
47	**Kalakadamba**	Landrace	Puri
48	**Damodarbhoga**	Landrace	Puri
49	**Gunjimanika**	Landrace	Puri
50	**Madhabi**	Landrace	Puri
51	**T 90**	Improved variety	EB-1, OUAT
52	**T 141**	Improved variety	EB-1, OUAT
53	**T 1242**	Improved variety	EB-1, OUAT
54	**Swarna**	High yielding variety	EB-1, OUAT
55	**Upahar**	High yielding variety	EB-1, OUAT
56	**Mrunalini**	High yielding variety	EB-1, OUAT

3.3 Character studied

Observations were recorded on the following characters during the course of investigation.

1. Days to 50% flowering (DF):

Number of days from sowing to the date on which 50% plants in the plot had started blooming, recorded on plot basis.

2.Plant height (before-after stagnant flooding):

Height from the base of the plant to the tip of the tallest tiller measured in centimetre.

2. Final Plant Height (PH):

Height from the base of plant to the tip of top most (tallest) panicle measured in centimetre recorded at maturity before and after flooding and also the final plant height at harvesting.

4.Tillers per plant(before and after stagnant flooding)

It was recorded as the number of tillers before and after flooding in each plot recorded on five competitive plants at the time of maturity.

3. Effective tillers per plant (EBT):

It was recorded as the number of ear bearing tillers in each plant recorded on five competitive plants at the time of maturity.

5. Panicle Length (PL):

Length of the panicle from the ciliate base to the tip of the panicle of the main culm measured in centimetre at the time of maturity.

6. Fertile grains per panicle (FGP):

It was recorded as the average number of fertile grains counted from the panicles of the main culm of five sample of the plants.

7. Grain fertility percentage (GF%):

It was computed as the ratio of number of fertile spikelets to total number of spikelets per panicle expressed in percentage and this was averaged over five sample of the panicles.

8. 100-grain weight (GW):

It was recorded as weight of well developed 100- grains taken at random from the panicles of each plant at about 14% grain moisture level and expressed in grams (g).

9. Grain yield per plant (GYP):

It was recorded as the weight of the grains from each plant after threshing, cleaning and 3 sundrying and measured in grams.

10. Harvest Index (HI):

It was deduced by taking the ratio of the economic yield (grain yield) to the total biological yield and was expressed in percentage.

11.Carbohydrate content before and after staganant flooding(CHO)

It was determined by taking sample of 5 plants per plot of before and after flooding in laboratory by Yosidha's method.

3.4 Statistical Analysis:

The data recorded were subjected to following statistical analysis based on sample mean of the various characters under observation.

3.4.1Analysis of variance:

The analysis of variance was carried out separately for each trait following the procedures of randomized block design analysis (Panse and Shukhatme, 1954). The analysis of variance was done on the basis of the following model:

$Yij= M+g_i+r_j+e_{ij}$

Where,

Y_{ij}= phenotypic observation of the ith genotype in jth replication

M=general mean

g_i= effect of the ith genotype

r_j= effet of the jth replication

e_{ij}= random error associated with ith genotype and jth replication.

The structure of analysis of variance is as follows:

ANOVA for RBD with expectation of mean sum of squares(EMS)

Source of variation	**Degree of freedom(d.f.)**	**Mean sum of square(MS)**	**Expected mean sum of square (EMS)**	**F-value**
Replication	(r-1)	M_r	$\sigma_e^2+g\sigma_r^2$	M_r/M_e
Genotypes	(g-1)	M_g	$\sigma_e^2+r\sigma_g^2$	M_g/M_e
Error	(r-1)(g-1)	M_e	σ_e^2	
Total	(rg-1)			

Where,

r = number of replication,

g = number of genotypes

M_r, M_g,, M_e stand for mean sum of squares due to replication, genotype, and error respectively.

Estimation of genetic parameters from ANOVA :

The phenotypic, genotypic and environmental variance components for different characters were estimated from the mean square in ANOVA according to A1-Jibouri *et al.* (1958) as follows:

From the structure of analysis of variance

Environmental variance $= \sigma_e^2 = M_e$

Genotypic variance $= \sigma_g^2 = (M_g - M_e) / r$

Phenotypic variance $= \sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where Mg and Me are mean sum of squares due to genotype and error, respectively, and 'r' is the number of replication.

3.4.2 Estimation of mean, range, standard error and critical differences:

Mean value of each character was worked out by dividing the total by the corresponding number of observations. The lowest and the highest values for each character was taken as the range. Standard error of mean (SEm) = √(EMS / r).

The test of significance of difference between means of two lines (genotypes) was done by using critical difference (CD at 5%) which was calculated as follows:

Critical difference (CD)= √(2EMS / r) × 't' value at error degree of freedom at 5% level of

significance

Where, r = number of replications,

EMS= error mean sum of square.

3.4.3 Coefficient of Variation(CV):

The coefficient of variation is a basis for comparing the extent of variation between different characters measured on different scales.

$$C.V = \frac{S.D.(\sigma)}{Mean\ (\bar{x})} \times 100$$

Where, S.D = Standard deviation

$\bar{x}$= General mean of the character

The phenotypic, genotypic and environmental coefficients of variation for different characters were estimated as follows:

Phenotypic coefficient of variation (PCV) = $\frac{\sigma p}{\bar{X}} \times 100$

Genotypic coefficient of variation (GCV) = $\frac{\sigma g}{\bar{X}} \times 100$

Environmental coefficient variance (ECV) = $\frac{\sigma_e}{\bar{x}} \times 100$

Where σp & σg are square root of phenotypic, genotypic and environmental variance, respectively and $\bar{x}$ is grand mean for the character.

3.4.4 Heritability (broad sense):

Heritability (h^2) estimate was worked out by using the formula suggested by Lush (1949) and Burton and de Vane (1953)

$$h^2_{(bs)} = \frac{Genotypic\ Variance(\sigma_g^2\ )}{Phenotypic\ Variance(\ \sigma_p^2\ )} \times 100$$

3.4.5 Expected genetic advances:

Genetic advance or genetic gain as a result of selection at 5% intensity among genotypes for different characters was estimated as per the formula suggested by Johnson, Robinson and Comstock (1955).

$GA = K \times h^2 \times \sigma_p$

Where, K= Standarized selection differential which is 2.06 for 5% selection intensity

h^2= heritability in broad sense

σ_p= Phenotypic standard deviation.

GA expressed as percentage of mean = $\frac{\text{GA}}{\text{Mean}} \times 100$

3.4.6 Analysis of covariance:

The analysis of covariance between all possible pairs of characters was done on the mean values following the procedure of randomized block design analysis (Panse and Sukhatme, 1954). The structure of analysis of covariance is as follows.

Analysis of covariance (ANCOVA) in RBD with expectations of mean sum of products (MSP)

Source	d.f.	MSP	Expected MSP
Replication	(r-1)	MSP_r	$\sigma_{e(xy)}+g\sigma_{r(xy)}$
Genotypes	(g-1)	MSP_g	$\sigma_{e(xy)}+r\sigma_{g(xy)}$
Error	(r-1)(g-1)	MSP_e	$\sigma_{e(xy)}$

Where,

r = number of replication
g = number of genotypes

MSP_r, MSP_g, MSP_e stand for mean sum of products between pairs of characters due to replication, genotype and error, respectively. From the structure of analysis of covariance the following estimates were computed.

Error covariance = $\sigma_{e\,(xy)} = MSP_e$
Genotypic covariance = $\sigma_{e\,(xy)} = (MSP_g - MSP_e)/r$
Phenotypic covariance = $\sigma_{p(xy)} = \sigma_{g(xy)} + \sigma_{e(xy)}$

3.4.7 Estimation of correlation coefficients:

Using the covariance components as described in 3.4.6 the genotypic and the phenotypic and environmental correlations between pairs of characters were computed adopting the following formula as given by AL- Jibouri et al (1958) .

Genotypic correlation (r_g) = $\frac{\sigma_{g(xy)}}{\sigma_{g(x)}\,\sigma_{g(y)}}$

Where $\sigma^2_{g(xy)}$ is the genotypic covariance between x and y and $\sigma^2_{g(x)}$ and $\sigma^2_{g(y)}$ are the genotypic standard deviation for the characters x and y, respectively.

Phenotypic correlation (r_p) = $\frac{\sigma_{p(xy)}}{\sigma_{p(x)}\,\sigma_{p(y)}}$

Where $\sigma^2_{p(xy)}$ were phenotypic covariance between x and y and $\sigma_{p(x)}$ and $\sigma_{p(y)}$ are phenotypic standard deviation of x and y, respectively.

$$\text{Environmental correlation } (r_e) = \frac{\sigma_{e(xy)}}{\sigma_{e(x)}\,\sigma_{e(y)}}$$

Where $\sigma_{e(xy)}$ is the environmental covariance.

Significance of correlation of co-efficient was tested by t- test with (n-2) degrees of freedom by the formula.

$$t = \frac{r}{\sqrt{(1-r^2)/(n-2)}}$$

Where, ‘r’ is the correlation coefficient, and ‘n’ is the number of genotypes and ‘t’ is the table ‘t’ value at (n-2) d.f. may be at 5% or at 1% level of significance.

3.4.8 Path Coefficient Analysis:

The path coefficient analysis is a type of cause and effect relationship among the various correlated characters. Path coefficient are standardized partial regression coefficients, which individually provide a measure of the direct effect of the casual factor on the effect variable. These permit partitioning of the correlation between a casual factor and the effect variable into components of direct and indirect effects, and thus give a better picture of the associations of the casual factors with the effect variable.

In the present investigation, grain yield per plant was taken as the ‘effect’ with other characters related to yield as the casual factors.

The path coefficients were obtained by solving the following simultaneous equations, which give the basic relationship between correlation and path coefficients in a system of correlated causes. (Wright, 1921; Dewey and Lu, 1959).

$$r_{1.12} = P_{1.12}+r_{1.2}P_{2.12}+ r_{1.3}P_{3.12}+\ldots\ldots\ldots\ldots\ldots\ldots+ r_{1.11}P_{11.12}$$

$$r_{2.12} = r_{2.1}P_{1.12}+r_{2.2}P_{2.12}+ r_{2.3}P_{3.12} +\ldots\ldots\ldots\ldots\ldots\ldots+ r_{2.11}P_{11.12}$$

....

$$r_{11.12} = r_{11.1}P_{1.12}+ r_{11.2}P_{2.12}+ r_{11.3}P_{3.12}+\ldots\ldots\ldots\ldots+P_{11.12}$$

Where,

r_{ij} is the correlation coefficient between i^{th} and j^{th} character and $p_{i,12}$ is the path coefficient (direct effect) of i^{th} character on yield (15^{th} character).

