MORPHOGENETIC VARIATION FOR LEAF FODDER QUALITY PARAMETERS IN POPULATIONS OF *Grewia optiva* DRUMMOND

Thesis

by

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(F-2019-11-D)

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FRONTISPIECE



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CERTIFICATE-I

This is certify that the thesis entitled **"Morphogenetic variation for leaf fodder quqlity parameters in populations of *Grewia optiva* Drummond",** submitted in partial fulfillment of the requirements for the award of degree of **DOCTOR OF PHILOSOPHY (FORESTRY)** in the discipline of **FOREST GENETIC RESOURCES** to Dr. Yashwant Singh Pamar University of Horticulture and Forestry, Nauni, Solan (HP) is record of bonofide research work carried out by **Ms. Jyoti Dhiman (F-2019-11-D)** daughter of Sh. Sher Singh under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of investigations have been fully acknowledged.

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CERTIFICATE-II

This is to certify that the thesis titled, **"Morphogenetic variation for leaf fodder quality parameters in populations of *Grewia optiva* Drummond"**, submitted by **Ms. Jyoti Dhiman (F-2019-11-D)** daughter of Sh. Sher Singh to Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (H.P.) – 173 230 India in partial fulfilment of the requirements for the award of degree of **DOCTOR OF PHILOSOPHY (FORESTRY) in the discipline of Forest Genetic Resources** has been approved by the Student's Advisory Committee after an oral examination of the student in collaboration with the External Examiner.

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ABBREVIATIONS USED

%	:	Per cent
($h^2_{b.s.}$)	:	Heritability (in Board Sense)
°C	:	Degree centigrade
AA	:	Amino acids
AFLP	:	Amplified Fragment Length Polymorphism
BD	:	Bulk density
bp	:	Base pair
Ca	:	Calcium
CD	:	Critical difference
Cm	:	Centimeter
Cm^2	:	Square centimeter
Cov	:	Covariance
D	:	Dominance
DNA	:	Deoxyribonucleic acid
dNTP	:	Di nucleotide tri phosphate
dSm^{-1}	:	decisiemens per meter
EC	:	Electrical conductivity
EMS	:	Error mean sum of square
GCV	:	Genotypic coefficient of variation
H.P.	:	Himachal Pradesh
ISSR	:	Inter simple sequence repeats
K	:	Potassium
Kg ha^{-1}	:	kilogram per hactare
mg	:	Milli grams
ml	:	Millilitres
mM	:	Milli molar
mm	:	Millimeter
ng	:	Nanograms
N	:	Nitrogen
P	:	Phosphorus
PC	:	Principal component

PCA	:	Principal componenet analysis
PCR	:	Polymerase chain reaction
PCV	:	Phenotypic coefficient of variation
PD	:	Particle density
RAPD	:	Random amplified polymorphic DNA
RBD	:	Randomized Block Design
RNA	:	Ribonucleic acid
SE	:	Standard error
SOC	:	Soil organic carbon
SS	:	Sum of square
SSR	:	Simple sequence repeats
Taq	:	*Thermus aquaticus*
TE	:	Tris EDTA (Ethylenediamine tetra acetic acid)
T-value	:	Tabulated-value
UK	:	Uttarakhand
UPGMA	:	Unweighted pair group mean average
UV	:	Ultra violet
µ	:	Micron
µl	:	Micro litre
TIGR	:	Tree Improvement and Genetic Resources
SAF	:	Silviculture and Agroforestry
COF	:	College of Forestry
UHF	:	Universty of Horticulture and Forestry

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Chapter-1

INTRODUCTION

Agriculture is directly responsible for providing a living for approximately 70 per cent of India's total population, making it one of the most important contributors to the country's economy. The Ministry of Statistics and Programme Implementation's quarterly estimates of GDP (for the fiscal year 2020-21) indicate that the contribution of agriculture and allied sectors to GDP is 20.19 per cent. In the mountainous regions of Himachal Pradesh and Uttarakhand, it is common to practice combining agricultural activities with raising livestock together. It has been estimated that India has a total livestock population of 535.78 million (20^{th} livestock census report, 2019). Livestock provides a means of subsistence for approximately 20.5 million people worldwide. Small farm households rely on livestock for 16 per cent of their income, which is significantly higher than the average of 14 per cent for rural households overall. Two-thirds of the people who live in rural areas make their living off of their livestock. Moreover, it employs about 8.8 per cent of India's population. The livestock industry is responsible for 4.11 per cent of the total GDP and 25.6 per cent of the total GDP generated by agriculture. The production in terms of meat, milk and wool does not meet the requirements of the country to the extent that it should be (ICAR, 2001). The significant decrease in the amount of palatable and nutritious green fodder that is available throughout the year is the primary factor contributing to this low production (Debroy *et al.,* 1980). According to the estimates on feed and fodder in India (million tonnes) by the standing committee on Agriculture, there will be a deficit of 40 per cent in green fodder and 21 per cent in dry fodder by the year 2025. According to the report titled "Revisiting National Forage Demand and Availability Scenario," which was published by the Indian Grassland and Fodder Research Institute (IGFRI), India is lacking 11.24 kg of green fodder for every one hundred kg that are required (Roy *et al*., 2019).

One of the most significant challenges confronting animal husbandry in the states of Himachal Pradesh and Uttarakhand is the shortage of readily available, nutrient-rich fodder due to the significantly larger demand for feeds and fodder for livestock than there is supply (Singh and Bimal, 2004). In the past, residents of these regions were required to travel daily distances of several kilometres in order to gather fodder from nearby forest areas to meet the needs of their livestock. In the same breath, the prevalent rainfed conditions of hilly areas,

small land holdings, and poverty of the farmers make it impossible for them to either buy concentrated feeds or resort to the cultivation of nutritious leguminous fodder. Not only will the judicious cultivation of fast-growing multipurpose broad leave species in the pasture and agricultural land of hilly areas of the country fill the gap of fodder requirement, but it will also protect the livestock against the hot wind and scorching sun during the summer (Debroy *et al.,* 1980). Additionally, the ecosystem will be preserved and restored as a result. (Bhat *et al.,* 2018).

Tree fodder leaves are valuable fodder (Roder, 1992), especially during the winter months when the availability of green fodder is limited, both in quantity (Khanal and Subba, 2001) and quality (Vishvakarma *et al.,* 1998, Roder *et al.,* 2003). Several important tree species such as *Grewia optiva, Quercus leucotrichophora, Quercus semicarpifolia, Celtis australis, Bauhinia variegata, Bauhinia rugulosa, Ficus roxburghii, Ficus palmata, Morus alba, Robinia pseudoacacia* and others, are relied upon heavily by farmers during the harsh winter months.

Grewia optiva Drummond also known as *G. oppositifolia*, is regarded as one of the most significant multifunctional, lean season, nutritious fodder species in Himachal Pradesh and Uttarakhand. This fodder tree species belongs to the family "Tiliaceae" (Singh *et al.,* 2018). Locally, *G. optiva*, is known as Bhimal, Bihul, Biul, etc., having chromosome number 2n =18 (Coleman, 1982). Because of its versatility as feed, fuel, and fibre, it is a highly well-liked agroforestry tree that is planted in low and mid-hills regions in the western and central Himalayas. It is indigenous fodder tree species to India.

Grewia optiva Drummond is a small to medium-sized tree with a spreading crown that can grow up to 12 metres tall, with a clear bole of 3 to 4 metres and a girth of about 80 cm. The branches are smooth and pale silvery-brown, and the bark is dark brown, thick, and roughish, with small woody scales that exfoliate. The leaves are opposite, ovate, acuminate, closely serrated, rough and hairy above, base rounded, slightly oblique, and 3-nerved, measuring 5-13 cm x 3.6 cm. The petiole 0.3-1 cm long, stout and tomentose. Flowers are grouped in groups of 1-8 and peduncles are solitary. Sepals are 1-1.5 cm long, linear oblong, three-ribbed and green on the outside and white, pale yellow or red on the inside. Petals are either yellow or white. The fruit is a fleshy drupe, 2-4 lobed, olive green when immature and black when ripe (Singh *et al.,* 2018). It sheds its leaves in the months of March and April and flowers appear with the new flush of leaves in the month of April-May and fruits formed

shortly after flowering (Brandis, 1906). Depending on the local environment, the fruits attain their full size by September and ripen from October to December. Trees that have been totally lopped do not produce fruits because flowers are not produced on the shoots of the current year. The fruits grow on the shoots from the previous year. Fruits are enjoyed by birds, the main agent of dispersal. (Singh *et al.,* 2018; Orwa *et al.,* 2009).

Grewia optiva is distributed naturally from foothills of the western Himalayas in Jammu and Kashmir to Nepal at elevations of up to 2000 m. (Brandis *et al.,* 1972). It is usually found near villages, along agricultural field boundaries and on terraces. It is a subtropical tree with a maximum temperature 38°C and a minimum -2°C and frost is common during the autumn and winter seasons. The species is common in areas with annual rainfall ranging from 1200 to 2500 mm, primarily in the summer. It can grow in a variety of soils, but it grows best in sandy loam soil with adequate moisture supply. The growth of trees along irrigated field bunds is significantly greater than that of trees growing in rainfed conditions. This species is a heavy light demander and requires complete overhead light to thrive. The tree can be reproduced through cuttings or seeds. It has great coppicing and pollarding skills and can resist heavy pruning. The tree has great potential in agroforestry combinations in Himachal Pradesh and Garhwal Himalayan regions of India, as no crop loss has been reported under the shade of *G. optiva* bordering irrigated fields (Troup, 1921). *G. optiva* can be grown in an intercropping system with taro (*Colocasia esculenta*) and turmeric (*Curcuma longa*) (Bijalwan and Dobriyal, 2014).

In tropical and subtropical regions of Pakistan, India, China, Malaysia, South Africa, Australia, Northern Thailand, and Nigeria, around 159 species of *Grewia* are cultivated. In India, 42 species of *G. optiva* have been reported, while in Himachal Pradesh, five species have been recorded. Some *Grewia* species produce edible fruit, including *G. asiatica*, *G. optiva*, *G. mollis, G. occidentalis,* and *G. tenax*. (Qamar *et al.,* 2021). *G. optiva* is usually cultivated in Punjab, Haryana, Himachal Pradesh, Uttarakhand, Bihar and other northern Indian states and territories. *G. optiva* is found in Himachal Pradesh between 30 22′44″ N and 33 12′40″ N latitude and 75 45′55″ E and 79 04′20″ E longitude, alongside *Bombax ceiba*, *C. australis*, *Acacia s*pecies, *T. ciliate* and *B. variegata*. (Gamble, 1972).

G. optiva is favoured by the majority of hill farmers in Uttarakhand, Himachal Pradesh, Nepal etc., because it is superior to other fodder tree species in terms of palatability, growth rate, propagation ease and forage yield (Mukherjee *et al.,* 2018). It supplies winter

(lean season) fodder when there is no other green fodder available. *G. optiva* is categorised as a high-quality fodder tree (Sahoo *et al.,* 2016) because its leaves contain a significant amount of nutrients (Katoch *et al.,* 2017). It has a potential dry matter (DM) digestibility of over 70 per cent and an effective degradability of 56.7 per cent, making it a good energy source for ruminants (Singh *et al.,* 1989). Its leaves include 17.4-21.0 per cent crude protein, 17.0-21.5 per cent crude fibre, 10.4-21.5 per cent total ash, 4.2-6 per cent ether extract and 40.4-50.2 per cent nitrogen-free extract (Sankhyan and Bhagta, 2016). A 16-year-old tree is claimed to produce 13.50 kg of leaf feed when lopped in the winter.

According to reports, the Bhimal-based feeding packages for goat production are suitable, sustainable and advantageous for farmers in the central and western hill regions of Nepal (Pandey *et al.,* 2017). *G. optiva* leaf fodder is nearly as nutritious as that of leguminous crops due to its high digestibility, high vitamin and mineral content and its ability to promote microbial growth and the digestion of cellulosic biomass in the rumen of animals (Singh, 1982). The absence of tannins in the leaves of *G. optiva* (Orwa *et al*., 2009) makes it more appropriate for use as fodder. In terms of crude protein, crude fibre, calcium and phosphorus content, green fodder made from the leaves and green succulent branches of beul is comparable to green fodder made from barseem, alfa and cowpea. Additionally, the pruned branches of *G. optiva* have the ability to regain their biomass and carbon-storing capacity. (Rana *et al.,* 2020).

Grewia optiva plant extract is also reported with medicinal properties (Rosa, 2006). As tree is used in the treatment of dysentery, typhoid, diarrhoea, fever, cough and smallpox as "folk" medicine (Ullah *et al.,* 2012). Its different parts are also used to treat skin diseases, hypertension, cancer, malaria and other conditions (Asolkar *et al.*, 1992; Pfau and Skog, 2004). Additionally, wood is used to make axe handles, paddles, cot frames, shoulder poles and tools. The delicate soft branches of this plant are used to make baskets (Gill *et al*., 2016). *G. optiva* shoots are source of natural fibres extracted by processes (Rana *et al*., 2021). Another, fibre can also be obtained from its stem bark is known as ‘bast fibre’. Villagers extract these fibres through the retting process and use them for making ropes, mats, nets, etc. (Kiran *et al*., 2021).

Grewia optiva grows in a wide range of environmental and climatic conditions, which makes it a great plant to study in order to find nutrient-rich strains that can help fill the gap between the need for feed for livestock and the amount that is available. Understanding tree

variation in nature and preserving such variation for future use are required for effective tree breeding. Variation refers to the occurrence of differences among populations and individuals within them as a result of differences in their genetic composition and the environment in which they grow. Variations occur in natural populations of a species due to geographical differences. High genetic variation has been demonstrated within and between populations, and the distribution of variation resulting from histories forms the basis of breeding programmes (Namkoong, 1984). Significant genetic variation is seen in the morphological and physiological features both within and between plant populations (Stebbins, 1950; Stern and Roche, 1974). Even in species that are cited as lacking populational differentiation, there is enough genetic diversity due to environmental influences to anticipate segregation of various genotypes as a response to elevation-related effects (Campbell, 1979).

Although good amount of work has been done on this species, even open pollinated seedling seed orchard and clonal seed orchard have been established of best families and genotypes by the Department of Tree Improvement and Genetic Resources in College of Forestry, UHF Nauni, Solan. But still there was need of screening of *G. optiva* genotypes in different altitudinal ranges of Himachal Pradesh and Uttarakhand to identify further morpho variants and superior nutritive strains/selections of *G. optiva* Drummond. As no work had been done on selection of species in the farmland settings and tree improvement asks for screening of best genotypes by employing morphometric and DNA-markers. The objective of molecular characterisation is to determine the genetic properties of the plants and establish the identity of the accessions and detect genetic link among genotypes. As the use of markers helps us to estimate extent of genetic variation within and among species and gives basis for conservation of superior strains (Gudeta, 2018). It also allows the easy and reliable identification of breeding lines, hybrids and cultivars. The knowledge of the genetic diversity of tree crops is essential for the rational planning of conventional, modern breeding and improvement programmes to increase crop production and quality (Rufai *et al.,* 2013).

The selected sites in Uttarakhand and Himachal Pradesh were explored for variations and a broader base of the species' germplasm in order to establish a germplasm bank. The creation of a germplasm bank aid in the mass-multiplication of superior genotypes as well as the transfer of genetically improved material to end-users. The identification of genetically distinct and superior seed sources of *G. optiva* Drummond in various geographical regions of

Himachal Pradesh and Uttarakhand will aid tree breeders in the development of improved nutritive strains of *G. optiva* via hybridization between distant superior genotypes.

The progeny has been raised from seeds collected from various locations in Himachal Pradesh and the Uttarakhand. Progeny testing is required to estimate the genetic worth of parents while screening the naturally available genetic variations in order to isolate good genotypes rather than simply selecting good phenotypes (Kedarnath, 1982). Progeny testing is a fairly accurate selection approach that selects parent trees based on the performance of their offspring and enables for the direct assessment of breeding values to be used in the selection process.

In light of the information presented previously, the current investigation, which is referred to as "Morphogenetic variation for leaf fodder quality parameters in populations of *Grewia optiva* Drummond," has been carried out with the following objectives:

OBJECTIVES:

i) To study morphological and genetic diversity of *Grewia optiva* Drummond among different populations.
ii) To study physiochemical properties of soil of different populations.
iii) To study variation in fodder quality parameters among different populations.
iv) Molecular markers-based analysis of best studied material.

Chapter-2

REVIEW OF LITERATURE

A brief summary of the work done on various aspects of the current investigations is reviewed under the following headings:

2.1 Morphological and Genetic diversity of *Grewia optiva* Drummond.
2.2 Physiochemical characteristics of soil.
2.3 Evaluation of fodder quality parameters among different populations.
2.4 Molecular markers-based assessment of Genetic Diversity

2.1 Morphological and Genetic diversity

The initial step in any breeding programme is to investigate variation. Variations in morphological expressions can be interpreted as direct evidence of different evolutionary processes taking place within species populations. These can be caused by genetic, physiological, or environmental factors. Differences in morphology between populations are more noticeable than differences within populations.

Genetic diversity refers to the genetic variation of an entire species. It is range of different inherited traits within a species. Many individuals with a wide range of different traits would exist in a species with high genetic diversity. Genetic diversity is essential for a population's ability to adapt to changing environments. Genetic diversity serves several important purposes:

(a) As a resource for tree breeding and improvement programmes aimed at developing well-adapted tree species varieties and increasing genetic gain for a wide range of useful traits
(b) To ensure the overall vitality of forest trees through their ability to withstand a variety of biotic and abiotic stresses under changing and unpredictable environmental conditions.
(c) The livelihoods of indigenous and local communities

Rich genetic diversity within and between species populations is thus a critical foundation for ensuring food security and enabling sustainable development (FAO, 2014). With a few exceptions, forest tree species appear to have allelic variation in the upper ranges of plant species (Fowler and Morris, 1977; Hamrick *et al*., 1981) Trees differ in their ability to grow on different microsites (Campbell, 1979) and they respond to selection for a variety of traits in almost all breeding programmes (Namkoong, 1978). The following literature on Morphological and Genetic variation is reviewed:

Papadool (1970) discovered that the variations in leaf area and petiole length demonstrated diagnostic significance for identifying one-year plants while dealing with poplar clones.

Dicke and Bagley (1980) found discontinuous variation in the morphological characteristics of *Quercus macrocarpa* between different provenances. In addition to this, they discovered a high rate of variation in the growth characteristics of the different sources.

According to Srivastava (1995), who examined the morphological characteristics of *Bauhinia variegata* in several provenances within the states of Himachal Pradesh, Punjab, and Haryana. The Solan provenance excelled in terms of seedling height and number of leaves. Additionally, he came to the conclusion that the best provenances were Palampur for the majority of the nutritional features and Ropar for collar diameter.

Gupta *et al*. (2000) evaluated geographically separated best population of *Grewia optiva* in Himachal Pradesh, India. For this purpose, geographically isolated four populations of *G. optiva* (Nauni, Palampur, Kandaghat and Tattapani) were selected. The investigation found that the fruits from Kandaghat population had the maximum seed length (6.17 mm), seed weight (10.65 g) and seed viability (63.78 %) while Tattapani populations had the lowest values for the studied seed characteristics.

Sankhyan *et al*. (2004) explored morphological variation in different species of seabuckthorn in cold deserts of Himachal Pradesh. Different species showed variation in branch, leaf, thorns and fruit characters under natural conditions. As regards the variation with age in both the species of seabukthorn viz., *Hippophae salicifolia* and *Hippophae rhamnoide,* it was reported that branch, leaf and fruit characters showed increasing trend up to the age of nine years, thereafter it starts declining. In general, the ninth year age was

suggested as the best for harvesting the fruits in both species of seabuckthorn, where all of the characters showed maximum value.

Turna (2004) compared 25 populations taken from natural stands in Turkey based on phenotypic variation of cone, seed and wing morphology, as well as two geographic parameters (altitude and watershed) to study the pattern of natural variation of Oriental spruce. ANOVA revealed that morphological characteristics differed between populations. Furthermore, cluster modelling on morphological characteristics revealed that geographic parameters (watershed and altitude) were divided into distinct group.

In 32 plus *Bauhinia variegata* trees, Wani (2005) examined the reproductive biology and morphological diversity in both greenhouse and field settings. According to the investigations, Pinjore, Kandaghat and Giripul plus tree progenies surpassed all other superior tree progenies in terms of morphological traits like height, diameter, number of branches, leaf area, etc. in a glasshouse. In contrast, for the aforementioned characters under study, the progeny of Renuka plus tree showed the best performance, followed by Subathu, Kunihar and Narag.

Loha *et al*. (2006) investigated the genetic variation pattern in *Cordia africana* (a tropical timber species) at the population level. Bulk seed samples from six natural populations in Ethiopia were collected and analysed for variation in seed morphometric traits, seed germination and seedling growth at the nursery stage. After 4 months of growth, the analysis of variance revealed significant differences between provenances in all studied attributes except root collar diameter. The provenance effect was 71-98 per cent for seed morphometric traits, 80 per cent for germination capacity, 42 per cent for germination energy, 57-58 per cent for seedling height and 3-13 per cent for root collar diameter, as determined by broad sense heritability.

Morphological variations in *Grewia laevigata* Vahl. revealed that some of the traits, *viz.,* branch length, number of leaves per branch, branch nodal length, leaf length, leaf area and seed weight, exhibited variation between the sites but not among the trees. However, leaf width, number of seeds per fruit, seed length and seed width showed non-significant variations. Genotypic correlation coefficients were found greater than phenotypic one for almost all the morphological traits Sankhyan *et al*. (2008).

Wani *et al.* (2009) demonstrated that genotypic correlation coefficient was stronger than the phenotypic correlation coefficient for all morphological traits in *Bauhinia variegata*. According to their findings, shoot fresh weight had a positive and very significant relation with seedling biomass at the phenotypic, genotypic and environmental levels. Leaf area showed a positive and highly significant correlation with seedling biomass at both the phenotypic and genotypic levels.

In the subtropical Garhwal Himalayas, Ashutosh *et al.* (2009) looked at the growth traits of various native fuelwood and fodder tree species. It was determined that *Grewia optiva, Bauhinia variegate* and *Albizia lebbeck* were the best tree species for plantations in the subtropical region of the Garhwal Himalayas based on the results of the seed and growth characteristics.

Bhat (2010) used cluster analysis and dendrograms to investigate genetic divergence. Families namely, HA-2 (PattaBalakar), CH-3 (Balu), SI-8 (Dotliji), SI-11 (Adgu), SI-13 (Sarpadol), and SO-12 (Kasauli) were best in terms of morphometric traits while as SI-3 (Deothal), SO-6 (Amberkothi), HA-1 (Bharari) and SI-5 (Deoltikkeri) were good with respect to seed and seedling traits. On basis of variability and divergence studies, he suggested that variation can be used for any breeding programme of *Grewia optiva* in accordance with its important characteristics in order to obtain heterotic vigour through hybridization. Also he necessitated that improvement in the quality of fodder and production of higher quality planting stock was demanded, which could be accomplished through breeding programmes and selection.

Divakara, 2010 screened twenty-four candidate plus trees from naturally accessible *Pongamia pinnata* genetic resources to determine the genetic variation and relationship of pod and seed features on germination capacity and pick the optimum planting material for improved productivity. Variability experiments showed that genotype CPT-19 had the greatest pod length (65.64 mm), 100-pod weight (542.35 g), 2D surface area (351.18 mm^2), seed length (27.93 mm), 100-seed weight (202.89 g), and total oil content (44.33 %). All characteristics had comparable phenotypic and genotypic coefficients of variation however, 100-pod weight and 100-seed weight had greater values. Seed length had the lowest broad sense of heritability, while 100-pod weight had the highest. Genetic progress as a percent of the mean ranged from 12.30 per cent to 46.04 per cent.

Poonam *et al*. (2012) evaluated the plus tree progenies of *Bauhinia variegata* for morphometric fodder characteristics and their findings revealed that morphometric traits varied significantly among progenies. The best performance was shown by P30 (Dehradun) followed by P15 (Subathu).

Gupta (2012) performed variability analysis on the morphological and fodder quality features of *Anogeissus latifolia* in Himachal Pradesh. The *A. latifolia* was found to be a mild fodder tree species, and if its leaves were coupled with dry fodder grass, it might be a better winter staple meal for feeding cattle and buffaloes.

Wani *et al.* (2012) evaluated morphological and biomass traits of seeds of *Albizzia lebbeck* Benth. from 20 seed sources of different eco-geographic regions of Uttar Pradesh. The traits included under the study were seedling height, collar diameter, internodal length, branches or seedlings, leaf area, fresh weight and dried weight of the shoots and roots, root-shoot ratio and seedling biomass. It was discovered that collar diameter, leaf area, shoot fresh weight and root dry weight all significantly correlated with seedling height. Additionally, there was a significant positive association between seedling biomass and shoot and root dry weights.

Sharma and Kumar (2013) assessed the variation in fruit and seed characteristics between eleven phenotypically superior *Jatropha curcas* plants in Himachal Pradesh. In a study, they determined the range, average, phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic gain. It was determined that there were statistically significant variations in all of the parameters examined. The variation in number of seeds or fruit and seed weight was greater than that of fruit width, seed width, fruit length and seed length. Due to the high heritability of seed length (79.04 %), fruit length (66.61 %), fruit width (66.33 %), and seed weight (47.55 %), it was also determined that there would be significant genetic gain through individual plant selection.

Pyakurel and Wang (2013) conducted leaf morphological variation among different genotypes of paper birch (*Betula papyrifera* Marsh.) and found that leaf area ranged 1.60 cm^2 to 1.84 cm^2. Both the leaf length and leaf width affect the leaf area and ultimately, leaf size.

Provenance variation in seed morphological characteristics, germination and early seedling growth of *Faidherbia albida* (an important agroforestry tree species widely

distributed across parklands and agricultural systems in Africa) was examined by Fredrick *et al.,* 2015. This study revealed highly significant differences among provenances in all studied parameters except for seedling height at month 2 to 5. Highest variation among provenances in seed traits was observed in seed weight while seed thickness had the lowest variation. Overall mean germination among provenances was 70.2 per cent varying from 32.7 to 93.3 per cent. Significant correlation was found between seed length and collar diameter and between temperature and collar diameter.

Prajapati *et al*. (2016) investigated variation in leaf morphology, i.e., petiole length, number of lateral veins, leaf length, maximal leaf width and leaf blade area of *Grewia optiva* at different altitudes. The study was done in an altitudinal range of 1000 m to 2000 m, which was further divided into three different ranges, *viz.,* 1000 to 1300 m, 1301 to 1600 m and 1601 m and above. Three sites in each altitudinal range were selected randomly and in each site one tree under three diameter classes (10-20 cm, 20-30 cm and > 30 cm) each was chosen. The results showed wide variation in all the leaf morphological parameters and most of them were significantly negatively correlated with altitudes except length of petiole. These results indicated that altitudinal gradient largely shapes the leaf morphology of *Grewia optiva* due to humid-hot condition at lower altitude and cool condition at higher altitude which may affect light, nutrients and moisture availability.

Bhat *et al.* (2018) examined different seed and seedling characters of 35 open pollinated progenies of *Grewia optiva* from Himachal Pradesh, for which significant variations were observed. Progeny SI3 (Deothal) was excelled in almost all traits followed by SO-6 (Amberkothi), HA-1 (Bharari), SI-5 (Deyoltikkeri) and CH5 (Rajpura). Seed weight was highly correlated with germination capacity (rg=0.980 and rp=0.642) and germination energy (rg=0.967 and rp= 0.551). Variability estimates were highly significant ($P<0.01$) and genetic traits exhibited high variability for these traits.

Kaur (2018) examined biomass related characteristics of *Grewia optiva* Drummond. High genotypic and phenotypic coefficients of variation were observed in this study for biomass, height, forage yield and number of branches, indicating a wide range of variation. This increased the potential for development through selection. In addition, cluster analysis was conducted and families were separated into five clusters.

The variability characteristics, correlation, and genetic divergence of half-sibling progenies of *Toona ciliata* M. Roem were studied by Kundal *et al*. (2020) under field conditions. For all of the characteristics, phenotypic coefficient of variation (PCV) values were found to be higher than genotypic coefficient of variation (GCV). Moderate heritability and genetic gain were developed for branch angle and plant height. Highly significant and positive genotypic and phenotypic correlations were examined for plant height with collar diameter and stem straightness and collar diameter with number of branches per plant. The genotypes were clustered into three distinct groups with the highest diversity (30.68) found between clusters I and cluster III.

Correlation studies between morphological characters and proximate principles of leaves of *Grewia optiva* Drummond were conducted by Prajapati *et al*., 2020. Leaves from *G. optiva* trees were collected in order to determine correlations among the morphological characters and proximate principles. In the current investigation, a total of 55 correlations were discovered. 13 of these were significant at $p<0.05$ and 5 of them were significant at $p<0.01$.

In the field conditions of Punjab, India, Kundal *et al.* (2020) investigated the juvenile development performance of half-sibling progenies of 24 genotypes of *Toona ciliata* M. Roem. Seed source (S3) Ludhiana demonstrated outstanding performance for growth metrics. The best growth characteristics were found in the progenies of the genotypes S3G7 (Ludhiana), S3G8 (Ludhiana), S1G1 (Talwara), and S2G4 (Kamahi Devi).

Sankhyan *et al*. (2021) examined thirty populations of superior plus trees (20-30 cm diameter) of *Grewia optiva* Drummond (Beul) in six districts of Himachal Pradesh *viz.* Solan, Sirmour, Una, Mandi, Hamirpur and Kangra, to study the variation in morphological descriptors among different populations to study qualitative characteristics, On the basis of overall scoring index of useful desired traits, in bark feature, silver brown has the maximum percentage value (56.11 %), in leaf characteristics, ovate leaf shape (95 %), leaf colour 135-A (Dark green) (26.11 %), leaf serrate margin (87.77 %) and leaf apex acuminate has the maximum percentage value i.e. (85.55 %) among all other qualitative traits studied.

2.1.1 Seed and Seedling Characteristics:

Diokov (1973), who studied the seed weight and seedling characteristics of *Abies alba*, reported a slight tendency of 1000 seed weight to decrease with decreasing latitude of

the provenances, but seed weight was not found to be obviously related to provenances. From the most northern to the most southern provenances, the development index increased gradually.

In India and Nepal, Devagiri *et al.* (1998) studied seed source variation in pod and seed characteristics of *Dalbergia sissoo*. Significant discontinuous variation was observed between seed sources for pod and seed characteristics, particularly seed weight and seed number per pod.

Thakur *et al.* (2000) examined six months old seedlings of *Alnus nitida* (Kosh). He discovered that high heritability with high genetic advance for traits such as number of branches per plant, number of leaves per plant, collar diameter and shoot height, indicating the presence of additive gene effect. In *Alnus nitida,* there was a significant positive correlation for leaf length, leaf breadth, and number of leaves per plant at both the genotypic and phenotypic levels.

Jha (2001) examined 59 open-pollinated, two-year-old families of *Dalbergia sissoo* f. The investigations found that for seedling height, collar diameter, dry leaf weight, leaf area, nitrogen, phosphate, potassium, total phenol and total sugars, the genetic gain for within-family selection was higher than that of family selection. The maximum heritability within family was observed for collar diameter and total phenols and minimum heritability for phosphorus content. Also, remarkable diversity amongst the fifty-nine families of *D. sissoo* was recorded based on non-hierarchical Euclidean analysis at two year age.

Anand (2003) evaluated the progeny of plus trees of *Bauhinia variegata* under nursery conditions. He noticed that genotypic correlation coefficients were greater than the phenotypic correlation coefficients for morphological traits, biomass, mineral nutrients and proximate principles for *Bauhinia variegata*. Highly significant and positive genotypic and phenotypic correlations were observed for morphological and biomass traits such as seedling height, collar diameter, number of nodes, number of leaves, leaf area and fresh shoot weight, whereas only leaf fresh weight was positive and significant among proximate principles.

Singh and Bhat (2008) investigated provenance variation in pods, seeds and seedling characteristics of *Dalbergia sissoo* in the Central Himalayas. For their investigation, they collected seeds from 19 sources located between 120 and 1130 m altitudinal range. In a

nursery and field trial, pods, seed morphology, seed weight, seed germination and seedling growth characteristics were also evaluated. Pod and seed characteristics, such as germination, plant height and collar diameter, exhibited morphological and physiological differences between provenances and seed origins. Numerous parameters, including seed weight and plant height were found to have a high heritability, as well as a high genetic advance and genetic gain. It was determined that characters with greater genetic influence could be directly screened or selected to increase the potential of this species in the Central Himalayas to produce high-quality planting material and increase its productivity.

In order to conduct their research on *Grewia optiva* (Bhimal), Tewari *et al.* (2008) obtained one-year-old seeds from the Indian Grassland and Fodder Research Institute in Jhansi and treated them before sowing. It was discovered that soaking seeds in water for 24 hours after being treated with concentrated sulfuric acid for 15 minutes resulted in 44 per cent germination, which was higher than other treatments.

Hooda *et al.* (2009) selected 30 plus trees of *Pongamia pinnata* (Karanj) and concluded that superior plus trees from cluster III and cluster V could be used as superior parents due to their high cluster mean and wide genetic distance. Progenies showed significant variation in germination percentage, seedling biomass, collar diameter, shoot length, and root length. Heritability and genetic advance were also moderate to high for parameters such as seed weight, collar diameter, root length, shoot length, oil and protein content as a percentage of mean, indicating the efficacy of selecting for these characters in developing productive trees.

Singh *et al.* (2010) examined provenance variation in seed and seedling characteristics of *Quercus glauca* Thunb. A significant difference in seed and seedling attributes with population. The altitude of the seed source had a significant inverse correlation with seed length, seed weight, and seedling weight. However, there was a positive correlation between altitude and seedling root collar diameter and percentage germination. There was also a significant positive correlation between seed weight and seedling weight.

2.2 Physiochemical Characteristics of Soil:

Soil has unique chemical, physical, mineralogical and biological properties that make it an ideal medium for plant growth (Thakre *et al.,* 2012). To determine the available nutrient status in soil and its relationship with tree growth characteristics, it is also necessary to

understand the physiochemical properties of soil, such as organic carbon, available Nitrogen (N), Phosphorus, Potassium, pH, electrical conductivity and bulk density (Sumithra *et al.,* 2013). Plants are stressed by nutrient deficiency when the availability of soil nutrients is less than what is required to sustain metabolic processes during a specific growth stage. This could be due to the inherently low nutrient status of the soil, low nutrient mobility within the soil, poor solubility of the given form of the nutrient or soil-microbe-plant interactions (Rengel, 2015). The following literature on soil physiochemical properties are reviewed:

Verma *et al.* (1976) noted that the cultivated soils of Kangra region of Himachal Pradesh were deficient in available Nitrogen. Verma and Tripathi (1982) reported that available nitrogen concentration in Una and Hamirpur districts varied from 113 to 228 kg ha^{-1} while it ranged from 295 to 503 kg ha^{-1} in Kangra, Mandi, Bilaspur, Shimla and Sirmaur districts of Himachal Pradesh.

Verma *et al.* (1976) reported that the cultivated soils of Kangra region of Himachal Pradesh were short in available phosphorus. Ghosh and Hasan (1979) discovered that available P content of Indian soils was medium, low and high to the extent of 52, 46 and 2 per cent, respectively. Verma *et al.* (1985) characterized the soils of Kangra, Kullu, Mandi and Sirmour regions of Himachal Pradesh and found available P level ranged from 2.69 to 28.22 kg ha^{-1}.

Ghosh and Hasan (1976) categorised the vast majority of Indian soils as medium, high and low in available K, with proportions of 42 per cent, 38 per cent and 20 per cent respectively. According to Verma *et al.* (1976), the cultivated soils in the Kangra region of Himachal Pradesh were deficient in available potassium. Verma *et al.* (1985) characterized the soils of Kangra, Kullu, Mandi and Sirmaur regions of the Himachal Pradesh and found the available K content ranging from 4.26 to 1507 kg ha^{-1}.

Bishnoi *et al*. (1983) found organic carbon contents under different locations in Himachal Pradesh varied between 0.19 to 5.43 per cent. The studies carried out by Singh and Datta (1988), Lahiri and Chakravarti (1989), Gangopadhyay *et al*. (1990) and Mandal *et al* (1990) indicated an increase in organic carbon content with the increase in elevation. It was further observed that organic carbon content was high in the surface horizons which sharply decreased in the sub-surface horizons of the profiles.

Several reasearchers (Gangopadhyay *et al*, 1990; Sahu and Patnaik, 1990; Verma *et al*, 1990; Walia and Chamuah, 1990) reported that soil pH values ranged from 4.3 to 9.9 in various parts of the country. In the central Himalayas of Himachal Pradesh (Kaistha and Gupta, 1993), the pH varied from 6.7 to 7.7. Whereas, in the mid altitude of outer Himalayas pH ranged from 6.5 to 8.4 (Singh *et al.,* 1991) and 5.1 to 9.8 in the soils of North-Western Himalayas (Kaistha *et al*., 1990; Sahu and Patnaik, 1990).