The solutions for path coefficients, direct and indirect effects of the casual factors were estimated as the value of the individual terms of above equation in the R.H.S.

The coefficient of determination (R^2) and residual effect ($P_{11}.R$) were calculated as follows.

$1=P^2_{11}.R_{1.} + P_{iy}.r_{iy}$

$R^2 = \sum P_{iy}\, r_{iy}$

$PR_{11} = \sqrt{1-\sum p_{iy}\, r_{iy}}$

$= \sqrt{1-(p_{1.11+})}$

Hence, $PR_{11} = \sqrt{1-R^2}$

The path analysis at the phenotypic level with the same cause and effect relationship was computed using the phenotypic correlation as stated earlier.

3.3.9 Analysis of genetic diversity among genotypes:

Genetic divergence analysis with regard to thirteen quantitative traits among 56 lowland rice genotypes was done by the following methods:

- D^2 analysis of genetic divergence.

D^2 analysis of genetic divergence:

Thirteen morpho-metric observations were recorded in five consecutive plants in each entry and replications and the mean value of 56 entries were used for the analysis of genetic divergence using Mahalonobis's D^2 statistics.

Mahalonobis's D^2 statistics (Rao, 1952) was used for estimation of genetic divergence among the 56 genotypes of lowland rice for thirteen characters. Genetic divergence (D^2) between any two genotype is given by the formula:

$$D^2_p = \sum_{i=1}^{p} \sum_{j=1}^{p} w_{ij}\, d_i\, d_j$$

Where, w_{ij} is the inverse of the common dispersion matrix (w_{ij}), d_i and d_j are the difference in the means of the 2 genotypes for ith and jth characters.

The computations of D^2 using the formula is complicated and laborious when more number of mutually correlated character is involved in the divergence analysis. So the character means were transformed into set of uncorrelated variable using pivotal condensation of common dispersion matrix following Rao (1952). After this transformation, the formula for genetic divergence becomes:

$$D^2_p = \sum_{i=1}^{p} d_i^2$$

Where d_i is the difference between the transformed means of any two genotypes for the ith character. All possible D^2 among the 56 genotypes were computed, the relative contribution of individual characters to divergence was assessed by (a) ranking of components D^2 as well as (b) percentage contribution to total D^2 over all combinations.

(a) Rank average: In all the D^2 combination, the characters were combinations, the characters were ranked 1 to 13 on the basis of their contribution to the D^2. Then ranks of each character are summed over all the D^2 combinations to get rank total and then rank average is estimated.

(b) Average D^2: Average contribution of each character to all the D^2 combinations is worked out.

Grouping of genotypes into different clusters

Tocher's method: Usually a cluster is defined as a group of genotypes of varieties of lines such that any two genotypes belonging to the same cluster, on an average, show a smaller D^2 than those belonging to the different clusters. A simple device suggested by Tocher (Rao, 1952) for construction of clusters is to start with two most closely related genotypes (having the smallest D^2) from the first two and so on. At certain stage when it is felt that after adding a particular population, there is a disrupt increase in the average D^2, this population is not added to the cluster. Similarly, construction of 2nd and 3rd and other clusters are formed till all the genotypes are included in one or the other cluster. Singh and Choudhari (1977) suggested a method for determining cut off value for addition of a genotype/population to a cluster. In that the D^2 values of each genotype with all others are to be arranged from lowest to highest value in matrix form.

The highest value of the lowest column is taken as cut off value for deciding on inclusion a genotype in the cluster. After construction of clusters, average intra-cluster and inter-cluster D^2 value were estimated.

3.4.10 Construction of selection indices:

Application of discriminate functions as a basis for making selection of several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. The selection index for different character combination were constructed considering grain yield per plant as the ultimate criterion. The indices were of the following form

$$l_x = b_1 x_1 + b_2 x_2 + b_3 x_3 + \dots\dots + b_n x_n$$

Where

x_s = character mean of particular genotype included in the index

b_s= relative weights to be assigned to the characters in computing the single index value l_x for each genotype on which the selection is based

The b value which would maximize the expected genetic advance in yield from index selection were obtained by solving the following simultaneous equation as suggested by Smith (1936) and Hazel (1943).

$$b_1p_{1.1} + b_2p_{1.2} + b_3p_{1.3} + \dots\dots + b_np_{1.n} = G_1y$$

$$b_1p_{2.1} + b_2p_{2.2} + b_3p_{2.3} + \dots\dots + b_np_{2.n} = G_2y$$

$$b_1p_{3.1} + b_2p_{3.2} + b_3p_{3.3} + \dots\dots + b_np_{3.n} = G_3y$$

$$\dots\dots\dots\dots\dots\dots\dots\dots$$

$$\dots\dots\dots\dots\dots\dots\dots\dots$$

$$b_1p_{n.1} + b_2p_{n.2} + b_3p_{n.3} + \dots\dots + b_np_{n.n} = G_ny$$

Where,

P = phenotypic variance/covariance

G = genotypic covariance between a particular character and grain yield

3.4.11 Character combination and group of indices

Since grain yield is a complex trait, controlled by non-additive gene action and is believed to have low heritability, hence direct selection for grain yield *per se* is often not reliable and effective. Further integer-genotypic competition and a large experimental error associated with yield measurements often bias the outcome for selection of higher yield. Therefore several workers in different crop plants have emphasized the importance of indirect selection for yield through the use of component traits governed by genes with strong correlation on grain yield. As no single trait can be taken as adequate criterion of selection for yield, therefore selection indices provide a useful method by making use of several correlated characters for greater efficiency of selection in yield. During the present investigation selection indices were constructed with grain yield per plant as the economic criterion and twelve different characters, days to 50% flowering, final plant height, tillers before flooding, tillers after flooding, effective tillers per plant, panicle length, fertile grains per panicle, grain fertility percentage, 100-grain weight, harvest index, carbohydrate content before flooding, carbohydrate content after flooding were chosen for the construction of thirteen selection indices. The thirteen character index including all the thirteen traits was used for the selection of genotypes. The genotypes which occupied better rankings in the above selection indices were selected for their future use. The following thirteen characters namely grain yield per plant (x_1), days to 50% flowering (x_2), final plant height (x_3), tillers before flooding (x_4), tillers after flooding (x_5), effective tillers per plant (x_6), panicle length (x_7), fertile grains per panicle (x_8), grain fertility percentage (x_9), 100-grain weight (x_{10}), harvest index (x_{11}), carbohydrate content before flooding (x_{12}), carbohydrate content after flooding(x_{13}), were chosen on the basis of heritability and phenotypic correlation for the construction of thirteen selection indices. The number of characters in the combination one after the other such that the indices varies from single character to a complete thirteen character index.

3.4.12 Genetic advance and relative efficiency in indices

The expected genetic advance from selection indices was computed on the basis of model suggested by Smith (1936) in the following manner

$$GA = K\sqrt{\sum b.\ G_{iy}} \quad \text{(in general)}$$

$$GA = K\sqrt{b_1\ G_{1y} + b_2\ G_{2y} + b_3\ G_{3y} + \cdots \ldots\ldots\ldots\ldots\ldots\ldots\ldots + b_n\ G_{ny}}$$

(in particular)

Where,

K= standardized selection differential which takes the value of 2.06 to 5% selection intensity

G_{iy}= genotypic covariance between i^{th} character and yield.

b_i= index value of the i^{th} character.

The relative efficiency of an index was estimated as the ratio of the expected genetic advance from index selection to that form direct selection on the basis of yield and was expressed in percentage.

3.4.13 Criteria of selection

On the basis of genetic advance values the selection indices including grain yield per plant as single character and combination of all the thirteen characters were used for the selection of genotypes from the present set of material. Those cultures which occupies better rankings in the complete thirteen character index were selected during the course of the present investigation for their future use.

3.5 Estimation of Carbohydrate of plant:

Carbohydrate content of plant samples was determined by following procedure (Yosidha et al.,2005). 100 mg of powdered dry sample was taken and extracted using 80 % ethanol (v/v). The extract was then used for sugar analysis by adding anthrone reagent, followed by measurement of absorbance at 630nm using a spectrophotometer. In case of simple carbohydrate estimation the sample was kept in a boiling tube and hydrolyzed by keeping in a boiling water for three hours with 5 ml of 2.5N HCl and then cooled to room temperature. The sample was neutralized with sodium carbonate till the effervescence ceases and transferred it to 100 ml volumetric flask and the volume was made up to 100 ml. 10 ml of this was taken in a centrifuge tube and was centrifuged for 10 minutes. The supernatant was collected and 0.2 to 0.3 aliquats were taken for analysis. 12 ml of anthrone reagent was added and heated for eight minutes in a boiling water bath. Then the content was cooled and absorbance (OD) of the content was recorded at 630 nm. The quantity of glucose was calculated from the standard curve prepared from glucose stock solution.

Amount of carbohydrate present in 100 mg of sample = (mg of sugar from graph/ml of aliquot sample) x (Total volume of extract in ml of sample in mg) x 100

CHAPTER-4

RESULTS

RESULTS

The present investigation was undertaken to evaluate the extent of variability available in a collection of 50 lowland rice landraces of Odisha along with 3 improved and 3 high yielding rice genotypes. The test entries were grown in rainfed lowland situation during kharif 2015. Different morphological and yield attributing traits of 56 genotypes were examined to study the variability in yield and yield contributing characters, nature and magnitude of character association among yield and other yield attributing traits, direct and indirect effects of different component traits on yield through path analysis and genetic divergence among the genotypes. The experimental findings has been presented under the following heads:

i) Study of variability
ii) Character association
iii) Path coefficient analysis
iv) D^2 analysis
v) Selection indices

4.1 Study of variability

The genetic variability in respect of a trait present in a population indicates as to how far the character could be manipulated in a desired direction. So it is necessary to carry out analysis of variance for various traits to study the genetic variability. In the present study analysis of variance along with other simple parameters like mean, range, phenotypic co-efficient of variation, heritability and genetic advance were used to study the variability among the test genotypes.

4.1.1 Analysis of variance

The analysis of variance in respect of 15 different characters are presented in Table 2. From the analysis of variance it was observed that there existed a highly significant difference among the test genotypes for the characters namely days to 50% flowering, plant height before and after flooding, final plant height, effective tillers/plant, panicle length, number of fertile grains/panicle, grain fertility %, harvest index, carbohydrate content after flooding and grain yield/plant. The magnitude of genetic variance of replication was high for days to 50% flowering, plant height before and after flooding and for the rest characters block effect is not significant.

Table 2. Analysis of variance of 15 characters (mean sum of squares) for 56 lowland rice genotypes

Sl No.	Character	Source of variation(df)		
		Replication(1)	Genotype(55)	Error(55)
1	Days to 50% flowering	25.179**	21.300**	3.347
2	Plant height before flooding(cm)	74.683**	198.872**	34.854
3	Plant height after flooding(cm)	301.500**	526.032**	35.091
4	Final plant height(cm)	0.179	539.991**	27.274
5	Tillers/plant before flooding(No.)	2.116	0.980	0.117
6	Tillers/plant after flooding(No.)	3.968	1.166	0.131
7	Effective tillers/plant(No.)	0.014	2.015**	0.228
8	Panicle length(cm)	0.556	14.181**	3.727
9	Fertile grains/panicle(No.)	2.063	1139.578**	163.533
10	Grain fertility%	0.973	175.391**	15.232
11	100 -grain weight(g)	0.016	0.401	0.022
12	Harvest index(%)	1.624	58.953**	2.266
13	Carbohydrate content before flooding(%)	0.006	1.004	0.037
14	Carbohydrate content after flooding(%)	0.003	1.599*	0.004
15	Grain yield/plant(g)	0.486	9.210**	0.425

4.1.2 Mean performance of the genotypes

The magnitude of variability in respect of range and mean for 9 characters are presented in Table 3 and 4. The data on mean and range indicated considerable amount of variability for majority of the characters under study.

Days to 50% flowering

The overall mean was 108.36 days with a range of variation 102.00 days to 121.00 days. Ratnachudi and Kadalipendi was the earliest landrace with 102.00 days to 50% flowering while the high yielding variety Upahar was the late maturing one with 121.00 days to 50% flowering.

Final plant height

Almost all the local landraces were intermediate to tall so far plant height was concerned, but the high yielding genotypes were semi dwarf in nature. The lowest height of 99.88cm was recorded in the high yielding variety Swarna where as the landrace Jalagudi was found to be the tallest one with 173.99 cm height. The mean height of the test genotypes at maturity was 147.98 cm.

Effective tillers per plant

The range of variability for number of effective tillers per plant among the test genotypes was 1.87 to 7.14 with an overall mean of 3.31. Among the genotypes Budidhan had the lowest number of effective tillers per plant and the highest number was present in case of Swarna.

Panicle length

The observed range of variability for panicle length in the present study was 21.15 cm (Mrunalini) to 36.15 cm (Kalakadamba) with overall mean of all the genotypes was 26.17 cm. The high yielding genotypes were having intermediate panicle length (21.50cm-27.65cm)

Fertiles grains/panicle

The lowest number of fertile grains per panicle was 40.94 in case of Budidhan and the highest number of fertile grains was recorded in case of Badashabhoga (157.28) with a mean number of 95.87.

Table 3.Mean performance of 56 lowland rice genotypes with respect to nine characters

Sl No.	Name of the Genotype	DF	FPH	EBT	PL	FGP	F%	GW	HI %	GYP
1	**Mahipal**	108.50	147.17	2.73	26.47	69.81	73.01	2.82	23.16	4.52
2	**Nadiarasi**	109.00	157.14	4.53	29.82	89.72	82.55	2.21	27.54	8.69
3	**Machakanta**	108.75	158.96	3.14	26.40	110.04	81.02	1.65	28.11	5.91
4	**Seulapana**	108.00	147.25	3.58	32.22	104.59	81.96	2.27	34.77	7.24
5	**Dhinkiasali**	106.00	162.46	3.90	25.23	96.27	82.63	2.34	27.12	7.78
6	**Kanthakamal**	110.00	161.26	2.85	26.57	97.08	62.30	2.37	24.38	5.90
7	**Ganjamgedi**	108.00	120.98	4.17	23.82	130.10	86.61	2.11	29.27	9.51
8	**Dhulia**	106.00	154.09	3.49	26.90	85.12	78.88	2.36	34.84	6.18
9	**Julpaya**	104.00	165.27	2.90	27.57	120.17	72.71	1.86	27.30	4.89
10	**Nilarpati**	106.00	143.99	4.46	25.82	107.46	78.11	2.77	32.78	7.78
11	**Haladichudi**	104.00	114.96	4.31	24.90	97.43	74.87	2.23	31.44	8.01
12	**Ratanmali**	107.25	145.74	3.17	27.90	87.77	80.13	1.93	28.49	5.24
13	**Badashabhoga**	110.00	137.15	3.40	28.98	**157.28**	69.58	**1.13**	28.03	5.73
14	**Juiphoola**	108.00	163.15	2.35	25.48	113.08	72.91	1.27	14.61	3.57
15	**Karpurakranti**	104.00	173.24	2.55	29.48	117.62	89.89	1.29	31.97	4.12
16	**Ganjeijata**	107.25	164.38	2.58	25.73	152.94	**90.27**	1.65	28.27	5.07
17	**Kalachampa**	113.00	152.33	3.50	22.07	77.06	89.54	2.45	26.49	5.45

18	Baudiachampa	109.00	159.16	2.72	24.73	89.13	72.46	2.55	27.71	4.40
19	Ghumusara	108.00	154.27	4.09	24.23	67.38	73.35	2.45	23.49	5.29
20	Bagudi	109.50	146.65	2.69	25.23	109.57	73.95	2.17	32.47	4.24
21	Baiganmanji	104.50	147.48	2.85	24.15	131.23	82.54	1.81	21.49	4.26
22	Mayurakantha	106.25	166.17	2.50	26.57	60.39	58.83	2.50	27.42	3.71
23	Kadaliachampa	110.00	148.84	2.23	26.07	92.79	78.85	2.45	20.49	4.21
24	Champeisiali	108.50	161.94	2.76	28.07	73.94	72.19	2.85	27.49	4.98
25	Landi	107.00	157.03	3.08	23.73	65.59	69.03	2.24	28.49	4.29
26	Bhutia	110.00	161.66	3.57	29.40	81.59	60.03	2.23	32.20	5.49
27	Ranisaheba	107.25	156.58	3.36	24.90	153.62	83.48	1.23	27.49	5.28
28	Kusuma	107.00	160.04	3.06	26.57	78.80	67.08	2.28	24.55	5.07
29	Basabhoga	104.00	146.58	2.67	24.32	108.79	78.37	1.70	24.49	4.27
30	Jaladubi	107.00	159.23	2.25	27.23	72.01	85.59	2.94	25.76	4.22
31	Laxmi	110.00	148.04	2.84	28.40	102.96	57.70	1.69	24.49	4.83
32	Sunakathi	107.25	156.26	3.15	27.23	118.59	76.90	1.61	26.63	3.34
33	Khandasagar	110.00	149.91	3.06	27.23	93.92	82.83	2.27	**8.78**	4.75
34	Budidhan	107.00	160.42	**1.87**	24.48	**40.94**	**33.18**	2.56	32.05	2.33
35	Bagdachinamla	108.00	142.25	2.13	24.73	90.80	79.78	2.10	24.32	3.97
36	Ratnachudi	**102.00**	142.86	2.09	26.90	93.63	82.63	2.50	28.49	4.39
37	Jalagudi	111.00	**173.99**	3.28	27.82	96.81	79.63	2.24	30.70	6.43
38	Desijhilli	108.00	156.70	2.95	26.07	99.81	68.78	2.08	33.50	5.78
39	Kadalipendi	**102.00**	147.58	3.67	24.32	125.50	85.73	1.97	29.49	8.68

40	**Champa**	107.00	154.86	2.76	22.32	107.90	69.33	2.41	31.46	6.10
41	**Bankoi**	107.25	146.64	4.34	25.48	82.27	78.08	2.55	24.49	8.45
42	**Biradiabankoi**	107.25	140.55	2.21	28.65	92.02	74.50	2.88	27.50	5.37
43	**Habira**	107.00	137.93	2.56	25.65	81.44	71.65	2.58	26.49	4.99
44	**Kakudimanji**	105.25	145.65	4.57	23.65	63.61	70.71	2.23	33.22	6.40
45	**Jagabalia**	111.00	153.23	3.89	25.15	76.10	73.46	2.52	31.94	5.54
46	**Dhoiabankoi**	109.00	151.79	2.61	24.77	82.60	73.40	2.83	29.38	4.72
47	**Kalakadamba**	111.50	152.37	2.49	**36.15**	86.62	82.55	**3.04**	28.49	4.77
48	**Damodarbhoga**	109.50	136.70	2.91	24.52	97.28	83.45	2.45	26.29	5.07
49	**Gunjimanika**	112.25	160.76	2.99	29.40	114.44	78.80	2.08	26.43	5.37
50	**Madhabi**	109.00	148.07	3.85	30.02	104.18	81.05	2.21	13.49	7.45
51	**T 90**	114.25	138.86	2.15	27.65	55.13	78.65	1.37	39.18	**1.94**
52	**T 141**	109.25	123.11	5.39	21.52	80.21	81.85	2.14	**39.49**	9.06
53	**T 1242**	108.25	109.90	4.63	24.40	84.22	80.65	2.53	30.24	9.63
54	**Swarna**	115.25	**99.88**	**7.14**	21.40	70.10	74.37	1.88	27.49	9.11
55	**Upahar**	**121.00**	106.97	5.23	25.90	115.32	79.68	2.15	31.19	**12.35**
56	**Mrunalini**	114.50	105.98	5.35	**21.15**	113.96	80.24	2.03	35.49	12.16
	Grand mean	108.36	147.98	3.31	26.17	95.87	76.11	2.19	27.90	5.86

Table 4. Range & mean for nine characters of 56 lowland rice genotypes

Sl No.	Characters	Range	Mean
1	Days to 50% flowering	102.00-121.00	108.36
2	Final plant height(cm)	99.88-173.99	147.98
3	Effective tillers/plant(No.)	1.87-7.14	3.31
4	Panicle length(cm)	21.15-36.15	26.17
5	Fertile grains/panicle(No.)	40.94-157.28	95.87
6	Grain fertility%	33.18-90.27	76.11
7	100 -grain weight(g)	1.13-3.04	2.19
8	Harvest index	8.78-39.49	27.90
9	Grain yield/plant(g)	1.94-12.35	5.86

Grain fertility%

The overall mean of fertility % was 76.11 and the range was from 33.18 in Budidhan to 90.27 in Ganjeijata.