The pH values were noticed to increase with depth, possibly due to leaching of bases (Kaistha *et al*. 1990, Sahu and Patnaik, 1990 and Walia and Rao, 1996). Minhas *et al.* (1997) found that the pH in the cultivated soils of Palampur (Kangra district) and Ahju (Mandi district) ranged from 5.3-6.5.

Nitrogen is the fourth most abundant nutrient taken up by plants, after carbon, oxygen, and hydrogen. The total N content of a soil is directly proportional to its organic carbon content and it ranges between 0.03 and 0.04 per cent by weight in cultivated soils (Mengel and Kirkby, 1987; Tisdale *et al*., 1995).

According to Kaistha *et al.* (1990), the organic carbon content of the soils in various parts of Himachal Pradesh ranged from 0.3 to 8.33 per cent. According to Tripathi *et al.* (1992), the organic carbon content of soils in the Mandi district ranges from 0.20 to 2.6 per cent. With a rise in altitude, the organic carbon content of soil surface horizons rose (from 0.9 % to 3.6 %). Low levels of organic carbon were present in the agricultural soils in the Kangra district of Himachal Pradesh (Minhas *et al.,* 1997).

Khan *et al.* (1997) examined that available phosphorus was greatest at the surface and decreased with depth. Pandey *et al.* (2000) discovered that the availability of P in various soil associations of Uttar Pradesh's Kanpur district varied widely. Available P contents ranged from 7.7 to 55.4 kg ha^{-1} and correlation studies revealed that organic matter and finer soil particles considerably and positively influenced P availability.

According to Sharma *et al.* (1998), the soils in the Loon basin of Kangra district have a medium availability of potassium. 52 per cent, 39 per cent and 9 per cent of Indian soils, respectively, had high, medium and low levels of potassium that was readily available (Anonymous, 2001). According to Mahajan (2001), the soils in the Mandi district have a medium level of available K (231 to 235 kg ha^{-1}).

In Indo-Gangetic plains of the Bihar, Sarkar and Sahoo (2000) discovered that the organic carbon content of the soils ranged from 0.08 to 0.86 per cent and gradually decreased with depth. Verma and Tripathi (2007) investigated the condition of the mid-Shivalik hills in Himachal Pradesh and found that the organic carbon content of these soils generally ranged from 0.10 to 2.77 per cent.

Sharma *et al*. (2002) found that soils in Fatepur block of the Himachal Pradesh ranged from low to high in available nitrogen. According to Sharma and Kumar (2003), agricultural lands in the mid-hill zone of Himachal Pradesh had medium to high levels of available Nitrogen. Tandon (2004) reported that approximately 63 per cent of Indian soils were deficient in available nitrogen.

Out of 3,650,004 samples of Indian soil, Motsara (2002) found that 13 per cent, 37 per cent and 50 per cent respectively, fell into the low, medium and high categories for potassium (K) availability. Sharma *et al*. (2002), showed that soils in the Fatepur block of Himachal Pradesh contained low to medium quantities of readily available K. In the hill soils of the North-Western Himalayas, nitrogen, phosphorus, and potassium levels were examined by Tripathi *et al*. (2007). The average potassium concentration, according to their report was 289 kg ha^{-1}.

Sharma and Kumar (2003), in their study, reported poor to high range of available potassium in the soil of mid-hill region of Himachal Pradesh. Tandon (2004) showed that approximately 21 per cent of Indian soils were low in available potassium.

Tripathi *et al*. (2005) examined the soils from four agro-climatic zones covering the districts of Kangra, Kinnaur, Sirmour, Chamba and Bilaspur of Himachal Pradesh. The average EC of soils of different districts were: Bilaspur 0.24 $dSm-^{1}$, Chamba 0.26 dSm^{-1}, Kangra 0.15dSm^{-1}, Kinnaur 0.37dSm^{-1} and Sirmour 0.20 dSm^{-1} and the average of all soils was recorded to be 0.24 dSm^{-1}. In Himachal Pradesh, soil of the mid Shiwalik hills had very low soluble salt concentrations with EC ranged from 0.01 to 0.15 dSm^{-1}, according to Verma and Tripathi (2007).

Paoli *et al.* (2007) investigated the relationship between soil fertility and aboveground biomass in lowland tropical forests. They quantified the impact of soil variation on the stand structure of mature Bornean forest across a lowland watershed using categorical and bivariate

methods (8-196 m a msl).Trees ≥ 10 cm (diameter at breast height, dbh) were enumerated in 30 (0.16 ha) plots (sample area = 4.8 ha). Six soil samples (0-20 cm) were collected from each plot and analysed for physiochemical properties. Allometric equations were used to calculate aboveground biomass. Across all plots, stem density averaged 521± 13 stems ha^{-1}, basal area 39.6 ± 1.4 m^2 ha^{-1} and aboveground biomass 518 ± Mg ha^{-1} (mean ± SE). Although stand structure did not differ significantly across substrates, but it did show a clear trend toward larger stature on nutrient-rich alluvial, with a higher density and larger maximum size of emergent trees. Across all plots, surface soil phosphorus (P), potassium, magnesium and percentage sand content were significantly related to stem density and aboveground biomass ($R_{Pearson}$= 0.368-0.416). Regression analysis on size classes showed that the abundance of emergent trees > 120 cm dbh was positively related to soil P and exchangeable bases, whereas trees of 60-90 cm dbh were negatively related to these factors. Thus, soil fertility had a significant influence on both total aboveground biomass and its distribution among size classes.

A study done by Muche *et al.* (2015) to assess the physiochemical properties of soil under various Land use types, including natural forest, cultivated land, plantation forest and grazing land. The result showed that soils in the natural forest had significantly higher soil pH and lower exchangeable acidity. Similarly, natural forest soil had significantly higher exchangeable bases, total nitrogen, organic matter, available potassium, CEC and clay content than other land use types. The study also discovered a significant difference in available phosphorus among different land use types.

Kumar *et al.* (2016) examined the effects of growing medium and seed size on germination and seedling growth of *Pinus gerardiana.* The seeds were divided into two sizes *viz.,* small and large and five growing medium treatments were used, *viz.*, Soil: Sand: Moss: FYM; Soil: Moss: Vermicompost; Soil: Sand: Vermicompost and Soil: Sand: Moss: Vermicompost, for assessing their impact on germination and seedling growth. Higher germination and seedling growth parameters were recorded among different growing medium treatments when Soil: Sand: Moss: Vermicompost was used for the study.

Edori and Iyama (2017) evaluated physiochemical parameters of soils from selected Abattoirs in Port Harcourt, Rivers state Nigeria. The pH of the soils was found to be acidic, ranging from 4.59 ± 0.03–4.99 ± 0.14, temperature from 33.14 ± 1.29 -35.04 ± 0.96°C, while

salinity had a range of 27.531.91-58.65 ± 2.25. Total nitrogen and nitrogen-based parameters were all very low in concentration in the soil. Extractable phosphorus content in the soil ranged from 0.66 ± 0.03-1.34 ± 0.33 per cent, total organic carbon ranged from 12.81 ± 0.15-16.41 ± 0.49 per cent and total organic matter ranged from 22.33 ± 0.86-29.58 ± 0.72 mg/Kg. The results showed that human activities within the Abattoir had an impact on the physicochemical speciation of the Abattoirs.

2.3 Evaluation of Fodder Quality Parameters:

Animals can get their fodder from the leaves of trees and shrubs and the fodder that comes from these sources is just as nutritious as the fodder that comes from leguminous fodder crops. If we want to see an improvement in the overall output of cattle, we absolutely must ensure that we have access to high-quality tree fodder. An overview of the work that has been done on this subject is as follows:

According to the study conducted by Negi in 1979, the chemical composition of *Grewia optiva* leaves on oven dry basis was reported to be as follows: crude protein 17 to 20 per cent, ether extract 2.17 to 6.70 per cent, crude fiber 18.88 to 22.12 per cent, N free extract 41.73 to 48.9 per cent, total ash 9.60 to 14.30 per cent, calcium 2.79 to 3.55 per cent and phosphorus 0.14 to 0.30 per cent. Young leaves had a high crude protein content, which then steadily reduced as the wet season progressed and then increased once more in the winter. The percentage of crude fibre was likewise greatest during the monsoon season. Over the course of the year, there was not a significant shift in the total amount of ash, calcium, or phosphorus.

Khosla (1992) reported leaf production, leaf fall, leaf protein and net primary productivity for 4-year-old fodder trees in the mid-western Himalaya (altitude 1350 m; rainfall 1100 mm). The species include; *Grewia optiva, Robinia pseudoacacia* and *Celtis australis* growing in the open and *Quercus glauca, Q. leucotrichophora* and *Ilex odorata* growing in the forest. *G. optiva, R. pseudoacacia*and *C. australis* exhibited two distinct phases of leaf flush and the lifespan of its leaves ranged from 180 to 360 days, in contrast to the other three species, each of which maintained its leaves for more than two years and exhibited only a single flush period between the months of March and April. The open site species showed much higher leaf production and the leaves contained a significantly higher

protein content, compared with the forest group. Net primary productivity of *G. optiva, C. australis* and *R. pseudoacacia* was significantly higher than the forest species.

Sharma *et al.* (1966) discovered that leaves of *Grewia optiva* contains 19.69 per cent crude protein, 4.55 per cent ether extract, 19.33 per cent crude fiber, 10.77 per cent total ash content and 45.66 per cent nitrogen free extract.

Manga and Sen (2000) investigated the nutrient content of *Prosopis cineraria* and found that crude protein ranged from 18.02-22.71 per cent, Sodium 0.245-0.708 per cent, potassium 0.646-1.573 per cent, calcium 1.042-2.208 per cent and phosphorus 0.260-0.346 per cent.

Yan *et al.* (2000) collected leaves from four strains of *Morus alba* (Mulberry) that were propagated in China. The leaves were sampled at three stages of maturity in spring and autumn. The nutritional value of leaves was assesed in terms of chemical composition, amino acid content and *in vitro* gas production. Except for one strain that was slightly inferior to other strains, there was no significant difference in chemical composition among different strains regardless of season. Also a little seasonal difference was observed in content of crude protein (CP) and true protein (TP) of mulberry leaves.

Khanal and Subha (2001) examined the nutritional value of Nepalese fodder tree leaves. He found that fodder tree leaves had 22-53 per cent dry matter, 11-22 per cent crude protein, and 5-17 per cent ash. Most tree fodder leaves had Ca >1 per cent, K >1 per cent, Mg >0.25 per cent, and Na <0.06 per cent. Phosphorus was generally 0.16–0.40 per cent. Lignin content was high in most of the species with values more than 10 per-cent on DM basis. Tannin content in most of the species was more than one per cent, with highest values (>12 %) found in the genus *Terminalia*.

Jain *et al.* (2002) studied the chemical and biochemical properties of Neem leaves from eleven different agroclimatic regions of Madhya Pradesh, Chattisgarh and Orissa. It was correlated with soil properties under geographical ordinates in order to obtain maximum productivity of desired character from that site or to artificially induce a suitable environment for better suitable environment for better productivity and the desired characters. The amount of leaf protein ranged from 8.76- 15.48 per cent and polyphenols from 2.4-7.1 per cent. The

marginal variation in leaf nitrogen (1.35-2.47 %) of different sites indicated that nutrient uptake potential and availability are nearly identical.

Anoop and Sharma (2003) reported that the leaves of *Grewia optiva, Emblica officinalis, Leuceana leucocephala, Albizia lebbeck,* and *Browssonentia papyrifera* had high nutritive value.

Singh *et al.* (2004) recorded the higher value of crude protein in the leaves of *Abizia lebbeck* (21.52 %), *Robinia psudoacacia* (20.67 %), *Grewia optiva* (19.435 %), *Morus alba* (18.87 *%), Pongamia pinnata* (16.79 %), *Acacia catechu* (15.92 %), *Toona ciliata* (15.55 %), *Dalbergia sissoo* (15.265 %) and *Ficus religiosa* (15.17 %).

Bakshi and Wadhwa (2004) analysed leaf samples of 13 species fed to livestock in the semi-hilly arid zones of Punjab. For a period of 12 months, leaves were collected every 30 days to assess their nutritional value for livestock. The samples were collected during four distinct seasons: dry hot, hot humid, fall and winter. The predominant protein fraction in the majority of the leaves was globulin. In contrast to the summer, they discovered that leaves generally got more fibrous and lignified during the winter and fall. The leaves of *Grewia optiva, Morus alba*, *Leucaena leucocephala, Carrisa spinarum* and *Acacia nelotica* were rich in Ca, P and most of the trace elements. Additionaly the minimum rumen fill values also demonstrated that leaves of *Azardirachta indica, Ehretia leavis, G. optiva, M. alba,* and *L. leucocephala* had good potential for voluntary dry matter intake. Whereas, leaves of *Ougeinia oojeineusis, Dodonea vicose* and *C. spinarum* had higher rumen fill value indicating poor potential for voluntary dry matter intake. It was further concluded that the leaves of *M. alba, E. leavis, G. optiva* and *L. leucocephla* had great potential as livestock fodder, while feeding of leaves of *O. oojeineusis* and *D. viscose* should be avoided.

Pathak *et al*. (2005) observed the proximate composition of green leaves of 15 fodder trees of subtropical zone of Himachal Pradesh and found that *Grewia optiva, Albizia lebbeck, Leucaena leucocephala, Dalbergia sissoo, Robinia pseudoacacia, Zizypus maurtiana* had a good percentage of crude protein and also indicated that these species had almost higher nutrient content. The foliage leaves of these species were comparable to the nourishing legume feed berseem (*Trifolium alexandricum*) in terms of nutritional components.

Danny *et al*. (2006) examined the adaptability, chemical composition, nutritional value and secondary metabolites level of ten fodder legume species, including *Albizia caribaea, Albizia lebbeck, Cassia fistula, Cassia grandis, Pithecellobium dulce, Pithecellobium saman, Gliricidiasepium, Leucaena macrophylla* and *Enterolobium contortisilicum*. The results showed that the species with the highest levels of polyphenolic chemicals and saponins were not browsed. All of the tested legume species had leaves and foliage that were acceptable in terms of nutrient content. To feed ruminants, the best supplements were found to be *Albizia lebbeck, Pithecellobium dulce, Gliricidia sepium*, and *Enterolobium contortisilicum.*

Lavania *et al.* (2006) studied that the farmers prefer to plant tree species like *Grewia optiva, Bauhinia variegata, Celtis australis, Morus alba* which gives nutritive and highly digestible fodder, especially during the lean periods when other sources of green fodder are not available.

Datt *et al.* (2008) assessed the leaf fodder quality of 12 multipurpose trees and shrubs of subtropical humid climate of India that were cultivated in agroforestry arboretum. The evaluation was carried out in order to assess their nutritional qualities. The average values noted were as follows 92.02 ± 0.30 per cent for organic matter, 16.00 ± 0.74 per cent for crude protein, 3.05 ± 0.13 per cent for ether extract, 18.97 ± 1.07 per cent for crude fibre, 54.00 ± 1.12 per cent for nitrogen free extract and 7.98 ± 0.30 per cent for total ash on Dry Matter basis. It was observed that leguminous trees had high crude protein, *viz.,* 18.30 per cent as compared to non-leguminous, *viz.,* 13.70 per cent and on this basis, it was concluded that *Leucaena leucocephala* was a good quality fodder, while *Gliricidia maculate, Morus alba, Azadirachta indica, Dalbergia sissoo and Samanea saman* were of medium type while the rest, *i.e.*, *Acacia auriculiformis, Albizzia procera, D. sissoo, Eucalyptus hybrids, Gmelina arborea, Michelia champaca* and *Tectona grandis* were of poor quality.

Thakur *et al.* (2008), studied variation and correlation for leaf dry matter and mineral nutrients in *Grewia optiva* Drummond. Studies were conducted on three diameter classes, at three sites that were located at three different altitudes in Himachal Pradesh. Leaf dry matter and mineral nutrient content for nitrogen (N), phosphorus (P) and potassium (K) among different diameter classes was found between 42.29 to 57.26 per cent, 2.40 to 2.95 per cent, 0.14 to 0.33 per cent and 2.37 to 2.64 per cent, respectively. The presence of significant

correlations between different character pairs indicated the possibility of indirect selection in the species.

There were various ranges for the leaf and fodder qualities were observed by Sankhyan *et al*. (2009) while analysing *Grewia laevigata* from Shiwaliks. 73.34–83.40 g, 32.82–40.13 g, 16.08–17.43 per cent, 13.17–14.47 per cent, 2.79–3.124 per cent, 8.226–10.04 per cent and 54.95–58.79 per cent respectively for 100 leaf fresh weight, 100 leaf dry weight, crude protein, crude fibre, ether extract, ash content and nitrogen free extract.

Singh *et al*. (2009) evaluated chemical composition of *Acacia catechu, Bauhinia variegata, Ficus religiosa, Grewia optiva, Leucaena leucocephala, Melia azedarach, Morus alba and Salix alba*. The tree leaves were examined for contents of Organic matter (OM), Ether extract (EE), Crude fibre (CF), Crude protein (CP), Total Ash (TA), Nitrogen free extract (NFE), Neutral detergent fibre (NDF), Acid detergent fibre (ADF), Calcium (Ca) and Phosphorous (P). In *Acacia catechu* (Khair) the contents were as follows: (91.36 %) OM, (3.65 %) EE, (12.63 %) CF, (19.06 %) CP, (8.64 %) TA, (56.02 %) NFE, (37.44 %) NDF, (20.27 %) ADF, (2.95 %) Ca and (0.21 %) P. In *Albizia lebbeck* the contents were (92.82 %) OM, (6.63 %) EE, (22.97 %) CF, (27.42 %) CP, (7.18 %) TA, (35.81 %) NFE, (41.77 %) NDF, (28.46 %) ADF, (1.95 %) Ca and (0.27 %) P. In *Bauhinia variegata* the contents were as follows: (93.38 %) OM, (2.89 %) EE, (19.32 %) CF, (16.47 %) CP, (6.62 %) TA, (54.71 %) NFE, (40.30 %) NDF, (30.56 %) ADF, (2.15 %) Ca and (0.25 %) P. In *Ficus religiosa* the contents were (84.78 %) OM, (3.4 7%) EE, (23.18 %) CF, (13.48 %) CP, (15.22 %) TA, (44.66 %) NFE, (43.53 %) NDF, (33.73 %) ADF, (3.65 %) Ca and (0.26 %) P. In *Grewia optiva* the nutrient contents were (90.17 %) OM, (21.13 %) CP, (2.88 %) EE, (14.25 %) CF, (9.84 %) TA, (51.92 %) NFE, (35.46 %) NDF, (22.40 %) ADF, (2.73 %) Ca and (0.29 %) P. In *Melia azedarach* the contents were as follows (90.83 %) OM, (3.82 %) EE, (9.77 %) CF, (22.30 %) CP, (9.17 %) TA, (54.95 %) NFE, (24.26 %) NDF, (18.28 %) ADF, (1.32 %) Ca and (0.29 %) P. In *Morus alba* the contents were (85.33 %) OM, (5.49 %) EE, (14.67 %) CF, (19.94 %) CP, (8.64 %) TA, (51.26 %) NFE, (28.92 %) NDF, (22.71 %) ADF, (2.96 %) Ca and (0.30 %) P. In *Salix alba* the contents estimated were (93.62 %) OM, (2.94 %) EE, (12.12 %) CF, (12.55 %) CP, (6.38 %) TA, (66.01 %) NFE, (46.49 %) NDF, (29.65 %) ADF, (1.71 %) Ca and (0.22 %) P.

Bhat (2010) examined the proportion of proximate fodder in 35 families including ether extract, crudefibre, crude protein, ash content, and nitrogen free extract with percentage

ranging from 18.01 to 22.03 per cent, 18.33 to 21.75 per cent, 10.32 to 13.26 per cent, 4.30 to 5.74 per cent and 39.42 to 45.63 per cent, respectively. Based on these criteria, the best families were identified to be families SI-8 (Dotliji), SI-13 (Sarpadol), HA-1 (Bharari), HA-2 (Patta Balakhar) and SI-11 (Adgu).

Azim *et al.* (2011) assessed the nutritional value of leaves from various fodder tree and found that *Acacia nilotica* contained (44.78 %) Dry Matter, (11.8 %) Crude Protein, (13.91 %) Crude Fibre, (7.86 %) Ash content, (2.73 %) Ether Extract and (63.69 %) Nitrogen Free Extract. While, *Albizia lebbeck* contained (37.24 %) Dry Matter, (19.50 %) Crude Protein, (26.5 %) Crude Fibre, (10.41 %) Ash content, (5.04 %) Ether Extract and (38.60 %) Nitrogen Free Extract. Whereas, *Grewia optiva* contained (38.17 %) Dry Matter, (19.37 %) Crude Protein, (17.83 %) Crude Fibre, (13.91 %) Ash content, (2.52 %) Ether Extract and (6.37 %) Nitrogen Free Extract. *Melia azedarach* contained (21.70 %) Dry Matter, (14.09 %) Crude Protein, (18.96 %) Crude Fibre, (5.30 %) Ash content, (4.04 %) Ether Extract and (57.61 %) Nitrogen Free Extract. Whereas, *Morus alba* contained (54.69 %) Dry Matter, (15.43 %) Crude Protein, (18.49 %) Crude Fibre, (12.17 %) Ash content, (6.45 %) Ether Extract and (47.46 %) Nitrogen Free Extract.

Sheikh *et al*. (2011) investigated the nutritional value of the leaves of *Acacia nilotica*, *Morus alba* and *Salix tetragonal*. The results illustrated that for *A. nilotica* Dry matter content was (88.45 %), Crude Protein (15.53 %), Ether extract (6.3 %), Crude Fibre (18.03 %), Nitrogen Free Extract (55.14 %), Ash content (5.0 %), Ca (3.41 %) and P (0.15 %). While, *Morus alba* contained (87.76 %) DM, (15.79 %) CP, (7.0 %) EE, (14.67 %) CF, (51.04 %) NFE, (32.09 %) NDF, (23.78 %) ADF, (11.5 %) Ash content, (3.45 %) Ca and (0.46 %) P. Whereas, *S. tetragonal* had (91.53 %) DM, (16.40 %) CP, (5.80 %) EE, (15.33 %) CF, (59.38 %), NFE, (43.76 %) NDF, (24.84 %) ADF, (8.0 %) Ash content, (2.03 %) Ca and (0.22 %) P.

Singh and Todaria (2012) conducted research on the variations in the nutritional composition of *Quercus semicarpifolia* leaves at various altitudes and seasons. In 2008-2009, leaves were collected from five geologically isolated sites ranging in altitude from 2450 to 2725m a msl for the purpose of evaluating their chemical composition between four seasons, *i.e.,* prior to the growing season, following the growing season, during the growing season, and upon late maturation, respectively. Seasonal variability was found in the chemical composition of the *Q. semecarpifolia* foliage. On average, the ash per cent in the foliage

varied from 3.36 to 4.47, with the greatest value in the April (growing season). The crude protein content concentration was significantly higher in July (after growing season), whereas ether extract was higher before growing season (January). The crude fiber content concentration was maximum (54.78 %), during the growing season, and a significant decrease was recorded from July (33.21 % after growing season) to October (37.58 % late maturity). The Phosphorus concentration in leaves was maximum (0.16 %) in July (after growing season) which later decreased to 0.12 per cent in October, the lowest value of 0.10 per cent was observed in January. The Ca concentration decreased during growing season and leaf fall. Nitrogen free extract (52.01 %) and organic matter (96.64 %) were higher in July. Ash contents, CP (crude protein), EE (ether extract), phosphorus exhibited significant variation among populations. CP was significantly higher in middle to higher altitudinal populations. P significantly decreased with increasing altitude. The rest of the studied mineral contents did not show any trend in the present study. The nutritive value of the leaves of *Q. semicarpifolia* was continually changing, especially CP and soluble protein. *Q. semicarpifolia* harvested at the proper stage of maturity (winter months) offers considerable potential as high-quality forage for livestock to fulfill the deficiency of protein.

Hashmi and Waqar (2014) assessed nutritional variation in *Grewia populifolia* and *Grewia optiva* at different sites during different seasons. Leaf samples of both the species were taken for nutritional analysis. The findings demonstrated that both the species were good source of fodder for animals and have high nutritive value.

Takele *et al*. (2014) evaluated the potential yield and chemical makeup of selected indigenous multipurpose fodder trees in three districts of Wolayta zone, Southern Ethiopia. A total of 28 indigenous MPFT species were identified. The five important MPFT species *viz*; *Erythrina brucei, Vernonia amygalina, Ehertia cymosa, Cordia africana* and *Dovylasa byssinica* from identified indigenous fodder tree species were taken for biomass estimation and laboratory analysis. Potential yield of the selected MPFTs ranges from 25 kg for *D. byssinica* in Humbo district to 959 kg for *Erythrina brucei* in Sodo Zuria district and vary significantly ($P < 0.05$) among the selected MPFTs and among the districts. The five selected indigenous MPFT species had chemical composition of 11–21 per cent crude protein, 8-14 per cent ash, 38-56 per cent neutral detergent fiber, 33-51 per cent acid detergent fiber and 9-17 per cent lignin, indicating their wide variability among species ($P < 0.05$). It can be

concluded that the indigenous MPFT species can be considered to be a potential source of CP to supplement poor quality roughages to fill the gap especially in dry season.

Bhandari *et al*. (2015) studied fourteen species of Bamboo for genetic evaluation of nutritional and fodder quality. The results showed that the 14 species of bamboo were grouped into four clusters based on divergence analysis of pooled data. Cluster I had maximum number of species (7), Cluster III had four species whereas, Cluster II and Cluster IV had maximum of (2) and (1) species respectively. Maximum intra-cluster distance was in Cluster II (46.03) and maximum inter-cluster distance was between cluster II and IV (96.84). Correlation analysis revealed that leaf:stem ratio, biomass, crude protein content, dry matter digestibility had major contribution in determining the nutritive potential of green and dry forage yield.

A study was conducted by Prajapati (2015) on assessment of fodder quality and morphological variation of *Grewia optiva* Drummond in parts of Garhwal Himalaya at three different altitudinal ranges. The study concluded that the population of altitudinal range 1300 to 1600 m amsl was found best suited for optimum growth. He also found that nutritional potential of *G. optiva* was high in this altitudinal range.

The results of a study that was carried out by Prajapati *et al*. (2019) on the variation in proximate principles and correlation studies in *Grewia optiva* along altitudinal gradient in Garhwal Himalaya showed that the altitudinal gradient had a significant impact on the proximate principles. The correlation coefficient indicated significant positive relation between altitude and dry matter and negative with ash contents. Diameter class showed significant positive relation with ether extract and crude fibre while negative relation with dry matter, crude protein and ash content. Highest crude protein (14.70 %) and low crude fibre (16.17 %) contents were observed at the mid-altitude and the higher altitude had better dry matter (57.11 %), ether extract (3.56 %), crude fibre (17.64 %) and nitrogen free extract (59.47 %) contents.

Sankhyan and Bhagta (2016) examined various seed and germination parameters, morphometric and fodder quality characteristics, of the 20 best seed bearing families of *Grewia optiva*. The percentage for these proximate fodder analysis, namely crude protein, crude fiber, ash content, ether extract, and nitrogen free extract, varied between 17.35-20.99 per cent, 17.00-21.51 per cent, 10.42-21.50 per cent, 4.21-5.99 per cent and 40.41-50.24 per

cent respectively. For seed parameters families, SO-6 (Amberkothi), KA-3 (Varal), HA-1(Bharari), KA-2 (Bhalun) excelled as the best one.

Pandey (2017) developed four types of experimental diets which were having various levels (0 to 100 %) of bhimal (*G. optiva*) leaves as fodder. Experimental animals of Treatment 1 were fed with seasonal fodder + 100 g concentrate mixture, Treatment 2 with 100 per cent bhimal fodder + 100 g concentrate mixture, Treatment 3 with 75 per cent bhimal fodder + 25 per cent seasonal fodder + 100 g concentrate mixture, while Treatment 4 with 50 per cent bhimal fodder + 50 per cent season fodder + 100 g concentrate mixture. The diets offered and refusal was measured daily and weight change was observed fortnightly. The result showed that fodder intake (g/d/animal) and total dry matter intake (TDMI g/kg live weight) of goats differed significantly ($P<0.01$), but concentrate intake was not differed significantly ($P<0.01$) among treatments. The highest dry matter intake per animal /day was in Treatment 2 (52.75 g/kg live weight) followed by Treatment 4, Treatment 3 and Treatment 1 (51.7, 48.56 and 32.69 g/kg live weight, respectively). The average daily gain in body weight was observed highest in Treatment 2 (66.66 g/d) followed by Treatment 3 (31.66 g/d) and Treatment 4 (30.83 g).

Luske and Eekeren (2018) observed the effect of soil type and season on the nutritional potential of leaves from *Fraxinus excelsior, Alnus glutinosa* and *Salix viminalis*. Leaf samples were collected at 10 sites in the Netherlands on clay and on sandy soil in June, July and September and were evaluated for digestibility, crude protein, macro and micro element concentrations. They concluded that the nutritional value of tree leaves differed between the studied tree species. Regarding the seasonal variation, they found a main effect of sampling period on the crude protein, calcium, phosphorus, copper and selenium concentration of leaves. No main effect of soil type was found on nutritional values of leaves. Significant interactions were found for species x soil (digestibility, calcium). For the zinc and selenium concentration in tree leaves, a significant species x soil x sampling period interaction were found.

Das (2019) qualitatively evaluated fodder trees and grasses in hill region and found that dry matter production was highest in Kharak (37.22 %) and Lemon grass (19.25 %). The organic matter was highest in ravines (92.15 %) and broad leaf Pasfelum (71.48 %). Manganese content was high in Utish (145.86 ppm). Calcium was found maximum in Betain

(1.84 %) and (180.43 ppm). The protein content was highest in Fanead (19.24 %) and *Cetorai cajungula* (16.85 %).

The results of a study that was carried out by Prajapati *et al*. (2019) on the variation in proximate principles and correlation studies in *Grewia optiva* along altitudinal gradient in Garhwal Himalaya showed that the altitudinal gradient had a significant impact on the proximate principles. The correlation coefficient indicated significant positive relation between altitude and dry matter and negative with ash contents. Diameter class showed significant positive relation with ether extract and crude fibre while negative relation with dry matter, crude protein and ash content. Highest crude protein (14.70 %) and low crude fibre (16.17 %) contents were observed at the mid-altitude and the higher altitude had better dry matter (57.11 %), ether extract (3.56 %), crude fibre (17.64 %) and nitrogen free extract (59.47 %) contents.

2.4 Molecular Markers-based Assessment of Genetic Diversity:

In the long history of plant breeding, there have been three primary areas that have always been important for molecular marker applications: (a) the determination of genetic diversity within and among populations (b) the verification and characterization of genotypes (c) marker-assisted selection.

Triest (2001) investigated morphology and molecular variation using RAPDs among 23 staminate and 14 pistillate individual of *Salix fragilis* and *Salix alba* from Belgium. Species-diagnostic RAPD markers were identified in progenies obtained from controlled crosses between *S. alba* and *S. fragilis* parents. A thorough screening of full-sib progenies of inter- specific controlled crosses was made to select homologous amplification products. The selected amplified products proved to be useful in a principal coordinate analysis for the estimation of variability of hybrid progenies. The RAPD analysis also revealed that the *S. fragilis* genotypes mainly consisted of staminate individuals, whereas most of the pistillate trees belonged to the *S. alba* genotype cluster.

Hossain *et al*. (2002) examined the genotype characteristic of cultivars, along with varieties of both of the jute species, *Corchorus olitorius and Corchorus capsularis*, in the germplasm collection at the Bangladesh Jute Research Institute (BJRI). DNA fingerprinting was generated for 9 different varieties and 12 accessions of jute cultivars by using random amplified polymorphic DNA (RAPD). They 29 arbitrary oligonucleotide primers. Out of

these seven primers gave polymorphism within the varieties, and 6 primers detected polymorphism within the accessions that were tested. A dendrogram was engendered from 13 these data, and this gave a distinct clustering of the cultivated species of jute. Therefore, they generated RAPD markers, which were species-specific. These primers can distinguish between *C. olitorius* and *C. capsularis.*

Using 15 Inter Simple Sequence Repeat (ISSR) and 15 Random Amplified Polymorphic DNA (RAPD) primers, Vijayan *et al.* (2003) attempted a experiment to determine the genetic relationships between 18 mulberry genotypes from India and Japan. ISSR primers produced 81.13 per cent polymorphism while RAPDs produced 71.78 per cent polymorphism.

A study conducted by Nanda *et al.* (2004) on identification and genetic relationships in six tree species of *Acacia* using Random amplified polymorphic DNAs (RAPD) markers. A total of two hundred and fifty-three distinct DNA fragments (bands), ranging from 0.1–3.1 kb was amplified by using selected 17 random 10-mer primers. The genetic similarity analysis was conducted on the basis of presence or absence of bands which revealed a wide range of variability within the species. The cluster analysis clearly showed that there was high degree of diversity (~70 %) within the six tree species of *Acacia.* Three major clusters were obtained belonging to 6 species of *Acacia*. First and second clusters were represented by only one species each *i.e., Acacia mollissima* and *Acacia arabica* respectively, whereas third cluster was represented by four species, *i.e*., *A. farnesiana*, *A. catechu, A. auriculiformis, A. concinna. A. farnesiana* and *A. catechu* were the closest member sharing about 30 per cent similarity. *A. auriculiformis* and *A. concinna* shared about 28 and 18 per cent similarity, respectively, with the cluster formed by *A. farnesiana* and *A. catechu*.

Goodall-Copestake *et al.* (2005) utilised RAPD and ISSR markers to elucidate the identification of samples in order to ensure that *ex-situ* collections of European elms (*Ulmus* spp.) contain a representative range of taxonomic diversity.

Roy *et al.* (2006) analysed genetic diversity of 20 exotic germplasm lines and 20 commercial varieties of the two cultivated species (*Corchorus olitorius* and *C. capsularis*) and two wild relatives of jute (*C. aestuans* and *C. trilocularis*) using sequence tagged microsatellite site (STMS), inter simple sequence repeat (ISSR) and random amplified polymorphic DNA (RAPD) markers. The level of intraspecific polymorphism revealed by

these markers was very low. The four ISSR and 22 RAPD primers employed in the study revealed 98.44 per cent and 100 per cent polymorphism, respectively, across all the species, while the level of polymorphism was significantly low within a species.

Sultana *et al*. (2006) constructed the first and very preliminary linkage map of the jute genome with eight ISSR (Inter Simple Sequence Repeat) markers and their different combinations using an F_2 population developed from a cross between jute cultivars O-9897 and Acc. 1805 which differed in cold tolerance. The polymorphisms between the parents were detected and the progenies were scored. The screening of parents (O-9897 and Acc. 1805) with ISSR primers revealed, 3 single primers and 2 primer pairs were polymorphic between the parents, which collectively produced 10 clear and reproducible markers for mapping. Thus, a total of 10 segregating markers were used to construct the Jute linkage map. The size of the markers varied from approximately 500 bp to 1,400 bp.

Gao *et al.* (2006) employed the Inter-Simple Sequence Repeat (ISSR) for genetic fingerprinting and identification of 28 significant *Populus L*. (poplar) cultivars (varieties/clones), as well as determination of the genetic relationships between these cultivars. These 28 cultivars belonged to the Aigeiros, Tacahamaca, Leuce and Turanga sections, as well as hybrids between the Aigeiros and Tacahamaca sections. Eight primers out of the 27 ISSR primers tested generated unambiguous multiplex profiles. The three best primers generated 154 readily detectable fragments, of which 129 (84 %) were polymorphic between cultivars. Each of these three primers generated fingerprint profiles that were unique to each of the examined accessions and could therefore be used exclusively for their identification. Detection of twenty-five markers unique to ten cultivars studied. In accordance with the ancestry of the sampled cultivars, the results demonstrated a distinct separation of cultivars within various sections of poplar.

Zhuang and Adams (2007) determined the allelic variation in gene expression in *Populus trichocarpa* X *P. deltoides* F1 hybrids. The results suggest differential regulation of the two parental alleles in the hybrids. Thirteen of 19 genes showed allelic expression ratios in the hybrid that were significantly different from the ratios of the parental species. The *P. deltoides* allele of one gene was silenced in the hybrid. Modes of gene regulation were inferred from the hybrid–parent comparisons. This study indicates that hybridization between plant species can have extensive effects on allelic expression patterns, some of which may result in phenotypic modifications.

Using eight inter simple sequence repeat (ISSR) primers, Feyissa *et al.* (2007) examined genetic diversity within and among 12 populations of the dioecious tropical tree species *Hagenia abyssinica* (Bruce) J.F. Gmel. in Ethiopia. A total of 104 clearly scorable bands were generated, among which 84 (81 %) were polymorphic. Jaccard similarity coefficient was calculated for pairwise comparisons among all 120 individuals and ranged from 0.30 to 0.88 while average within-population similarity ranged from 0.53 to 0.66. Within-population variability was estimated as percentage polymorphic loci (ranging from 52 % to 87 %), Shannon's information index (0.30-0.50) and Nei's genetic diversity (0.21-0.35). The highest variability values were obtained for one recently planted population and for one wild population growing in an undisturbed primary forest area. Significant overall differentiation among populations was detected by both Shannon's information index (0.26) and G_{ST} (0.25). Relatedness among samples was estimated with a principal coordinate analysis and relatedness among populations was estimated with a cluster analysis (UPGA). A Mantel test indicated a significant association between genetic and geographical distances, and an autocorrelation analysis showed significant evidence of gene flow over distances up to 30 km.

Bhau *et al.* (2007) quantified genetic diversity in the existing populations of *Tecomella undulata* by using amplified fragment length polymorphism (AFLP) markers in the assessment of genetic diversity and phenetic relationship among 42 *T. undulata* plants collected from different regions of India. Eight AFLP primer combinations generated a total of 338 bands across the 42 *T. undulata* accessions screened. On an average, 42 AFLP fragments were amplified per reaction. Of the total 338 AFLP fragments, 71.7 per cent was polymorphic across all the accessions. From the AFLP data, a similarity matrix based on Jaccard's coefficient was calculated which was used for constructing a phenetic dendrogram using UPGMA analysis. *T. undulate* accessions represented high levels of genetic variation as indicated by GS values ranging from 0.721 to 0.83, at which 42 *T. undulata* accessions grouped together.

Collevatti *et al*. (2008) reported the population genetic structure of the endangered tropical tree species *Caryocar brasiliense*, based on variability at 10 microsatellite loci. Additionally, they compared heterozygosity and inbreeding estimates for continuous and fragmented populations and discussed the consequences for conservation. For a total of 314 individuals over 10 populations, the number of alleles per locus ranged from 20 to 27 and

expected and observed heterozygosity varied from 0.129 to 0.924 and 0.067 to 1.000, respectively. Significant values of θ and R_{ST} showed important genetic differentiation among populations. θ was much lower than R_{ST}, suggesting that identity by state and identity by descent have diverged in these populations. Although a significant amount of inbreeding was found under the identity by descent model (f = 0.11), an estimate of inbreeding for microsatellite markers based on a more adequate stepwise mutation model showed no evidence of nonrandom mating (R_{IS} = 0.04). Differentiation (pairwise F_{ST}) was positively correlated with geographical distance, as expected under the isolation by distance model.

Thawaro and Te-chato (2009) reported the use of randomly amplified polymorphic DNA (RAPD) and simple sequence repeat (SSR) primers to assess the hybrid verification and somaclonal variation of the cross 366 (D) x 72 (P) of *Elaeis quineensis* Jacq (Oil palm). After isolation of genomic DNA from mature zygotic embryo (MZE) RAPD and SSR analysis was carried out using seven RAPD and eight SSR primers separately. RAPD and SSR analysis revealed that all the primers were able to amplify and provided polymorphic patterns of parents. But only one RAPD and SSR primer (OPT06 and EgCIR1772) provided a clear banding pattern which was used to distinguish hybrid between 366 (D) x 72 (P) of *Elaeis quineensis*. All hybrids showed the DNA patterns between the two parents.

In order to examine the genetic diversity of *Dalbergia sissoo*, Arif *et al.* (2009) compared two DNA-based molecular marker techniques, inter simple sequence repeat (ISSR) and random amplified polymorphism DNA (RAPD). There was a total of 30 polymorphic primers (15 ISSR and 15 random) were used. Amplification of genomic DNA of 22 genotypes, using ISSR analysis, yielded 117 fragments, of which 64 were polymorphic. Number of amplified fragments with ISSR primers ranged from five to ten and varied in size from 180 to 1,900 bp. Percentage polymorphism ranged from 0 to 87.5. The 15 RAPD primers produced 144 bands across 22 genotypes, of which 84 were polymorphic. The number of amplified bands varied from five to 13, with size range from 180 to 2,400 bp. Percentage polymorphism ranged from 0 to 100, with an average of 58.3 across. RAPD markers were relatively more efficient than the ISSR assay. Clustering of isolates remained more or less the same in RAPD and combined data of RAPD and ISSR. The similarity coefficient ranged from 0.734 to 0.939, 0.563 to 0.946, and 0.648 to 0.920 with ISSR, RAPD, and combined dendrogram, respectively.

Ogunkanmi *et al*. (2010) studied, inter and intra genetic diversity analysis of 40 genotypes from *Corchorus olitorius* and 40 genotypes from *C. incisifolus* using sixteen RAPD markers. The molecular study of the two species classified *C. olitorius* into two main clusters with five genotypes unresolved while there are three clusters with all the genotypes clearly separated in *C. incisifolus*. The results of both inter and intra genetic diversities revealed a higher level of allelic diversity in *C. incisifolus* than in *C. olitorius.*

The OPI16 RAPD profile as those generated by OPG10 revealed polymorphisms among the amplification products of different homo and heterozygote genotypes. About 73 percent of fragments showed absence/presence polymorphism, which could be particularly useful for discriminating most of the hybrids along with their parents. The clustering of hybrids and their parental lines into 3 clusters of genotypes: CMS lines (except Drofa CMS), Rf and F1 genotypes. The closest relationships within the group were ascertained for paternal lines than maternal and hybrids. Such findings could help in distinguishing the hybrid pedigree. Considering these reasons, it was compared the data of yield components for commercial and experimental F1 sunflower hybrids to establish the relationship between these as indices of hybrid performance and genetic distances among parental genotypes of hybrid combinations (Maria *et al*., 2010).

Bhat (2012) evaluated genetic divergence among various open-pollinated families of *Grewia optiva* Drummond seedling seed orchard for a variety of seed and seedling parameters. The investigation was conducted in RBD in order to determine the clustering pattern of these thirty-five families. The genetic divergence was estimated using Mahalanobis D2 statistics, and the families were grouped using Tocher's method based on minimal generalised distances. The families were clustered into four clusters: Cluster I-(CH2, HA-4, SH-5, SI-13, SI-15, SO-9, SO-10, SO-12), Cluster II-(CH-5, CH-6, HA-5, SH-1, SH-3, SO-2, SO-5, SO-11), Cluster III-(BI-4, BI-5, CH-1, HA-1, HA-3, KA2, MA-2, SI-6, SO-1, SI-10) and Cluster IV-(CH-3, HA2, KA-1, KA-3, SI-3, SI-5, SI-7, SO-6, SO-8). The generalized inter cluster distances were 5.665 (between I and IV), 4.486 (between I and II), 3.276 (between III and IV), 3.103 (between I and III), 2.941 (between II and III) and 2.217 (between II and IV). The relative divergence of each cluster from other clusters (inter cluster distance) indicated high order of divergence between I and IV, followed by I and II, III and IV, I and III, II and III and II and IV.

Samal *et al.* (2012) investigated the level and pattern of diversity in 65 mango (*Mangifera indica* L.) genotypes of India, including 20 commercial cultivars, 18 hybrids, 25 local genotypes and two exotic cultivars, using qualitative and quantitative fruit characters as well as RAPD and ISSR profiles. 15 RAPD primers generated 27 monomorphic and 129 polymorphic bands with an average polymorphism percentage of 82.7 per cent. Eight ISSR primers generated a total of 70 ISSR bands, of which 60 bands (85.71 %) were found to be polymorphic. Cumulative band data from these two techniques precisely classified accessions into eight clusters that correspond to their pedigree relationship. Using RAPD, ISSR, and cumulative data, UPGMA dendrograms demonstrated highly similar classification of genotypes based on their parental origin.

The molecular markers based paternity analysis in *Grewia optiva* revealed high similarity between F1 and their male parents. The 14 RAPD markers data showed that 23 out of 24 hybrids were highly similar to their male parents, whereas, eleven ISSR markers disclosed that 20 out of 24 hybrids were highly similar to their male parents (Saresh 2013).

Abdelhamid *et al.* (2014) employed four DNA markers to detect genetic variation between and within *Castanea* species and to compare the efficacy of each system for estimating genetic variation. Using 12, 5, 4 and 5 primer combinations, they amplified 106 random amplified polymorphic DNA (RAPD), 228 amplified fragment length polymorphism (AFLP), 42 inter simple sequence repeat (ISSR), and 36 simple sequence repeat (SSR) polymorphic markers, respectively. Each marker system classified the investigated species into distinct but indistinguishable clusters; however, only the RAPD method obtained partial agreement regarding species relationships. The comparison of the correlation coefficient of RAPD marker data and the other markers showed a higher correlation [($r = 0.69$, $P < 0.01$), ($r = 0.77$, $P < 0.01$), and ($r = 0.47$, $P < 0.01$) with AFLP, ISSR, and SSR, respectively.

The Jaccard's similarity coefficients for molecular diversity among 30 genotypes ranged from 0.17 to 0.83 for the RAPD assay and from 0.30 to 0.84 for the ISSR assay using 25 RAPD and 18 ISSR primers respectively. It was determined that genotype SO-12 (Kasauli) was the most divergent genotype that could be used to establish a number of combinations in *Grewia optiva* seed orchards and as a parent in hybridization programmes (Verma, 2015).

RAPD, ISSR, and SSR markers were used to characterize twenty genotypes of sandalwood (*Santalum album* L.). 225 and 208 bands were amplified among twenty genotypes of sandalwood using twenty-five RAPD and twenty-one ISSR primers that produced unambiguous and reproducible patterns. Polymorphism was found in 181 (83.13 %) of the 225 RAPD bands and 156 (75.77 %) of the 208 ISSR bands. For RAPD and ISSR, the average polymorphism informed content (PIC) was 0.84 and 0.86, respectively. The matrices created by RAPD and ISSR primers had a strong correlation (0.96). Despite considerable genotype similarity (0.79 by RAPD and 0.70 for ISSR), the observed genetic diversity was sufficient for classification of sandalwood genotype (Patel *et al.,* 2016).

Rellstab *et al*. (2016) assessed 13 leaf morphological characters and applied eight nuclear microsatellite markers in almost 1400 trees of 71 oak populations across Switzerland. Performed two multivariate approaches with three variable sets (morphology, genetics, combined) and assessed their performance in separating the taxa. They also compared the taxon assignment to a model-based clustering approach (STRUCTURE) based on genetic data alone. Found that joint use of morphological and genetic variables led to an improved taxon assignment. Whereas *Q. robur* could clearly be separated from the two other taxa, there was a certain overlap between *Q. petraea* and *Q. pubescens*. The STRUCTURE clustering led to the same taxon assignment in 85 (%) of the individuals.

Ghaidaminiharouni *et al.* (2017) used ISSR markers to determine genetic diversity among thirty clones of willow (*Salix acmophylla*, *S. excelsa*, *S. alba* and *S. triandra*). The mean percentage of polymorphic loci was found to be 59.86 and genetic similarity pairwise varied from the range of 0.18 to 0.65. Nei's gene diversity varied from 0.12 to 0.18 and average heterozygosity was obtained at 0.15. Values obtained from genetic diversity and genetic differentiation revealed a low level of genetic differentiation among the examined population of Salix.

Wang *et al.* (2019) explored the genetic diversity and population structure of *Magnolia sinostellata,* by using sequence tag-simple sequence repeat (EST-SSR) markers based on transcriptome data of *M. sinostellata*. In total, 25472 SSR_S were identified among 110644 unique assembled sequence with a total of 90.83 Mb and an average frequency of 23.02 per cent. The mononucleotide (35.53 %) and dinucleotide (42.08 %) motifs appeared to be the most abundant. In total, 150 potential loci were randomly selected to validate the quality of the developed SSR markers; an effective PCR rate of 32.00 per cent and a

polymorphism rate of 15.33 per cent were obtained for these loci. After performing sequencing and cloning for validation, 23 pairs of SSR primers were retained and used to characterize the genetic diversity and population structure of *M. sinostellata.* Overall, 204 alleles were amplified. The results of Shannon's information index (*I*), heterozygosity (H_0), heterozygosity (H_e) and Nei's expected heterozygosity (H) indicated rich genetic diversity in *M. sinostellata.*

Lissambou *et al*. (2019) tested species delimitation within *Greenwayodendron* sp. by combining morphological and population genetics data. First, a visual inspection of about a thousand specimens suggested the existence of seven morphogroups: four of them occur in Central Africa and overlap in Gabon, while three others are allopatric, occurring respectively in West Africa, East Africa, and the islands of Sao Tome and Principe. Their morphological differentiation was confirmed by analysis of 27 morphological characters coded from 233 herbarium specimens. Second, after genotyping 800 samples at eight nuclear microsatellites, Bayesian clustering analyses (STRUCTURE) identified four genetic clusters corresponding to the well sampled morphogroups but failed to separate the three remaining morphogroups represented by few samples. However, they showed that this is an inherent limit of the STRUCTURE algorithm, whereas factorial correspondence analysis (FCA) and pairwise F_{ST} and R_{ST} measures confirmed the genetic differentiation of all morphogroups.

Sharma *et al.* (2022) assessed the genetic diversity and population structure analysis using RAPD and ISSR molecular markers in diverse genotypes of Indian willow (*Salix tertrasperma* Roxb.) from five populations. The average number of effective alleles, gene diversity and Shannon information index were estimated with RAPD and ISSR markers, and were found to be 1.38±0.013, 0.35±0.010, and 0.23±0.007, respectively. Within-population genetic variation was found to be higher (87 %) than among-population genetic variation (13 %). Between RAPD and ISSR markers, there was a significant Mantel correlation (r=0.551). Structure software revealed four gene pools using a Bayesian clustering pattern. Based on the genetic information obtained by combining the RAPD and ISSR marker systems with respect to Indian willow, it is proposed that an individual tree be selected within populations rather than among populations for the improvement of Indian willow economic traits while also conserving entire ecological populations.

Chapter-3

MATERIALS AND METHODS

The present investigation entitled **"Morphogenetic variation for leaf fodder quality parameters in populations of *Grewia optiva*"** has been carried out in the Department of Tree Improvement and Genetic Resources, College of Forestry, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan (Himachal Pradesh). This study was conducted in the four altitudinal ranges (400 to 800 m, 801-1200 m, 1201-1600 m and 1601-2000 m above mean sea level (a msl), of Himachal Pradesh (H.P.) and Uttarakhand (U.K.) (Table 3.1) to assess the magnitude of variations in morphological, leaf and fodder characteristics of *Grewia optiva* Drummond along an altitudinal gradient. The physiochemical characteristics of the soil samples collected underneath different selected populations of *Grewia optiva* Drummond were analysed to determine their correlation with leaf, fodder and morphometric characteristics of *G. optiva*. Half-sib progenies of *G. optiva* Drummond were also evaluated for 18 months finally in nursery conditions to study genetic parameters and screen out the top growing half sib progeny of best genotypes of *G. optiva*. During the months of March-April 2020, an ecogeographical survey of *Grewia optiva* populations was conducted in eight districts of Himachal Pradesh and Chamba block of district Tehri-Garhwal of Uttarakhand to identify sites occurring at four different altitude ranges where species occur almost in abundance. In each altitudinal zone, five populations (4 from H.P. and 1 from U.K.) were selected for evaluation of variations in morphometric, leaf and fodder quality characteristics between and among selected populations. As a result, the total populations/sites under study were twenty (sixteen populations from H.P. and four from U.K).The four superior individuals (20-30 cm diameter class) of *Grewia optiva* Drummond were identified at minimum 100 m and maximum 200 m distances and chosen for further study using the check tree method at each selected site. As a result, a total of eighty trees/genotypes (Table 3.2) were recognised for collecting seeds and assessing variation in morphometric and fodder characteristics among and between selected populations. Half sib Progeny were also raised in Shilli nursery experimental farm under the Department of Tree Improvement and Genetic Resources and evaluated for different seedling growth characteristics, over a 18 months period. The high-performing half sib progenies of the best identified genotypes were further analysed using ISSR molecular markers.

Table 3.1 Detail of populations selected from four altitudinal ranges in Himachal Pradesh and the Chamba block of District Tehri Garhwal, Uttarakhand.

Altitudinal Zone (a msl)	Populations	District	Altitude (amsl)	Latitude	Longitude
A1(400-800m)	P1(Harsar)	Kangra	482m	32.1046^0 N	76.0387^0 E
	P2(Sujanpur Tihra)	Hamirpur	515m	31.8339^0 N	76.5055^0 E
	P3(Dramman)	Kangra	740m	32.2246^0 N	76.1653^0 E
	P4(Ghumarwii)	Bilaspur	700m	31.4491^0 N	76.7048^0 E
	P5(Daggar)	Uttarakhand	785m	30.3718^0 N	78.1809^0 E
A2(800-1200m)	P6 (Kalanjri Devi)	Hamirpur	854 m	31.6662^0 N	76.5410^0 E
	P7 (Sihunta)	Chamba	900 m	32.3017^0 N	76.0882^0 E
	P8 Dodar	Mandi	982m	31.6990^0 N	76.7324^0 E
	P9(Kuthar)	Solan	1127m	30.9731^0 N	76.9672^0 E
	P10(Kutuldi)	Uttarakhand	1136m	30.1839^0 N	78.2255^0 E
A3 (1200-1600m)	P11(Awah devi)	Hamirpur	1219m	31.5871^0 N	76.5110^0 E
	P12 (Dharot)	Solan	1500m	30.9495^0 N	77.0949^0 E
	P13(Neri)	Shimla	1520m	31.0922^0 N	77.1269^0 E
	P14(Basni)	Sirmaur	1552m	30.8033^0 N	77.2275^0 E
	P15(Jagdhar)	Uttarakhand	1585m	30.3233^0 N	78.3984^0 E
A4 (1600-2000m)	P16 (Shoghi)	Shimla	1712m	31.0421^0 N	77.1198^0 E
	P17 (Sangrah)	Sirmaur	1830m	30.6957^0 N	77.4257^0 E
	P18 (Ghanahatti)	Shimla	1900m	31.1385^0 N	77.0838^0 E
	P19 (Garhkhal)	Solan	1800m	30.9019^0 N	76.9809^0 E
	P20 (Ranichauri)	Uttarakhand	1730m	30.3212^0 N	78.4064^0 E

Table 3.2 Detail of selected genotypes within each Population.

Population	Genotypes	Genotype Code
Harsar (P1)	Harsar (T1)	HR 1
	Harsar(T2)	HR 2
	Harsar(T3)	HR 3
	Harsar(T4)	HR 4
Sujanpur Tihra (P2)	Sujanpur Tihra(T1)	ST 1
	Sujanpur Tihra(T2)	ST 2
	Sujanpur Tihra(T3)	ST 3
	Sujanpur Tihra(T4)	ST 4
Dramman (P3)	Dramman(T1)	DR 1
	Dramman(T2)	DR 2
	Dramman(T3)	DR 3
	Dramman(T4)	DR 4
Ghumarwii (P4)	Ghurmarwii(T1)	GH 1
	Ghurmarwii(T2)	GH 2
	Ghurmarwii(T3)	GH 3
	Ghurmarwii(T4)	GH 4

Daggar (P5)	Daggar(T1)	DA 1
	Daggar(T2)	DA 2
	Daggar(T3)	DA 3
	Daggar(T4)	DA 4
Kalanjri Devi (P6)	Kalanjri Devi(T1)	KD 1
	Kalanjri Devi(T2)	KD 2
	Kalanjri Devi(T3)	KD 3
	Kalanjri Devi(T4)	KD 4
Sihunta (P7)	Sihunta (T1)	SI 1
	Sihunta (T2)	SI 2
	Sihunta(T3)	SI 3
	Sihunta(T4)	SI 4
Dodar(P8)	Dodar(T1)	DO 1
	Dodar(T2)	DO 2
	Dodar(T3)	DO 3
	Dodar(T4)	DO 4
Kuthar (P9)	Kuthar(T1)	KT 1
	Kuthar(T2)	KT 2
	Kuthar(T3)	KT 3
	Kuthar(T4)	KT 4
Kutuldi(P10)	Kutuldi(T1)	KU 1
	Kutuldi(T2)	KU 2
	Kutuldi(T3)	KU 3
	Kutuldi(T4)	KU 4
Awah Devi (P11)	Awah Devi(T1)	AD 1
	Awah Devi(T2)	AD 2
	Awah Devi(T3)	AD 3
	Awah Devi(T4)	AD 4
Dharot (P12)	Dharot (T1)	DH 1
	Dharot (T2)	DH 2
	Dharot (T3)	DH 3
	Dharot (T4)	DH 4
Neri(P13)	Neri (T1)	NR 1
	Neri (T2)	NR 2
	Neri (T3)	NR 3
	Neri (T4)	NR 4
Basni(P14)	Basni (T1)	BA 1
	Basni (T2)	BA 2
	Basni (T3)	BA 3
	Basni (T4)	BA 4
Jagdhar(P15)	Jagdhar (T1)	JG 1
	Jagdhar(T2)	JG 2
	Jagdhar(T3)	JG 3
	Jagdhar(T4)	JG 4
Shogi (P16)	Shogi (T1)	SH 1
	Shogi (T2)	SH 2
	Shogi (T3)	SH 3
	Shogi (T4)	SH 4

Sangrah (P17)	Sangrah (T1)	SN 1
	Sangrah (T2)	SN 2
	Sangrah (T3)	SN 3
	Sangrah (T4)	SN4
Ghanhatii(P18)	Ghanhatii (T1)	GT 1
	Ghanhatii (T2)	GT 2
	Ghanhatii (T3)	GT 3
	Ghanhatii (T4)	GT 4
Garhkhal (P19)	Garhkhal(T1)	GR 1
	Garhkhal(T2)	GR 2
	Garhkhal(T3)	GR 3
	Garhkhal(T4)	GR 4
Ranichauri (P20)	Ranichauri(T1)	RA 1
	Ranichauri(T2)	RA 2
	Ranichauri(T3)	RA 3
	Ranichauri(T4)	RA 4

3.1 EXPERIMENTAL SITES

Experimental Sites	Altitude	Latitude	Longitude
Shilli (Solan, H.P.)	1300 m amsl	30̊.90′ N	77̊.09′ E
Nauni(Solan, H.P.)	1250 m amsl	30̊ 51′ N	76̊ 11′ E

(Source): Survey of India, Toposheet No. 55F/1)

3.2 EXPERIMENT METHODOLOGY

The research work has been carried out under four experiments, detailed below:

3.2.1 EXPERIMENT I: Morphological and Genetic Diversity of *Grewia optiva* Drummond among different populations. This experiment was conducted in two parts, *i.e.,* Experiment Ia and Experiment Ib.

3.2.1.1 EXPERIMENT Ia: Selection of *Grewia optiva* Drummond genotypes from populations on the basis of morphometric characters.

Altitudinal zones	**:**	**4**
No. of populations selected in each altitudinal zone	:	5 (4 from HP, 1 from UK)
Total populations	:	20 (4× 5)
No. of trees (genotypes) selected in each population	:	4
Total number of trees (genotypes)	:	80(20× 4)
Diameter class	:	20-30cm
Design	:	RBD

OBSERVATIONS RECORDED:

A) Methodology for Morphological Characters:

The morphometric characteristics of populations selected from four altitudinal ranges were recorded as per the following methodology:

i) Tree height (m):

Tree height was measured from ground level to topmost portion in tree canopy center exactly above the main trunk. It was registered using Ravimultimeter.

ii) **Tree diameter (cm):** The diameter of each tree was measured with the help of vernier calliper at a height of approximately 70 cm from the ground level. Two observations of tree diameter were taken at right angles to each other and mean diameter was observed.

iii) **Crown spread (E-W & N-S):** The crown spread was measured with the help of measuring tape. It was measured in two directions East-West (E-W) and North -South (N-S).

iv) **Number of primary branches:** Number of primary branches that were emerging out of main stem were recorded for all the selected trees.

v) **Number of secondary branches:** Number of secondary branches that were emerging out of primary branches were recorded for all the selected trees.

vi) **Internodal distance (cm):** Internodal distance was measured with a scale as the distance between the consecutive nodes.

vii) **Leaf shape:** The composite samples of 40 leaves per population (10 leaves per genotype) were taken, and leaf shape was observed by following the Standard Cyclopedia of Horticulture.

B) Leaf Morphometric Characteristics:

For this study, samples of leaves were collected from the entire crown at different heights (top, middle, and base) of each tree, including leaves of all sizes, as per the methodology given by Suri and Dalal (1963).

i) Leaf length (cm)

Leaf length was measured using a scale from the base to the tip of the leaf blade. It was recorded as the mean length of 12 leaves from each genotype.

ii) Leaf width (cm)

Leaf width was measured using a scale and mean value was expressed in centimeters (cm). It was recorded on same leaves used for the measurement of leaf length. Width was measured at the widest portion of the leaf.

iii) Leaf area (cm^2)

Leaf area was measured in $cm^2$with the help of a leaf area meter (leaf area meter model CI-202, CID, Inc.). It was also recorded on same leaves used for the measurement of leaf length leaf width.

iv) Petiole length (cm):

It was measured with the help of a scale. It was also recorded for same 12 leaves which were collected from different portion of the crown. Their mean value was recorded.

3.2.1.2 EXPERIMENT Ib: Nursery evaluation for selection of best genotypes of *Grewia optiva* Drummond.

Seeds were collected from selected populations in Himachal Pradesh (HP) and Uttarakhand (UK) during the month of December 2020. In the laboratory of the Department of Tree Improvement and Genetic Resources, the seed was first depulped, then dried, packaged, and finally labelled before being stored. Morphometric characteristics of the seeds, such as seed length and seed width, were measured and analysed. The sowing of seed was done during the month of May 2021. The seeds were pretreated with hot water for 24 hours. Seeds were sown in polybags containing a potting mixture of sand, clay and FYM (2:1:1). The sown seeds were watered on a consistent basis until the seedlings gained sufficient vitality. Regular weeding was done in order to protect the young seedlings that were being grown. The seeds from each of the 80 genotypes were sown in three separate replications, and in each replication, 10 seedlings were taken for recording observations on nursery-related parameters. The growth performance of seedlings was evaluated for 18 months.

No. of populations	**:**	**20**
No. of genotypes per population	:	4
Total no. of genotypes	:	80
Number of replications	:	3
No. of seedlings were taken in each replication for recording observations on nursery related parameters	:	10
Total number of seedlings under study were	:	2400 (80 x30)
Statistical design	:	RBD

OBSERVATIONS RECORDED:

A) Methodology adopted for measurements of seed parameters

i) Seed size : The length and width of seeds were measured using a digital vernier calliper.

ii) 100 Seed weight (gm): Hundred seeds were weighed to calculate the seed weight in grams (gm) as per ISTA (1966).

B) Methodology adopted for measurements of germination and seedling growth parameters

i) Germination percentage (%): The number of seeds germinated to the total number of seeds sown were calculated and expressed as germination percentage.

ii) Germination value: It was calculated by the following formula:
Germination value (GV) = Mean daily germination (MDG) x Peak value at mean daily germination (PV).

iii) Germination energy: The proportion of germination which had occurred up to the time of peak germination was noted.It was taken to 12 days.

iv) Germination index: It was calculated by the following formula: Germination index (GI) = $\sum$(G/T) where G is the percent of seed germinated per day and T is the germination period.

v) Survival percentage (%): The total number of plants that survived after six months of germination was calculated as a survival percentage.

vi) Seedling height (cm): The height of seedlings was recorded at the age of 6 month, 12 month and 18 months. It was recorded from ground level to the apex of the leading shoot by using a measuring scale and expressed in cm.

vii) Collar diameter (mm): The collar diameter of seedlings was measured at the ages of six months, 12 months, and 18 months. It was measured above ground level at the collar region with the help of a digital calliper and expressed in mm.

viii) Internodal length (cm): The internodal length was measured as distance between two nodes and expressed in cm.

ix) Petiole length (mm): The petiole length was measured with the help of measuring a scale and expressed in mm.

x) Leaf area (cm^2): The full-grown leaves were collected randomly from the lower, middle and upper portions of the seedlings, and leaf area was measured with the help

of a leaf area metre and expressed in cm^2. The leaf area was also recorded for 18 months (at an interval of six months).

xi) **Fodder quality and Mineral nutrient characteristics:** A composite sample of leaves was taken from different heights of 18-month-old seedlings. These samples were taken during the last week of the month of October 2021. The method used for the examination of the fodder quality and mineral nutrient parameters for mother trees (in Experiment 3) was also used for these parameters.

EXPERIMENT 2: Physiochemical Properties of Soil of different Populations

Methodology: Two composite soil samples representative of the different population were drawn from the two depths *i.e.,* 0-15cm (Surface layer) and 15-30cm (subsurface layer).These samples were collected to know the nutritional status of surface layers underneath the selected populations of *Grewia optiva* Drummond. Each sample was air dried, grounded with wooden pestle and mortar, sieved through 2 mm sieve and stored in plastic containers. The soil samples were then analysed for morphological (soil colour), physiochemical (bulk density, particle density, porosity, pH, EC), and available nutrient status.

Total Populations	**:**	**20**
No. of composite samples of soil from each Population(Site)	:	2 (at two depth: 0-15 cm and 15-30cm)
Total number of soil composite samples /treatments	:	40(20× 2)
Soil Depth	:	0-15 and15-30cm
Design	:	RBD(Factorial)

OBSERVATIONS RECORDED :

i) **Soil Colour:** It was observed with the help of Munsell colour chart.

ii) **Bulk density (BD):** It was determined by core method using following formula:

$$BD\ (g\ cm^{-3}) = \frac{\text{wt.of oven dry soil in the core (g)}}{\text{volume ofcore/soil } (cm^3)}$$

iii) **Particle density (PD):** It was determined with the help of Pychnometer method.

$$PD\ (g\ cm^{-3}) = \frac{10}{W_{pw}+10-W_{psw}}$$

Where, W_{pw} = weight of water filled in pycnometer

W_{psw} = weight of Pycnometer + water + soil

iv) **Porosity:** It was determined by using bulk density and particle density empirical formula:

$$\text{Porosity} = 1-\frac{BD}{PD} \times 100$$

v) **Soil pH:** It was measured with the help of Digital pH meter as per the method reported by Jakson, 1973.

vi) **Electrical conductivity (dSm^{-1}):** It was measured with the help of digital EC meter (Jakson, 1973).

vii) **Organic carbon (%):** It was measured with the help of chromic acid titration method given by Walkley and Black, 1934.

viii) **Available N (kg ha^{-1}):** It was measured with the help of alkaline permanganate method of Subbiah and Asija, 1956.

ix) **Available P (kg ha^{-1}):** It was measured with the help of 0.5 M sodium bicarbonate ($NaHCO_3$) at 8.5 pH method of Olsen *et al*., 1954.

x) **Available K (kg ha^{-1}):** It was measured with the help of flame photometric method (1N NH_4OAC extractable) (Merwin and Peech, 1951).

Experiment 3: Variation in fodder quality parameters among different populations

Methodology:

Number of Populations	:	20
Number of Genotypes	:	80 (4 per population)
Number of Replication	:	3
Statistical Design	:	RBD

A composite sample of 100 leaves were taken randomly from upper, middle and lower plant parts from all the four directions from selected parent trees in population and weighed with the help of top pan balance to calculate leaf fresh weight and dry weight. Beside this 500 g of fresh foliage in the form of composite samples were taken during I^{st} week of December from the entire crown of each tree including the leaves of each size as reported by Suri and Dalal (1963). Considering composite sample as one replication, three composite samples were taken from each tree. These samples were washed and treated with 0.1N HCl followed by washing with distilled water. These samples were dried till they attained constant weight and all moisture was evaporated. The dried samples were grinded to make fine powder and stored with proper labels for further analysis of proximate principles, i.e., DM (Dry matter), EE (Ether extract), CF (Crude fiber), CP (crude protein), AC (Ash

content) and NFE (Nitrogen free extract), Mineral nutrients (N, P, Na, K, Ca) and biochemical estimation (total amino acids).

i) Leaf Fresh weight (g)

A composite sample of 100 leaves were taken randomly from upper, middle and lower crown parts from all the four directions and weighed with the help of top pan balance.

ii) Leaf Dry Weight (g)

Fresh leaves were oven dried at 60°C till they lose moisture and attained a constant dry weight. The dry weight was recorded on an electric top balance.

iii) Leaf dry matter content (%)

The percentage difference in leaf weight due to loss of moisture content before and after drying was recorded as leaf dry matter content (%).

$$\text{Dry matter content (\%)} = \frac{\text{weight of dried leaf samples}}{\text{weight of fresh leaf samples}} \times 100$$

iv) Crude protein (%)

Crude protein content was estimated by Microkjeldahl method (Sankaram, 1966). For crude protein estimation, nitrogen content in leaves was estimated and crude protein was obtained by multiplying the nitrogen by 6.25.

For nitrogen estimation 1gram dried grinded leaf samples were taken in 500ml Micro- kjeldahl's flask in which 10 g of digestion mixture (10 g copper sulphate + 20 g ferrous sulphate + 200 g potassium sulphate + 3g HgO) and 20 ml of concentrated sulphuric acid was added. Small pieces of calcium carbonate were added, so as to check bumping. The flask was then kept on the electric heater till the colour of the digested material become light bluish-green. The flask was cooled overnight and the material was diluted with distilled water to make the aliquot of 100 ml in a volumetric flask.

Total nitrogen in the leaves was estimated by Micro-Kjeldahl method. The 10 ml of saturated sodium hydroxide (40 %) solution was taken in micro Kjeldahl's flask. Thereafter aliquot (5ml) was added and kept on the electric heater with distillation unit connected through tap to the condenser. The lower end of the condenser was dipped in a solution of 20 ml of boric acid (4 %) containing mixed indicator in a 250 ml beaker. Distillation was carried out for 30 minutes during which all the ammonia released was trapped in the boric

acid solution, which was then titrated against 0.1N H_2SO_4 to get pink to yellow colour. Total nitrogen was calculated by the standard value, i.e., 1ml of 0.1N H_2SO_4 = 0.0014 mg of nitrogen.

$$\text{Crude protein (\%)} = \frac{100 \times Y \times 0.0014 \times 6.25}{X \times W} \times 100$$

Where,

Y = Aliquot volume made of digested sample (100ml)

T = Titre value (ml)

X = Volume taken for distillation (5ml)

W = Weight of sample taken for digestion (1g)

v) Ether extract (%)

Two grams of grinded sample was extracted with petroleum ether (B.P. 60-80°C) in a Soxhlet Apparatus. Solvent was allowed to evaporate to a constant dryness and the weight of the abstract was expressed as percentage of the weight of the sample taken.

$$\text{Ether extract (\%)} = \frac{\text{Weight of fat}}{\text{Orignal weight of sample}} \times 100$$

vi) Crude fibre (%)

Crude fibre content was estimated by acid-alkali digestion (ashing) as described by AOAC (1995) and Sankaram (1966). A 2 g fat free sample (after ether extraction) was transferred to a beaker and 200 ml of 1.25 percent H_2SO_4 was added to it. Beaker was put on hot plate and allowed to reflux for 30 minutes. After boiling, the beaker was removed from hot plate and filtered through a muslin cloth using vacuum pump. The residue was washed with hot water till it became free from acid. Then the material was transferred to the same beaker and 200 ml of 1.25 per cent NaOH solution was added to it and the content was again refluxed for 30 minutes. The content was filtered again through muslin cloth using vacuum pump and the residue was washed with hot water till it became free from alkali. Then the total residue was shifted in a crucible and placed in hot air oven, allowed to dry to a constant weight at 100^{o}C and its weight was recorded thereafter. The residue was ignited in muffle furnace at 550-600^{o}C for 3-4 hours, and then cooled and weighed again. The loss of weight due to ignition was weight of crude fibre. The percentage of crude fibre was calculated by the following formula:

$$\text{Crude fibre (\%)} = \frac{\text{Weight of crude fibre}}{\text{Original weight of sample}} \times 100$$

vii) Total ash (%)

Ash content was analyzed as per the procedure given by AOAC (1995) and Sankaram (1966). Two gram of oven dried powdered sample was taken in a crucible. The sample was heated on an electric heater till the smoke ended up. The crucible was then transferred to a muffle furnace and the temperature was raised to 600^0C for two hours. The crucible from furnace was removed and cooled in desiccators and weighed. The previously recorded empty crucible weight was not subtracted and weight of ash thus determined. The total ash content in percentage was calculated by the following formula:

$$\text{Total ash (\%)} = \frac{\text{Weight of ash}}{\text{Original weight of sample}} \times 100$$

viii) Nitrogen free extract (%)

Nitrogen free extract was determined by subtracting the sum of crude protein, crude fibre, ether extract and total ash content from hundred as reported by AOAC (1995) and Sankaram (1966).

$$\text{NFE (\%)} = 100 - (\text{CP\%} + \text{CF\%} + \text{EE\%} + \text{Total ash \%})$$

ix) Mineral nutrients (P,Na,K,Ca): Powdered sample of leaves were also used for estimation of mineral nutrients Phosphorus (P) by Vanadomolybdate method and Na, K and Ca by Flame photometer (AOAC, 1980).

x) Biochemical Estimates (Amino acids): The Amino acids were estimated as per method given by Lee and Takahashi method (1966).