100-grain weight

The range of variability for 100-grain weight among the test genotypes were observed between 1.13 gm and 3.04 gm with overall mean 2.19 gm. Among the genotypes low grain weight was recorded in case of Badashabhoga (1.13 gm) and where as high grain weight was observed in Kalakadamba (3.04 gm).

Harvest index

The magnitude of variability for harvest index ranged from 8.78 to 39.49 with an overall mean of 27.90. Among the test entries Khandsagar was having low harvest index where as T 141 was having high harvest index. The mean harvest index per plant among the test genotypes was 27.90.

Grain yield per plant

The overall mean grain yield per plant was 5.86 gm with a range of 1.94 to 12.35 gm. Among the genotypes the low yielders were T 90 (1.94 gm),Budidhan (2.33 gm) ,Bagdachinamala (3.97 gm) where as high yield was obtained from Upahar(12.35 gm) and Mrunalini(12.16gm).

4.1.3 Comparison of characters before and after stagnant flooding

Characters like plant height, tillers/plant and the physiological characters i.e. carbohydrate content were recorded critically before and after stagnant flooding and the result is presented in table 5 and 6. The mean plant height before flooding was 64.56cm which reached to 137.04 cm after the receding of standing water. On the other hand the iller number/plant decreased after the receding of standing water. The mean tiller number efore flooding was 6.43 which came down to 6.08 after flooding. Similarly the hysiological character i.e. carbohydrate content of the plants showed tremendous eduction from 3.16%-0.76% after receding of stagnant water.

Plant height before flooding

The lowest height of 38.43 cm was recorded in the local landrace Haladichudi where as the landrace Jalagudi was found to be the tallest one with 83.79 cm height before stagnant flooding. The mean height of the test genotypes before stagnant flooding was 64.56 cm.

Plant height after flooding

The lowest height of 89.07cm was recorded in the high yielding variety Swarna where as the landrace Karpurakranti was found to be the tallest one with 162.93 cm height after stagnant flooding. The mean height of the test genotypes after stagnant flooding was 137.04 cm.

Tillers per plant before flooding

The range of variability for number of tillers per plant before stagnant flooding among the test genotypes was 4.65 to 7.85 with an overall mean of 6.43. Among the genotypes, Dhulia had the lowest number of effective tillers per plant and the highest number was present in case of T90.

Tillers per plant after flooding

The range of variability for number of tillers per plant before stagnant flooding among the test genotypes was 4.26 to 7.93 with an overall mean of 6.08. Among the genotypes, Dhulia had the lowest number of effective tillers per plant and the highest number was present in case of T1242.

Carbohydrate content before flooding

The range of variability for carbohydrate content in percentage before stagnant flooding among the test genotypes were observed between 2.20% and 4.90% with overall mean 3.16%. Among the genotypes low carbohydrate content was recorded in case of Baudiachampa(2.20%) and where as high carbohydrate content was observed in T1242 (4.90%).

Carbohydrate content after flooding

The range of variability for carbohydrate content in percentage before stagnant flooding among the test genotypes were observed between 0.11% and 3.49% with overall mean 0.76%. Among the genotypes low carbohydrate content was recorded in case of T90 (0.11%) and where as high carbohydrate content was observed in Swarna (3.49%).

Table 5.Comparison of mean performance of 56 lowland rice genotypes for three characters before and after flooding

Sl No.	Name of the Genotype	PHBF	PHAF	TBF	TAF	CHOBF	CHOAF
1	Mahipal	61.69	137.36	6.30	5.89	2.83	0.16
2	Nadiarasi	67.59	144.18	6.95	6.56	2.79	1.14
3	Machakanta	70.62	149.92	7.15	6.76	3.01	0.29
4	Seulapana	58.57	135.08	6.15	5.74	3.34	1.15
5	Dhinkiasali	70.71	151.36	6.35	5.96	2.73	1.23
6	Kanthakamal	76.36	151.96	5.85	5.48	2.92	0.49
7	Ganjamgedi	43.17	111.67	6.05	5.64	3.41	1.23
8	Dhulia	69.85	144.95	**4.65**	**4.26**	3.18	0.38
9	Julpaya	74.32	154.22	6.10	5.73	3.51	0.19
10	Nilarpati	61.68	134.71	5.20	4.79	3.63	1.10
11	Haladichudi	**38.43**	104.75	5.75	5.36	3.38	1.23
12	Ratanmali	58.42	134.44	7.60	7.20	2.89	0.28
13	Badashabhoga	52.85	125.94	7.70	7.31	3.32	0.35
14	Juiphoola	73.20	152.40	5.90	5.53	3.26	0.19
15	Karpurakranti	77.66	**162.93**	7.55	7.16	3.17	0.31
16	Ganjeijata	77.66	153.57	7.00	6.56	3.16	0.48
17	Kalachampa	68.74	141.53	6.75	6.36	3.10	0.12
18	Baudiachampa	72.40	148.35	5.75	5.37	**2.20**	0.19
19	Ghumusara	70.38	143.47	7.00	6.58	2.66	0.24
20	Bagudi	62.75	135.84	5.85	5.46	3.04	0.14
21	Baiganmanji	65.67	137.91	6.40	6.01	3.23	0.23
22	Mayurakantha	74.75	152.55	5.25	4.84	2.49	0.17
23	Kadaliachampa	78.98	135.79	6.70	6.31	2.37	0.16
24	Champeisiali	74.76	151.77	6.30	5.91	3.18	0.26
25	Landi	67.20	145.94	6.85	6.43	2.77	0.24
26	Bhutia	73.56	151.25	6.95	6.56	2.79	0.30
27	Ranisaheba	69.13	144.85	6.95	6.56	3.13	0.33
28	Kusuma	73.77	147.55	6.95	6.55	3.09	0.23
29	Basabhoga	60.11	136.29	6.30	5.91	3.33	0.17
30	Jaladubi	71.21	147.49	5.65	5.26	2.93	0.20
31	Laxmi	64.73	138.50	6.75	6.34	2.59	0.39
32	Sunakathi	70.67	145.44	6.20	5.81	2.83	0.18
33	Khandasagar	65.09	139.60	7.00	6.61	2.63	0.24
34	Budidhan	72.63	148.02	6.70	6.31	3.17	0.12
35	Bagdachinamla	58.36	132.26	7.10	6.71	2.39	0.19
36	Ratnachudi	58.23	131.95	6.40	6.01	2.30	0.17
37	Jalagudi	**83.79**	161.18	7.05	6.66	3.65	0.64
38	Desijhilli	69.26	147.03	6.75	6.36	2.52	0.38
39	Kadalipendi	64.54	137.64	6.15	5.76	3.19	2.17
40	Champa	70.58	144.91	6.10	5.71	3.21	1.25
41	Bankoi	59.86	135.51	6.50	6.11	2.24	1.59
42	Biradiabankoi	56.15	129.24	6.40	6.01	2.35	0.17

43	**Habira**	54.14	126.66	5.45	5.05	4.43	0.22
44	**Kakudimanji**	61.79	134.43	6.40	6.01	3.28	1.27
45	**Jagabalia**	69.38	142.01	5.75	5.36	3.15	0.93
46	**Dhoiabankoi**	63.03	136.12	4.85	4.46	3.53	1.97
47	**Kalakadamba**	68.42	141.56	6.75	6.36	2.59	0.32
48	**Damodarbhoga**	54.51	127.61	5.70	5.31	2.75	0.43
49	**Gunjimanika**	73.52	146.61	5.95	5.54	2.41	0.17
50	**Madhabi**	64.74	137.83	5.35	4.96	2.43	1.34
51	**T 90**	55.57	128.66	**7.85**	7.46	4.57	**0.11**
52	**T 141**	52.76	112.30	6.85	7.05	4.88	3.01
53	**T 1242**	50.81	99.09	7.15	**7.93**	**4.90**	3.21
54	**Swarna**	43.60	**89.07**	7.00	7.04	4.82	**3.49**
55	**Upahar**	44.87	96.16	7.00	6.78	4.87	3.11
56	**Mrunalini**	48.09	95.17	6.85	6.84	4.78	2.71
	Grand mean	64.56	137.04	6.43	6.08	3.16	0.76

Table 6. Range and Mean of 56 lowland rice genotypes for three characters before and after flooding

Sl No.	Characters	Range	Mean
1	**Plant height before flooding(cm)**	**38.43-83.79**	**64.56**
2	**Plant height after flooding(cm)**	**89.07-162.93**	**137.04**
3	**Tillers/plant before flooding(No.)**	**4.65-7.85**	**6.43**
4	**Tillers/plant after flooding(No.)**	**4.26-7.93**	**6.08**
5	**Carbohydrate content before flooding(%)**	**2.20-4.90**	**3.16**
6	**Carbohydrate content after flooding(%)**	**0.11-3.49**	**0.76**

4.1.4 Variability, heritability and genetic advance

The coefficients of variability, heritability and genetic advance for all the 15 characters were studied and the result is presented in Table 7.

In general, phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) in all the characters. Among 15 characters studied PCV ranged from 3.01 for days to 50% flowering to 116.94 for carbohydrate content of plant after flooding . Similarly, GCV ranged from 2.77 to 116.81 for carbohydrate content of plant after flooding respectively. All other characters had moderate to high PCV and GCV estimates.

The estimate of heritability in broad sense for different characters ranged from 73.72 in case of panicle length to 99.78 in case of carbohydrate content after flooding. All the characters exhibited high degrees of heritability.

Improvement in mean genotypic value of selected plants over the parental population is known as genetic advance. It is a measure of genetic gain under selection. Genetic advance as percentage of mean ranged from 0.74 in case of 100 grain weight to 35.98 recorded in case of fertile grain/panicle. Genetic advance was low in case of days to 50% flowering, tillers/plant before flooding, tillers/plant after flooding, effective tillers/plant, panicle length, 100-grain weight, carbohydrate content of plant before and after flooding and grain yield/plant ; moderate in case of plant height before flooding, grain fertility %, harvest index and high in case of plant height after flooding, final plant height and fertile grains per panicle.

4.2 Character association

Due to influence of environment, selection on the basis of *per se* yield performance is not reliable. Therefore selection through yield attributing characters is important to improve grain yield. Hence, study of character association is important to find out the strength and direction of various characters with the economic characters, i.e grain yield. This relationship is measured by the correlation coefficient and is represented by "r". In the present investigation an attempt has been made to estimate the nature and magnitude of association of characters at genotypic and phenotypic levels and are presented in Table 8.