Extraction

10 mg acetone dried powdered material was heated in 5 ml of 70 per cent etylalcohol on a water bath at 60^oC for 10 minutes. The material was centrifuged at 2000 rpm for 10 minutes and the supernatant collected and made to 5 ml with 70 per cent ethyl alcohol.

Estimation

Amino acids determined after Lee and Takahashi (1966). Added 2 ml of supernatant in the test tubes which were heated on water bath and evaporated to dryness while dried

residue was still hot, 2 ml of ninhydrin reagent (0.1% ninhydrin in 70 % ethylalcohol) was added and the solution boiled for 10 minutes with constant shaking. After cooling, the solution was diluted to 5 ml by iso-propylalcohol and the optical density of the blue colour was read at 520 nm on UV-VIS spectrophotometer. Amino acid content was calculated from standard caliberation curve obtained from glycine and expressed as mg/gm on dry weight basis.

STATISTICAL ANALYSIS

Statistical analysis is an important tool for collection, evaluation and interpretation of data. The data was analyzed statistically by using RBD and RBD factorial. Analysis of variance (ANOVA) for morphological, leaf morphometric, physiochemical characteristics of soil and proximate principles were calculated as method described by Panse and Sukhatme (1967). The table for analysis of variance (ANOVA) was set as explained by Gomez and Gomez (1984).

ANOVA

Source of variation	Degree of freedom	Sum of square	Mean sum of square	Variance ratio (F value)
Replications (r)	*r-1*	*Sr*	$\frac{Sr}{r-1} = Mr$	$\frac{Mr}{Me}$
Treatment (t)	*t-1*	*St*	$\frac{St}{t-1} = Mt$	$\frac{Mt}{Me}$
Error (e)	*(r-1)(t-1)*	*Se*	$\frac{Se}{(r-1)(t-1)} = Me$	

Where,

r = No. of replications of each treatment.

t = No. of treatments

Mr = Mean sum of squares due to replication

Mf = Mean sum of squares due to treatments

Me = Mean sum of squares due to error

The calculated ‘F’ values were compared with tabulated ‘F’ value for test of significance. Standard Error (SE), Critical Differences (CD) and Coefficient of Variation (CV) were calculated to find out the superiority of one genotype over the others with the help of following formulae:

$$SE\ (m) \pm = \sqrt{\frac{Me}{r}}$$

$$SE\ (d) \pm = \sqrt{\frac{2Me}{r}}$$

$CD_{(0.05)}$ = SE (d) × table value of $t_{(0.05)}$ at error degree of freedom.

where,

SE (m)± = Standard error of mean

SE (d)± = Standard error of difference

$CD_{(0.05)}$ = Critical difference at 5% level of significance

$CV = \frac{\sigma}{\bar{x}} \times 100$ (σ is standard deviation and $\bar{x}$ is mean)

All the characters, which showing significant differences among different populations were further subjected to analysis for the following genetic parameters:

1. Coefficient of variability (%)

Coefficient of variability was worked out by the formula given by Burton and De Vane, (1953).

$$PCV\ (\%) = \frac{\sqrt{Vp}}{\bar{x}} \times 100$$

$$GCV\ (\%) = \frac{\sqrt{Vg}}{\bar{x}} \times 100$$

$$ECV\ (\%) = \frac{\sqrt{Ve}}{\bar{x}} \times 100$$

Where,

PCV = Phenotypic Coefficients of variability

GCV = Genotypic Coefficients of variability

ECV = Environmental Coefficients of variability,

$\bar{x}$ = General mean of population

$$Vg = \frac{MSt - MSE}{r}$$

Ve = MSE

Vp= Vg + Ve

$$\bar{x} = \frac{Grandtotal}{r \times t}$$

Where,

Vp = Phenotypic variance

Vg = Genotypic variance

Ve = Environmental variance

MSt = Mean sum of squares due to treatments

MSE = Mean sum of squares due to error

r = Number of replications

$\frac{Grandtotal}{r \times t}$

2. Heritability (%)

Heritability (H^2) in broad sense was calculated as suggested by Burton and De Vane (1953) and Johnson *et al*., (1955).

$$H^2(\%) = \frac{Vg}{Vp} \times 100$$

Where,

H^2 = Broad Sense Heritability

Vg = Genotypic variance

Vp = Phenotypic variance

3. Genetic Advance

The expected genetic advance resulting from selection of five per cent superior individuals were worked out as suggested by Lush (1940) and further used by Burton and De vane (1953) and Johnson *et al*. (1955).

$$\text{Genetic advance} = h^2 \times \sqrt{Vp} \times K$$

Where,

h^2 = Heritability in broad sense

$\sqrt{Vp}$ = Phenotypic variance deviation

K = Selection differential at 5% selection intensity

The value of K = 2.06 (at 5 % selection intensity, Allard, 1960).

4. Genetic gain (%)

Genetic gain was calculated as suggested by Johnson *et al.,* (1955).

$$\text{Genetic gain (\%)} = \frac{Genetic\ advance}{General\ mean\ of\ population\ (\bar{X})} \times 100$$

For categorizing the magnitude of different parameters the limits used, are given below:

PCV and GCV > 30 % - High

15 – 30 % - Moderate

< 15 % - Low

Heritability (h^2) > 80 % - High

50 – 80 % - Moderate

< 50 % - Low

Genetic gain (GG) >30 % - High

15 – 30 % - Moderate

< 15 % - Low

5. Covariance : Covariance can be portioned due to environment and genotypic factors.

Environmental covariance $Cov_{xy(e)} = MSP_{EXY}$

Genotypic covariance $Cov_{xy(g)}) = \frac{MSP_{GXY} - MSP_{EXY}}{r}$

Phenotypic covariance $Cov_{xy(e)} = Cov_{xy(e)} + (Cov_{xy(g)})$

6. Correlation coefficient

The correlation between all characters under study, at genotypic, phenotypic and environmental levels were estimated as per the method described by Robinson *et al*. (1951) and Searle (1961).

1. Phenotypic correlation between character X and Y

$$r_{xy(p)} = \frac{Cov_{xy(p)}}{\sqrt{Var_{x(p)} \times Var_{y(p)}}}$$

2. Genotypic correlation between character X and Y

$$r_{xy(g)} = \frac{Cov_{xy(g)}}{\sqrt{Var_{x(g)} \times Var_{y(g)}}}$$

3. Environmental correlation between character X and Y

$$r_{xy(e)} = \frac{Cov_{xy(e)}}{\sqrt{Var_{x(e)} \times Var_{y(e)}}}$$

where,

$Cov_{xy(p)}$, $Cov_{xy(g)}$ and $Cov_{xy(e)}$ denote phenotypic, genotypic and environmental covariance between characters X and Y, respectively.

$Var_{x(p)}$, $Var_{y(g)}$ and $Var_{x(e)}$ denote phenotypic, genotypic and environmental variances for character X, whereas

$Var_{y(p)}$, $Var_{y(g)}$ and $Var_{y(e)}$ denote phenotypic, genotypic and environmental variances for character Y, respectively.

7. Path Coefficient Analysis

The path coefficient analysis of component traits with biomass was done by following Dewey and Lu (1959). The direct and indirect effects were calculated by solving the following set of simultaneous equations.

$P y_1 + P y_2\, r_{12} + P y_3 r_{13} + \ldots\ldots\ldots\ldots\ldots\ldots + P y_n r1_n = r y_1$

$P y_1\, r_{12} + P y_2 + P y_3 r_{23} + \ldots\ldots\ldots\ldots\ldots\ldots + P y_n\, r2_n = r y_2$

$P y_1\, r_{1n} + P y_2\, r2_n + P y_3 r3_n + \ldots\ldots\ldots\ldots\ldots\ldots + P y_n = r y_n$

Where

$P y_1$, $P y_2$, $P y_3$ ..., $P y_n$ are the direct path effects of 1,2,3, …n variables on dependent variable ‘y’.

r_{12}, r_{13} ……, r_{1n} are the genotypic coefficients of correlation between various independent variables.

$r y_1$, $r y_2$….., $r y_n$ are the genotypic correlation coefficients of independent variables with dependent variable ‘y’.

$P y_1\, r_{12}$, $P y_3\, r_{23}$ ….. $P y_n\, r_{2n}$ are the indirect effects.

The variation in the independent variable, which remained undetermined by including all variables, was assumed to be due to variable (s) not included in the present investigation. The degree of determination (p^2_{yx}) of such variable (s) on dependent variable was calculated as follows:

$$P^2_{yx} = 1- (P^2y_1 + 2Py_1\ Py_2 r_{12} + 2Py_1\ Py_3\ r_{13} \ldots\ldots$$
$$+ P^2y_2\ + 2Py_2\ Py_3\ r_{23} + \ldots\ldots\ldots\ldots\ldots\ldots$$
$$+\ P^2y_3\ + 2Py_3\ Py_4\ r_{34}\ + \ldots\ldots\ldots\ldots + P^2y_n)$$

and

Residual effect (R^2) = $\sqrt{p2_{yx}}$

8. Principal Component Analysis

It is a multivariate statistical technique to reduce the data with large number of correlated variables in to a substantially smaller set of new variables. A principal component analysis is concerned with explaining the variance- covariance structure of a set of variables through a few linear combinations of these variables. Its general objectives are:

1. Data reduction
2. Interpretation

It does not require the assumption of multivariate normality. It deals with the internal structure of the variables involved. Its aim is to sacrifice some information contained in the original variables in order to keep as few variables as possible, but the lost information is kept as minimum as possible.

The aim of principal component analysis is to ascertain new variables, called principal components, which carry most of the information present in original variables. Principal components are generally estimated from either the correlation matrix (R) or sample variance-covariance matrix (S). When the variables are measured in different units, scale effect can influence the composition of the derived components. In order to overcome such situation it is desirable to standardize the variable. Also correlation matrix should be used. The first few principal components usually account for most of the variation of the original variables and the variation described by following principal components is relatively little, it is often useful to retain only those first few principal component and drop all subsequent

components from the analysis. It is so because the variable they express is largely random and is of no use in the analysis. Several thumb rules have been proposed for the number of principal components of the correlation matrix with eigen roots less than one. The principal component's with the variance less than one contains less information.

Various steps involved in worked out of principal components are summarized as below:

i. First of all Keyse-meyer-olkin measure for sampling adequacy is computed. If the value of KMO comes out to be more than 0.5 only then we should go for principal component analysis.
ii. After that find the eigen value of variance-covariance matrix of correlation matrix.
iii. Arrange eigen values in decreasing order. Let these values in decreasing order be λ_1, λ_2,. . . . . , λ_p, and corresponding variability be V_1, V_2…. V_p, Where V_p is variability for λ_p.
iv. Starting from first principal component, go on adding the variance or first few principal components whose value is more than unity. The variability described by them is of greater use. Discard the remaining principal components.
v. From the eigen vectors of chosen principal components variables which load the respective principal components are found.

The output desired for interpretation and grouping include:

i. Eigen value and percentage of total variation explained by each principal component.
ii. The eigen vector for each principal component.
iii. The principal component scores
iv. The correlation between original Standardized variable and the corresponding principal component scores (occasionally called loading).

9. Cluster Analysis

Cluster analysis is one of the methods of data reduction technique which reduces the number of observation. For a set of individuals (or objects), the cluster analysis is performed to see the existence of any possible groups or subsets of closely associated individuals based on some “similarities” in the recorded observations of sample objects. Those samples objects which are “similar” in their recorded information may form a group. “Dissimilar” objects fall in different groups. In general, the objects that share similar characteristic are found together.

There are two clustering approaches viz. Hierarchical and Non-Hierarchical. In present investigation Hierarchical clustering approach was used. Ward's method is a criterion applied in hierarchical cluster analysis. Ward's minimum variance method is a special case of the objective function approach originally presented by Joe H. Ward, Jr. Ward suggested a general agglomerative hierarchical clustering procedure, where the criterion for choosing the pair of clusters to merge at each step is based on the optimal value of an objective function. This objective function could be "any function that reflects the investigator's purpose."

Experiment 4: Molecular markers-based analysis of best studied material

Methodology:

The best growing half sib progenies in terms of morphometric, fodder quality and germination parameters from different populations of beul were selected and used for molecular markers analysis. The 10 ISSRs molecular markers were selected for molecular characterization of selected progenies of *Grewia optiva*.

The experimental details of material used and methodology adopted during the entire course of study are given under the following headings:

4.1 Source of plant material

4.2 Isolation and purification of genomic DNA

4.3 Qualitative and quantitative assessment of genomic DNA

A. Agarose gel electrophoresis

B. DNA quantification

4.4 ISSR studies for genetic divergence

4.5 Data analysis

4.1 Source of Plant Material

Fresh and disease free leaves were collected from selected half sib progenies of *Grewia optiva* growing under nursery conditions of Shilli (Solan).

4.2 Isolation and Purification of Genomic DNA

Collection of leaf material

Fresh, green leaves were separately excised from different plants. Before plucking, the leaves were wiped off the soil with tissue paper and then wrapped in aluminum foil and brought to the laboratory in ice-box and stored in deep freezer at -20^{o}C till further use.

Isolation of genomic DNA

Genomic DNA from the collected leaves of top performing progenies separately isolated using CTAB method of Doyle and Doyle, 1987 with some modifications wherever required.

The following reagents were used for DNA isolation:

Reagents:

a) 10% CTAB	10 gm of CTAB (Cetyl Trimethyl Ammonium Bromide) was dissolved in 100ml of distilled water by warming at 65^0C.
b) 0.5M EDTA (pH 8.0)	18.61 gm of EDTA was dissolved in 80ml distilled water and pH of the solution was adjusted to 8.00 with 1NHCl. Final volume of the solution was made to 100 ml with distilled water and the solution was sterilized by autoclaving.
c) 4M NaCl	23.37 gm of NaCl was dissolved in minimum amount of distilled water and the final volume was made to 100 ml using distilled water and followed by sterilization by autoclaving.
d) 1M Tris HCl (pH 8.0)	15.76 gm of Tris HCl was dissolved in 80 ml distilled water. Then the pH was adjusted to 8.0 with 1NNaOH. The final volume was made to 100 ml with distilled water and the solution was sterilized by autoclaving.
e) DNA extraction buffer	100 ml of the extraction buffer contained 1. 10 ml 1M Tris HCl 2. 4 ml 0.5M EDTA 3. 20 ml 10 (%) CTAB 4. 35 ml 4M NaCl 5. 31 ml distilled water 6. 0.2 (%) β-mercaptoethanol
f) Chloroform: Isoamyl	96 ml of chloroform and 4ml of isoamyl alcohol were mixed (24:1,v/v) thoroughly and the mixture was then kept in a closed container at room temperature.
g) 70% ethanol	70 ml of absolute alcohol was mixed with 30 ml of distilled water to make it 100 ml.

h) TE buffer	0.1576 gm of Tris HCl and 0.0372 gm of EDTA were dissolved in 100 ml of distilled water followed by adjustment of pH to 8.0 with 1N NaOH.

Procedure:

Step 1	About 2 gm of collected leaves were homogenized to fine powder with liquid nitrogen using prechilled pestle and mortar.
Step 2	The leaf powder was transferred to 50 ml centrifuge tube containing 10 ml pre-warmed (at 65^0C) DNA extraction buffer. Leaf powder should not get moist because under wet condition DNase digests total DNA.
Step 3	Incubated the tubes for one to two hours at 65^0C in a water bath. During incubation the samples were mixed well by inverting the tubes every five minutes.
Step 4	10 ml of chloroform : isoamyl alcohol (24:1, v/v) was added to each tube followed by mixing gently by hand inversions till the colour in the lower portion of the tube turned dark green.
Step 5	Centrifuged the above suspension at 12000 rpm for ten minutes at room temperature (25^0C).
Step 6	Transferred the aqueous phase gently without disturbing the inter phase to fresh autoclaved centrifuge tubes.
Step 7	Added equal volume of prechilled isopropanol to the aqueous phase taken, mixed gently by hand inversions and incubated at -20^0C for 1hour or overnight so that DNA gets precipitated.
Step 8	The precipitated DNA was spooled out with the help of sterilized glass hook or pelleted it by centrifugation at 10000 rpm for ten minutes at 4^0C.
Step 9	Washed the DNA with 500µl of 70% ethanol and centrifuged at 5000 rpm for five minutes at 4^0C.
Step 10	Supernatant was decanted and dried the pellet overnight to completely evaporate the alcohol.
Step 11	Dissolved the DNA pellet in 500 µl TE buffer.

Purification of genomic DNA

Isolated DNA was purified by successive RNase treatment followed by phenol: chloroform extraction.

Reagents:

a) RNase (10mg/ml)	10 mg of RNase was dissolved in 1 ml of autoclaved distilled water and vortexed to mix thoroughly and stored at -20^{o}C.
b) Phenol : chloroform	Mixed 50 ml phenol and 50 ml chloroform(1:1v/v) properly. Stored at 4^{0}C in a covered container.
c) Chloroform : isoamyl	96 ml of chloroform and 4 ml of isoamyl (24:1v/v) alcohol were mixed together and the mixture was kept in a closed container at room temperature.
d) 3M sodium acetate	24.60 gm of sodium acetate was dissolved in 80 ml distilled water and the pH was adjusted to 4.8 using glacial acetic acid. The final volume was made to 100 ml with distilled water.
e) Absolute ethanol (95%)	The solution was procured from Merck chemicals.
f) 70% ethanol	70 ml of absolute alcohol was mixed with 30 ml of distilled water to make it 100 ml

Procedure:

Step 1	0.5 µl (10mg/ml) of RNase was added to the isolated DNA samples followed by incubation at 37^{0}C for 1 hour.
Step 2	Equal volume of phenol: chloroform was added and mixed thoroughly.
Step 3	Centrifugation was done at 11000 rpm for two minutes at room temperature and aqueous phase was transferred to fresh eppendorf microfuge tubes.
Step 4	Extraction was done twice with equal volume of chloroform: isoamyl alcohol (24:1, v/v) followed by 11000 rpm spin for two minutes.
Step 5	The aqueous phase was separated to which 1/10th volume of 3M sodium acetate and 2.5 volume of absolute ethanol was added. It was mixed properly and incubated at 4^{0}C.

Step 6 Pelleted the DNA by centrifugation at 11000 rpm for five minutes.

Step 7 The supernatant was decanted off followed by washing of pellet with 70% ethanol, and the pellet was then air dried.

Step 8 Resuspended the pellet in 100 µl TE buffer.

4.3 Quantification of Purified DNA

A) Agarose gel electrophoresis

The isolated genomic DNA was electrophoresed on 0.8 per cent agarose gel (stained with 0.5µg/ml of ethidium bromide) at 80V –100V and 70mA for two hours in 1X TAE buffer (Appendix II) and then observed on UV-transilluminator. Quality of DNA samples was judged on the basis of whether sample DNA formed a single high molecular weight band or smear.

B) DNA quantification

The quantity of DNA was assessed by UV/VIS spectrophotometer (Perkin Elmer, Hyderabad, India). Concentration of DNA was quantified using following formula:

$$\text{DNA } (\mu g/ml) = \frac{\text{OD}(260) \text{ x dilution factor x } 50}{1000}$$

The ratio of absorbance at 260 nm and at 280 nm was measured to check the contamination of protein.

Purity check of DNA on the basis of A_{260}:A_{280} ratio

Sr. No.	A_{260}:A_{280} ratio (Absorbance ratio)	Indication
1.	Above 1.8	Protein contamination
2.	1.4 to 1.8	Good quality DNA
3.	Below 1.4	RNA contamination

4.4 Inter Simple Sequence Repeat (ISSR) studies for genetic divergence

1. DNA amplification

DNA amplification was carried out for ISSR analysis. A total of eighteen ISSR primers synthesized by M/S Banglore Genei, India Limited were used in the present study (Table 3.3).

Table 3.3 Nucleotide sequences of ISSR primers

Sr. No.	Primer name (ISSR)	Base sequence (5'-3')
1	UBC 809	AGAGAGAGAGAGAGAGG
2	UBC 810	GAGAGAGAGAGAGAGAT
3	UBC 811	GAGAGAGAGAGAGAGAC
4	UBC 812	GAGAGAGAGAGAGAGAA
5	UBC 825	CACACACACACACACC
6	UBC 830	TGTGTGTGTGTGTGTGG
7	UBC 834	AGAGAGAGAGAGAGAGYT
8	UBC 835	AGAGAGAGAGAGAGAGYC
9	UBC 850	GTGTGTGTGTGTGTGTYA
10	UBC 820	GTGTGTGTGTGTGTGTC

2. Standardization of PCR amplification conditions

Tests were performed for standardizing polymerase chain reaction amplification conditions mainly the annealing temperature**.**

Sr. No.	Reactions		Temperature and Time Specifications	Number of Cycles
1.	Initial Denaturation		94°C-for 3min	1
2.	A	Denaturation	92°C-for 45 sec	45
	B	Annealing of Primer	55°C-for 1min	
	C	Primer amplification	72°C-for 2min	
3.	Final amplification		72°C-for 10min	1
After completion			4°C- till electrophoresis	

3. Amplification of DNA by PCR using ISSR primers

The amplification reactions were performed in a total volume of 24 µl containing

Sr. No.	Constituents	Quantity
1.	Sterile distilled water	15 µl
2.	Taq buffer (10X)	2.5 µl
3.	dNTPs (2.5 mM)	1.25 µl
4.	Primer (10 ng)	1.0 µl
5.	Taq DNA Polymerase (3U/µl)	0.25 µl
6.	DNA (5 ng/µl)	4 µl
	Total for 1 reaction	24 µl

The reagents were mixed thoroughly in a 2 ml Eppendorf tube and vortexed for few seconds. 20 µl of mixture was distributed to each PCR tube and 4.0 µl of template DNA (5

ng/µl) was added to each tube for each amplification reaction in thermal cycler (Corbett Thermal Cycler) (Williams *et al*., 1990) programmed as above.

4. Electrophoresis using agarose gel

The amplified DNA was mixed thoroughly with 6X loading dye (Appendix III) and then electrophoresed in 2 per cent agarose gel in 1X TAE buffer (Appendix II). The gel was run at constant voltage at the rate of 5V/cm under submerged conditions for about two hours. Ethidium bromide at the rate of 0.5µg/ml was incorporated in the gel. Stock solution of ethidium bromide @ 10 mg/ml was kept ready. DNA profiles were visualised on UV Transilluminator and photographed on Gel Documentation System (Syngene, Cambridge, UK).

ISSR Fingerprints

1. Viewing of amplified DNA

After the run was over, the gel was viewed under the UV light using Gel Documentation system and was photographed.

2. Scoring of bands

The amplified bands after separation were visualized using Gel Documentation system. Further the bands were scored for percentage polymorphism for each set of primer amplified product using NTSYS 2.2.

4.5 Analysis of ISSR Data

The scored bands were analyzed in the form of binary system to prepare the similarity index. The bands with same molecular weight and mobility were treated as identical fragments. Data matrices were prepared in which the presence of a band was coded as 1 whereas the absence as zero. The data matrices were analyzed by the SIMQUAL Program of NTSYS-PC (Version 2.2) and similarities between Families were estimated using Jaccard similarity coefficient, calculated as J = A / (N-D), where A is the number of positive matches (*i.e.* presence of band in both samples), D is the number of negative matches (*i.e.* absence of band in both samples) and N is the total sample size including both the number of matches and unlatches. Dendrogram was produced from the resultant similarity matrices using the UPGMA method.

Chapter-4

RESULTS AND DISCUSSION

The current study, which was given the title **"Morphogenetic variation for leaf fodder quality parameters in populations of *Grewia optiva* Drummond"** was conducted in the research field and laboratory of the Department of Tree Improvement and Genetic Resources, College of Forestry, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan (Himachal Pradesh) during the years 2020–2023. The goal of this investigation was to evaluate various morphological, seedling growth and fodder quality characteristics of twenty different selected populations of *Grewia optiva*. After observing the development of seedlings for a period of 18 months in a nursery setting, the top performing half-sib progenies of the 15 best genotypes were put through a genetic study using molecular markers. The findings of the current investigations are presented in this chapter and they are arranged under the following headings:

4.1 Morphological and Genetic diversity

4.1.1 Morphometric characteristics

4.1.1.1 Morphological characteristics

4.1.1.2 Leaf morphometric characteristics

4.1.2 Nursery Evaluation

4.1.2.1 Seed and germination characteristics

4.1.2.2 Seedling growth characteristics

4.1.2.3 Fodder quality and mineral nutrient characteristics

4.2 Physiochemical properties of soil

4.3 Variation in fodder quality parameters of mother trees

4.4 Variations in mineral nutrients and biochemical estimates of mother trees

4.5 Genetic estimates

4.6 Correlation studies

4.7 Path analysis

4.8 Principal component analysis

4.9 Cluster analysis

4.10 Molecular- markers based analysis

4.1 Morphological and Genetic Diversity

Twenty populations of *G. optiva* Drummond were evaluated for the selection of the finest genotypes based on morphometric characteristics.

4.1.1 Morphometric characteristics

4.1.1.1 Variation in Morphological characteristics

Different tree morphological characteristics, such as height, diameter, crown spread (both east-west and north-south), number of primary branches, number of secondary branches, branch nodal length and leaf shape were observed among the different genotypes and populations of the *G. optiva*. The altitudinal variations in the mean values of these morphological features among the populations were also observed in this study.

A. Variation in Morphological characteristics among genotypes of *G. optiva* Drummond.

The findings presented in Table 4.1 showed the variation in tree morphological characteristics, such as height (m), diameter (cm), crown spread (E-W and N-S) (m), number of primary branches, number of secondary branches and branch internodal length (cm) among eighty genotypes of populations of *G. optiva*.

Table 4.1. Variations in morphological characters among genotypes of populations of *Grewia optiva* Drummond.

Sr. No.	Genotypes	Tree height (m)	Diameter (cm)	Crown spread (N-S)	Crown spread (E-W)	No. of primary branches per tree	No. of secondary branches per primary branch	Branch internodal length (cm)
1	HR 1	8.0	24.50	4.32	4.22	5	7	6.17
2	HR 2	7.7	24.97	4.16	4.26	5	6	6.32
3	HR 3	8.5	27.11	3.85	4.15	5	6	6.73
4	HR 4	9.0	28.64	4.11	4.38	5	8	7.15
5	ST 1	8.5	23.45	3.65	3.85	6	8	6.73
6	ST 2	8.3	25.31	3.88	3.50	5	9	7.09
7	ST 3	8.4	23.65	4.47	3.82	5	10	6.04
8	ST 4	7.8	24.00	4.12	4.02	5	11	6.20
9	DR 1	10.5	29.55	4.09	4.14	5	5	7.28
10	DR 2	10.0	28.64	4.17	4.46	6	7	7.33
11	DR 3	9.8	27.77	4.29	5.11	5	6	7.17
12	DR 4	9.9	26.75	5.04	5.05	5	7	6.55
13	GH 1	8.0	27.44	4.18	4.34	4	7	7.25
14	GH 2	9.0	27.65	4.07	4.25	4	8	7.09
15	GH 3	9.3	26.50	3.38	4.00	4	9	6.12
16	GH 4	9.5	29.45	3.55	4.15	4	8	7.19

17	DA 1	8.2	24.69	4.65	3.92	5	8	6.42
18	DA 2	8.3	26.59	4.05	3.65	5	9	7.06
19	DA 3	8.8	24.71	4.64	4.02	5	8	5.91
20	DA 4	8.5	25.50	3.04	3.75	5	10	6.79
21	KD 1	6.5	25.19	3.45	4.08	5	10	6.03
22	KD 2	7.1	26.05	3.33	3.75	5	9	6.12
23	KD 3	7.5	23.85	4.50	3.98	6	9	6.33
24	KD 4	7.3	23.45	5.21	4.35	6	8	7.11
25	SI 1	9.5	28.87	5.23	4.52	8	11	7.32
26	SI 2	8.4	27.94	5.14	5.43	7	11	6.78
27	SI 3	10.5	27.50	4.20	5.35	8	10	7.26
28	SI 4	9.0	29.82	4.33	3.76	8	10	6.91
29	DO 1	6.5	24.45	2.92	3.12	5	9	5.22
30	DO 2	6.8	22.55	3.05	3.25	6	8	5.79
31	DO 3	6.5	23.19	3.45	4.25	6	9	5.98
32	DO 4	7.0	22.50	3.07	3.37	6	7	6.16
33	KT 1	8.8	26.45	2.78	4.45	6	10	6.76
34	KT 2	9.1	25.78	4.05	3.95	6	12	6.47
35	KT 3	8.6	27.74	3.08	3.84	5	11	6.88
36	KT 4	9.2	25.75	3.15	4.05	6	13	7.11
37	KU 1	7.0	27.76	5.52	4.12	7	10	6.07
38	KU 2	7.5	28.33	4.93	5.25	6	10	6.98
39	KU 3	7.5	25.67	5.50	4.82	6	10	6.22
40	KU 4	7.0	28.88	4.76	4.76	7	12	6.44
41	AD 1	7.3	27.60	4.51	3.53	5	10	6.56
42	AD 2	7.2	26.24	5.22	3.54	5	11	5.49
43	AD 3	7.1	26.50	4.24	2.92	5	11	5.22
44	AD 4	7.5	24.55	3.83	3.03	5	10	6.98
45	DH 1	7.3	26.78	4.76	5.16	7	13	6.34
46	DH 2	6.5	24.45	4.50	4.20	6	11	5.97
47	DH 3	8.5	25.09	5.50	4.50	5	16	6.72
48	DH 4	8.0	25.31	5.45	4.55	6	16	6.57
49	NR 1	6.5	22.90	3.84	4.05	5	11	5.37
50	NR 2	7.6	22.70	3.36	5.52	4	11	6.18
51	NR 3	7.0	23.50	4.15	2.74	5	13	5.87
52	NR 4	6.5	26.51	4.25	2.73	5	11	4.73
53	BA 1	8.0	23.44	4.19	4.04	6	7	5.92
54	BA 2	7.5	26.07	3.23	3.94	7	10	5.43
55	BA 3	8.5	24.50	5.07	3.75	6	10	6.93
56	BA 4	9.0	25.09	3.50	3.75	7	8	7.12
57	JG 1	7.0	26.16	3.96	4.05	5	11	6.09
58	JG 2	7.2	25.12	5.50	3.93	5	10	5.79
59	JG 3	7.5	29.76	5.42	4.75	4	13	6.86
60	JG 4	8.0	27.55	4.66	4.88	5	13	6.97
61	SH 1	6.5	23.44	3.55	3.05	6	11	5.61
62	SH 2	6.0	24.53	3.42	2.92	5	11	5.43
63	SH 3	6.0	24.03	4.09	3.95	4	12	6.14
64	SH 4	5.6	22.11	3.15	2.75	4	9	5.82
65	SN 1	7.0	25.62	2.84	4.34	5	7	6.07
66	SN 2	6.5	24.87	3.15	4.50	5	8	5.63
67	SN 3	7.5	26.01	3.58	3.88	6	7	6.29
68	SN4	5.7	24.10	3.09	4.44	5	9	5.05
69	GT 1	6.1	20.09	4.34	3.34	4	8	5.85

70	GT 2	5.5	22.20	3.88	2.78	3	9	5.52
71	GT 3	5.8	23.11	3.98	4.08	4	10	6.90
72	GT 4	5.5	20.50	3.15	3.55	5	10	5.22
73	GR 1	6.5	24.33	2.78	3.28	4	6	5.77
74	GR 2	7.5	25.02	2.99	3.45	5	7	6.05
75	GR 3	6.0	23.04	3.35	4.05	5	7	5.17
76	GR 4	6.2	22.09	3.29	3.59	5	8	4.91
77	RA 1	6.5	23.11	4.14	3.50	4	9	5.23
78	RA 2	7.5	22.61	3.89	4.05	4	9	5.99
79	RA 3	7.3	20.17	4.00	4.21	5	8	4.56
80	RA 4	7.0	22.06	3.50	3.75	4	10	5.20
Mean		**7.6**	**25.26**	**4.03**	**4.00**	**5.29**	**9.46**	**6.25**
Range		5.5-10.5	20.09-29.82	2.78-5.52	2.72-5.52	3.00-8.00	5.00-16.00	5.25-7.08
CV(%)		15.76	8.97	18.70	15.87	19.08	22.62	8.61

The height of the tree varied from 5.5 to 10.5 m. The DR1 and SI3 genotypes were reported as the tallest, measuring 10.5 m in height, while the GT2 genotype was the shortest, measuring 5.5 m in height. The diameter of the tree ranged from 20.09 cm to 29.82 cm (at a height of 70 cm). The SI4 genotype had the maximum diameter, whereas the RA3 genotype had the smallest diameter. The width of the crown from north to south was measured to be between 2.78 and 5.52 m. The KU1 genotype had the highest crown spread (N-S) value with 5.52 m, while the GR1 genotype had the lowest, *i.e.,* 2.78 m. The crown spread (from east to west) varied from 2.72 to 5.52 m. The NR4 genotype had the narrowest crown spread (2.73 m), whereas, the NR2 genotype had the widest crown spread (5.52 m). The SI1, SI3, and SI4 genotypes each had a maximum of 8 primary branches, while the RA4 genotype had a minimum of 3 primary branches. There could be anywhere from 5 to 16 secondary branches on each individual tree. The DH3 and DH4 genotypes had the maximum number of secondary branches per tree, which was 16, whereas, the DR1 genotype had the lowest possible number of secondary branches per tree, which was 5. The length of the branch nodes ranged from 4.73 cm to 7.33 cm, with the DR1 genotype reported with the maximum branch nodal length and the NR4 genotype reported with the shortest branch nodal length.

B. Variation in Morphological characteristics among populations of *G. optiva* Drummond.

The data illustrated in Table 4.2 and Fig 4.1 pertained to the differences in tree morphological characteristics, such as height (m), diameter (cm), crown spread (E-W & N-S) (m), number of primary branches, number of secondary branches and branch internodal length (cm) between different populations of *G. optiva*.

Table 4.2 Variations in morphological characters among populations of *Grewia optiva* Drummond.

Altitudinal Zone (a msl)	Populations	Tree Height (m)	Diameter (cm)	Crown spread (N-S) (m)	Crown spread (E-W) (m)	No. of primary branches per tree	No. of secondary branches per primary branch	Branch internodal length (cm)
A1(400-800 m)	P1(Harsar)	8.30	26.31	4.11	4.25	4.91	7.05	6.59
	P2(SujanpurTihra)	8.25	24.10	4.03	3.80	5.45	9.69	6.52
	P3(Dramman)	10.03	28.18	4.40	4.69	5.38	5.86	7.08
	P4(Ghumarwii)	8.96	27.76	3.80	4.19	3.98	8.20	6.91
	P5(Daggar)	8.43	25.37	4.10	3.84	4.96	8.89	6.55
A2(800-1200 m)	P6 (Kalanjri Devi)	7.09	24.64	4.12	4.04	5.75	9.15	6.40
	P7 (Sihunta)	9.33	28.53	4.73	4.77	7.69	10.42	7.07
	P8(Dodar)	6.69	23.17	3.12	3.50	5.52	8.14	5.79
	P9(Kuthar)	8.91	26.43	3.27	4.07	5.67	11.62	6.81
	P10(Kutuldi)	7.25	27.66	5.18	4.74	6.76	10.63	6.43
A3 (1200-1600 m)	P11(Awah devi)	7.26	26.22	4.45	3.26	4.88	10.55	6.06
	P12 (Dharot)	7.58	25.41	5.05	4.60	5.94	14.01	6.40
	P13(Neri)	6.90	23.90	3.90	3.76	4.66	11.43	5.54
	P14(Basni)	8.25	24.78	4.00	3.87	6.73	8.83	6.35
	P15(Jagdhar)	7.43	27.15	4.89	4.40	4.72	11.69	6.43
A4 (1600-2000 m)	P16 (Shogi)	6.02	23.53	3.55	3.17	4.87	10.70	5.75
	P17 (Sangrah)	6.69	25.15	3.17	4.29	5.32	7.93	5.76
	P18 (Ghanahatti)	5.72	21.48	3.84	3.44	4.12	9.27	5.87
	P19 (Garhkhal)	6.55	23.62	3.10	3.59	4.64	7.16	5.48
	P20 (Ranichauri)	7.08	21.99	3.88	3.88	4.17	9.18	5.25
Mean		**7.63**	**25.26**	**4.03**	**4.01**	**5.31**	**9.52**	**6.25**
$CD_{0.05}$		0.73	1.85	0.72	0.69	0.70	1.41	0.76

A glance at Table 4.2 and Fig 4.1 revealed the substantial differences in tree height among the various populations. Population P3 reported with maximum tree height (10.03 m) which was statistically at par with P7. Population P18 reported with minimum tree height (5.72 m) which was statistically at par with population P16.