Table 7. PCV, GCV, h^2 and GA estimates for various characters of 56 lowland rice genotypes

Sl No.	Characters	PCV	GCV	h^2	GA	GA(% of Mean)
1	Days to 50% flowering	**3.01**	**2.77**	84.29	4.84	**4.47**
2	Plant height before flooding	15.45	14.03	82.47	14.47	22.42
3	Plant height after flooding	11.83	11.43	93.33	26.64	19.44
4	Final plant height	11.10	10.82	94.95	27.46	18.56
5	Tiller/plant before flooding	10.89	10.22	88.09	1.09	16.89
6	Tiller/plant after flooding	12.56	11.83	88.80	1.19	19.63
7	Effective tillers/plant	30.30	28.54	88.70	1.57	47.30
8	Panicle length	10.18	8.74	**73.72**	3.45	13.20
9	Fertile grains/panicle	24.90	23.04	85.65	**35.98**	37.53
10	Fertility %	12.30	11.76	91.32	15.05	19.77
11	100 grain weight	20.41	19.83	94.41	**0.74**	33.92
12	Harvest index(%)	19.46	19.08	96.16	9.19	32.93
13	CHO before flooding	22.39	21.98	96.34	1.20	37.96
14	CHO after flooding	**116.94**	**116.81**	**99.78**	1.57	**205.35**
15	Grain yield/plant	36.61	35.76	95.38	3.60	61.46

Table 8. Estimates of phenotypic and genotypic correlation co-efficient among various characters for 56 lowland rice genotypes

Characters		DF	PHBF	PHAF	FPH	TBF	TAF	EBT	PL	FGP	F%	GWP	HI	CHO BF	CHO AF
PHBF	r_p	-0.212													
	r_g	-0.275*													
PHAF	r_p	-0.392**	0.918**												
	r_g	-0.435**	0.966**												
FPH	r_p	-0.378**	0.924**	0.097											
	r_g	-0.415**	0.975**	1.000**											
TBF	r_p	0.280*	-0.061	-0.111	-0.114										
	r_g	0.341*	-0.033	-0.105	-0.115										
TAF	r_p	0.314*	-0.155	-0.253	-0.254	0.970**									
	r_g	0.370**	-0.153	-0.258	-0.265*	0.984**									
EBT	r_p	0.356**	-0.521**	-0.644**	-0.641**	0.107	0.229								
	r_g	0.422**	-0.607**	-0.705**	-0.701**	0.126	0.273*								
PL	r_p	0.012	0.286*	0.380**	0.387**	0.062	-0.022	-0.356**							
	r_g	-0.040	0.388**	0.470**	0.002	0.090	-0.018	-0.400**							
FGP	r_p	-0.109	-0.034	-0.002	-0.015	0.073	0.042	0.015	0.080						
	r_g	-0.171	-0.021	0.021	-0.185	0.081	0.037	0.084	0.062						
F%	r_p	0.002	-0.170	-0.157	-0.168	0.095	0.112	0.195	0.033	0.428**					
	r_g	-0.004	-0.212	-0.180	-0.185	0.113	0.129	0.132	0.071	0.478**					
GWP	r_p	-0.002	0.023	-0.022	-0.009	-0.461**	-0.415**	-0.053	0.057	-0.581**	-0.140				
	r_g	-0.012	0.006	-0.023	-0.007	-0.502**	-0.456**	-0.031	0.055	-0.638**	-0.149				
HI	r_p	0.079	-0.226	-0.221	-0.217	0.087	0.136	0.238	-0.120	-0.118	-0.060	0.006			
	r_g	0.086	-0.259	-0.238	-0.232	0.081	0.140	0.267*	-0.137	-0.144	-0.065	0.002			
CHOBF	r_p	0.381**	-0.507**	-0.632**	-0.628**	0.170	0.314*	0.544**	-0.373**	0.002	0.099	-0.188	0.457**		
	r_g	0.437**	-0.549**	-0.655**	-0.646**	0.193	0.347**	0.580**	-0.443**	0.021	0.108	-0.192	0.490**		
CHOAF	r_p	0.334*	-0.562**	-0.719**	-0.708**	0.032	0.204	0.817**	-0.382**	0.015	0.184	0.056	0.297*	0.666**	
	r_g	0.365**	-0.614**	-0.743**	-0.726**	0.031	0.213	0.863**	-0.445**	0.017	0.192	0.058	0.302*	0.680**	
YIELD	r_p	0.319*	-0.540**	-0.647**	-0.648**	0.032	0.154	0.840**	-0.246	0.208	0.302*	0.069	0.243	0.492**	0.843**
	r_g	0.341*	-0.589**	-0.670**	-0.671**	0.036	0.165	0.882**	-0.286*	0.234	0.331*	0.079	0.244	0.516**	0.859**

* Significant at 5% level, ** Significant at 1% level

4.2.1 Correlation of component characters with grain yield

In general, the estimates of genotypic correlation were higher than that of phenotypic correlation. Grain yield per plant exhibited positive correlation with, days to 50% flowering, effective tillers/plant, carbohydrate content before flooding, carbohydrate content after flooding but negatively correlated with plant height. The highest correlation was between grain yield per plant and carbohydrate content after flooding ($r_p = 0.843$, $r_g = 0.859$). This was followed by effective tillers/plant ($r_p =0.840$, $r_g = 0.882$), carbohydrate content before flooding ($r_p = 0.492$, $r_g= 0.516$) ,days to 50% flowering($r_p = 0.319$, $r_g = 0.341$), grain fertility% ($r_p = 0.302$, $r_g = 0.331$). Negative correlation of yield was noticed with plant height before flooding , plant height after flooding ,final plant height. The rest of the characters showed non-significant correlation with yield.

4.2.2 Correlation among other component characters

Days to 50% flowering is positively correlated with number of tillers in all stages and carbohydrate content before and after flooding.

Plant height was positively correlated with panicle length but negatively correlated with effective tillers/plant and carbohydrate content before and after flooding.

There was a high positive correlation between tiller number before and after flooding.

Tiller number after flooding showed positive correlation only with the character i.e. carbohydrate content before flooding.

Effective tiller number is significantly correlated with carbohydrate content before and after flooding; however it was negatively correlated with panicle length.

Fertile grains per panicle was positively correlated with fertility % , while negatively correlated with 100 grain weight.

There was a strong positive correlation observed between HI and carbohydrate content before as well as after flooding.

4.3 Path coefficient analysis

Path analysis has been used to organize the relationship between predicted variable ınd responsible variables. To understand the direct and indirect effects of each character on grain yield and the application of selection pressure in a better way for yield improvement, partitioning of correlation coefficient into direct and indirect effects through path coefficient analysis is very important. The phenotypic correlations coefficients were used for carrying out path coefficient analysis and presented in Table 9. The results obtained are presented below.

In the present investigation on direct and indirect effects of character on grain yield, it reveled that effective tillers and carbohydrate content after flooding had high positive effect of 0.840, 0.843, respectively on grain yield. These character also had high direct effects on grain yield. Number of tillers before flooding(0.399), fertile grains per panicle(0.366) and 100 grain weight(0.321) had moderate direct effect on grain yield. The effective tillers also contributed indirectly to grain yield through carbohydrate content after flooding(0.349). The value of residual effect was calculated to be 0.34 which indicates that 66% of the total variability can be explained by these 12 characters.

4.4 D^2 analysis

Mainly to assess the genetic diversity that exist among the materials studied, in D^2 statistics is used in plant breeding trials. As because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents, so genetic diversity plays an important role.

The analysis of variance revealed significant differences among the genotypes for all the characters studied, there by indicating the presence of ample variability among the genotypes. On the basis of magnitude of D^2 value (Table 10), all the 56 genotypes of rice for 13 characters, showed that the generalized distance (D^2) between two genotypes varied from 18.76 to 3908.49 which were indicators of considerable diversity available in the materials evaluated.

The smallest D^2 estimate (18.76) observed between Baiganmanji and Basabhoga, indicated that these genotypes were much similar in many traits. The largest D^2 (3908.49) was obtained between Khandsagar and Swarna which indicated the maximum diversity, between these two genotypes.

Relative contributions of 13 characters to D^2 among the genotypes were estimated by average D^2 and presented in Table 11. On the basis of average D^2, Carbohydrate content of plant after flooding contributed maximum to divergence (147.80) followed by Carbohydrate content of plant before flooding (43.94%) and Harvest index (33.07).

Table 9. Direct and indirect effects of component traits on yield for 56 lowland rice genotypes

GENOTYPE	DF	PH	TBF	TAF	EBT	PL	FGP	F%	GWP	HI	CHO BF	CHO AF	GYP
DF	**0.010**	0.027	0.112	-0.106	0.179	0.000	-0.040	0.000	-0.001	0.004	-0.009	0.143	0.319
PH	-0.004	**-0.070**	-0.046	0.086	-0.322	0.016	-0.005	-0.001	-0.003	-0.011	-0.016	-0.303	-0.648
TBF	0.003	0.008	**0.399**	-0.328	0.054	0.002	0.027	0.001	-0.148	0.004	-0.004	0.014	0.032
TAF	0.003	0.018	0.387	**-0.338**	0.115	-0.001	0.015	0.001	-0.133	0.007	-0.008	0.087	0.154
EBT	0.004	0.045	0.043	-0.077	**0.503**	-0.014	0.005	0.001	-0.017	0.012	-0.013	0.349	0.840
PL	0.000	-0.027	0.025	-0.007	-0.179	**0.040**	0.029	0.000	0.018	-0.006	0.009	-0.163	-0.246
FGP	-0.001	0.001	0.029	-0.014	0.008	0.003	**0.366**	0.002	-0.187	-0.006	0.000	0.006	0.208
F%	0.000	0.012	0.038	-0.038	0.098	0.001	0.157	**0.006**	-0.045	-0.003	-0.002	0.079	0.302
GWP	0.000	0.001	-0.184	0.140	-0.027	0.002	-0.213	-0.001	**0.321**	0.000	0.005	0.024	0.069
HI	0.001	0.015	0.035	-0.046	0.120	-0.005	-0.043	0.000	0.002	**0.049**	-0.011	0.127	0.243
CHOBF	0.004	0.044	0.068	-0.106	0.274	-0.015	0.001	0.001	-0.060	0.022	**-0.025**	0.285	0.492
CHOAF	0.003	0.050	0.013	-0.069	0.411	-0.015	0.005	0.001	0.018	0.015	-0.016	**0.428**	0.843