It is apparent from Table 4.2 and Fig 4.1 that the maximum diameter was recorded for population P7 (28.53 cm) which was statistically at par with P3 and P10. The minimum tree diameter was recorded for P18 (21.48 cm) which was statistically at par with P3 and P10.

The data illustrated in Table 4.2 and Fig 4.1 revealed that the population P10 had the widest crown spread (N-S) (5.18 m), whereas, population P19 had the narrowest crown

spread (3.10 m). The maximum value of crown spread (N-S) was statistically at par with P12, P3 and P7, while, minimum value was statistically at par with P4, P8, P9, P16, and P17

Persual of Table 4.2 and Fig 4.1 showed that maximum crown spread (E-W) was recorded in population P7 (4.77 m) which was statistically at par with P1, P3, P4, P10, P12, P15 and P17. Moreover, the minimum crown spread (E-W) was reported in population P16 (3.17 m) which was found to be statistically at par with P2, P5, P8, P11, P13 and P18.

Table 4.2 and Fig 4.1 showed that maximum number of primary branches per tree were recorded in P7 (7.69) which was followed by P10 and P14, while, minimum number of primary branches per tree were recorded in P4 (3.98) which was statistically at par with P18 and P20. The maximum number of secondary branches per tree were observed in P12 (14.01) which followed by P9, P13 and P15, while, minimum number of secondary branches per tree was recorded in P3 (5.86) which was statistically at par with P1 and P19.

It is evident from Table 4.2 and Fig 4.1 that the population P3 reported with maximum branch nodal length (7.08 cm) which was statistically at par with P7, P4, P9, P1, P2, P5, P6, P10, P12 and P15, while, P20 reported with minimum branch nodal length (5.25 cm) which was statistically at par with P8, P13, P16, P17, P18 and P19.

The supporting explanations for the vast differences in morphological characteristics have been reported by numerous researchers in a number of species: height, diameter and number of branches in *Cedrela* species (Whitmore, 1971); plant height, diameter, number of branches, branch length and internodal distance in *Acacia nilotica* (Shivkumar and Banerjee, 1986) and *Acacia mangium* (Salazar, 1989); plant height and diameter in *Populus* species (Jha and Gupta, 1992); Sehgal and Jaswal (1996) in *G. optiva,* Rathore (1997) in *G. optiva,* Bhat (1999) in *Albizia lebbeck* and Choudhary (2000) in *Toona ciliata.* Pant *et al*. (2003) in *G. optiva*; Marriapan (2007) in *Grewia laevigata* Vahl., Wani *et al.* (2009) in *Bauhinia variegata*; Sankhyan *et al.* (2009) in *G. laevigata*; Bhat (2010), Bhagta (2015), Prajapati (2015) and Sushmita (2021) in *G. optiva*. Poonam *et al.* (2012) documented plant height ranged between 2.00 m and 3.82 m in *B. variegata*. Diameter measurements are the most essential tree attribute since they can be readily measured and used to compute basal area and timber volume. Sankhyan *et al.* (2013) in *Anogeissus latifolia* reported a substantial variation in tree diameter among sites. Gupta (2012) found that mean diameter varied from 10.50 cm to

37.10 cm in *A. latifolia* at different sites and diameter classes. The number of branches per tree is the most important feature of fodder trees. They provide the necessary support for leaves, fruits and flowers throughout their development into their final structures. They are also the vessels that take water from the earth to the leaves and food from the leaves to the rest of the tree. In the current study, the variation in number of branches per tree among populations of different altitudinal ranges might be attributed to the frequency of lopping done by local people. Alternatively, the variation could be attributable to the effects of some elements that cause variation, such as climate, tree age, genetic factors, stage of growth, etc. Poonam *et al.* (2012) during the course of their research on evaluation of plus tree progenies of *B. variegata*, number of branches ranged anywhere from 3.67 to 9.67 among a number of different locations. Wani (2005) also carried out research on morphological variation and discovered that the progenies from Pinjore, Kandaghat and Giripul showed exceptional performance in terms of the number of branches when compared to all of the superior tree progenies in the glass house. Gupta (2012) carried out the research on *A. latifolia* and discovered that the number of tree branches varied among sites.

C. Altitudinal Variation in Morphological characteristics among populations of *G. optiva* Drummond.

Table 4.3 and Fig 4.2 displayed the results pertaining to altitudinal variations (mean value) in tree morphological characteristics including height (m), diameter (cm), crown spread (E-W & N-S) (m), number of primary branches, number of secondary branches, and branch nodal length (cm) among *G. optiva* populations.

Table 4.3 Altitudinal variations (mean value) (of Table 4.2) in morphological characters among populations of *Grewia optiva* Drummond.

Altitudinal Zone (a msl)	Tree Height (m)	Diameter (cm)	Crown spread (N-S)(m)	Crown spread (E-W) (m)	No. of primary branches per tree	No. of secondary branches per primary branch	Branch internodal length (cm)
A1 (400-800 m)	8.8	26.34	4.09	3.93	4.84	7.94	6.73
A2 (800-1200 m)	7.9	26.09	4.08	4.30	6.20	9.94	6.50
A3(1200-1600 m)	7.5	25.49	4.34	4.06	5.12	11.35	6.16
A4(1600-2000 m)	6.4	23.15	3.55	3.80	4.66	9.20	5.62

The mean observations for morphological characters (of populations) that are displayed in Table 4.3 and Fig 4.2 demonstrated that the height of the tree, diameter, crown spread (N to S), crown spread (E to W), number of primary branches per tree, number of secondary branches and branch nodal varied with the fluctuation in altitude zone. The

populations of the A1 (400–800 m a msl) altitudinal zone were found to have the highest mean tree height (8.8 m), diameter (26.34 cm) and branch nodal length (6.73 cm). On the other hand, the populations of the A4 (1600–2000 m a msl) altitudinal zone were found to have the minimum tree height (6.41 m), diameter (23.15 cm) and branch nodal length (5.62 cm).

The mean value for crown spread (N-S) recorded a maximum (4.34 m) in the A3 (1200–1600 m a msl) altitudinal zone and a minimum (3.55 m) for the A4 (1600–2000 m a msl) altitudinal zone. In a similar fashion, the maximum mean values for crown spread (E-W) (4.30 m) and for number of primary branches per tree (6.20) were recorded for the A2 (800–1200 m a msl) altitudinal zone, whereas, the minimum was recorded for the A4 (1600–2000 m a msl) altitudinal zone. The highest mean number of secondary branches per tree was 11.35 in the A3 (1200–1600 m a msl) altitudinal zone, while, the lowest number was 7.94 in the A1 altitudinal zone.

There are studies that were uncovered by researchers that demonstrated how altitudinal gradients and contemporaneous factors influence the height of plants. High-altitude plants face many environmental stresses that alters plant characteristics, especially temperature and radiation extremes (Hatfield and Prueger, 2015; Wang *et al*., 2020; Dongdong *et al*., 2020), soil and water stresses (Magnani and Borghetti, 1995). Low-altitude plants endure high temperatures, dry climates, harsh radiation and limited precipitation, while, high-altitude plants endure low temperatures, high irradiance, etc. (Paridari *et al*., 2013; Mao *et al*., 2018). Higher elevations are frequently regarded as more stressful for plant development and survival, as the competition for light and nutrients at higher elevations favours undersized trees (Reif *et al*., 2004; Xu *et al*., 2012) and reduces tree growth (Coomes and Allen, 2007). The crown spread also changed as the altitude zone changed. It increased from altitude zone A1 to altitude zone A3 and then decreased from altitude zone A3 to altitude zone A4. Similarly, the morphological characteristics of *Boswellia* trees in Eritrea were found to vary significantly along altitudinal ranges. It revealed that as altitude increased, tree height, crown width and depth all decreased in *Boswellia* species (Pi *et al*., 2020; Ogbazghi *et al*., 2006).

D. Variation in leaf shapes among populations of *G. optiva* Drummond.

Table 4.4 showed the variations in leaf shape for different populations. Among populations, three leaf shapes were observed: narrowly ovate, ovate and broadly ovate.

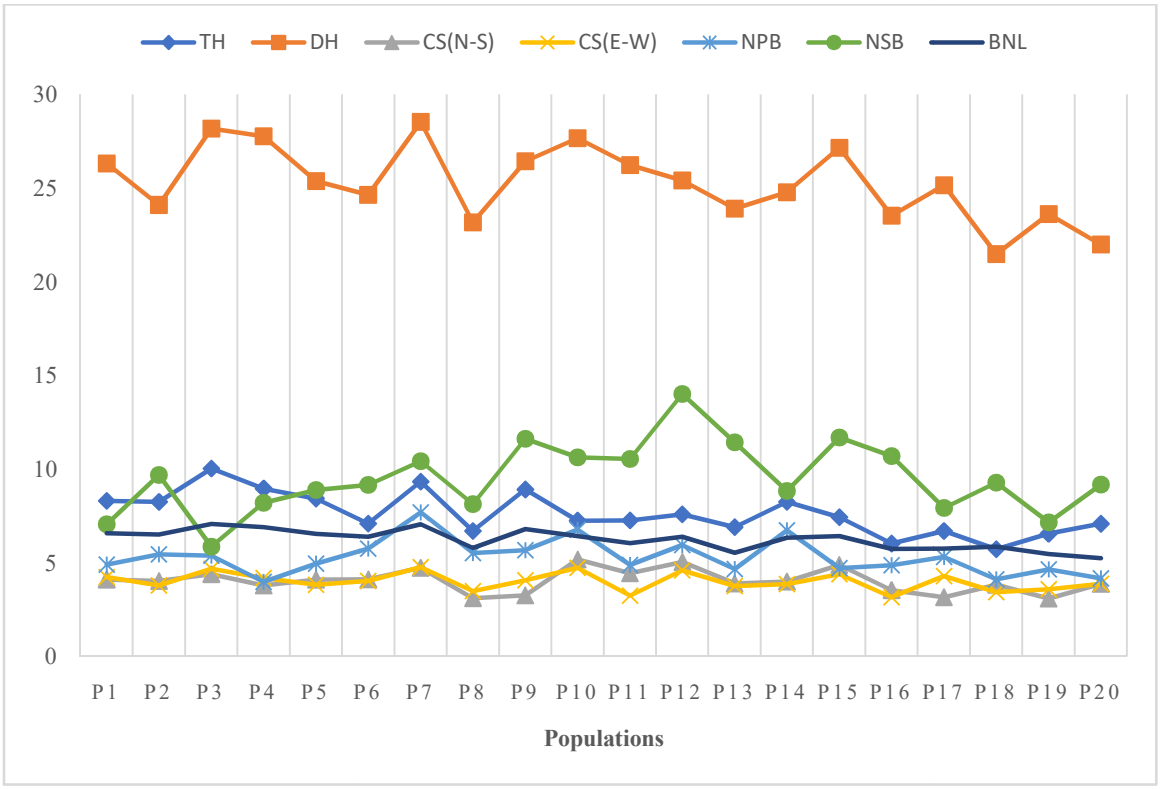


Fig 4.1 Variations in morphological characters among populations of *Grewia optiva* Drummond.

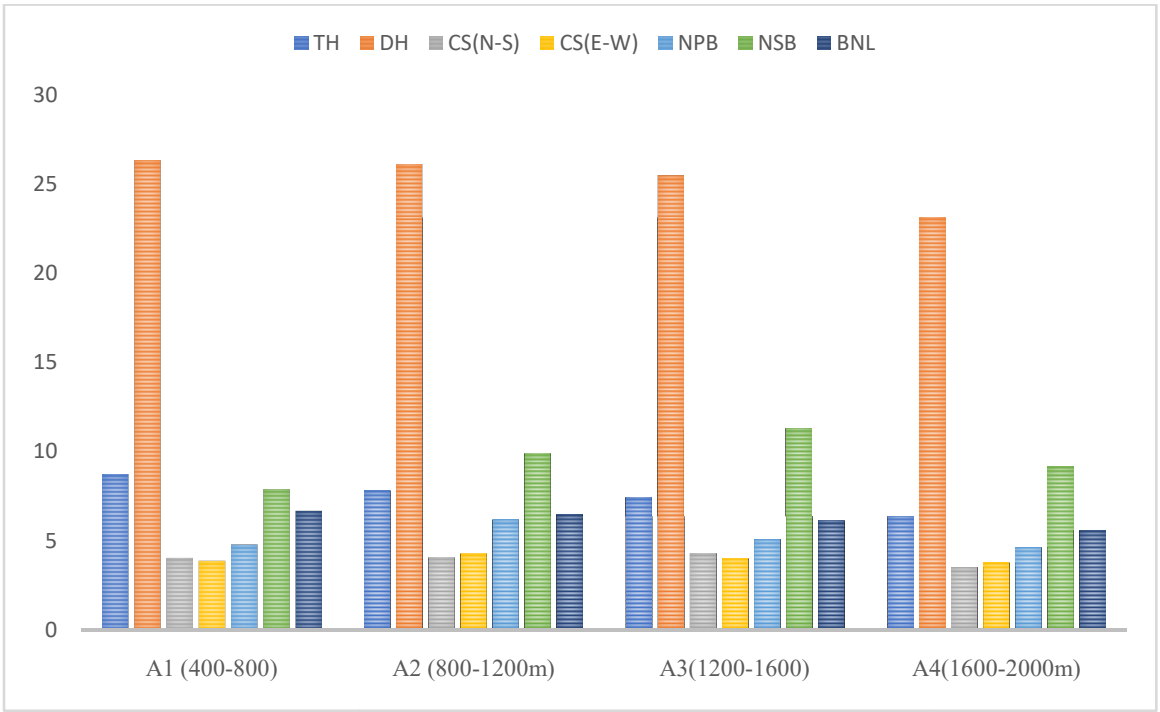


Fig 4.2 Altitudinal variations in morphological characters among populations of *Grewia optiva* Drummond.



No. of branches



Tree diameter



Branch Internodal length



Variation in leaf shape

Plate 1. Recording observations on Tree morphological characters.

Variations in leaf apex were also seen between populations. The leaf apex was narrowly acuminate, abruptly acuminate and broadly acuminate. The morphology of leaves is an important indicator of plant response to climate change. Leaf size and shape are related to how plants exchange carbon, water and energy with their surroundings. The results of current study are supported by the findings of Sankhyan *et al*., 2021 in *G. optiva*, where they discovered three types of leaf shape in distinct genotypes and populations of *G. optiva*, namely ovate and acuminate.

Table 4.4. Variations in leaf shape among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Leaf shape	Leaf apex
A1(400-800 m)	P1(Harsar)	Narrowly Ovate	Abruptly acuminate
	P2(SujanpurTihra)	Ovate	Abruptly acuminate
	P3(Dramman)	Narrowly Ovate	Narrowly acuminate
	P4(Ghumarwii)	Ovate	Narrowly acuminate
	P5(Daggar)	Ovate	Narrowly acuminate
A2(800-1200 m)	P6 (Kalanjri Devi)	Ovate	Broadly acuminate
	P7 (Sihunta)	Narrowly Ovate	Abruptly acuminate
	P8(Dodar)	Ovate	Narrowly acuminate
	P9(Kuthar)	Ovate	Abruptly acuminate
	P10(Kutuldi)	Narrowly Ovate	Abruptly acuminate
A3(1200-1600 m)	P11(Awah devi)	Ovate	Narrowly acuminate
	P12 (Dharot)	Narrowly Ovate	Abruptly Acuminate
	P13(Neri)	Ovate	Abruptly Acuminate
	P14(Basni)	Narrowly Ovate	Abruptly Acuminate
	P15(Jagdhar)	Narrowly Ovate	Abruptly acuminate
A4(1600-2000 m)	P16 (Shogi)	Ovate	Broadly acuminate
	P17 (Sangrah)	Broadly Ovate	Broadly acuminate
	P18 (Ghanahatti)	Broadly Ovate	Broadly acuminate
	P19 (Garhkhal)	Ovate	Broadly acuminate
	P20 (Ranichauri)	Broadly Ovate	Broadly acuminate

4.1.1.2 Leaf Morphometric characteristics

A. Variation among genotypes

The genotypes of selected populations of *G. optiva* differed significantly in leaf morphometric features such as leaf length (cm), leaf width (cm), leaf area (cm^2) and petiole length (cm). Table 4.5 presented a critical assessment of the data among genotypes.

Data exhibited in Table 4.5 revealed that maximum leaf length was recorded for SI1 genotype (18.12 cm), while, minimum leaf length was estimated for RA3 genotype (9.22 cm) which was statistically at par with the GR2, GT2, GT1, SH3, and BA1. The maximum leaf width was recorded for KT4 (11.11 cm) which was statistically at par with KT3 and KT2. The minimum leaf width was recorded for RA2 genotype (4.7 cm).

Data demonstrated in the Table 4.5 depicts that the genotype SI1 had the maximum leaf area (133.23 cm^2) which was statistically at par with SI2, while, the genotype RA3 had the smallest leaf area (55.44 cm^2) which was found to be statistically at par with RA4.

The data shown in Table 4.5 revealed that the genotype KT2 had the longest petiole length (1.33 cm), whereas, the genotype DO4 had the shortest petiole length (0.83 cm) which was statistically at par with the genotypes GR3, GT3, GT1, NR3, BA1 and BA4.

Table 4.5. Variations in leaf morphometric characteristics among genotypes of populations of *Grewia optiva* Drummond

Sr. No.	Genotypes	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2)	Petiole length (cm)
1	HR 1	15.28	9.54	107.78	0.93
2	HR 2	15.52	8.75	100.67	1.04
3	HR 3	16.55	9.21	103.56	1.03
4	HR 4	15.09	10.34	102.07	1.11
5	ST 1	14.42	10.22	100.71	1.08
6	ST 2	13.89	9.87	99.56	0.94
7	ST 3	14.3	9.94	101.76	1.21
8	ST 4	10.21	10.08	95.88	1.07
9	DR 1	10.04	9.17	79.85	0.92
10	DR 2	11.32	8.97	80.11	0.90
11	DR 3	13.54	8.88	97.21	0.89
12	DR 4	9.88	10.03	82.32	0.91
13	GH 1	13.82	8.12	90.22	1.01
14	GH 2	12.21	9.55	82.07	0.92
15	GH 3	11.15	10.22	82.12	0.93
16	GH 4	10.88	10.10	85.15	0.88
17	DA 1	13.55	7.50	94.53	0.96
18	DA 2	11.66	8.23	79.23	1.01
19	DA 3	11.32	7.05	75.34	1.10
20	DA 4	10.11	6.11	76.98	0.97
21	KD 1	10.23	9.22	72.31	1.01
22	KD 2	9.95	10.08	70.56	1.07
23	KD 3	12.67	7.98	75.18	1.12
24	KD 4	13.34	9.95	80.45	0.98
25	SI 1	18.12	9.33	133.23	1.05
26	SI 2	17.22	9.82	130.34	1.11
27	SI 3	17.42	10.70	128.43	1.23
28	SI 4	16.98	10.20	120.60	1.17
29	DO 1	10.04	9.67	67.89	0.96
30	DO 2	12.22	7.49	80.77	0.87
31	DO 3	9.82	8.32	72.34	0.95
32	DO 4	9.78	9.16	69.79	0.85
33	KT 1	16.21	10.39	122.12	1.02
34	KT 2	14.11	10.99	124.54	1.33
35	KT 3	17.22	10.98	127.21	0.99
36	KT 4	17.45	11.11	125.34	1.12
37	KU 1	13.09	10.45	104.34	1.11

38	KU 2	12.55	9.14	99.97	0.84
39	KU 3	14.23	8.83	100.67	0.88
40	KU 4	16.76	9.54	101.99	1.30
41	AD 1	13.32	9.56	99.35	0.98
42	AD 2	10.45	8.89	79.89	1.01
43	AD 3	13.67	9.17	100.24	0.89
44	AD 4	11.34	9.88	82.45	0.94
45	DH 1	13.54	10.22	99.86	1.12
46	DH 2	13.31	10.11	97.67	0.98
47	DH 3	11.95	10.05	87.09	0.89
48	DH 4	13.32	9.63	95.34	1.13
49	NR 1	10.12	9.43	77.54	1.06
50	NR 2	13.09	10.80	81.34	0.95
51	NR 3	11.32	9.05	83.99	0.86
52	NR 4	10.11	8.22	83.87	0.91
53	BA 1	9.57	9.64	70.45	0.87
54	BA 2	10.07	8.98	72.38	0.93
55	BA 3	10.33	9.22	73.27	0.99
56	BA 4	11.59	9.05	70.89	0.86
57	JG 1	13.45	7.30	100.60	0.99
58	JG 2	12.08	9.56	98.55	0.96
59	JG 3	13.51	8.10	100.98	1.01
60	JG 4	10.33	6.75	97.33	1.07
61	SH 1	9.89	9.33	69.75	0.99
62	SH 2	10.11	8.85	67.89	0.94
63	SH 3	9.60	9.07	70.23	0.89
64	SH 4	11.02	9.21	71.24	0.98
65	SN 1	12.45	10.03	89.60	1.10
66	SN 2	14.63	9.68	100.21	1.19
67	SN 3	11.32	9.86	93.22	0.89
68	SN4	15.43	8.54	95.16	1.03
69	GT 1	9.54	7.39	59.98	0.82
70	GT 2	9.43	6.64	60.19	0.92
71	GT 3	10.65	7.36	60.22	0.86
72	GT 4	10.76	7.98	61.67	0.99
73	GR 1	12.65	8.32	83.21	0.95
74	GR 2	9.69	7.89	64.22	0.88
75	GR 3	10.04	8.32	65.09	0.85
76	GR 4	10.11	8.97	60.12	0.91
77	RA 1	11.22	6.50	70.34	0.89
78	RA 2	12.90	4.70	67.38	0.99
79	RA 3	9.22	7.20	55.44	0.88
80	RA 4	10.78	5.50	58.09	0.97
Mean		**12.40**	**9.00**	**87.52**	**0.99**
$CD_{0.05}$		0.49	0.38	3.40	0.04

B. Variation among populations

The results pertaining to variation in leaf morphometric characteristics *viz.,* leaf length (cm), leaf width (cm), leaf area (cm^2) and petiole length (cm) are shown in Table 4.6 and Fig. 4.3.

Table 4.6. Variations in leaf morphometric characters among populations of *Grewia optiva* Drummond.

Altitudinal Zone (a msl)	Populations	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2)	Petiole length (cm)
A1(400-800 m)	P1(Harsar)	15.61	9.46	103.52	1.03
	P2(SujanpurTihra)	13.21	10.03	99.48	1.08
	P3(Dramman)	11.20	9.26	84.87	0.91
	P4(Ghumarwii)	12.02	9.50	84.89	0.94
	P5(Daggar)	11.66	7.22	81.52	1.01
A2(800-1200 m)	P6 (Kalanjri Devi)	11.55	9.31	74.63	1.05
	P7 (Sihunta)	17.44	10.01	128.15	1.14
	P8(Dodar)	10.47	8.66	72.70	0.91
	P9(Kuthar)	16.25	10.87	124.80	1.12
	P10(Kutuldi)	14.16	9.49	101.74	1.03
A3 (1200-1600 m)	P11(Awah devi)	12.20	9.63	90.48	0.96
	P12 (Dharot)	13.03	10.00	94.99	1.03
	P13(Neri)	11.16	9.38	81.69	0.95
	P14(Basni)	10.39	9.22	71.75	0.91
	P15(Jagdhar)	12.34	7.93	99.37	1.01
A4 (1600-2000m)	P16 (Shogi)	10.16	9.12	69.78	0.95
	P17 (Sangrah)	13.46	9.53	94.55	1.05
	P18 (Ghanahatti)	10.10	7.34	60.52	0.90
	P19 (Garhkhal)	10.62	8.38	68.16	0.90
	P20 (Ranichauri)	11.03	5.98	62.81	0.93
Mean		**12.40**	**9.01**	**87.52**	**0.99**
$CD_{0.05}$		1.99	1.05	7.64	0.13

It is evident from Table 4.6 and Fig. 4.3 that population P7 exhibited maximum leaf length (17.44 cm) which was statistically at par with P1 and P9, whereas, minimum value (10.10 cm) was recorded in population P18 which was statistically at par with P3, P5, P6, P8, P11, P13, P14, P16, P19 and P20.

It was found that population P9 showed the maximum leaf width (10.87 cm) which was statistically at par with P2, P7 and P12, whereas, the minimum leaf width (5.98 cm) was exhibited by P20 (Table 4.6).

A perusal of data presented in Table 4.6 and Fig 4.3 showed that maximum leaf area (128.12 cm^2) was recorded in P7 which was statistically at par with P20. Moreover, the minimum value of leaf area was (60.52 cm^2) noted in P18 which was statistically at par with P20. The maximum petiole length (1.14 cm) was reported in P7 which was statistically at par with P15 and P17, whereas, minimum petiole (0.90 cm) was recorded in P18 and P19 which was statistically at par with P3, P4, P8, P11, P13, P14, P16 and P20.

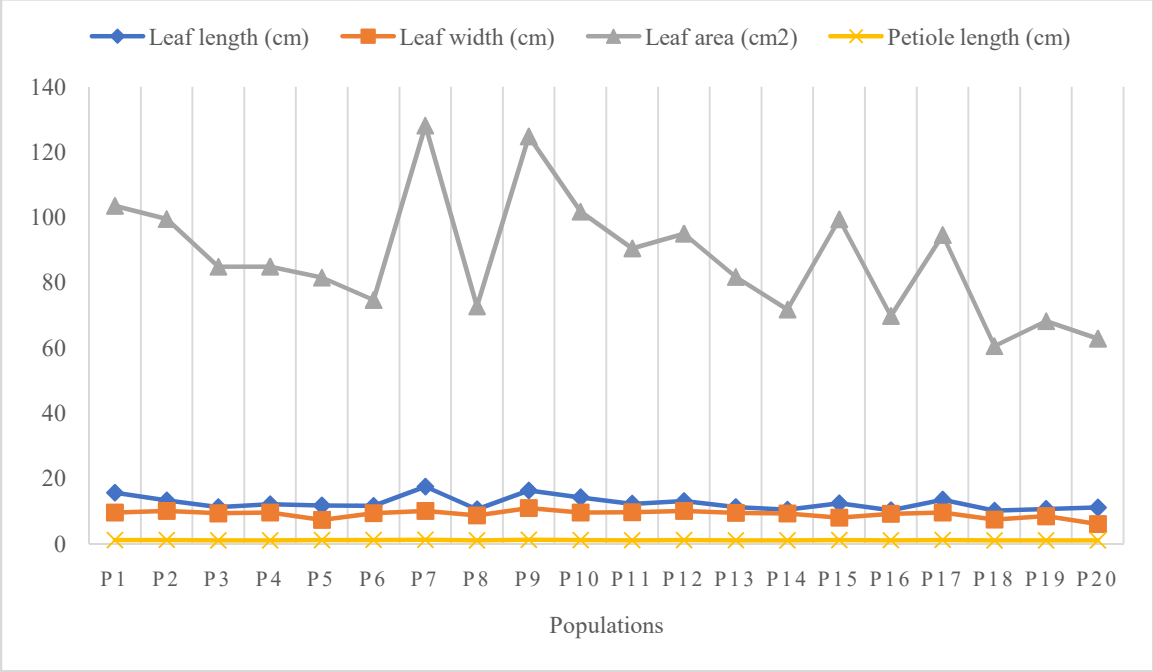


Fig 4.3 Variations in leaf morphometric characters among populations of *Grewia optiva* Drummond

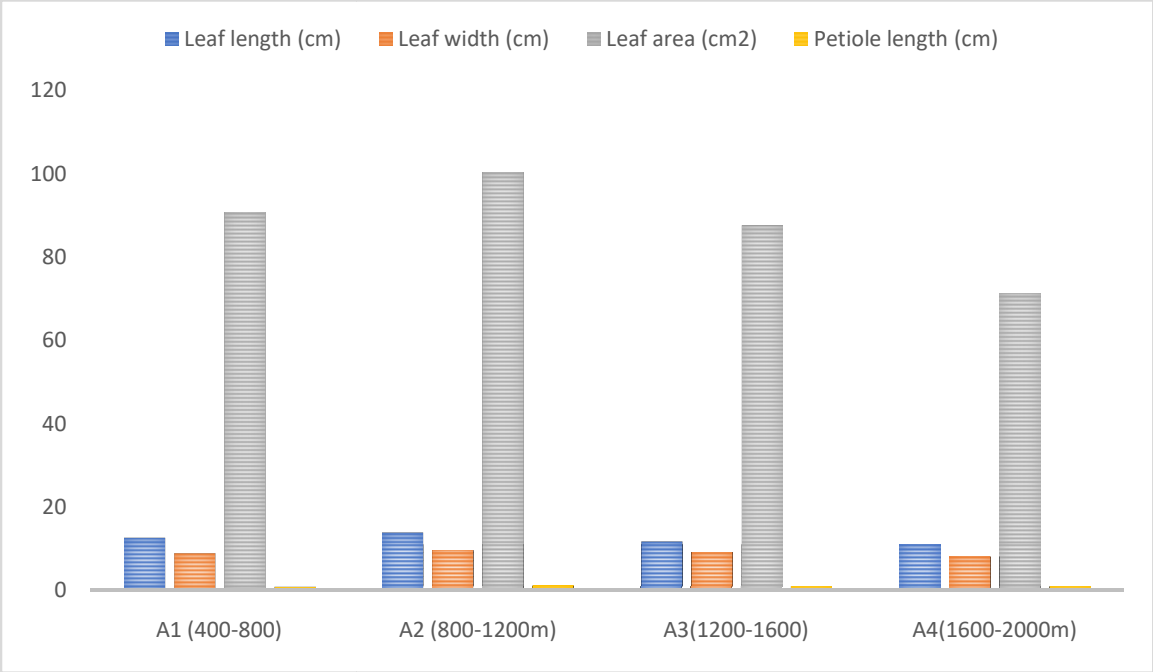


Fig 4.4 Altitudinal variations in (mean value) leaf morphometric characteristics among populations of *Grewia optiva* Drummond





Plate 2. Recording observations on leaf morphometric (leaf length, leaf width, leaf area, fresh weight of 100 leaves, dry weight of 100 leaves) characteristics in the Laboratory.

The above observations on leaf morphometeric characteristics are in accordance with findings of Dixon (1988) in *Juglans nigra*; Bhatt (2010), Bhagta (2015) and Sushmita (2021) in *G. optiva*. Calagari and Modirrahmati (2006) conducted research on the morphological diversity in the leaf characteristics of *Populus euphratica* at eleven different locations. They found that the length of the leaf varied from 4.28 cm to 8.06 cm. Rajendra and Finkeldey (2008) observed, the morphological diversity in needle among the population of *Pinus merkusii*, that the length of the needles varied ranging from 7.6 cm at Burni Telong to 23.3 cm at Hakim Bale Dedalu. Gupta (2012), who also investigated the variation in leaf length with changes in sites, altitude and trees, found that the leaf length ranged from 4.40 cm to 13.28 cm and exhibited substantial differences across sites, altitude, trees and their interaction. Leaf functional features, such as leaf size, are associated with diversity in plant ecological strategies and ecosystem functioning (Westoby *et al.,* 2002). Leaf size also effects leaf temperature effecting photosynthesis, transpiration and respiration (Leigh *et al.*, 2017)

C. Altitudinal variations among populations

The altitudinal variation in leaf morphometric characteristics of *G. optiva* among populations has been documented in Table 4.7 and Fig 4.4. These features include leaf length (cm), leaf breadth (cm), leaf area (cm^2) and petiole length (cm).

Table 4.7 Altitudinal variations in (mean value) leaf morphometric characteristics among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Leaf length (cm)	Leaf width (cm)	Leaf area (cm^2)	Petiole length (cm)
A1 (400-800 m)	12.74	9.09	90.86	0.99
A2 (800-1200 m)	13.97	9.67	100.40	1.05
A3(1200-1600 m)	11.82	9.23	87.65	0.97
A4(1600-2000 m)	11.07	8.07	71.16	0.95

Changes in the altitudinal zone were found to cause variations in the mean values of leaf morphometric parameters such as leaf length, leaf width, leaf area and petiole length. The highest value for the leaf morphometric characteristics was shown by populations in the A2 altitudinal zone, while, the lowest value was shown by populations in the A4 altitudinal zone.

Yuksek *et al.* (2013) studied the variations in leaf length of *Vaccinium arctophylos* present at different altitude and found that the most extended leaf length was measured at the second altitude, while the lowest leaf length was found at the first altitude. The difference in leaf length can be attributed to a number of different causes, including environmental conditions, high pressure, and low air temperature, as well as the gradient in altitude. Yuksek *et al*. (2013) studied variations in leaf width in *V. arctophylos* and documented that the average variation in leaf width (2.92-0.036 cm) was lowest at higher altitude, which matches the current study's findings. In current study we observed that leaf area increased with increasing altitudinal range from A1 to A2 and then further decreased from A2 to A4 (Table 4.7 and Fig 4.4). The present investigation supported by Milla and Reich (2011), they found that as elevation increased, leaves became thicker and water content reduced; However, Guo *et al*. (2018) found that as elevation increased, leaves size became smaller. Plants can develop adaptive strategies in response to environmental change produced by an elevational gradient (Rudgers *et al*., 2019; Cui *et al*., 2020; Cubino *et al*., 2021). According to Pan *et al*. (2013) and Sun *et al*. (2017), when elevation increases, the temperature always drops, limiting leaf area (LA) expansion due to heat and energy availability. However, according to our findings, the LA steadily increases up to 800-1200 m a msl (A2 altitudinal zone). This counterintuitive pattern could be explained by the impact of precipitation and temperature fluctuations on LA.

4.1.2 Nursery Evaluation

4.1.2.1 Seed and Germination characteristics

Seed characteristics, including seed length, seed width, seed thickness and 100 seed weight, as well as germination characteristics, including germination percentage, germination value, germination energy, germination index and survival percentage, were evaluated for variation among *G. optiva* genotypes and populations.

A. Variation among genotypes

The data illustrated in Table 4.8 presented a critical analysis of variations in seed and seed germination characteristics among genotypes.

Table 4.8. Variations in seed and germination characteristics among genotypes of populations of *Grewia optiva* Drummond

Sr. No.	Genotypes	Seed length (mm)	Seed width (mm)	100 seed weight (gm)	Germination percentage (%)	Germination value	Germination energy	Germination index	Survival percentage (%)
1	HR 1	6.24	4.71	10.07	100.00 (90.00)	20.70	76.67	65.67	96.67(83.86)
2	HR 2	5.98	4.56	11.49	83.33(70.07)	15.36	63.33	43.67	92.50(76.95)
3	HR 3	5.99	5.19	12.57	73.33(59.00)	11.85	50.00	41.00	91.07(75.70)
4	HR 4	6.27	5.08	13.22	76.67(61.22)	13.28	50.00	38.33	86.90(68.79)
5	ST 1	6.09	4.89	11.07	83.33(66.15)	13.17	46.67	54.00	96.30(83.51)
6	ST 2	6.25	5.11	12.04	70.00(57.00)	11.54	50.00	24.67	91.67(80.00)
7	ST 3	5.44	5.08	13.56	66.67(54.78)	11.94	53.33	29.67	90.48(75.19)
8	ST 4	5.86	5.05	12.65	73.33(59.00)	13.12	43.33	34.00	86.31(68.29)
9	DR 1	6.16	5.04	11.35	90.00(75.00)	22.62	66.67	43.33	100.00(90.00)
10	DR 2	6.83	4.99	12.39	73.33(59.00)	15.48	66.67	40.33	91.67(80.00)
11	DR 3	5.87	5.19	11.19	63.33(52.78)	11.98	56.67	31.67	90.48(79.23)
12	DR 4	5.99	5.21	12.02	70.00(56.79)	9.70	50.00	51.33	90.48(75.15)
13	GH 1	5.53	3.71	8.6	56.67(48.85)	4.62	26.67	42.33	88.89(73.94)
14	GH 2	5.79	5.07	9.09	46.67(43.08)	3.95	30.00	20.67	80.56(68.25)
15	GH 3	4.16	4.79	8.5	46.67(43.08)	4.73	36.67	34.00	80.56(68.25)
16	GH 4	5.39	4.96	9.1	43.33(41.15)	3.34	26.67	27.00	76.67(61.15)
17	DA 1	5.83	4.85	11.99	70.00(56.79)	15.79	63.33	38.33	90.48(75.19)
18	DA 2	6.96	3.66	11.65	73.33(59.00)	15.74	60.00	33.33	95.83(83.10)
19	DA 3	4.97	4.62	12.52	73.33(59.00)	13.94	63.33	40.33	91.07(75.70)
20	DA 4	5.95	3.68	10.49	80.00(63.93)	17.91	70.00	42.67	100.00(90.00)
21	KD 1	5.84	4.18	8.12	60.00(50.85)	4.85	33.33	51.33	84.92(71.20)
22	KD 2	6.03	4.93	7.82	53.33(46.92)	4.44	30.00	41.33	70.00(57.29)
23	KD 3	4.56	4.66	9.16	53.33(46.92)	4.23	30.00	42.67	87.78(73.11)
24	KD 4	5.41	4.73	9.33	60.00(50.77)	4.59	23.33	44.33	88.89(73.94)
25	SI 1	5.54	4.39	14.01	70.00(56.79)	16.61	70.00	35.67	90.48(75.19)
26	SI 2	6.19	4.23	13.13	83.33(66.15)	22.76	83.33	42.00	100.00(90.00)
27	SI 3	6.54	5.05	13.09	76.67(61.71)	21.97	76.67	33.67	96.30(83.51)
28	SI 4	5.96	5.12	12.43	70.00(56.79)	14.77	63.33	28.33	95.24(82.60)
29	DO 1	5.09	3.66	7.69	53.33(46.92)	5.40	40.00	35.33	68.89(56.31)
30	DO 2	5.07	3.96	6.53	46.67(43.08)	5.04	36.67	23.67	78.33(62.29)
31	DO 3	4.86	4.91	7.25	46.67(43.08)	4.53	33.33	26.00	78.33(66.92)
32	DO 4	5.11	4.81	6.36	46.67(43.08)	5.25	33.33	29.33	78.33(66.29)
33	KT 1	5.91	4.10	12.81	86.67(72.29)	22.11	80.00	45.67	100.00(90.00)
34	KT 2	6.18	4.16	13.16	90.00(71.57)	22.44	73.33	50.00	96.30(83.51)
35	KT 3	5.87	4.32	13.08	80.00(63.44)	16.47	63.33	37.67	95.83(83.10)
36	KT 4	5.98	4.67	14.02	66.67(54.78)	11.93	46.67	33.67	90.48(75.19)
37	KU 1	7.13	5.11	12.01	86.67(68.86)	15.56	56.67	57.67	92.59(77.02)
38	KU 2	5.48	5.04	13.01	76.67(61.71)	11.26	50.00	58.00	96.30(83.51)
39	KU 3	5.71	4.99	9.89	83.33(66.15)	12.80	60.00	59.00	83.80(66.61)
40	KU 4	6.03	5.21	10.74	80.00(63.93)	17.28	66.67	44.33	92.13(76.61)
41	AD 1	5.43	4.85	7.01	60.00(50.77)	6.70	43.33	43.67	77.78(66.49)
42	AD 2	5.63	4.82	9.21	50.00(45.00)	3.43	30.00	45.67	73.33(63.85)
43	AD 3	5.09	5.14	8.09	53.33(46.92)	4.38	36.67	45.00	94.44(81.97)
44	AD 4	4.98	5.08	7.53	63.33(52.86)	6.48	36.67	63.00	85.71(71.83)
45	DH 1	7.07	4.85	13.21	93.33(77.71)	20.03	73.33	52.67	100.00(90.00)
46	DH 2	6.61	5.05	13.16	86.67(68.86)	19.23	76.67	48.67	96.30(83.51)
47	DH 3	5.48	5.09	12.96	73.33(59.00)	11.16	53.33	51.33	95.83(83.10)
48	DH 4	6.09	5.11	13.58	83.33(66.15)	18.34	76.67	45.00	100.00(90.00)

49	NR 1	5.19	4.59	10.45	73.33(59.00)	11.03	53.33	48.00	91.67(80.00)
50	NR 2	4.71	4.16	10.69	63.33(52.78)	9.86	53.33	37.67	89.68(74.57)
51	NR 3	5.45	4.93	11.57	66.67(54.78)	9.00	46.67	49.67	90.48(75.19)
52	NR 4	6.04	5.63	12.09	83.33(66.15)	21.20	76.67	40.33	87.96(80.00)
53	BA 1	6.75	4.55	13.87	76.67(61.22)	17.61	73.33	45.33	95.83(74.57)
54	BA 2	6.51	5.48	14.24	83.33(66.15)	11.83	50.00	62.33	92.13(75.19)
55	BA 3	5.86	5.21	13.97	86.67(68.86)	21.05	76.67	58.67	96.30(69.71)
56	BA 4	5.66	5.05	14.19	76.67(61.22)	12.52	56.67	51.67	95.83(83.10)
57	JG 1	5.73	4.76	12.19	50.00(45.00)	3.69	30.00	40.33	80.00(63.44)
58	JG 2	5.48	4.73	11.66	46.67(43.08)	3.76	33.33	39.33	80.00(68.07)
59	JG 3	5.31	4.18	9.91	43.33(41.15)	2.88	20.11	30.33	78.33(66.92)
60	JG 4	4.19	3.90	12.07	53.33(46.92)	4.22	30.00	46.67	94.44(81.97)
61	SH 1	5.09	3.95	10.33	60.00(50.77)	7.52	46.67	61.33	94.44(81.97)
62	SH 2	4.89	3.90	10.79	63.33(52.78)	6.69	43.33	59.00	90.48(79.23)
63	SH 3	4.87	3.95	9.33	56.67(48.85)	5.44	40.00	56.00	88.89(73.94)
64	SH 4	5.31	3.88	11.03	60.00(50.85)	5.02	33.33	52.00	84.92(71.20)
65	SN 1	5.95	4.34	12.78	60.00(50.85)	5.63	33.33	50.00	90.48(79.23)
66	SN 2	5.99	4.63	12.32	56.67(48.85)	6.99	36.67	44.00	83.33(75.00)
67	SN 3	6.08	5.26	13.54	63.33(52.78	6.80	36.67	48.33	90.48(79.23)
68	SN4	6.04	4.39	11.28	60.00(50.77)	5.33	30.00	52.33	83.33(65.91)
69	GT 1	5.41	4.11	8.12	56.67(48.85)	4.82	30.00	45.67	88.89(78.25)
70	GT 2	5.31	4.09	7.36	63.33(53.07)	6.22	33.33	48.67	95.83(83.10)
71	GT 3	5.92	3.87	7.98	56.67(48.85)	5.10	33.33	48.33	88.89(78.25)
72	GT 4	4.51	4.11	9.65	60.00(50.85)	5.79	36.67	49.00	90.48(79.23)
73	GR 1	5.47	4.14	9.19	63.33(52.86)	6.58	30.00	44.33	85.71(71.83)
74	GR 2	4.96	4.04	8.67	66.67(54.78)	7.18	40.00	60.67	90.48(75.19)
75	GR 3	5.13	4.17	10.99	60.00(50.77)	6.18	40.00	60.33	77.78(66.49)
76	GR 4	5.32	4.09	11.07	60.00(50.77)	6.88	40.00	42.00	90.48(79.23)
77	RA 1	5.08	4.31	7.89	46.67(43.08)	3.61	23.33	32.33	78.33(66.92)
78	RA 2	4.79	3.99	8.41	43.33(41.15)	3.27	26.67	27.67	78.33(66.92)
79	RA 3	4.55	4.56	7.05	36.67(37.22)	2.37	20.00	22.00	83.33(70.00)
80	RA 4	5.11	4.02	8.25	40.00(39.23)	3.65	30.00	19.00	75.00(65.00)
Mean		**5.64**	**4.61**	**10.84**	**66.04**	**10.31**	**47.63**	**43.30**	**88.74**
$CD_{0.05}$		0.25	0.19	0.50	8.51	3.92	11.77	22.39	NS

The maximum seed length (7.13 mm) was found in the KU1 genotype which was statistically at par with DR2, DA2 and DH1. Minimum seed length (4.16 mm) was recorded for the GH3 genotype, which was statistically at par with JG4 (Table 4.8).

Persual of Table 4.8 showed that maximum seed width (5.63 mm) attained by genotype NR4 which was statistically at par with BA2, whereas, minimum seed width (3.66 mm) was recorded in DA2 which was statistically at par with GH1 and DA4.

The data presented in Table 4.8 delineates that the maximum 100 seed weight (14.24 gm) was attained by genotype BA2 which was statistically at par with BA1, BA3 and BA4. The minimum 100 seed weight was recorded in DO4 genotype (6.36 gm) which was statistically at par with DO2.

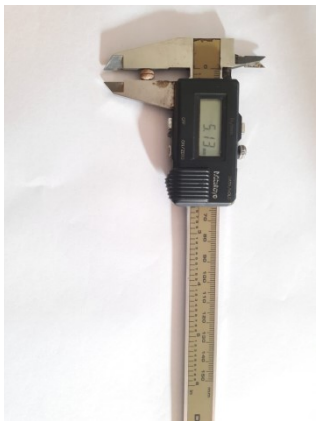




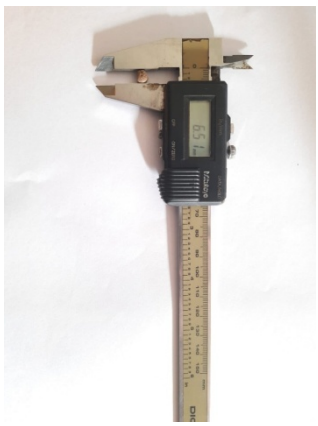
Seed collection



100 seed weight



Seed width



Seed length



Collected seeds of different locations



Variation in seed size

Plate 3. Seed collection and recording observation on seed traits

The HR1 genotype had the highest germination percentage (100 %) while, RA3 genotype had lowest value of germination percentage (36.67 %) (37.22) which was statistically at par with RA2, RA1, RA4, JG3 and JG2. (Table 4.8).

Data depicted in Table 4.8 showed that the maximum germination value (22.76) and maximum germination energy (83.33) was recorded for S12 genotype, while, the minimal germination value (2.37) and minimum germination energy (20) was estimated for RA3 genotypes. Maximum germination value was at par with the BA3, BA1, NR4, DH1, HR1, HR2, HR3, HR4, ST1, ST3, ST4, DR1, DR2, DR3, DA1, DA2, DA3, DA4, SI1, SI2, SI3, SI4, KT1, KT2, KT3, KT4, KU1, KU3, KU4, whereas, maximum germination energy was at par with HR1, SI3, KT1, KT2, DH1, DH2, DH4, NR4, BA1 and BA3 The minimum germination value was at par with the GH1, GH2, GH3, GH4, KD1, KD2, KD3, KD, DO1, DO2, DO3, DO4, AD2, AD3, AD4, JG1, JG2, JG3, JG4, SH3, SH4, SN1, SN4, GT1, GT3, GT4, RA1, RA2 and RA4, while RA4, RA1, GR1, SN4, SN3, JG4, JG3, JG1, ST2, GH2, GH4, SI4, DO2 and DO3.

B. Variation among populations

The data pertaining to variations in seed and germination characteristics among populations of *G. optiva* is shown in Table 4.9 and Fig 4.5.

Significant variations in seed length were observed among populations (Table 4.9 and Fig 4.5). The maximum seed length (6.31 mm) was reported in P12 which was found to be statistically at par with P1, P2, P3, P5, P7, P10, P9 and P14. Moreover, minimum seed length (5.03 mm) was reported in P8 which was statistically at par with P4, P6, P11, P13, P15, P16, P18 and P19 populations.

Data exhibited in the Table 4.9 elucidated significant variation among populations for seed width. The maximum seed width (5.11 mm) was recorded in P3 which was statistically at par with P2, P10, P12, and P14. However, the minimum seed width (3.92 mm) was recorded in P16 which was statistically at par with the P5, P9, P18, P19 and P20.

Table 4.9 Variations in seed and germination characteristics among populations of *Grewia optiva* Drummond.

Altitudinal Zone (a msl)	Populations	Seed length (mm)	Seed width (mm)	100 seed weight (gm)	Seed thickness (mm)	Germination percentage (%)	Germination value	Germination energy	Germination index	Survival percentage (%)
A1 (400-800 m)	P1(Harsar)	6.12	4.89	11.84	4.69	83.33(68.98)	15.30	60.00	47.17	91.79(73.75)
	P2(SujanpurTihra)	5.91	5.03	12.33	5.25	73.33(59.08)	12.44	48.33	35.58	91.19(73.11)
	P3(Dramman)	6.21	5.11	11.74	5.47	74.17(60.00)	14.94	60.00	41.67	93.15(76.82)
	P4(Ghumarwii)	5.22	4.63	8.82	4.29	48.33(44.04)	4.16	30.00	31.00	81.67(64.83)
	P5(Daggar)	5.93	4.20	11.66	4.35	74.17(59.51)	15.84	64.17	38.67	94.35(78.22)
A2 (800-1200 m)	P6 (Kalanjri Devi)	5.46	4.63	8.61	4.85	56.67(48.84)	4.53	29.17	44.92	82.90(66.00)
	P7 (Sihunta)	6.06	4.70	13.17	5.32	75.00(60.15)	19.03	73.33	34.92	95.50(79.58)
	P8(Dodar)	5.03	4.34	6.96	4.03	48.33(44.04)	5.06	35.83	28.58	75.97(60.72)
	P9(Kuthar)	5.99	4.31	13.27	4.78	80.83(64.58)	18.24	65.83	41.75	95.65(79.79)
	P10(Kutuldi)	6.09	5.09	11.41	4.84	81.67(64.76)	14.23	58.33	54.75	91.20(73.27)
A3 (1200-1600 m)	P11(Awah devi)	5.28	4.97	7.96	5.08	56.67(48.85)	5.25	36.67	49.33	82.82(66.24)
	P12 (Dharot)	6.31	5.03	13.23	5.00	84.17(67.11)	17.19	70.00	49.42	98.03(84.28)
	P13(Neri)	5.35	4.83	11.20	4.72	71.67(58.07)	12.77	57.50	43.92	89.95(71.55)
	P14(Basni)	6.20	5.07	14.07	4.59	80.83(64.18)	15.75	64.17	54.50	95.02(77.26)
	P15(Jagdhar)	5.18	4.39	11.46	5.24	48.33(44.04)	3.64	28.33	39.17	83.19(66.37)
A4 (1600-2000 m)	P16 (Shogi)	5.04	3.92	10.37	4.81	60.00(50.78)	6.17	40.83	57.08	89.68(71.52)
	P17 (Sangrah)	6.02	4.66	12.48	5.02	60.00(50.78)	6.19	34.17	48.67	86.90(68.96)
	P18 (Ghanahatti)	5.29	4.05	8.28	3.81	59.17(50.29)	5.48	33.33	47.92	91.02(72.83)
	P19 (Garhkhal)	5.22	4.11	9.98	4.02	62.50(52.25)	6.71	37.50	51.83	86.11(68.43)
	P20 (Ranichauri)	4.88	4.22	7.90	3.45	41.67(40.19)	3.23	25.00	25.25	78.75(62.61)
Mean		**5.64**	**4.61**	**10.84**	**4.68**	**66.04**	**10.31**	**47.63**	**43.30**	**88.74**
$CD_{0.05}$		0.65	0.49	1.22	0.56	6.79	4.09	11.28	10.11	7.91

Persual of Table 4.9 and Fig 4.5 showed that the population P14 had the highest 100 seed weight (14.07 g), while, population P20 had the lowest value (7.90 g). The maximum value of 100 seed weight was statistically at par with P7 and P9, whereas, minimum value was statistically at par with the P11.

Table 4.9 and Fig 4.5 clearly demonstrated that seed thickness (mm) varied significantly between populations. The population P3 had maximum seed thickness (5.47 mm), while, P20 had minimum seed thickness (3.45 mm). The maximum value of seed thickness was at par with P2, P7, P11, P12, P15 and P17 and minimum value was statistically at par with P8 and P19.

Data appended in the Table 4.9 and Fig 4.5 revealed that maximum germination percentage (84.17 %) was recorded in P12 which was statistically at par with P1, P7, P9, P10 and P14, whereas, minimum value of germination percentage (41.67 %) was reported in P20 which was found to be statistically at par with the P4, P8 and P15.

Data exhibited in the Table 4.9 and Fig 4.5 elucidated that maximum germination value (19.03) was noted in P7 which was statistically at par with P1, P5, P9, P12 and P14. The minimum germination value (3.23) was noted in P20 which was found to be statistically at par with P4, P6, P8, P11, P16, P17 and P19.

The data on germination energy has been presented in Table 4.9 and Fig 4.5. The maximum value of germination energy (73.33) was recorded in P7 which was statistically at par with P5, P9, P12 and P14, whereas, minimum value of germination energy (25.00) was reported in P20 which was statistically at par with the P4, P6, P15, P17 and P18.

Data demonstrated in the Table 4.9 and Fig 4.5 depicts that P16 population showed the highest value of germination index (57.08), while, P20 had the lowest value of germination index (25.25). The maximum value was statistically at par with P1, P10, P11, P14, P17, P18 and P19, while, minimum of germination index was statistically at par with P4, P7 and P8.

The survival percentage of six-month-old seedlings was observed (Table 4.9 and Fig 4.5). The percentage of seedlings that survived (at the age of 6 months) in each population of *G. optiva* varied significantly. The maximum survival rate (98.03 %) was recorded for

seedlings of P12, while the lowest survival rate (75.97 %) was recorded for seedlings of P8. The maximum value of survival percentage was statistically at par with P3, P5, P7, P9 and P14, while, minimum value was at par with P4 and P11.

C. Altitudinal variations

The variations in seed and seed germination characteristics of population of different altitudinal zones were observed and outlined in Table 4.10 and Fig. 4. It depicts the average values for seed and germination characteristics for populations that were selected from each altitudinal zone.

Table 4.10 Altitudinal variations in (mean value) seed and germination characteristics among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Seed length (mm)	Seed width (mm)	100 seed weight (gm)	Seed thickness (mm)	Germination percentage (%)	Germination value	Germination energy	Germination index	Survival percentage (%)
A1 (400-800 m)	5.88	4.77	11.28	4.81	70.67	12.54	52.50	38.82	90.43
A2 (800-1200 m)	5.72	4.61	10.68	4.76	68.50	12.21	52.50	40.98	88.25
A3(1200-1600 m)	5.66	4.86	11.58	4.93	68.33	10.92	51.33	47.27	89.80
A4(1600-2000 m)	5.29	4.19	9.80	4.22	56.67	5.55	34.17	46.15	86.49

Data depicted in Table 4.10 and Fig 4.6 showed that the seed length (mm) and germination percentage (%), germination value, and germination index all decreased as we move from the A1 to the A4 altitudinal zone (a msl). However, the opposite tendency was found for the germination index. Maximum mean seed length (5.88 mm) and germination percentage (70.67), germination value (12.54) and germination energy (52.55) were reported for populations of A1 (400–800 m a msl) altitudinal zone, whereas, minimum seed length (5.29 mm) and germination percentage (56.67 %), germination value (5.55) and germination energy (34.77) were recorded for populations of A4 (1600–2000 m a msl) altitudinal zone. Germination index values ranged from a high of 47.27 for populations located in the A4 altitudinal zone (1600–2000 m a msl) to a low of 38.82 for populations located in the A1 altitudinal zone. The population of the A1 altitudinal zone recorded the highest survival percentage (%), while the population of the A4 zone recorded the lowest value.

It is clear in Table 4.10 and Fig 4.6 that seed width (mm), 100 seed weight (gm) and seed thickness (mm) increased as we move from the A1 (400–800 m a msl) altitudinal zone to the A3 (1200–1600 m a msl) altitudinal zone. These parameters further went down as we went up from the A3 (1200–1600 m a msl) to the A4 (1600–2000 m a msl) altitudinal zone.

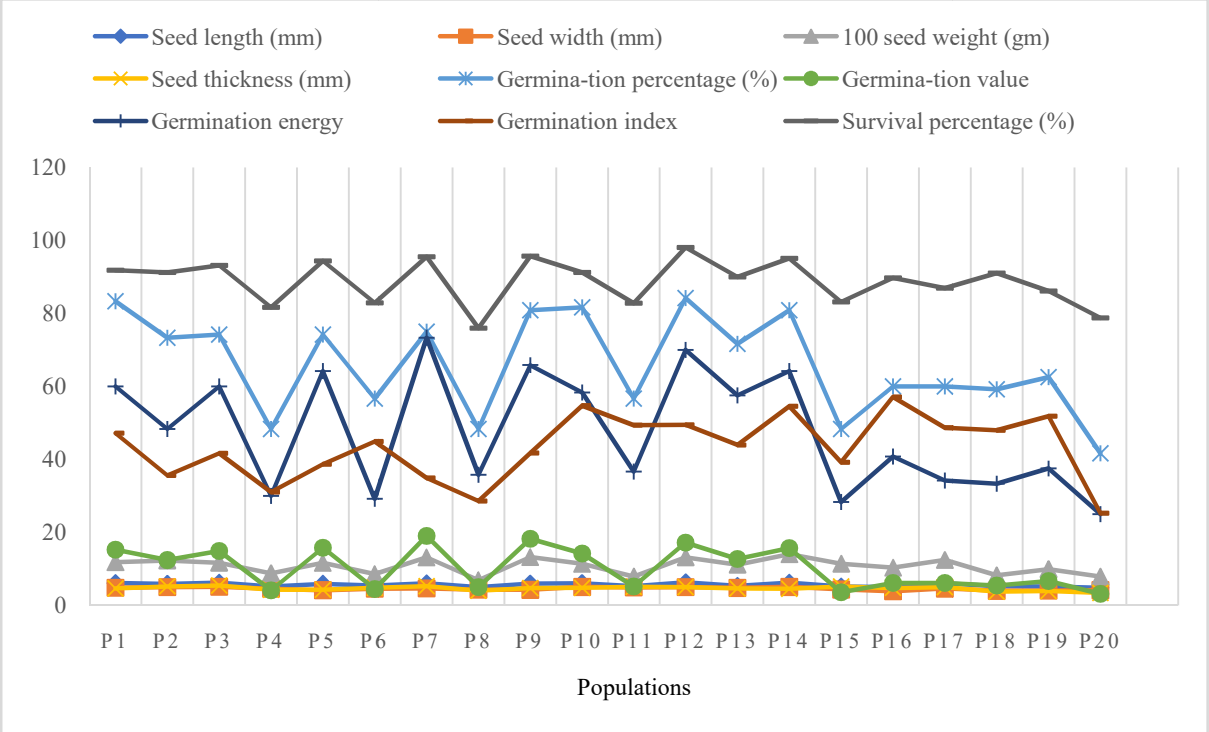


Fig 4.5 Variations in seed and germination characteristics among populations of *Grewia optiva* Drummond

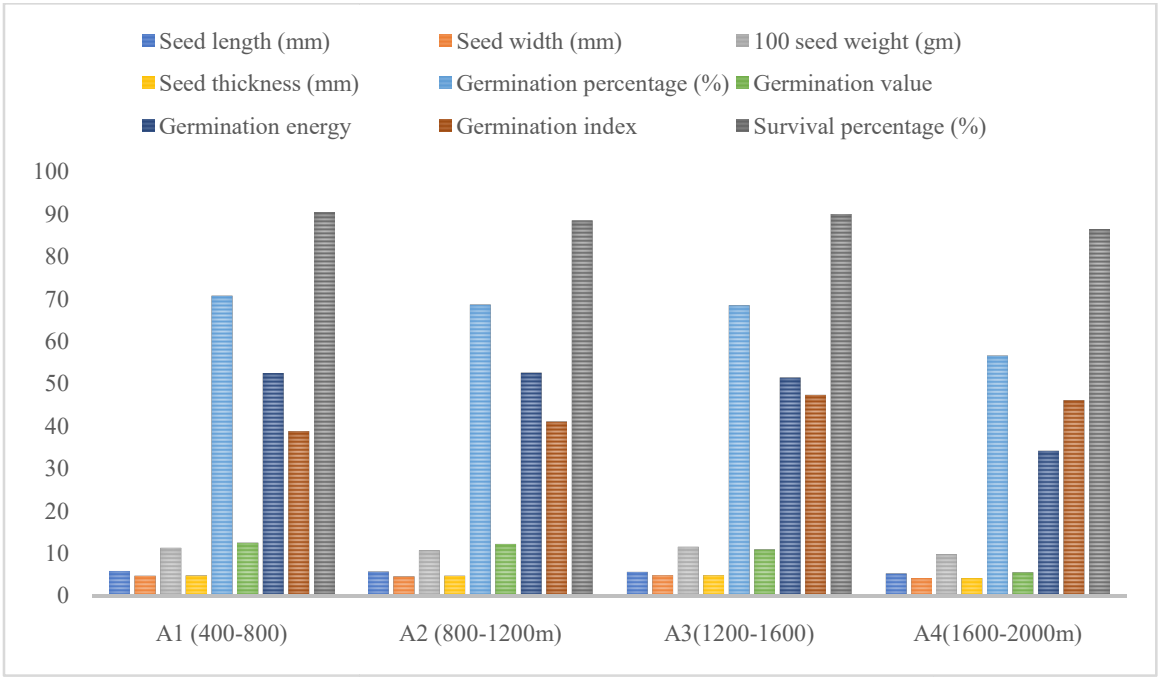


Fig 4.6. Altitudinal variations in (mean value) seed and germination characteristics among populations of *Grewia optiva* Drummond

4.1.2.2 Seedling growth characteristics

Seedling growth parameters such as height (cm), collar diameter (mm), internodal length (cm), petiole length (cm) and leaf area (cm^2) were examined for a period of 18 months. The growth of these seedlings was examined at regular intervals of every six months.

4.1.2.2.1 Seedling growth at the age of six months

A. Variations in seedling growth characteristics among genotypes (at the age of six months)

Variation in seedling growth parameters among genotypes of *G. optiva*, is shown in Table 4.11 (at the age of six months). The analysis of variance for seedling growth characteristics *viz.,* seedling height (cm), collar diameter (mm), internodal length (cm), petiole length (cm) and leaf area (cm^2), exhibited significant variations.

Table 4.11. Variations in seedling growth characteristics (at the age of 6 months) among genotypes of populations of *Grewia optiva* Drummond

Sr. No.	Genotypes	Seedling Height (cm)	Collar diameter (mm)	Seedling internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
1	HR 1	62.53	6.32	3.41	0.43	49.77
2	HR 2	56.67	4.27	2.83	0.45	40.78
3	HR 3	53.98	4.36	2.66	0.41	42.28
4	HR 4	51.87	5.16	2.55	0.42	41.86
5	ST 1	64.13	6.96	3.73	0.49	43.33
6	ST 2	53.98	5.76	2.71	0.59	42.5
7	ST 3	57.67	5.47	2.96	0.41	38.69
8	ST 4	54.23	5.80	3.06	0.53	40.15
9	DR 1	64.08	6.05	3.53	0.48	49.21
10	DR 2	63.23	6.02	3.72	0.45	45.04
11	DR 3	55.93	5.98	3.09	0.56	40.86
12	DR 4	56.99	5.17	3.11	0.57	39.54
13	GH 1	50.58	4.54	2.98	0.54	35.07
14	GH 2	42.03	5.21	2.14	0.49	42.93
15	GH 3	39.48	4.37	2.21	0.46	37.42
16	GH 4	44.32	4.39	2.36	0.49	40.20
17	DA 1	52.99	4.66	2.91	0.59	40.34
18	DA 2	56.11	5.68	3.19	0.62	50.07
19	DA 3	58.78	5.54	3.21	0.60	43.99
20	DA 4	61.15	6.19	3.88	0.57	48.54
21	KD 1	40.69	4.61	2.79	0.56	39.21
22	KD 2	44.77	4.71	2.85	0.53	41.04
23	KD 3	39.19	3.98	2.54	0.54	40.07
24	KD 4	42.88	4.14	2.34	0.49	34.54
25	SI 1	55.77	5.29	2.99	0.51	43.38
26	SI 2	70.98	7.04	4.09	0.49	47.37
27	SI 3	68.14	6.83	3.70	0.48	43.68
28	SI 4	57.12	5.74	3.07	0.44	40.31
29	DO 1	46.98	4.12	2.52	0.50	34.39

30	DO 2	39.98	3.81	1.65	0.49	30.45
31	DO 3	43.13	4.04	2.86	0.48	38.85
32	DO 4	50.88	4.78	2.98	0.41	36.86
33	KT 1	58.32	6.38	3.92	0.56	50.73
34	KT 2	69.44	7.08	3.53	0.59	53.68
35	KT 3	60.02	5.74	3.19	0.52	40.28
36	KT 4	59.38	5.58	2.82	0.56	41.11
37	KU 1	67.09	7.04	3.29	0.49	49.13
38	KU 2	56.75	5.15	2.85	0.43	40.74
39	KU 3	55.33	4.88	2.77	0.41	39.57
40	KU 4	58.03	5.52	2.77	0.43	40.52
41	AD 1	47.61	4.69	1.79	0.55	40.18
42	AD 2	46.50	4.75	2.56	0.49	40.34
43	AD 3	42.55	3.99	1.83	0.54	39.54
44	AD 4	50.15	5.11	2.36	0.58	40.89
45	DH 1	75.33	7.11	4.26	0.63	53.44
46	DH 2	76.63	7.78	4.12	0.56	53.07
47	DH 3	60.11	5.41	3.62	0.61	43.39
48	DH 4	75.18	7.36	4.45	0.62	47.75
49	NR 1	53.98	4.52	2.71	0.49	31.42
50	NR 2	59.98	5.67	2.41	0.54	33.86
51	NR 3	57.77	5.49	2.76	0.53	36.97
52	NR 4	61.08	7.05	3.31	0.52	44.92
53	BA 1	59.77	6.25	2.94	0.46	40.33
54	BA 2	73.98	7.33	4.22	0.48	45.53
55	BA 3	75.04	7.14	4.01	0.58	53.92
56	BA 4	60.02	6.01	3.01	0.51	42.53
57	JG 1	47.11	3.38	2.50	0.46	37.77
58	JG 2	51.88	5.16	2.80	0.44	35.45
59	JG 3	46.15	4.22	2.40	0.54	40.55
60	JG 4	50.49	5.89	2.85	0.52	40.77
61	SH 1	42.91	3.54	2.13	0.49	32.97
62	SH 2	40.19	3.33	2.01	0.53	41.68
63	SH 3	45.59	3.36	2.3	0.57	40.10
64	SH 4	50.93	5.09	2.12	0.59	40.44
65	SN 1	51.98	5.13	2.72	0.45	31.68
66	SN 2	50.55	4.11	2.87	0.49	31.73
67	SN 3	55.98	5.04	2.91	0.44	34.08
68	SN4	47.68	4.03	2.44	0.53	45.65
69	GT 1	41.02	3.97	2.66	0.41	33.59
70	GT 2	50.14	5.10	2.59	0.42	37.38
71	GT 3	39.23	3.89	2.89	0.38	29.44
72	GT 4	44.09	4.11	3.01	0.37	30.65
73	GR 1	55.98	4.10	3.21	0.42	31.24
74	GR 2	58.77	4.08	2.56	0.34	28.74
75	GR 3	49.54	3.88	2.43	0.39	28.93
76	GR 4	50.85	5.97	2.98	0.41	31.42
77	RA 1	36.59	3.32	2.95	0.41	43.45
78	RA 2	43.45	5.18	2.09	0.42	30.44
79	RA 3	39.15	4.03	2.66	0.45	42.02
80	RA 4	41.33	4.11	2.83	0.39	33.88
Mean		**55.66**	**5.18**	**2.91**	**0.50**	**40.26**
$CD_{0.05}$		4.04	0.46	0.43	0.02	3.04

Data appended to Table 4.11 revealed the maximum seedling height for genotype DH2 (76.63 cm) which was statistically at par with DH1, DH4, BA2 and BA3. The minimum seedling height was recorded for genotype RA3 (39.15 cm) which was statistically at par with GH2, GH3, KD1, KD3, KD4, SH2 and GT1.

The maximum value of the collar diameter of seedlings was recorded for DH2 (7.78 mm) which was statistically at par with DH4. The minimum value was depicted by RA1 (3.32 mm), which was statistically at par with JG1, SH1, SH2, and SH3, as reported in Table 4.11.

Perusal of Table 4.11 showed that the maximum internodal length was recorded for DH4 (4.45 cm) which was statistically at par with DH1, DH2, BA2 and SI2. A minimum value was recorded for genotype DO2 (1.65 cm) which was statistically at par with AD1, AD3 and SH2.

An examination of the data in Table 4.11 revealed that DH1 had the longest petiole length (cm) (0.63 cm), which was statistically at par with DA2, DH3 and DH4. The genotype GR2 had the shortest petiole length (0.34 cm).

An appraisal of the data presented in Table 4.11 elucidated that BA3 attained the maximum leaf area (53.92 cm^2), which was statistically at par with KT2, DH1 and DH2. Genotype GR2 was recorded with a minimum leaf area of 28.74 cm^2. The minimum value was statistically at par with GT3, GR3 and RA2.

B. Variations in seedling growth characteristics among populations of *Grewia optiva* Drummond. (At the age of six months)

Data pertaining to variations in seedling (progeny) growth characteristics (at the age of 6 months) among populations of *G. optiva* is given in Table 4.12 and Fig 4.7. The analysis of variance revealed significant variations between the populations in terms of seedling growth characteristics *viz.,* seedling height, collar diameter, internodal length, petiole length and leaf area (cm^2)

Data demonstrated in Table 4.12 and Fig 4.7 depicts that the maximum seedling height (71.81 cm) was recorded for seedlings of P12 which was found to be statistically at par with P14. The minimum seedling height (40.13 cm) was recorded for P20 which was statistically at par with P4, P6, P8, P11, P16 and P18.

Data presented in the Table 4.12 and Fig 4.7 showed that the maximum collar diameter (6.92 mm) was reported in seedlings of population P12 which was statistically at par with P7, P9 and P14, whereas, minimum value of collar diameter (3.83 mm) was reported for seedlings of population P16 which was followed by P8 and P20.

Data exhibited in the Table 4.7 elucidated the maximum intermodal length (4.11 cm) was recorded in seedlings of population P12 which was statistically at par with the P14. The minimum value of internodal length (2.14 cm) was observed in seedlings of population P11 and P16 which was statistically at par with P4, P6, P8, 15, and 20.

The maximum petiole length (0.61 cm) was recorded for seedlings of P12 which was statistically at par with P5. The seedlings of population P19 reported with the minimum value of petiole length (0.39 cm) which was statistically at par with P1, P10, P18 and P19 (Table 4.12 and Fig 4.7).

Table 4.12 Variations in seedling growth characteristics (at the age of 6 months) among population of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Seedling Height (cm)	Collar diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
A1 (400-800 m)	P1(Harsar)	56.26	5.03	2.86	0.43	43.67
	P2(SujanpurTihra)	57.50	6.00	3.12	0.51	41.17
	P3(Dramman)	60.06	5.81	3.36	0.52	43.66
	P4(Ghumarwii)	44.10	4.63	2.42	0.50	38.91
	P5(Daggar)	57.26	5.52	3.30	0.60	45.74
A2 (800-1200 m)	P6 (Kalanjri Devi)	41.88	4.36	2.63	0.53	38.72
	P7 (Sihunta)	63.00	6.23	3.46	0.48	43.69
	P8(Dodar)	45.24	4.19	2.50	0.47	35.14
	P9(Kuthar)	61.79	6.20	3.37	0.56	46.45
	P10(Kutuldi)	59.30	5.65	2.92	0.44	42.49
A3 (1200-1600 m)	P11(Awah devi)	46.70	4.64	2.14	0.54	40.24
	P12 (Dharot)	71.81	6.92	4.11	0.61	49.41
	P13(Neri)	58.20	5.68	2.80	0.52	36.79
	P14(Basni)	67.20	6.68	3.55	0.51	45.58
	P15(Jagdhar)	48.91	4.66	2.64	0.49	38.64
A4 (1600-2000 m)	P16 (Shogi)	44.91	3.83	2.14	0.55	38.80
	P17 (Sangrah)	51.55	4.58	2.74	0.48	35.79
	P18 (Ghanahatti)	43.62	4.27	2.79	0.40	32.77
	P19 (Garhkhal)	53.79	4.51	2.80	0.39	30.08
	P20 (Ranichauri)	40.13	4.16	2.63	0.42	37.45
Mean		**53.66**	**5.18**	**2.91**	**0.50**	**40.26**
$CD_{0.05}$		**6.87**	**1.05**	**0.56**	**0.06**	**6.31**

The data pertaining to leaf area (Table 4.12 and Fig 4.7) showed that maximum leaf area (49.41 cm^2) was recorded in seedlings of P12 which was statistically at par with P9 and

P14. Population P9's seedlings had the minimum leaf area (30.08 cm^2) which was statistically at par with P8, P13 and P17.

4.1.2.2.2 Seedling growth at the age of 12 months.

A. Variations in seedling growth characteristics among genotypes (at the age of 12 months)

Data pertaining to differences in seedling growth characteristics (at the age of 12 months) among different genotypes of *G. optiva* is presented in Table 4.13. The analysis of variance revealed significant variations in seedling growth characteristics, encompassing seedling height (cm), collar diameter (mm), internodal length (cm), petiole length (cm) and leaf area (cm^2).