R=0.34

Table 10. D^2 value among 56 lowland rice genotypes

Between genotype	Lowest value	Highest value
1 and the rest	20.16(42)	3608.98(54)
2 and the rest	28.17(5)	2147.36(54)
3 and the rest	24.06(12)	3421.57(54)
4 and the rest	53.76(44)	1878.73(54)
5 and the rest	66.27(41)	1930.10(54)
6 and the rest	53.43(28)	2925.59(54)
7 and the rest	44.58(11)	1869.54(54)
8 and the rest	55.89(20)	3120.42(54)
9 and the rest	40.83(29)	3477.01(54)
10 and the rest	74.13(45)	1939.99(54)
11 and the rest	62.09(44)	1814.84(54)
12 and the rest	36.49(25)	3506.73(54)
13 and the rest	33.67(27)	3324.32(54)
14 and the rest	82.77(21)	3557.99(54)
15 and the rest	56.36(27)	3426.91(54)
16 and the rest	30.88(27)	3015.18(54)
17 and the rest	48.58(19)	3692.86(54)
18 and the rest	30.70(22)	3564.86(54)
19 and the rest	26.25(28)	3600.38(54)
20 and the rest	38.01(38)	3477.06(54)

Between genotype	Lowest value	Highest value
21 and the rest	**18.76(29)**	3512.72(54)
22 and the rest	44.28(25)	3527.60(54)
23 and the rest	23.42(35)	3727.14(54)
24 and the rest	26.21(30)	3318.39(54)
25 and the rest	25.38(28)	3418.76(54)
26 and the rest	20.50(38)	3342.64(54)
27 and the rest	44.74(32)	3373.18(54)
28 and the rest	45.41(49)	3491.46(54)
29 and the rest	25.07(32)	3531.81(54)
30 and the rest	43.49(42)	3491.64(54)
31 and the rest	63.76(38)	3227.72(54)
32 and the rest	38.86(49)	3526.29(54)
33 and the rest	170.76(35)	**3908.49(54)**
34 and the rest	179.56(38)	3524.31(54)
35 and the rest	43.61(36)	3654.59(54)
36 and the rest	22.83(42)	3775.04(54)
37 and the rest	124.69(45)	2666.11(54)
38 and the rest	59.88(49)	3222.49(54)
39 and the rest	146.72(46)	1355.53(42)
40 and the rest	45.07(44)	1621.52(54)
41 and the rest	91.62(50)	1580.39(54)

Between genotype	Lowest value	Highest value
42 and the rest	56.03(48)	3733.54(54)
43 and the rest	115.89(48)	3175.67(54)
44 and the rest	43.81(45)	1657.51(54)
45 and the rest	152.18(48)	2078.97(54)
46 and the rest	366.14(56)	1655.75(51)
47 and the rest	82.11(49)	3389.83(54)
48 and the rest	70.46(49)	3059.91(54)
49 and the rest	545.99(50)	3671.52(54)
50 and the rest	1228.47(56)	2020.19(54)
51 and the rest	2150.98(56)	3523.86(54)
52 and the rest	85.75(53)	182.33(54)
53 and the rest	111.81(55)	167.14(56)
54 and the rest	154.12(55)	313.55(56)
55 and the rest	99.21(56)	

NB: Name of the 56 genotypes are given in Table 1

Table 11.Relative contribution of each character to genetic divergence

Sl. No.	**Character**	**Average D^2 value**	**% Contribution**
1	Days to 50% flowering	6.36	0.97(XI)
2	Plant height(cm)	19.30	2.94(V)
3	TBF	8.99	1.37(X)
4	TAF	2.00	0.30(XIII)
5	Effective tillers/plant(No.)	10.64	1.62(IX)
6	Panicle length(cm)	4.26	0.65(XII)
7	Fertile grains/panicle(No.)	11.72	1.79(VIII)
8	Grain fertility%	14.28	2.18(VII)
9	100 -grain weight(g)	18.44	2.81(VI)
10	Harvest index	33.07	5.04(III)
11	CHOBF	43.94	6.70(II)
12	CHOAF	**147.80**	**69.83(I)**
13	Grain yield/plant(g)	24.82	3.79(IV)

On the basis of cut-off D^2 value (278.23) the 56 rice genotypes were grouped into seven clusters following Tocher's method and the composition of the genetic clusters is given in Table 12. Cluster I with 36 genotypes was the largest cluster followed by cluster II with 10 genotypes , cluster III with 5 genotypes, cluster IV with 2 genotypes and clusters V,VI,VII were mono genotypic in nature.

The average intra- and inter- cluster distances are presented in Table 13. Intra cluster distance values were lower than the inter cluster distances. Lowest intra cluster distance was observed in cluster V, VI, VII (0.00), where as highest intra cluster distance was recorded in cluster III (151.06) followed by cluster IV (146.71).

Inter cluster distance is the main criterion for selection of genotypes. Maximum inter cluster distance was observed between cluster III and V (2899.46) followed by cluster III and VI (2857.10).

Clusters means of 56 lowland rice genotypes for all the 13 characters are presented in Table 14. Cluster III recorded the highest mean value for grain yield per plant (10.46g),carbohydrate content of plant after flooding(3.10%), carbohydrate content of plant before flooding (4.85%), effective tillers/plant(5.54),days to 50% flowering(113.65) and second highest mean values for harvest index(32.78),tillers after flooding(7.13),tillers before flooding(6.97). Cluster V recorded high mean values for plant height(160.42) and 100 grain weight(2.56). Cluster VI recorded high mean values for tillers before flooding (7.85) and tillers after flooding(7.46), harvest index(39.18);where as cluster VII recorded high mean values for panicle length(30.02), fertile grain per panicle(104.18) and fertility %(81.05).

4.6 Selection indices

Smith (1936) suggested that a better way of exploiting genetic correlation with several traits having high heritability is to construct an index, called selection index, which combines information on all the characters associated with the dependent variable 'yield'. Thus, selection index refers to a linear combination of characters associated with yield. It is an useful method to make use of several correlated traits for greater efficiency of selection for yield.

In the present investigation, selection indices were constructed with grain yield as the economic criterion and 13 different characters namely as the component characters.

Table 12. Composition of genetic clusters using D^2 value

Clusters	No. of genotypes	Name of genotypes
I	36	Baiganmanji, Basubhoga, Sunakathi, Ranisaheba, Machakanta, Julpaya, Kadalipendi, Kusuma, Ratnamali, Bagadachinamala, Ghumusara, Kadalichampa, Ganjeijata, Damodarbhoga, Juiphoola, Mahipal, Ratanchudi, Landi, Badashabhoga, Baudiachampa, Kalachampa, Jaladubi, Laxmi, Bagudi, Biridibankoi, Champeisiali, Desijhilli, Kanthakamal, Karpurakranti, Habira, Bhutia, Mayurakantha, Kalakadamba, Khandasagar, Dhulia, Jalagudi
II	10	Nadiarasi, Dhinkiasali, Seulapana, Ganjamgedi, Jagabalia, Bankoi, Kakudimanji, Nilarpati, Champa, Haladichudi
III	5	T-141, T-1242, Mrunalini, Upahar, Swarna
IV	2	Dhoiabankoi, Kadalipendi
V	1	Budidhan
VI	1	T-90
VII	1	Madhabi

Cut-off D^2 value: 278.23

Table 13.Average intra and inter cluster D^2 values among clusters of rice genotypes

Clusters	I	II	III	IV	V	VI	VII
I	122.04						
II	389.05	108.25					
III	2776.50	1380.54	**151.06**				
IV	1245.31	410.78	555.26	146.71			
V	294.43	581.49	**2899.46**	1401.87	0.00		
VI	528.67	816.82	2857.10	1704.99	421.39	0.00	
VII	566.15	283.29	1651.64	503.37	954.94	1495.05	0.00

Table 14.Cluster means of 56 lowland rice genotypes for 13 characters

character	DF	PH	TBF	TAF	EBT	PL	FGP	F%	GWP	HI(%)	CHO BF	CHO AF	GYP
Cluster													
I	107.97	154.09	6.47	6.08	2.87	26.71	98.37	75.98	2.16	26.42	2.91	0.26	4.87
II	107.15	144.72	6.12	5.72	4.05	25.84	95.54	77.83	2.36	30.40	3.12	1.21	7.55
III	**113.65**	109.17	6.97	7.13	**5.54**	22.87	92.76	79.36	2.15	32.78	**4.85**	**3.10**	**10.46**
IV	105.50	149.68	5.50	5.11	3.14	24.55	104.05	79.57	2.40	29.43	3.36	2.07	6.70
V	107.00	**160.42**	6.70	6.31	1.87	24.48	40.94	33.18	**2.56**	32.04	3.17	0.11	2.33
VI	114.25	138.86	**7.85**	**7.46**	2.14	27.65	55.13	78.65	1.37	**39.18**	4.57	0.11	1.94
VII	109.00	148.07	5.35	4.96	3.85	**30.02**	**104.18**	**81.05**	2.20	13.49	2.43	1.34	7.45

The expected genetic advance selection index over direct selection on grain yield have been presented in Table 15. The predicted genetic advance from different indices at 10% selection intensity ranged from 3.60 in one character index to 3.63 in thirteen character index.

The promising genotypes occupying better ranking in the 13 character index with their grain yield and index score have been presented in Table 16. It is interesting to note that the top 2 entries with respect to their *per se* yield performance had the index score in the same order. Those are: Upahar and Mrunalini. These genotypes were selected for their use in future breeding programme. The varieties namely Swarna, T-1242 and Ganjamgedi having index score 3 to 5 are also having the yield rank in that range. So, these genotypes were also selected for their use in future breeding programme.

Table 15.Expected genetic advance selection index over direct selection on grain yield

Index no and no of characters	**Character**	**Expected GS***
1(One character index)	GYP	3.60
2(Two character index)	GYP+DF	3.60
3(Three character index)	GYP+DF+PH	3.60
4(Four character index)	GYP+DF+PH+ TBF	3.60
5(Five character index)	GYP+DF+PH+ TBF+TAF	3.60
6(Six character index)	GYP+DF+PH+ TBF+TAF+EBT	3.60
7(Seven character index)	GYP+DF+PH+ TBF+TAF+EBT+PL	3.60
8(Eight character index)	GYP+DF+PH+ TBF+TAF+EBT+PL+FGP	3.61
9(Nine character index)	GYP+DF+PH+ TBF+TAF+EBT+PL+FGP+GF%	3.61
10(Ten character index)	GYP+DF+PH+ TBF+TAF+EBT+PL+FGP+GF%+GW	3.61
11(Eleven character index)	GYP+DF+PH+ TBF+TAF+EBT+PL+FGP+GF%+GW+HI	3.61
12(twelve character index)	GYP+DF+PH+TBF+TAF+EBT+PL+FGP+GF%+GW+HI+ CHOBF	3.61
13(thirteen character index)	GYP+DF+PH+TBF+TAF+EBT+PL+FGP+GF%+GW+HI+ CHOBF+CHOAF	3.63

*** GS at 10% selection intensity**

Table 16. Selection of genotypes on the basis of 13 character index

Sl No.	Genotype	Index score	Grain yield/ plant (g)
1	**Upahar**	13.96(1)	12.35(1)
2	**Mrunalini**	13.33(2)	12.16(2)
3	**Swarna**	11.32(3)	9.11(5)
4	**T-1242**	11.10(4)	9.63(3)
5	**Ganjamgedi**	10.96(5)	9.51(4)
6	**T-141**	10.86(6)	9.06(6)
7	**Kadalipendi**	10.65(7)	8.68(8)
8	**Bankoi**	10.08(8)	8.45(9)
9	**Nadiarasi**	10.06(9)	8.69(7)
10	**Nilarpati**	9.70(10)	7.78(12)
11	**Haladichudi**	9.62(11)	8.01(10)
12	**Dhinkiasali**	9.40(12)	7.78(11)
13	**Madhabi**	9.08(13)	7.45(13)
14	**Seulapana**	9.07(14)	7.24(14)
15	**Kakudimanji**	8.21(15)	6.40(16)

Fig1: Rice plants under Stagnant flooding

Fig 2: Rice plants under Stagnant flooding

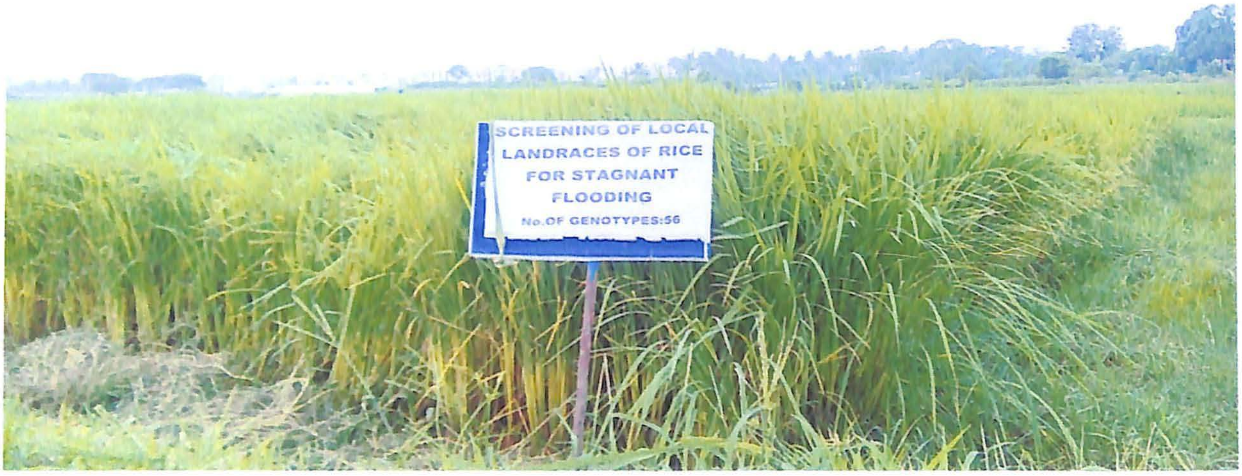

Fig :3 Increased plant height after removal of stagnant flood water

CHAPTER-5

DISCUSSION

DISCUSSION

Fifty local landraces of rice along with 3 improved and 3 high yielding varieties were evaluated in stagnant flooding situation at the Rice Research Station of Department of Plant Breeding and Genetics, OUAT, Bhubaneswar, during 2015 kharif season. Different yield attributing traits and physiological traits were examined to study the extent of genetic variability, nature and magnitude of character association in relation to yield and other traits, direct and indirect effects of component traits on grain yield, genetic diversity among the test entries and selection of genotypes based on multiple character index.

The importance of the study lies with the fact that flash-flooding and submergence adversely affect at least 16% of the rice lands of the world (~22 m ha). In eastern India, ~13 m ha of rice lands are unfavourably affected by excess water and periodically suffer from flash-floods and complete submergence. Genetic variability present in the germplasm is the key factor to bring about genetic improvement. In Odisha, a large number of local landraces of rice are available which contribute to genetic variability for different characters. Landraces are considered to be the store house of innumerable important genes (Mishra and Sinha,2012). Hence the experiment was carried out to assess variability, correlation, genetic diversity and select promising genotypes among local landraces of rice.

5.1 Study of variability

The genetic variability in respect of a trait is the direct measure as to how far the character could be manipulated in a desired direction.

5.1.1 Analysis of variance

From the analysis variance significant amount of genetic variation was displayed for 11 traits. Characters having higher magnitude of genetic variance such as fertile grains per panicle, final plant height, plant height after flooding , plant height before flooding and grain fertility %, effe tive tillers/pl, carbohydrate content after flooding maybe sorted out as important selection criteria for realization of higher productivity in rice in stagnant flooding condition.

5.1.2 Mean performance of the genotype

So far plant height is concerned, the local landraces were taller as compared to the high yielding varieties and they get even more increase in height after flooding. Tall height may be useful for getting long straw suitable for thatching purposes and in mushroom cultivation. But the more height is not beneficial under stagnant flooding, because the stored energy in the form of carbohydrate is utilized in height increment and ultimately a shortfall in yield is observed.

Highest number of tillers/plant after flooding (7.93) was present in the variety T-1242 and profuse tillering leads to high biomass production and beneficial for giving effective tillers to the plant and ultimately leads to higher productivity.

Highest number of effective tillers per plant (7.14) was observed in the high yielding variety 'Swarna'. Panicle bearing tillers after stagnant flooding usually leads to high biomass production and higher productivity. Most of the landraces were having very low number of effective tillers (2-4) and resulted in lower productivity.

Panicle length of the test entries varied from 21.15 cm to 36.15 cm which can grouped into medium to long type. This is a stable character. It has been observed that the longer panicle types are dominant over short panicle types and therefore, selection of genotypes with long panicle types might prove beneficial for realization of high yield (Mathur,2011).

Fertile grains per panicle ranged from 40.94-157.28. It has been reported by many workers that the grain yield has a direct correlation with the number of fertile grains per panicle. So the genotype with higher grain number should be sorted out for future breeding programme. In the present study Ranisaheba, Ganjamgedi, Kadalipendi, Badsabhoga, Ganjeijata and Baiganmanji were having more than 130 frertile grains per panicle after experiencing stagnant flooding condition.

It is also observed that when selection for higher grain number is carried out, there is a corresponding decrease in grain size. (Dey *et al.*2005) It is, therefore, suggested that in order to maintain higher productivity, a balance between grain number and grain weight should be made. The 100-grain weight of 2.02 to 2.50g is considered ideal in rice crop. In the present study 100-grain weight ranged from 1.13 – 3.04g . Among the genotypes tested Kalakadamba (3.04g), Biradiabankoi (2.88g), Champeishiali (2.85g), Dhoiabankoi (2.83g), Mahipal (2.82g) had high grain weight .So, this variety should be used in future breeding programme under stagnant flooding condition.

Grain fertility % varied from 33.18 to 90.27 % which shows that the character is highly variable and might fluctuate due to environmental condition. Stagnant flooding condition before flowering and low light intensity at reproductive and ripening phase induces spikelet sterility. Also high wind during flowering stage affects pollination and leads to chaffiness. It is indicated that low light stress affects the total dry matter production, production of spikelets per unit area and grain size considerably; and stress of stagnant flooding before flowering causes source sink imbalance and allocates stored carbohydrate in increasing plant height. As dry matter production is greatly reduced after flowering, the grain filling is largely affected due to poor mobilization and allocation of pre-flowering photosynthates from shoot to panicle causing spikelet sterility. Genotypes on the basis of grain fertility may be selected for realization of high yield in rice (Mathur,2011).

Harvest index is an indication of partitioning of the dry matter production. Higher the harvest index, higher will be the production and productivity. Harvest index reflects the physiological efficiency of a genotype. It is a highly heritable character and can be used for direct selection of genotypes. .(Mukherjee *et al.*2008) In the present study, harvest index(%) ranged from 8.78% to 39.49%. T 141, T90, Mrunalini, Dhulia, Seulapana , Desijhilli, Kakudimanji were having higher harvest index.

5.1.3 Variability, heritability and genetic advance

In the present study, phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient variation (GCV). In all the 15 characters indicating some influence of the environment in the expression of these characters. Characters namely carbohydrate content of plant after flooding, effective tillers per plant, fertile grains per panicle, carbohydrate content of plant before flooding, 100-grain weight had moderate to high PCV and GCV estimates. Similar findings were also reported by Chand *et al.*, 2004 for fertile grains per panicle; Sinha *et al.*, 2004 for grain weight; Shukla *et al.*, 2004 for fertile grains per panicle, grain weight; Sarkar *et al.*, 2007 for 100-grain weight; Kole *et al.*, 2008 for fertile grains per panicle; Fukrei *et al.*, 2011 for effective ear bearing tillers per plant, fertile grains per panicle and flag leaf area; Idris *et al.*, 2012 for fertile grains per panicle; Seyoum *et al.*, 2012 for 1000-grain weight and grains per panicle; Gangashetty *et al.*, 2013 for effective ear bearing tillers per plant; Prasad *et al.*, 2013 for effective ear bearing tillers per plant; Singh and Sharma 2013 for fertile grains per panicle and effective ear bearing tillers per plant and Srivastava *et al.*, 2014 for number of tillers per plant and number of spikelets per panicle.

Heritability is an estimate of the ratio of genotypic variance to the total phenotypic variance. It is also subjected to some experimental error. Hence, genetic advance along with heritability gives a more reliable information for consideration of a character under selection.

In the present study, all the 15 characters exhibited high degree of heritability and among those final plant height, 100-grain weight, harvest index, carbohydrate before flooding, carbohydrate after flooding and grain yield per plant had high heritability. Similar observations were also recorded by Das *et al.,* 2001 for harvest index and grain yield per plant; Yadav *et al.,* 2004 for grains per panicle and grain yield per plant; Jayasudha *et al.,* 2007 for grain yield per plant; Karim *et al.,* 2007 for fertile grains per panicle and 1000-grain weight; Kole *et al.,* 2008 for grain number and grain yield; Sarawgi 2008 for fertile grains per panicle, harvest index and grain yield per plant; Pandey *et al.*, 2009 for effective ear bearing tillers per hill, test weight, harvest index and grain yield; Subudhi *et al.*, 2009 for grains per panicle; Fukrei *et al.*, 2011 for grain yield per plant; Immanuel et al. 2011 for harvest index; Selvaraj *et al.*, 2011 for grain yield per plant; Pratap *et al.*, 2012 for flag leaf area; Gangashetty *et al.*, 2013 for grain yield per plant; Singh and Sharma 2013 for fertile grains per panicle and grain yield per plant; Akinwale *et al.*, 2011 for grains per panicle and grain yield.