Table 4.13. Variations in seedling growth characteristics (at the age of 12 months) among genotypes of populations of *Grewia optiva* Drummond

Sr. No.	Genotypes	Seedling Height (cm)	Collar diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
1	HR 1	85.21	8.08	4.07	0.55	56.85
2	HR 2	65.09	6.71	3.23	0.53	50.81
3	HR 3	66.32	6.75	3.94	0.66	50.30
4	HR 4	70.66	7.19	3.28	0.64	51.41
5	ST 1	88.89	8.25	5.10	0.68	52.34
6	ST 2	71.35	7.48	4.39	0.67	51.48
7	ST 3	65.12	7.58	3.92	0.69	46.85
8	ST 4	70.32	7.86	4.19	0.71	54.23
9	DR 1	95.22	9.19	5.07	0.59	51.68
10	DR 2	90.75	7.60	4.99	0.60	59.88
11	DR 3	62.76	6.42	3.66	0.70	50.31
12	DR 4	70.19	7.06	4.71	0.67	47.82
13	GH 1	56.87	6.04	3.63	0.68	43.26
14	GH 2	50.14	6.06	3.61	0.68	56.03
15	GH 3	47.87	5.13	3.40	0.67	45.48
16	GH 4	50.55	5.37	3.65	0.65	50.05
17	DA 1	63.88	5.49	3.69	0.79	51.52
18	DA 2	76.23	7.54	4.15	0.82	56.63
19	DA 3	71.75	7.25	4.35	0.81	54.41
20	DA 4	79.42	7.69	4.69	0.86	55.56
21	KD 1	60.21	6.11	3.01	0.74	48.06
22	KD 2	70.43	7.48	3.78	0.79	50.42
23	KD 3	50.33	5.54	3.39	0.71	51.4

24	KD 4	65.45	6.75	3.90	0.74	45.25
25	SI 1	63.99	6.86	3.96	0.78	59.61
26	SI 2	93.43	9.59	5.71	0.67	53.46
27	SI 3	90.95	8.52	5.79	0.78	55.94
28	SI 4	71.92	6.44	4.56	0.70	50.35
29	DO 1	50.88	5.73	3.25	0.77	49.34
30	DO 2	48.92	4.76	2.86	0.66	45.74
31	DO 3	50.44	5.41	3.37	0.75	50.71
32	DO 4	60.67	5.46	3.13	0.73	48.06
33	KT 1	80.44	7.74	5.02	0.68	56.57
34	KT 2	78.84	7.80	4.98	0.73	65.38
35	KT 3	69.21	6.69	4.03	0.65	51.98
36	KT 4	67.91	7.02	3.64	0.76	47.54
37	KU 1	80.11	7.98	5.14	0.75	53.52
38	KU 2	65.08	6.91	3.27	0.67	49.87
39	KU 3	63.32	5.92	3.36	0.66	45.62
40	KU 4	65.89	8.13	3.56	0.71	51.36
41	AD 1	51.25	5.36	2.98	0.64	52.94
42	AD 2	49.32	5.04	3.50	0.58	49.46
43	AD 3	46.96	4.99	2.88	0.69	50.38
44	AD 4	59.41	6.18	3.08	0.65	52.28
45	DH 1	96.05	8.89	6.98	0.82	60.57
46	DH 2	99.76	9.42	6.56	0.76	60.33
47	DH 3	68.19	7.99	4.92	0.89	50.13
48	DH 4	96.17	9.76	6.22	0.95	59.95
49	NR 1	57.22	5.39	3.51	0.66	48.45
50	NR 2	67.87	6.15	3.86	0.72	51.08
51	NR 3	65.53	5.55	3.29	0.71	50.97
52	NR 4	83.55	8.03	4.58	0.75	55.66
53	BA 1	83.9	8.95	4.07	0.72	51.83
54	BA 2	90.43	9.46	5.95	0.75	55.86
55	BA 3	88.15	9.68	5.72	0.70	60.59
56	BA 4	80.22	7.83	3.89	0.77	51.97
57	JG 1	66.34	6.04	3.51	0.58	46.19
58	JG 2	70.45	7.09	4.38	0.56	45.59
59	JG 3	53.24	5.42	3.05	0.61	55.24
60	JG 4	70.21	6.99	4.75	0.75	54.94
61	SH 1	62.09	6.35	3.90	0.66	47.65
62	SH 2	60.29	6.26	3.59	0.68	52.56
63	SH 3	50.18	5.04	3.27	0.62	52.96
64	SH 4	70.88	7.11	3.2	0.69	52.07
65	SN 1	59.92	5.96	3.18	0.68	48.24
66	SN 2	55.44	5.55	3.32	0.75	53.32

67	SN 3	69.67	6.97	3.40	0.80	54.62
68	SN4	55.44	5.14	3.26	0.95	51.50
69	GT 1	50.21	5.17	3.46	0.69	47.49
70	GT 2	68.64	6.85	3.93	0.83	57.33
71	GT 3	45.24	4.59	3.66	0.67	45.33
72	GT 4	50.91	5.24	3.57	0.62	40.87
73	GR 1	60.39	5.71	4.02	0.70	50.39
74	GR 2	63.29	5.44	3.78	0.64	47.43
75	GR 3	54.68	4.96	3.65	0.65	45.49
76	GR 4	60.24	6.74	3.49	0.71	50.80
77	RA 1	45.11	5.19	3.52	0.66	52.33
78	RA 2	67.88	6.94	3.25	0.68	49.55
79	RA 3	53.87	5.69	2.91	0.64	50.19
80	RA 4	53.14	5.93	3.29	0.59	39.88
Mean		**66.86**	**6.73**	**3.98**	**0.70**	**51.51**
$CD_{0.05}$		2.67	0.69	0.38	0.05	2.89

Data affix in Table 4.13 showed the maximum seedling height for genotype DH2 (99.76 cm) which was followed by DH1 and DH2. The minimum seedling height was recorded for genotype RA1 (45.11cm) which was statistically at par with GT3.

The maximum collar diameter (9.76 mm) was documented in seedlings of DH4 which was statistically at par with DR1, DH2, BA2 and BA3. The minimum collar diameter (4.59 mm) was documented in seedlings of GT3 which was statistically at par with GH3, AD2, AD3, SH3, SN4 and GT1 (Table 4.13).

Table 4.13 and Fig 4.8 revealed that the genotype DH1 had the maximum internodal length (6.98 cm) which was statistically at par with DH2. The seedlings of genotype DO2 had the minimum value of internodal length (2.86 cm), which was statistically at par with HR2, KD1, DO4, AD1, AD3, AD4 and SN1 genotypes.

A review of the information contained in Table 4.13 revealed that the seedlings of genotype DH4 and HR2 exhibited maximum petiole length (0.95 cm), while seedlings of HR2 genotype exhibited the minimum petiole length (0.53 mm) which was statistically at par with HR1 and JG2.

Appraisal of the data presented in Table 4.13 elucidated that seedlings of genotype KT2 showed maximum leaf area (65.38 cm^2) which was followed by DH1 and DH2. The seedlings of RA4 genotype marked with minimum leaf area (39.88 cm^2) which was statistically at par with GT4.

B. Variations in seedling growth characteristics among populations (At the age of 12 month)

The data on seedling growth characteristics (at the age of 12 months) has been presented in Table 4.14 and Fig 4.8, which showed significant variations in seedling growth characteristics among populations.

Table 4.14 and Fig 4.8 showed that population P12 had maximum seedling height (90.04 cm) which was statistically at par with P7 and P14. P4 had the minimum seedling height (51.36 cm) which was found to be statistically at par with P8, P11, P16, P17, P18 and P19.

Data demonstrated in the Table 4.14 and Fig 4.8 depicts that seedlings of population P12 had the highest value of collar diameter (9.02 mm) which was statistically at par with P14. The seedlings of P8 the minimum value of collar diameter (5.34 mm) which was statistically at par with P4, P11, P17 and P20.

Table 4.14. Variations in seedling growth characteristics (at age of 12 months) among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Seedling Height (cm)	Collar diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
A1 (400-800 m)	P1(Harsar)	71.82	7.18	3.63	0.60	52.34
	P2(SujanpurTihra)	73.92	7.79	4.40	0.69	51.23
	P3(Dramman)	79.73	7.57	4.61	0.64	52.42
	P4(Ghumarwii)	51.36	5.65	3.57	0.67	48.71
	P5(Daggar)	72.82	6.99	4.22	0.82	54.53
A2 (800-1200 m)	P6 (Kalanjri Devi)	61.61	6.47	3.52	0.75	48.78
	P7 (Sihunta)	80.07	7.85	5.01	0.73	54.84
	P8(Dodar)	52.73	5.34	3.15	0.73	48.46
	P9(Kuthar)	74.10	7.31	4.42	0.71	55.37
	P10(Kutuldi)	68.60	7.24	3.83	0.70	50.09
A3 (1200-1600 m)	P11(Awah devi)	51.74	5.39	3.11	0.64	51.27
	P12 (Dharot)	90.04	9.02	6.17	0.86	57.75
	P13(Neri)	68.54	6.28	3.81	0.71	51.54
	P14(Basni)	85.68	8.98	4.91	0.74	55.06
	P15(Jagdhar)	65.06	6.39	3.92	0.63	50.49
A4 (1600-2000 m)	P16 (Shogi)	60.86	6.19	3.49	0.66	51.31
	P17 (Sangrah)	60.12	5.91	3.29	0.80	51.92
	P18 (Ghanahatti)	53.75	5.46	3.66	0.70	47.76
	P19 (Garhkhal)	59.65	5.71	3.74	0.68	48.53
	P20 (Ranichauri)	55.00	5.94	3.24	0.64	47.99
Mean		66.86	6.73	3.98	0.70	51.52
$CD_{0.05}$		12.26	1.16	0.80	0.08	5.96

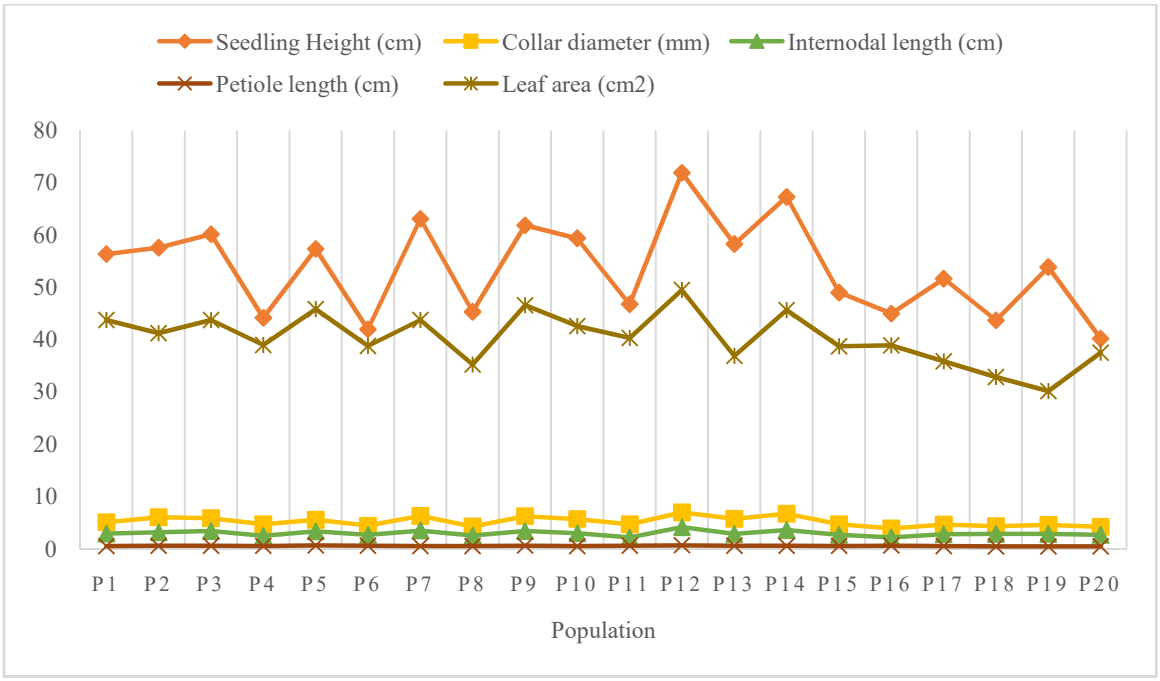


Fig 4.7.Variations in seedling growth characteristics (at the age of 6 months) among populations of *Grewia optiva* Drummond.

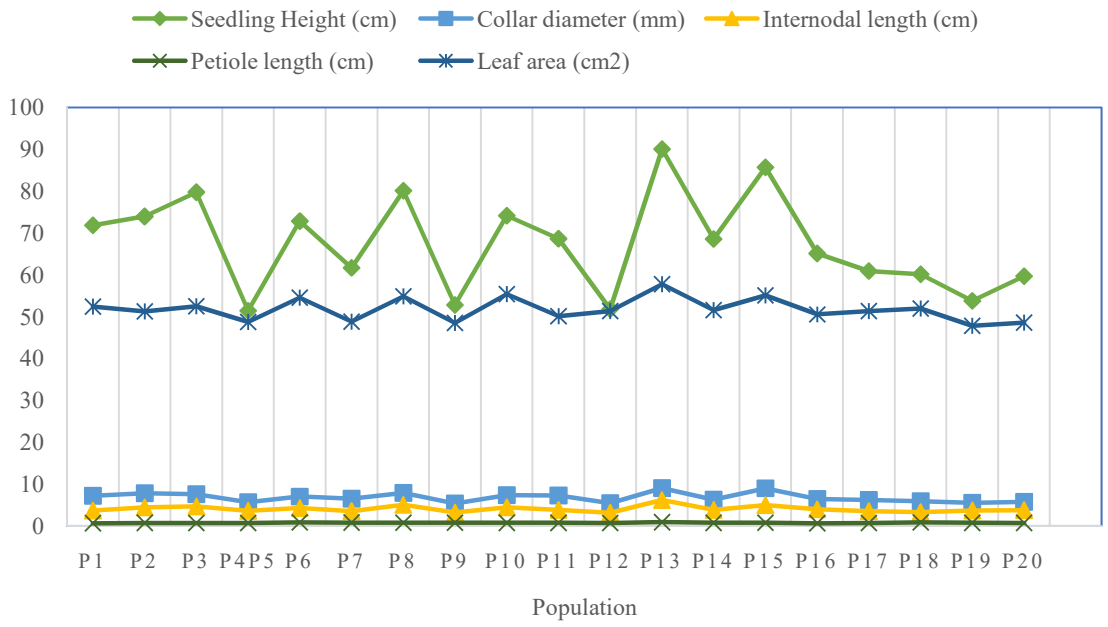


Fig 4.8 Variations in seedling growth characteristics (at age of 12 month) among population of *Grewia optiva* Drummond

Data appended in Table 4.14 and Fig 4.8 revealed that maximum internodal length (6.17 cm) was recorded in seedlings of P12 which was followed by P7. The minimum value of intermodal length (3.15 cm) was reported in seedlings of P8 which was statistically at par with P1, P4, P6, P16, P17, P18, P19 and P20.

Assessment of data presented in Table 4.14 and Fig 4.8 elucidated that maximum leaf area (57.75 cm^2) was recorded in seedlings of P12, which was statistically at par with P7, P9, and P14. The minimum leaf area (47.76 cm^2) was reported in seedlings of P18 which was statistically at par with P1, P2, P3, P10, P11, P13, P15, P16, P18, P19 and P20.

4.1.2.2.3 Seedling growth at the age of 18 months.

A. Variations in seedling growth characteristics among genotypes (At the age of 18 months)

Table 4.15 displayed the significant differences in height, collar diameter, internodal length, petiole length and leaf area (at 18 months of age) among genotypes of *G. optiva*.

Data appended to Table 4.15 revealed the maximum seedling height (118.76 cm) recorded for DH2 genotype which was followed by DR1. The minimum seedling height (53.22 cm) was recorded for DO2 which was statistically at par with GH3, DO2, AD2 and AD3.

The Table 4.15 elucidates that the maximum value of collar diameter (13.42 mm) was recorded for seedlings of DH2 genotype which was statistically at par with DH4, whereas, minimum value of collar diameter (5.24 mm) was recorded for seedlings of AD3 genotype which was statistically at par with GH3, DO2, AD1, GT3, GT4 and GR3.

Table 4.15 Variations in seedling growth characteristics (at the age of 18 months) among genotypes of populations of *Grewia optiva* Drummond

Sr. No.	Genotypes	Seedling Height (cm)	Collar diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
1	HR 1	99.61	10.79	6.31	0.73	72.55
2	HR 2	85.21	9.77	5.3	0.78	62.49
3	HR 3	76.83	7.87	4.72	0.8	58.82
4	HR 4	79.66	8.93	5.59	0.83	60.30
5	ST 1	97.66	10.70	6.03	0.81	70.88
6	ST 2	82.05	8.35	5.51	0.77	60.97
7	ST 3	89.22	8.82	5.73	0.80	51.13
8	ST 4	90.89	9.04	5.75	0.83	60.81

9	DR 1	112.57	12.30	7.02	0.67	69.94
10	DR 2	100.75	11.12	6.86	0.69	70.33
11	DR 3	88.76	8.78	5.79	0.75	61.71
12	DR 4	90.19	9.03	6.02	0.75	58.81
13	GH 1	61.78	8.94	4.63	0.75	50.19
14	GH 2	56.14	7.11	4.49	0.73	60.13
15	GH 3	54.87	6.02	4.75	0.74	50.17
16	GH 4	61.35	7.44	4.97	0.70	54.88
17	DA 1	75.09	8.04	5.07	0.86	57.28
18	DA 2	85.03	8.85	5.97	0.87	60.86
19	DA 3	88.02	9.15	6.28	0.89	62.14
20	DA 4	97.32	11.08	6.16	0.93	73.66
21	KD 1	73.11	7.89	5.13	0.87	52.51
22	KD 2	81.33	8.35	5.97	0.85	54.16
23	KD 3	68.33	6.50	4.95	0.80	55.82
24	KD 4	78.45	7.50	5.88	0.88	49.11
25	SI 1	90.19	8.95	6.13	0.96	64.07
26	SI 2	105.43	12.11	7.11	0.87	70.09
27	SI 3	100.45	11.79	6.93	0.93	69.57
28	SI 4	91.52	8.81	6.11	0.90	64.39
29	DO 1	57.58	6.37	4.67	0.79	53.38
30	DO 2	53.22	5.27	3.86	0.72	49.55
31	DO 3	58.94	6.47	4.93	0.80	58.44
32	DO 4	65.57	7.07	5.02	0.82	55.77
33	KT 1	97.94	10.82	6.94	0.78	73.78
34	KT 2	99.04	11.19	7.08	0.81	75.59
35	KT 3	78.71	9.69	6.97	0.75	60.24
36	KT 4	92.16	10.05	6.44	0.83	57.97
37	KU 1	100.71	12.19	7.03	0.85	70.09
38	KU 2	83.32	8.19	6.45	0.79	57.58
39	KU 3	79.79	7.18	5.38	0.77	56.67
40	KU 4	87.86	9.33	6.45	0.80	59.09
41	AD 1	59.15	6.02	3.84	0.73	57.19
42	AD 2	55.86	6.14	4.45	0.69	54.38
43	AD 3	53.66	5.24	3.52	0.76	55.38
44	AD 4	65.04	6.95	3.84	0.77	60.51
45	DH 1	107.75	11.82	7.10	0.93	70.29
46	DH 2	118.76	13.42	7.05	0.93	69.22
47	DH 3	94.19	9.97	6.31	0.99	60.44
48	DH 4	108.78	13.21	6.92	1.10	63.32
49	NR 1	80.57	8.11	5.44	0.89	55.38
50	NR 2	90.17	9.02	6.34	0.85	59.97
51	NR 3	83.33	7.86	5.29	0.92	60.92
52	NR 4	102.35	12.45	6.94	0.93	67.13
53	BA 1	98.99	11.66	5.89	0.95	62.11
54	BA 2	104.13	12.86	6.95	0.91	62.96
55	BA 3	101.45	12.07	7.14	0.89	69.05
56	BA 4	92.52	9.73	5.99	0.98	61.92
57	JG 1	86.13	8.09	5.46	0.79	50.38
58	JG 2	85.45	8.75	5.92	0.75	50.50
59	JG 3	67.62	7.83	5.14	0.81	61.07
60	JG 4	81.11	9.45	6.28	0.82	60.15
61	SH 1	70.32	6.55	5.52	0.82	55.55

62	SH 2	75.99	8.96	5.09	0.98	60.09
63	SH 3	65.09	6.89	5.21	0.94	61.89
64	SH 4	80.48	8.14	5.39	1.02	57.42
65	SN 1	65.29	7.95	4.32	0.84	55.45
66	SN 2	60.94	7.22	4.87	0.86	59.27
67	SN 3	78.57	8.12	5.44	0.93	61.44
68	SN4	65.64	6.65	4.9	1.01	60.76
69	GT 1	60.71	6.83	4.37	0.81	53.59
70	GT 2	70.34	8.42	5.82	0.89	63.52
71	GT 3	57.62	5.91	4.19	0.86	52.64
72	GT 4	65.31	6.01	5.67	0.88	46.01
73	GR 1	65.19	6.49	5.16	0.76	60.11
74	GR 2	70.09	7.01	5.19	0.70	53.33
75	GR 3	60.21	5.99	5.56	0.72	50.19
76	GR 4	67.32	8.04	4.08	0.78	56.39
77	RA 1	59.11	6.24	3.93	0.71	59.32
78	RA 2	73.02	7.45	4.11	0.76	53.55
79	RA 3	58.23	7.11	3.88	0.73	54.19
80	RA 4	59.63	7.43	3.94	0.69	45.88
	Mean	79.78	8.65	5.56	0.83	59.61
	$CD_{0.05}$	3.39	0.85	0.46	0.03	2.56

Table 4.15 revealed that seedlings of genotype BA3 showed the maximum internodal length (7.14 cm), while, seedlings of genotype AD3 showed the minimum value of intermodal length (3.52 mm). The maximum value was statistically at par with DR1, DR2, KT1, KT2, KT3, KU1, DH1, DH2 and NR4 whereas, minimum value was statistically at par with AD1, AD4, RA1, RA3 and RA4.

The perusal of Table 4.15 revealed that DH4 had the maximum petiole length (1.10 cm) which was statistically at par with SH4 and SN4. A minimum value was noted for genotype DR1 (0.67 cm) which was found to be statistically at par with DR2.

Data demonstrated in the Table 4.15 illustrated the maximum leaf area (73.78 cm^2) was recorded for seedlings of KT2 which was statistically at par with KT1 and DA4. The minimum leaf area (45.88 cm^2) was recorded for seedlings of RA4 genotype which was statistically at par with GT4.

B. Variations in seedling growth characteristics among populations (at the age of 18 months)

Data pertaining to variations in seedling growth characteristics (at the age of 18 months) among populations of *G. optiva* has been presented in Table 4.16 and Fig 4.8. There was significant variations observed among populations for seedling growth characteristics

namely seedling height (cm), collar diameter (mm), internodal length in (cm), petiole length (cm) and leaf area (cm^2).

Table 4.16. Variations in seedling growth characteristics (at the age of 18 months) among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Seedling Height (cm)	Collar diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
A1(400-800 m)	P1(Harsar)	85.33	9.34	5.48	0.79	63.54
	P2(SujanpurTihra)	89.96	9.23	5.76	0.80	60.95
	P3(Dramman)	98.07	10.31	6.42	0.72	65.20
	P4(Ghumarwii)	58.54	7.38	4.71	0.73	53.84
	P5(Daggar)	86.37	9.28	5.87	0.89	63.49
A2 (800-1200 m)	P6 (Kalanjri Devi)	75.31	7.56	5.48	0.85	52.90
	P7 (Sihunta)	96.90	10.42	6.57	0.92	67.03
	P8(Dodar)	58.83	6.30	4.62	0.78	54.29
	P9(Kuthar)	91.96	10.44	6.86	0.79	66.90
	P10(Kutuldi)	87.92	9.22	6.33	0.80	60.86
A3 (1200-1600 m)	P11(Awah devi)	58.43	6.09	3.91	0.74	56.87
	P12 (Dharot)	107.37	12.11	6.86	0.99	65.82
	P13(Neri)	89.11	9.36	6.00	0.90	60.85
	P14(Basni)	99.27	11.58	6.48	0.93	64.01
	P15(Jagdhar)	80.08	8.53	5.70	0.79	55.53
A4 (1600-2000 m)	P16 (Shogi)	72.97	7.64	5.30	0.94	58.74
	P17 (Sangrah)	67.61	7.49	4.88	0.91	59.23
	P18 (Ghanahatti)	63.50	6.79	5.01	0.86	53.94
	P19 (Garhkhal)	65.70	6.88	5.00	0.74	55.01
	P20 (Ranichauri)	62.50	7.06	3.97	0.72	53.24
Mean		79.78	8.65	5.56	0.83	59.61
$CD_{0.05}$		10.15	1.71	0.74	0.06	7.65

Data exhibited in Table 4.16 and Fig 4.9 clearly indicated the maximum seedling height (107.37 cm) was reported for P12 which was statistically at par with P3 and P14. The minimum seedling height (58.43 cm) was reported for P11 which was statistically at par with P4 and P8.

Persual of Table 4.16 and Fig 4.9 showed that maximum collar diameter (12.11 mm), was recorded in seedlings (progeny) of P12 which was statistically at par with P14. The minimum value of collar diameter (6.09 mm) was recorded in seedlings of P11 which was statistically at par with P4, P6, P8, P18, P19 and P20.

An examination of data presented in Table 4.16 and Fig 4.9 revealed that maximum internodal length (6.86 cm) was recorded in seedlings of P12 and P9 which was statistically

at par with P3, P7, P10 and P14. However, the minimum value of intermodal length (3.91 cm) was recorded in seedlings of P11 which was statistically at par with P8 and P20.

Appraisal of data presented in the Table 4.16 and Fig 4.9 demonstrated that maximum petiole length (0.99 cm) was recorded in seedlings of P12 which was statistically at par with P16. Moreover, the minimum value of petiole length (0.72 cm) was recorded in seedlings of P3 and P20 which was found to be statistically at par with P4, P11 and P19.

The maximum leaf area (67.03 cm^2) was recorded in seedlings of P7 which was statistically at par with P1, P2, P3, P5, P7, P10, P13 and P14. The minimum leaf area (52.90 cm^2) was reported in seedlings of P6 which was statistically at par with P4, P8, P11, P15, P16, P18, P19 and P20.

C. Altitudinal Variations in (mean value) seedling growth characteristics among populations (at the age of 18 months)

The average seedling growth performance of populations in each altitudinal zone is outlined in Table 4.17 and Fig 4.10, which may be seen here.

Table 4.17 Altitudinal variations in (mean value) seedling growth characteristics (at the age of 18 months) among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Seedling Height (cm)	Collar diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)
A1 (400-800 m)	83.65	9.11	5.65	0.78	61.40
A2 (800-1200 m)	82.18	8.79	5.97	0.83	60.39
A3(1200-1600 m)	86.85	9.53	5.79	0.87	60.61
A4(1600-2000 m)	66.46	7.17	4.83	0.83	56.03

Maximum mean seedling height and collar diameter were observed for seedlings raised from populations of the A3 (1600–2000 m a msl) altitudinal zone, while, minimum were observed for populations of the A4 (1600–2000 m a m s l) altitudinal zone. Maximum internodal length (5.97 cm) recorded for populations of the A2 (800–1200 m a msl) altitudinal zone and the highest value of leaf area (61.40 cm^2) for populations of the A1 altitudinal zone. Populations of A4 (1600–2000 m) were observed with minimum internodal length and leaf area.

Since the seedlings of all seed sources were grown under identical nursery conditions, variation in growth characteristics among seed sources can be attributed to genetic

differences and variation in seed attributes. Growth parameters have good positive relationships with seed size and weight (Chauhan and Raina, 1980; Dunlap and Barnett, 1983), according to Suri (1984) in *Tectona grandis*; consequently, the variation in the seed traits was reflected by significant variation in all growth parameters among the seed sources. Similarly, in the past, *Pinus strobus* (Demeritt and Hocker, 1974), *Acacia mangium* (Salazar, 1989) and *Acacia albida* (Sniezko and Stewart, 1989) had been observed to exhibit variation in seed dimensions (length, breadth and thickness) and weight among individual trees within a population. Seed size (length, width and thickness) and weight have a controlling influence on seed germination (Dunlap and Barton, 1983), collar diameter and leaves per plant in *Santalum album* seedlings (Veerendra and Sharma, 1990). Pathak *et al*. (1984) in 30 provenances of *Leuceana leucaenaphthala* and Sehgal and Jaswal (1996) in *G. optiva* also reported this kind of variations among seed sources. A few studies have demonstrated that larger seeds germinate more rapidly and completely than smaller ones due to a larger endosperm nutrient pool (Kandy, 1978). Therefore, variation in germination among genotypes and populations can be attributed to the significant differences observed in seed dimensions and weight. Seed germination, seedling and growth characteristics are interdependent processes governed by genetic structure, environment and seed characteristics (Dunlap and Barnett, 1983; Pathak *et al.,* 1984). Variation in seed germination reflects adaptations to site conditions (Grime *et al.*, 1981; Nishitani and Masuzawa, 1996), which have a substantial effect on seedling growth and survival. Variability in the germination response of seeds from various provenances, populations, individuals of the same population or different locations in the crown of the same individual tree is well documented (Silvertown 1984; Martin *et al.*, 1995 and Mamo *et al.,* 2006). In addition to age, vigour, crown exposure and genetic factors, the most influential factors on seed attributes are edaphic (such as soil fertility and moisture content) and climatic conditions prevalent in the seed source localities (Mathur *et al.*, 1984). The species originated from warmer climates (particularly deciduous species), are adapted to the extended growing season that occurs at lower elevations but suffer from early or late frosts when transplanted to higher elevations (Broadhurst and Boshier, 2014). Due to this polymorphic germination response, not all seeds may respond in same manner to a given stimulus. The germination value (GV) of seed also varied substantially among populations. The GV is a combination of germination rate and germination success (Czabator, 1962), which are functions of seed size and weight (Dunlap and Barnett, 1983). In turn, this led to variations in GV. In accordance with *Acacia* species (Mathur *et al.,* 1984) and *Albizia falcataria* (Bahuguna *et al.,* 1989), a population of trees

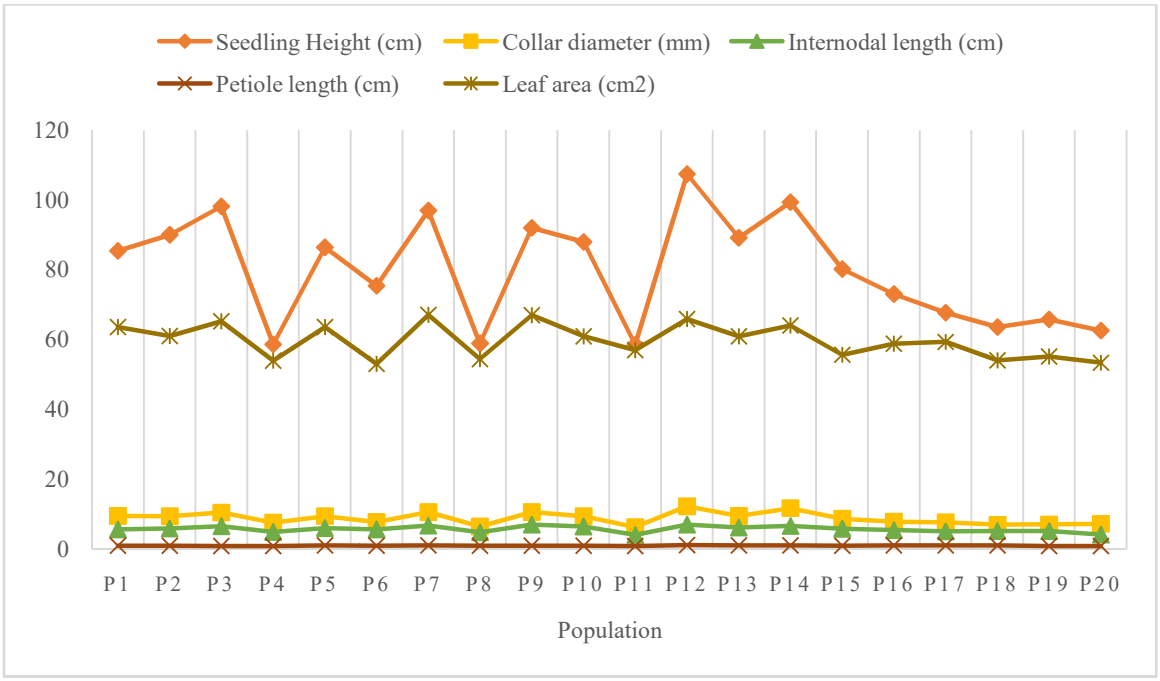


Fig. 4.9 Variations in seedling growth characteristics (At the age of 18 months) among populations of *Grewia optiva* Drummond

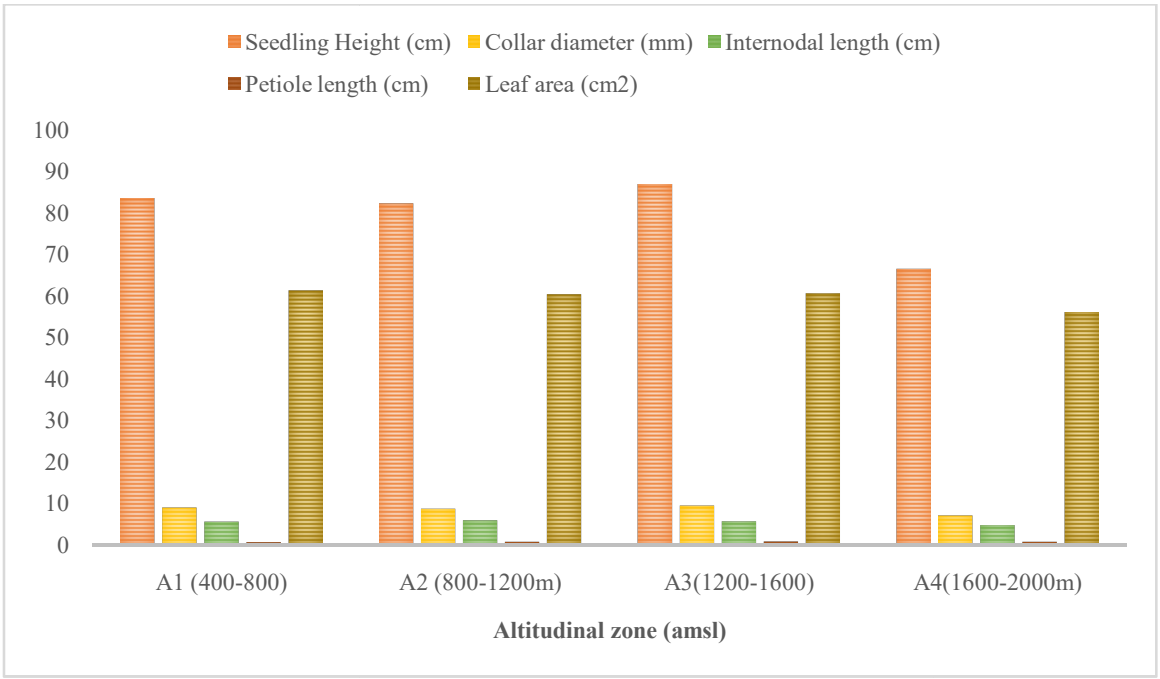


Fig 4.10 Altitudinal variations in (mean value) seedling growth characteristics (at the age of 18 months) among populations of *Grewia optiva* Drummond




Seedling growth at the age of 6 months





Seedling growth at the age of 12 months





Seedling growth at the age of 18 months

Plate 4. Seedling growth at different age under nursery conditions.

exhibits significant variation in germination value as well as germination percentage. According to Meyer *et al*. (1995), Grime *et al.* (1981) and Nishitani and Masuzawa (1996), the germination requirements of a species are adapted to the habitat in which the species exists. Moreover, the germination rate of seeds from distinct regions of a species' range is frequently variable (Baskin and Baskin 1973; Hardin 1984; Martin et al. 1995), due to genetic factors and climatic variation during seed ripening (Meyer and Allen 1999). Germination is also affected by the altitude at which seeds are gathered (Holm, 1994). According to Donoso (1979), marginal climates for seed development at higher elevations can result in incomplete seed maturation, which can be difficult to detect visually in the seed but is revealed during germination and subsequent seedling development (Edwards 1980). Moya *et al*. (2017) discovered that *Nothofagus glauca* populations at higher latitudes tend to have lower germination capacities than *Nothofagus glauca* populations at lower latitudes. The present analysis is also supported by Viveros *et al.* (2008), who found genetic variation in *Pinus hartwegii* at different altititude. Similarly, Lamchhaney (1985) in *Alnus nepalensis* and Ngulube, (1989) in *Gliricidia sepium* reported variations in survival percentage among different seed sources.