5.2 Character association

In plant breeding, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield (Singh and Narayanan,1993). Very often, selection for yield *per se* is not reliable and therefore, indirect selection through component traits become important for the ultimate output, the grain yield. Hence, studies on character association not only help to understand physical linkage, but also provide information on nature and direction of selection. An attempt has been made to estimate the nature and magnitude of correlation of character pairs, which would facilitate selection of genotypes where a balanced combination of characters is associated with increased productivity. In general, in the present investigation, the estimation of genotypic correlation were higher than that of phenotypic correlation, which indicated that environmental cause of correlation has affected the genetic cause (Chauhan *et al.*, 1996; Prasad *et al.,* 1998; Sawant *et al.,* 1996; B.Satish Chandra *et al.*, 2009; Sunayan Rathi *et al.*, 2010 and Prajapati *et al.*, 2011). Genotypic correlation may be either due to pleiotropic action of genes or due to linkage or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to manifold effects of a gene (Falconer,1960).

In the present study, grain yield per plant exhibited positive correlation with days to 50% flowering, carbohydrate content before flooding, carbohydrate content after flooding. Similar finding was observed by Das *et al,*2007 for carbohydrate.This reveals that selection on the basis of these characters bears relevance to grain yield.

The correlation of plant height with panicle length was found positive.Similar observation was made by Patil and Sahu,2009; Chandra *et al.*,2009; Singh *et al.*,2007.

5.3 Path coefficient analysis

In the present study, characters like effective tillers per plant, filled grains per panicle, 100 grain weight, carbohydrate content after flooding were having high direct effect on grain yield, which indicates true dependence of the effect on these character. Hence direct selection based on these character will be rewarding for yield improvement.

Out of the above characters, effective tillers per plant and carbohydrate content after flooding were having high positive effect on grain yield. So these two characters must be taken into consideration during selection. Similar finding was observed by Das *et al,*2007 for carbohydrate.

5.4 D^2 analysis

D^2 analysis is made to assess the genetic diversity of the breeding materials. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability. Fifty local landraces of lowland rice were collected from different geographical areas of Odisha which indicates the possible existence of diversity among the materials.

The smallest D^2 value (18.76) between Baiganmanji and Basabhoga and largest D^2 value (3908.49) between Khandsagar and Swarna indicated similarity and maximum diversity among those genotypes respectively. Study on genetic diversity among rice genotypes were also carried out by Rather *et al.*, 2001; Subudhi *et al.*, 2008; Mini and Mohanan,2009; Prasad *et al.*, 2009; Ahmed *et al.*, 2010; Ekka *et al.*, 2012.

Among the 13 characters the relative contributions of carbohydrate content of plant after flooding, carbohydrate content of plant before flooding, harvest index(%) was maximum to diversity. These findings are in agreement with published reports by Das *et* *al.*, 2007 for carbohydrate content ; Subudhi *et al.*, 2008 for 1000-grain weight;Medhabati *et al.*, 2013 for 100-grain weight and Monahara and Singh,2013 for 1000-grain weight.

The 56 genotypes, based on critical D^2 value, were classified into seven clusters. . Cluster I with 36 genotypes was the largest cluster followed by cluster II with 10 genotypes , cluster III with 5 genotypes, cluster IV with 2 genotypes and clusters V,VI,VII were mono genotypic clusters.

Lower values of intra cluster distance as compared to the inter cluster distances indicated that the genotypes included within the cluster tended to diverse less from each other.

Maximum inter cluster distance was observed between cluster III and V (2899.46) followed by cluster III and VI (2857.10). Since, the inter cluster distance was maximum between cluster III and V followed by cluster III and VI, genotypes with high mean value from cluster III may be selected as parents for hybridization with parents selected from cluster V and VI.

Thus, cross combination such as Khadsagar × Swarna, Ratnachudi × Swarna, Biradiabankoi × Swarna, Kadalichampa × Swarna, Kalachampa × Swarna may be made to get large variability in the early segregating generations.

5.5 Selection indices

Several workers in different crop plants have emphasized the need of indirect selection for yield through the use of component traits governed by genes with additive effect and having strong correlation with grain yield.

In the present study, in terms of predicted genetic advance, the 13 character index was found to be superior over direct selection for yield *per se*. This is in general agreement with those of Chakravarty and Hazarika, 1996; Surek and Beser, 2005; Bastia *et al.*, 2007 and Purohit and Majumdar, 2009.

The promising genotypes occupying better ranking in the 13 character index were selected for their future use in breeding programmes.

CHAPTER-6

SUMMARY & CONCLUSION

SUMMARY AND CONCLUSION

Rice is the staple food of India. It occupies the largest area among all the crops in India. It is grown in an area of about 44.6 million hectares with a production of 93.34 million tones and productivity level of 2066kg/ha. Flash-flooding and submergence adversely affect at least 16% of the rice lands of the world (~22 m ha). In eastern India, ~13 m ha of rice lands are unfavourably affected by excess water and periodically suffer from flash-floods and complete submergence. Improvement of germplasm is likely the best option to withstand submergence and stabilize productivity in these environments.

Keeping in view of the above points, the present research project entitled "Genetic variability in indigenous lowland rice under stagnant flooding" was undertaken with the objective of assessing competitive performances, genetic variability, character association, genetic divergence and direct and indirect effects of different characters on grain yield in the study material comprising 50 lowland rice landraces, 3 improved lowland varieties and 3 released high yielding varieties.

Field evaluation of the 56 genotypes was done at Rice Research station, Bhubaneswar during Kharif 2015 in Randomized Block design with 2 replications . After giving it more than 30days of stagnant flooding , observations were recorded on 15 characters such as days to 50% flowering, plant height before flooding, plant height after flooding, final plant height, tillers/ plant before flooding, tillers/ plant after flooding, number of effective tillers/ plant, panicle length, fertile grains/ panicle, fertility %, 100 grains weight, harvest index, carbohydrate content of plant before flooding, carbohydrate content of plant after flooding and grain yield/plant.

Analysis of variance revealed highly significant differences among the test genotypes in respect of all the characters under study in both the sets, indicating wide genetic variation which was also supported by mean performance and range of variation among the genotypes for all the characters.

Mean performance of lowland rice genotypes indicated that Upahar was promising with respect to the yield performance (12.35 g/plant) associated with more numbers of days to 50% flowering, lower plant height, higher effective tiller numbers, higher 100 grain weight, high havest index, high carbohydrate content before and after flooding. For yield attributing characters the promising genotypes were Swarna (for effective tillers), Badashabhoga (Fertile grains/panicle), Ganjeijata (Grain fertility %), Kalakadamba (100 grain weight), T-141(harvest index), T-1242(carbohydrate content before flooding), Swarna (carbohydrate content after flooding). So these varieties should be used in breeding programme.

Phenotypic and genotypic coefficient of varition maintained correspondence for the characters and both GCV & PCV were high for for characters like number of effective tillers per plant, number of fertile grains per panicle, 100 grains weight, carbohydrate content after flooding and yield/plant indicating selection for such characters will be more reliable.

The genetic advance in percentage of mean for lowland rice genotypes was high for plant height after flooding, final plant height and filled grains/panicle. And for all other characters it is low to moderate.

A moderate to high degree of heritability estimates were associated with high degree of genetic advance indicating presence of additive effect to all the associated characters including yield.

Genotypic and phenotypic correlation coefficients were calculated to study the association between characters. In general, the estimates of genotypic correlation were higher than that of phenotypic correlation. Grain yield per plant exhibited positive correlation with days to 50% flowering, effective tillers/panicle, grain fertility%, carbohydrate content before and after flooding. Negative correlation of grain yield was noticed with plant height and panicle length. Among other characters, positive correlation was observed between days to 50% flowering and carbohydrate content before as well as after flooding; plant height before flooding and plant height after flooding; and final plant height; plant height before flooding and panicle length; plant height after flooding and panicle length; final plant height and panicle length; number tillers before flooding and number tillers after flooding; number of tillers after flooding and carbohydrate content before flooding; number of effective tillers and carbohydrate content before and after flooding; fertile grains per panicle and fertility %; harvest index and carbohydrate content before and after flooding; carbohydrate content before flooding and carbohydrate content after flooding.

It was observed from the path coefficient analysis that the carbohydrate content after flooding exhibited maximum positive direct effect on grain yield followed by number of effective tillers/plant. Also days to 50% flowering, fertile grains per panicle, carbohydrate content before flooding, grain fertility% and harvest index were observed to be the major indirect contributors towards grain yield. The results of residual effect was found to be 0.343 indicating that 66% of total variability was contributed by the variables used in the study.

Considerable diversity is available in the materials evaluated, which was known by D^2 analysis. The generalized distance (D^2 value) between two genotypes varied from 18.76 to 3908.49. The 56 genotypes were classified into 7 clusters. Cluster I with 36 genotypes was the largest cluster followed by cluster II with 10 genotypes , cluster III with 5 genotypes, cluster IV with 2 genotypes. Clusters V, VI and VII were mono genotypic in nature.

Inter cluster distance was maximum between cluster III and V followed by cluster III and VI. Hence, genotypes from these clusters should be selected as parents for hybridization. Thus, the cross combinations such as (T-141, T-1242, Mrunalini, Upahar, Swarna) × Budidhan and (T-141, T-1242, Mrunalini, Upahar, Swarna) × T-90 may be attempted to get large variability in the early segregating generations.

During the present investigation selection indices were constructed with grain yield as the economic criterion and 13 different characters namely grain yield per plant, days to 50% flowering, final plant height, no. of tillers before flooding, no. of tillers after flooding, effective tillers per plant, panicle length, fertile grains per panicle, grain fertility%, 100-grain weight,harvest index, carbohydrate content before flooding, carbohydrate content after flooding, were chosen for the construction of 13 selection indices. The 13 character index including all the 13 traits was used for the selection of genotypes. The promising genotypes occupying better ranking in the thirteen character index namely Upahar, Mrunalini, Swarna, T-1242,Ganjamgedi and T-141 were selected for their future use in breeding programmes.

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