D. Variations in fodder quality and mineral nutrients characteristics (of 18 months old seedlings) among genotypes and populations of *Grewia optiva* Drummond

Fodder quality characteristics, *viz.,* crude protein (%), crude fibre (%), ether extract extract (%), total ash (%), NFE (%) and mineral nutrients; P (g/100 g), Na (ppm), K (g/100 g), and Ca (g/100 g), were observed for variation among genotypes (Table 4.18) and populations (Table 4.19). Statistical differences were observed among genotypes and populations of *G. optiva* for fodder quality and mineral nutrient characteristics and presented in Tables 4.18 and Table 4.19, respectively.

i) Variation among genotypes

A critical examination of the data appended to Table 4.18 revealed that the maximum value for crude protein (25.01 %) obtained for seedlings (progeny) of the SI1 genotype, which, was statistically at par with HR1, ST1 and SI2 genotypes. Minimum value of crude protein was registered for seedlings of RA2 (17.22 %) genotype.

An appraisal of the data presented in Table 4.18 elucidated that seedlings of SH1 attained the maximum ether extract percentage (4.11 %), which was statistically at par with

GH3, KT3, JG3, and SN2. Progeny of GR3 showed the lowest ether extract content (2.58 %) which was followed by AD3 and DH4.

Data exhibited in Table 4.18 revealed that seedlings of the DH3 genotype attained the maximum crude fibre content (20.20 %) which was statistically at par with JG4. The minimum value of crude fiber (15.02 %) was exhibited by seedlings of KU3 genotype which was statistically at par with SH3, DO2, NR2, SH3, SN3, RA3, and RA4.

Table 4.18. Variations in fodder quality and mineral nutrients characteristics (of 18 months old seedlings) among genotypes of populations of *Grewia optiva* Drummond

Sr. No.	Genotypes	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)	Phosphorus (gm/100gm)	Sodium (ppm)	Potassium (gm/100gm)	Calcium (gm/100g)
1	HR 1	24.35	3.36	17.02	9.56	45.71	0.27	303.61	2.14	3.08
2	HR 2	21.79	3.61	17.50	8.89	48.21	0.23	310.11	2.05	3.09
3	HR 3	21.89	2.96	16.89	9.11	49.15	0.24	339.89	2.08	3.06
4	HR 4	20.73	3.11	18.25	9.10	48.81	0.23	371.14	2.03	3.12
5	ST 1	24.18	3.12	17.50	9.23	45.97	0.24	267.19	2.18	3.11
6	ST 2	20.11	2.76	18.23	9.46	49.44	0.24	274.21	2.10	3.21
7	ST 3	21.03	3.19	16.69	8.64	50.45	0.24	319.28	2.23	3.07
8	ST 4	20.89	3.23	18.92	8.33	48.63	0.26	262.89	2.21	3.10
9	DR 1	23.47	3.06	19.11	9.23	45.13	0.30	309.32	1.99	3.00
10	DR 2	22.85	3.21	17.49	10.12	46.33	0.27	277.08	1.88	3.32
11	DR 3	20.49	3.16	16.05	9.33	50.97	0.20	328.11	2.01	3.01
12	DR 4	19.55	3.46	17.79	8.98	50.22	0.18	320.19	1.97	3.10
13	GH 1	18.39	3.49	18.50	9.22	50.40	0.27	406.21	2.27	2.46
14	GH 2	19.02	3.27	18.98	10.11	48.62	0.28	399.11	2.11	2.57
15	GH 3	20.22	4.05	19.07	9.22	47.44	0.21	413.18	2.04	2.55
16	GH 4	20.40	3.65	17.18	9.45	49.32	0.21	297.48	2.09	2.22
17	DA 1	22.05	3.13	17.45	8.78	50.59	0.20	316.11	2.11	3.11
18	DA 2	21.71	2.98	17.09	9.22	49.00	0.21	265.92	2.08	3.17
19	DA 3	22.61	3.16	18.49	8.65	50.61	0.18	299.18	2.19	2.94
20	DA 4	19.09	3.05	16.79	9.65	47.90	0.20	220.14	2.26	3.09
21	KD 1	20.81	3.39	19.20	9.45	47.15	0.21	424.81	2.21	2.59
22	KD 2	21.33	3.68	16.67	10.20	48.12	0.21	430.64	2.24	2.86
23	KD 3	19.55	2.96	16.45	8.79	52.25	0.21	370.19	2.12	2.28
24	KD 4	20.43	3.09	17.20	9.96	49.32	0.19	354.21	2.01	2.34
25	SI 1	25.01	3.28	16.54	10.22	45.74	0.29	272.19	2.02	3.08
26	SI 2	24.49	3.32	16.03	10.11	46.05	0.29	252.16	2.04	3.03
27	SI 3	22.14	3.05	15.29	9.89	49.63	0.28	248.31	2.14	3.12
28	SI 4	22.05	2.96	14.32	9.97	50.70	0.27	250.25	2.07	3.01
29	DO 1	16.21	3.22	16.21	8.23	56.13	0.19	333.22	2.13	2.92
30	DO 2	19.05	3.16	15.22	8.45	54.12	0.20	342.91	2.17	3.03
31	DO 3	19.75	3.09	17.31	8.76	51.09	0.19	335.32	2.22	2.91
32	DO 4	20.97	3.55	18.40	9.21	47.87	0.19	350.28	1.98	2.93
33	KT 1	22.75	3.38	16.10	10.34	47.43	0.23	294.80	2.11	3.09
34	KT 2	23.05	3.76	19.05	10.22	43.92	0.23	288.18	2.19	3.16

35	KT 3	21.51	4.05	18.38	9.97	46.09	0.24	291.23	2.02	3.08
36	KT 4	21.03	3.61	16.05	9.88	49.43	0.23	310.27	2.07	2.92
37	KU 1	23.96	3.41	17.45	10.22	44.96	0.25	252.65	2.39	3.16
38	KU 2	22.05	2.76	16.65	9.45	49.09	0.25	305.21	2.41	2.98
39	KU 3	21.88	3.09	15.02	9.43	50.58	0.26	349.23	2.34	3.09
40	KU 4	22.03	3.51	19.08	10.11	45.27	0.26	325.67	2.29	3.12
41	AD 1	21.08	3.13	18.50	9.55	47.74	0.25	422.64	2.13	3.09
42	AD 2	20.11	3.1	17.03	9.23	50.53	0.25	433.81	2.03	3.11
43	AD 3	21.43	2.83	18.25	9.67	47.82	0.25	419.29	2.19	3.05
44	AD 4	20.15	3.16	17.19	8.76	50.74	0.25	417.32	2.17	2.94
45	DH 1	22.98	3.44	17.22	9.70	46.66	0.30	389.68	2.12	2.95
46	DH 2	23.14	3.38	16.04	10.20	47.24	0.28	399.42	2.27	3.06
47	DH 3	21.19	2.87	20.20	9.14	46.60	0.27	370.12	2.05	2.48
48	DH 4	23.10	2.82	19.23	10.43	44.42	0.26	405.21	2.03	2.32
49	NR 1	21.89	3.17	16.75	8.97	49.22	0.19	353.91	1.94	3.08
50	NR 2	21.17	3.09	15.49	8.68	51.57	0.19	398.28	2.09	2.11
51	NR 3	20.99	3.38	18.12	9.10	48.41	0.20	329.52	2.11	2.27
52	NR 4	22.99	3.32	19.01	10.10	44.58	0.22	300.21	2.06	2.19
53	BA 1	21.79	2.88	17.11	9.32	48.90	0.23	299.13	1.95	2.36
54	BA 2	21.53	2.96	16.16	9.45	49.90	0.22	333.22	2.03	2.22
55	BA 3	22.03	3.03	18.38	9.79	46.77	0.22	318.29	2.13	2.19
56	BA 4	23.32	2.99	15.89	10.45	47.35	0.24	429.50	2.11	2.65
57	JG 1	21.11	3.19	18.75	8.59	48.36	0.28	403.10	2.01	2.96
58	JG 2	21.99	3.15	19.40	8.59	46.87	0.27	387.66	2.10	2.39
59	JG 3	20.09	4.06	17.33	8.11	50.41	0.22	373.82	2.04	2.93
60	JG 4	21.05	3.68	20.14	9.32	45.81	0.21	340.31	2.09	2.86
61	SH 1	20.13	4.11	17.17	8.65	49.94	0.19	260.70	1.95	2.69
62	SH 2	19.45	4.08	16.69	8.44	51.34	0.20	255.32	2.02	2.94
63	SH 3	18.49	3.71	15.54	7.98	54.28	0.20	247.16	2.01	2.91
64	SH 4	21.34	3.61	15.98	8.21	50.86	0.19	260.83	1.98	2.79
65	SN 1	21.11	3.87	17.14	9.29	48.59	0.21	345.40	2.02	3.01
66	SN 2	22.00	4.1	16.11	9.50	48.29	0.21	339.11	2.01	2.98
67	SN 3	21.04	3.79	19.33	8.88	46.96	0.21	401.09	2.15	2.93
68	SN4	22.07	3.69	15.64	8.97	49.63	0.21	391.25	2.10	2.94
69	GT 1	19.45	3.21	16.08	8.34	52.92	0.20	345.26	1.83	2.25
70	GT 2	18.73	3.76	18.30	7.89	51.32	0.20	359.43	1.78	2.59
71	GT 3	20.50	3.38	19.03	9.10	47.99	0.20	409.15	2.04	2.92
72	GT 4	19.05	3.19	15.33	7.69	54.74	0.21	340.21	1.82	2.94
73	GR 1	19.31	3.13	19.09	8.75	49.72	0.21	405.60	2.08	2.85
74	GR 2	19.22	3.11	17.12	8.77	51.78	0.18	469.37	2.01	2.69
75	GR 3	20.34	2.58	18.17	9.25	49.66	0.17	382.25	2.10	2.72
76	GR 4	20.12	2.99	16.24	9.65	51.00	0.18	369.63	2.03	2.44
77	RA 1	19.23	3.17	17.12	7.69	52.79	0.20	296.26	1.93	2.51
78	RA 2	17.22	2.99	17.05	7.98	54.76	0.21	319.11	1.99	2.93
79	RA 3	18.01	3.17	15.11	8.42	55.29	0.20	329.11	2.02	2.18
80	RA 4	18.42	3.29	15.21	8.31	54.99	0.19	300.70	1.99	2.12
Mean		**21.04**	**3.30**	**17.32**	**9.20**	**49.18**	**0.23**	**337.92**	**2.08**	**2.82**
$CD_{0.05}$		**0.88**	**0.14**	**0.66**	**0.39**	**2.01**	**0.01**	**13.723**	**0.08**	**0.11**

A critical rummage of Table 4.18 indicated the highest value of total ash (10.44 %) content for progeny of BA4 genotype which was statistically at par with DH4, KT1, DR2, GH2, SH1, SH2, KT2, KU1, KU4 and NR4. Progenies of GT4 and RA1 exhibited the lowest

value of total ash content (7.69%). It was also apparent from Table 4.18 that nitrogen free extract in progenies of DO1 accounted for the highest value (56.13 %) and showed parity with RA3. However, the lowest value of NFE was recorded for KT2 (43.92 %) which was statistically at par with DH4 and NR4.

Table 4.18 showed that the highest content of P (0.30 gm/100 gm) was observed in progeny of the DH1 genotype which was followed by SI1. However, the lowest value was recorded for GR3 (0.17 gm/100gm) which was followed by GR4.

Data depicted in Table 4.18 revealed that progeny of the GR2 genotype attained the maximum Na content (469.37 ppm). The minimum value (220.14 ppm) was shown by the progeny of DA4.

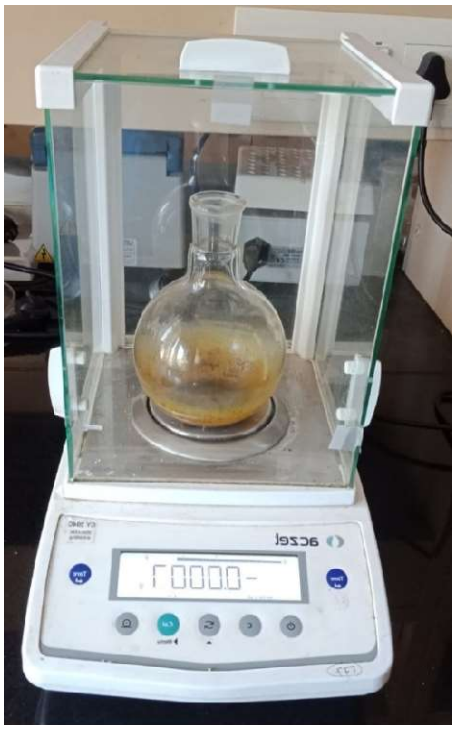
An appraisal of the data presented in Table 4.18 elucidated that seedlings of KU2 attained the maximum K content (2.41 gm/100 gm) which was statistically at par with the performance of progeny of KU1 and KU3. Seedlings of GT2 showed the minimum K content (1.78 gm/100 gm) which was at par with the potassium content of progeny of GT1.

A critical examination of Table 4.18 indicated the highest value of Ca for seedlings (progenies) of DR2 (3.32 gm/100 gm). The minimum Ca content (2.11 gm/100 gm) exhibited by NR2 which was statistically at par with progenies of NR4, BA3, RA3.

ii) Variations in fodder quality and mineral nutrient characteristics (of 18 months old seedlings) among populations of *Grewia optiva* Drummond

Significant differences were found among the population for crude protein (%) (Table 4.19, Fig 4.11). The progenies (seedlings) of the population P7 were found to have the highest crude protein content (23.40 %), while, the progenies of the population P20 had the lowest crude protein content (18.20 %). The maximum value was statistically at par with P12, while minimum value of crude protein was statistically at par with P8.

Data shown in Table 4.19 and Fig 4.11 revealed that the value of ether extract for progeny of population P16 was highest (3.83 %) which was statistically at par with P4, P9 and P17. However, the lowest value of ether extract (2.99 %) was recorded for P19 which was found to be statistically at par with P1, P2, P3, P5, P6, P7, P8, P10, P11, P13, P14 and P18.



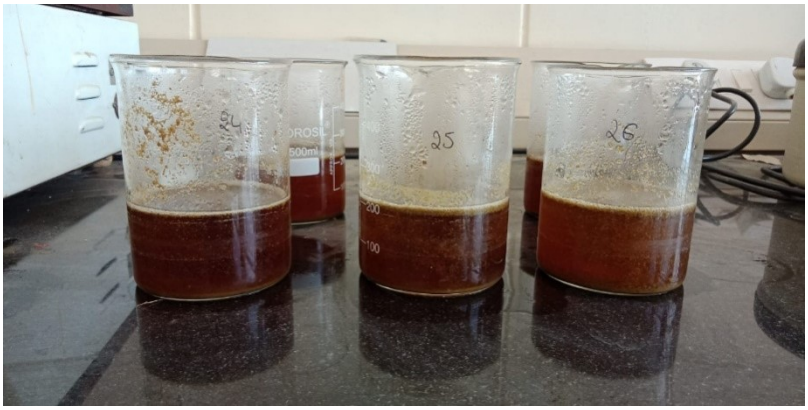




Plate 5. Estimation of fodder characteristics in the Laboratory

Data depicted in Table 4.19 and Fig 4.11 illustrated that the percentage of crude fibre displayed significant variation among the populations. It was determined that seedlings from population P4 had the highest percentage of crude fibre (18.43 %). The seedlings of P7 population had the lowest amount of crude fibre (15.55%). The maximum value of crude fibre was statistically at par with P2, P12, and P15, whereas, minimum value was at par with P16 and P20.

The total ash content (%) varied significantly among populations (Table 4.19 and Fig 4.11). The progenies of P9 had the highest observed total ash content (10.10 %) which was statistically at par with P7. The lowest percentage of total ash content (8.10 %) reported for progeny of population P20 which was statistically at par with P8, P15, P16 and P18..

As indicated in Table 4.19 and Fig 4.11, the progeny of the P7 and P12 populations had the highest P content (0.28 gm/100 gm) which was followed by P2. Despite this, the lowest value (0.19 gm/100 gm) recorded was for the progeny of population P19 which was statistically at par with P10 and P11.

Table 4.19 Variations in fodder quality and mineral nutrient characteristics (of 18 months old seedlings) among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)	Phosphorus (g/100gm)	Sodium (ppm)	Potassium (g/100gm)	Calcium (g/100gm)
A1(400-800m)	P1(Harsar)	22.20	3.28	17.42	9.17	47.97	0.24	331.19	2.08	3.09
	P2(SujanpurTihra)	21.60	3.18	17.84	8.92	48.62	0.25	280.89	2.18	3.12
	P3(Dramman)	21.60	3.17	17.61	9.42	48.16	0.24	308.68	1.96	3.11
	P4(Ghumarwii)	19.50	3.51	18.43	9.50	48.95	0.24	379.00	2.13	2.45
	P5(Daggar)	21.40	3.09	17.46	9.08	49.53	0.20	275.34	2.16	3.08
A2(800-1200m)	P6 (Kalanjri Devi)	20.50	3.18	17.38	9.60	49.21	0.21	394.96	2.15	2.52
	P7 (Sihunta)	23.40	3.16	15.55	10.05	48.03	0.28	255.73	2.07	3.06
	P8(Dodar)	19.00	3.25	16.79	8.66	52.30	0.19	340.43	2.13	2.95
	P9(Kuthar)	22.10	3.57	17.40	10.10	46.72	0.23	296.12	2.10	3.06
	P10(Kutuldi)	22.50	3.20	17.05	9.80	47.48	0.25	308.19	2.36	3.09
A3 (1200-1600m)	P11(Awah devi)	20.70	3.08	17.74	9.30	49.21	0.25	423.27	2.13	3.05
	P12 (Dharot)	22.60	3.19	18.17	9.87	46.23	0.28	391.11	2.12	2.70
	P13(Neri)	21.80	3.29	17.34	9.21	48.45	0.20	345.48	2.05	2.41
	P14(Basni)	22.20	3.03	16.89	9.75	48.23	0.23	345.04	2.06	2.36
	P15(Jagdhar)	21.10	3.63	18.91	8.65	47.86	0.25	376.22	2.06	2.79
A4 (1600-2000m)	P16 (Shogi)	19.90	3.83	16.35	8.32	51.61	0.20	256.00	1.99	2.83
	P17 (Sangrah)	21.60	3.72	17.06	9.16	48.37	0.21	369.21	2.07	2.97
	P18 (Ghanahatti)	19.40	3.30	17.19	8.26	51.74	0.20	363.51	1.87	2.68
	P19 (Garhkhal)	19.70	2.99	17.66	9.11	50.54	0.19	406.71	2.06	2.68
	P20 (Ranichauri)	18.20	3.13	16.12	8.10	54.46	0.20	311.30	1.98	2.44
Mean		21.04	3.30	17.32	9.20	49.18	0.23	337.92	2.08	2.82
$CD_{0.05}$		0.88	0.36	1.82	0.63	3.01	0.03	45.91	0.10	0.30

It is clear from Table 4.19 and Fig 4.11 that the progeny of population P11 had the highest level of Na content (423.27 ppm) which was statistically at par with P6, P12 and P19. The progeny of P16 had the lowest value, which was 256 ppm and it was statistically at par with P2, P5, P7 and P9.

Based on a review of the data that was shown in Table 4.19 and Fig 4.11 the seedlings from population P10 attained the highest level of K content (2.36 gm/100 gm) which was followed by P2. The P18 population's progeny were recorded with minimum K value (1.87 gm/ 100 gm) which was followed by P20.

A comprehensive examination of Table 4.19 and Fig 4.11 revealed that the Ca content of seedlings of P2 population had the highest value (3.12 gm/100 gm) which was statistically at par with P1, P3, P5, P7, P9, P10 and P11. The progenies of P14 was reported with minimum Ca concentration 2.36 gm/100 gm which was statistically at par with P4, P6, P12 and P13.

iii) Altitudinal variations (mean value) in fodder quality and mineral nutrient characteristics (of 18 months old seedlings) among populations of *Grewia optiva* Drummond

It is clear from Table 4.20 that the maximum mean value of crude protein (21.66 %), crude fibre (17.81 %), P (0.24 gm/100gm) and Na (376.22 gm/100gm) recorded for populations of A3 (1200-1600 m a msl) altitudinal zone. Populations of A4 altitudinal zone illustrated least value of crude protein (19.76 %), total ash (8.59 %), P (0.20 g/100gm) and K (1.99 g/100 gm). Minimum value of Na (319.09 ppm) and crude fiber (16.83 %) reported for populations of A2 (800-1200 m a msl) altitudinal zone.

Table 4.20 Altitudinal variations in (mean value) fodder quality and mineral nutrient characteristics (of 18 months old seedlings) among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)	Phosphorus (gm/100gm)	Sodium (ppm)	Potassium (gm/100gm)	Calcium (gm/100gm)
A1 (400-800 m)	21.24	3.25	17.75	9.21	48.65	0.23	315.02	2.10	2.97
A2 (800-1200 m)	21.50	3.32	16.83	9.64	48.75	0.23	319.09	2.16	2.94
A3(1200-1600 m)	21.66	3.18	17.81	9.36	48.00	0.24	376.22	2.08	2.66
A4(1600-2000 m)	19.76	3.45	16.87	8.59	51.34	0.20	341.35	1.99	2.72

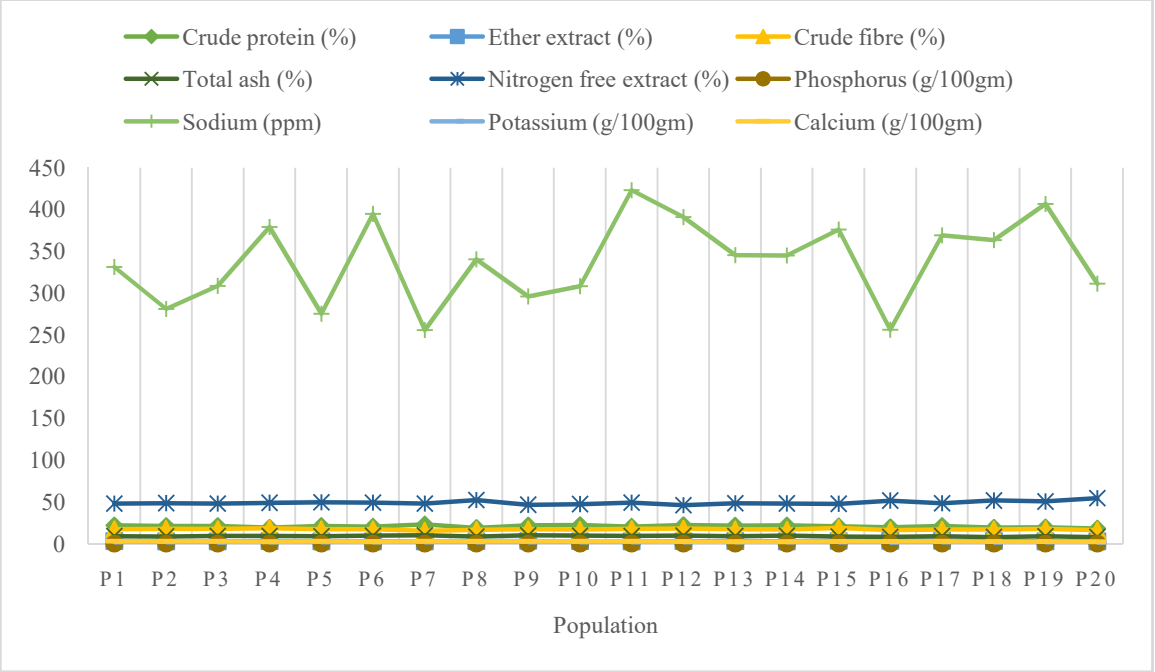


Fig 4.11 Variations in fodder quality and mineral nutrient characteristics (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Table 4.21 Identified 15 Best genotypes of *Grewia optiva* among eighty genotypes (on the basis of 18 months seedling growth and their fodder characteristics) within selected populations of *Grewia optiva* Drummond.

Sr. No.	Genotypes	Seedling Height (cm)	Collar diameter (mm)	Seedling internodal length (cm)	Petiole length (cm)	Leaf area (cm^2)	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)	Phasphorus (g/100gm)	Sodium (ppm)	Potassium (g/100gm)	Calcium (g/100g)
1	DH1	107.75	11.82	7.14	0.93	70.29	22.98	3.44	17.22	9.70	46.66	0.30	389.68	2.12	2.95
2	DH2	118.76	13.42	7.05	0.93	69.22	23.14	3.38	16.04	10.20	47.24	0.28	399.42	2.27	3.06
3	DH4	108.78	13.21	6.92	1.10	63.32	23.10	2.82	19.23	10.43	44.42	0.26	405.21	2.03	2.32
4	HR1	99.61	10.79	6.31	0.73	72.55	24.35	3.36	17.02	9.56	45.71	0.27	303.61	2.14	3.08
5	ST 1	97.66	10.70	6.03	0.81	70.88	24.18	3.12	17.50	9.23	45.97	0.24	267.19	2.18	3.11
6	DR1	112.57	12.3	7.02	0.67	69.94	23.47	3.06	19.11	9.23	45.13	0.30	309.32	1.99	3.00
7	DR2	100.75	11.12	6.86	0.69	70.33	22.85	3.21	17.49	10.12	46.33	0.27	277.08	1.88	3.32
8	NR4	102.35	12.45	6.94	0.93	67.13	22.99	3.32	19.01	10.10	44.58	0.22	300.21	2.06	2.19
9	DA4	97.32	11.08	6.16	0.93	73.66	22.61	3.05	16.79	9.65	47.90	0.20	220.14	2.26	3.09
10	BA3	113.65	12.80	7.10	0.89	69.05	23.32	3.03	18.38	9.79	46.77	0.22	318.29	2.13	2.19
11	KU1	100.71	12.19	7.03	0.85	70.09	23.96	3.41	17.45	10.22	44.96	0.25	252.65	2.39	3.16
12	SI2	105.43	12.11	7.11	0.87	70.09	24.49	3.32	16.03	10.11	46.05	0.29	252.16	2.04	3.03
13	SI3	100.45	11.79	6.93	0.93	69.57	25.01	3.05	15.29	9.89	49.63	0.28	248.31	2.14	3.12
14	KT1	97.94	10.82	6.94	0.78	73.78	22.75	3.38	16.10	10.34	47.43	0.23	294.80	2.11	3.09
15	KT2	99.04	11.19	7.08	0.81	75.59	23.05	3.76	19.05	10.22	43.92	0.23	288.18	2.19	3.16

It is evident from Table 4.20 that minimum mean percentage of ether extract (3.18 %) and Ca (2.66 gm/ 100 gm) observed for populations of A3 (1200-1600 m a msl) altitudinal zone and maximum ether extract percentage (3.45 %) recorded for A4 (1600 -2000m a msl) altitudinal zone. A4 altitudinal zone (1600-2000 m a msl) showed minimum value of nitrogen free extract for populations of this zone.

Based on the seedling growth and fodder quality characteristics of 18 months old seedlings, the 15 best genotypes, *i.e.,* DH1, DH2, DH4, HR1, ST1, DR1, DR2, NR4, DA4, BA3, KU1, SI2, SI3, KT1 and KT2 (Table 4.21) of *G. optiva* Drummond were identified among eighty genotypes within selected populations of *G. optiva*. These genotypes were selected on the basis of high level of crude protein, leaf area and seedling height, along with other grouping characteristics.

4.2 Physiochemical properties of soil

A. Variation among population

Underneath each of the twenty populations of *G. optiva*, two composite soil samples were taken from the surface (0–15 cm) and the subsurface layer (15–30 cm). The following physiochemical parameters, involving soil colour, bulk density, particle density, porosity, pH, electrical conductivity, organic carbon, available nitrogen, available phosphorus and available potassium, were observed and statistically analysed. The physiochemical characteristics of the soil were found to differ significantly, as laid forth in Tables 4.22, 4.23, and 4.25 respectively.

Soil collected underneath different populations of *G. optiva* showed variations in soil colour. The soils of the population of the A1 altitudinal zone (at 0-15 cm depth) varied from brown to dark brown, dark yellowish brown and greyish brown. These colours become lighter in colour as we moved from the 0–15 cm layer to the 15–30 cm soil layer. In A2 altitudinal zone (800-1200 m a msl), four soil colours were observed (at 0-15 cm depth): light brown, dark brown, yellowish brown and brown. Under the population of the A3 altitudinal zone, variation in soil colour was observed. In this altitudinal zone, there were four types of soil colour (at 0-15 cm depth): dark yellowish brown, dark brown, light brown, and dark greyish brown observed. The soil of A4 altitudinal zone acquaintance with light brown, brown and dark brown (at 0-15 cm depth).

Table 4.22. Variations in soil colour among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Soil depth	
		0-15 cm	15-30 cm
A1 (400-800 m)	P1(Harsar)	Brown	Light yellowish brown
	P2(SujanpurTihra)	Brown	Light brown
	P3(Dramman)	Dark brown	Brown
	P4(Ghumarwii)	Dark yellowish Brown	Light yellowish brown
	P5(Daggar)	Greyish brown	Greyish
A2 (800-1200 m)	P6 (Kalanjri Devi)	Light Brown	Yellowish brown
	P7 (Sihunta)	Dark brown	Light brown
	P8(Dodar)	Yellowish Brown	Light brown
	P9(Kuthar)	Brown	Light brown
	P10(Kutuldi)	Dark brown	Light Brown
A3 (1200-1600 m)	P11(Awah devi)	Dark yellowish brown	Yellowish brown
	P12 (Dharot)	Dark brown	Brown
	P13(Neri)	Light brown	Very light brown
	P14(Basni)	Dark brown	Brown
	P15(Jagdhar)	Dark Greyish brown	Brown
A4 (1600-2000 m)	P16 (Shogi)	Light brown	Very light brown
	P17 (Sangrah)	Dark Brown	Light Brown
	P18 (Ghanahatti)	Dark brown	Light Brown
	P19 (Garhkhal)	Brown	Light brown
	P20 (Ranichauri)	Dark brown	Light brown

Analysis of variance for soil bulk density (BD) (g cm^{-3}), particle density (PD) (g cm^{-3}) and soil porosity showed significant variation among populations, with soil depth and population x soil depth interaction, as presented in Table 4.23.

A critical observation of the data presented in Table 4.23 showed that among populations maximum mean value of bulk density (1.37 g cm^{-3}) was observed for soil of populations P1 and P5, whereas, minimum value (0.87 g cm^{-3}) observed underneath population P17. Between two soil depth, high bulk density (1.21 g cm^{-3}) was observed at 15-30 cm depth. In population and soil depth (0–15 and 15–30 cm) interaction, the maximum bulk density at depth of 0-15 cm obtained underneath the P5 population (1.35 g cm^{-3}) whereas, population P1 showed highest value of BD (1.44 g cm^{-3}) at soil depth of 15-30 cm.

Perusal of the data in Table 4.23 revealed that among the populations, the maximum soil particle density (2.65 g cm^{-3}) was observed for the soil of the P5 population, followed by P1, which was at par with the maximum and minimum value (2.12 g cm^{-3}) recorded for P19. Particle density showed significant variation with depth; it reached its maximum at 15-30 cm depth (2.38 g cm^{-3}**).** A critical analysis of interaction effects between population and soil depth (0-15 cm and 15-30 cm) revealed that the particle density was found to be maximum

for soil of population P5, i.e., 2.63 g cm^{-3} at depth 0-15 cm and 2.67 **g** cm^{-3} at depth 15-30 cm and minimum obtained for population P19 for both soil depths (2.09 g cm^{-3} at depth 0-15 cm and 2.14 g cm^{-3} for 15-30 cm depth).

A critical examination of Table 4.23 elucidated that among populations, the maximum porosity was observed for the soil of population P17 (62.59) and the minimum for population P20 (43.11), which was at par with P10. While examining variation in soil porosity with depth, the maximum was found at 0–15 cm depth (53.27) and decreased at 15–30 cm depth (49.20). Data pertaining to the interaction effects of population and soil depth showed maximum porosity for the soil of population P17 for 0–15 cm depth (69.43) and 55.75 at 15–30 cm soil depth. Population P20 is acquainted with the minimum soil porosity at both soil depths, i.e., 43.61 at 0–15 cm and 42.61 at 15–30 cm subsurface layer.

Table 4.23 Variations in soil Bulk Density (BD) (g cm^{-3}), Particle density (PD) (g cm^{-3}), soil porosity among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	(BD) (g cm^{-3}) Soil Depth		Mean (Population)	(PD) (g cm^{-3}) Soil Depth		Mean (Population)	Soil porosity Soil Depth		Mean (Population)
		0-15 cm	15-30 cm		0-15 cm	15-30 cm		0-15 cm	15-30 cm	
A1(400-800m)	P1(Harsar)	1.30	1.44	1.37	2.57	2.60	2.59	49.41	44.61	47.01
	P2(SujanpurTihra)	1.22	1.36	1.29	2.54	2.59	2.57	51.97	47.49	49.73
	P3(Dramman)	1.11	1.34	1.23	2.32	2.47	2.40	52.15	45.75	48.95
	P4(Ghumarwii)	1.17	1.25	1.21	2.45	2.51	2.48	52.24	50.20	51.22
	P5(Daggar)	1.35	1.39	1.37	2.63	2.67	2.65	48.67	47.94	48.31
A2(800-1200m)	P6 (Kalanjri Devi)	1.13	1.20	1.16	2.31	2.38	2.35	51.08	49.58	50.33
	P7 (Sihunta)	0.99	1.09	1.04	2.22	2.39	2.31	55.40	54.39	54.90
	P8(Dodar)	1.25	1.32	1.29	2.36	2.43	2.40	47.03	45.68	46.36
	P9(Kuthar)	1.04	1.11	1.08	2.28	2.33	2.30	54.38	52.36	53.37
	P10(Kutuldi)	1.31	1.35	1.33	2.34	2.40	2.37	44.02	43.75	43.88
A3 (1200-1600m)	P11(Awah devi)	1.09	1.16	1.13	2.39	2.43	2.41	54.39	52.26	53.33
	P12 (Dharot)	1.04	1.13	1.09	2.11	2.17	2.14	50.71	47.93	49.32
	P13(Neri)	0.96	1.10	1.03	2.26	2.32	2.29	57.52	52.59	55.05
	P14(Basni)	0.89	1.09	0.99	2.31	2.39	2.35	61.47	54.39	57.93
	P15(Jagdhar)	1.30	1.33	1.32	2.33	2.37	2.35	44.20	43.88	44.04
A4 (1600-2000m)	P16 (Shogi)	0.82	1.05	0.94	2.12	2.15	2.14	61.32	51.16	56.24
	P17 (Sangrah)	0.70	1.04	0.87	2.29	2.35	2.32	69.43	55.75	62.59
	P18 (Ghanahatti)	0.76	1.07	0.91	2.21	2.26	2.23	65.61	52.65	59.13
	P19 (Garhkhal)	1.03	1.09	1.06	2.09	2.14	2.16	50.72	49.06	49.89
	P20 (Ranichauri)	1.28	1.32	1.30	2.27	2.30	2.28	43.61	42.61	43.11
Mean (Depth)		1.09	1.21		2.32	2.38		53.27	49.20	
		$CD_{0.05}$	SE(d)	SE(m)	$CD_{0.05}$	SE(d)	SE(m)	$CD_{0.05}$	SE(d)	SE(m)
Population		0.04	0.02	0.01	0.07	0.03	0.02	1.58	0.79	0.56
Soil Depth		0.01	0.01	0.01	0.02	0.01	0.01	0.50	0.25	0.18
Population x Soil Depth		0.05	0.03	0.02	0.04	0.03	0.02	2.23	1.12	0.79

In Table 4.24, the results of the analysis of variance for soil pH, electrical conductivity (EC) (dSm^{-1}) and organic carbon (%) showed significant variation among populations, with soil depth and between population x soil depth interactions.

Table 4.24 Variations in soil pH, electrical conductivity, organic carbon of soil samples collected underneath different populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	pH		Mean (Population)	Electrical conductivity (EC) (dSm^{-1})		Mean (Population)	Organic carbon (%)		Mean (Population)
		Soil Depth			Soil Depth			Soil Depth		
		(0-15 cm)	(15-30 cm)		(0-15 cm)	(15-30 cm)		(0-15 cm)	(15-30 cm)	
A1(400-800m)	P1(Harsar)	6.85	6.90	6.88	0.19	0.13	0.16	2.06	1.75	1.91
	P2(SujanpurTihra)	7.38	7.44	7.41	0.80	0.60	0.70	2.22	1.44	1.83
	P3(Dramman)	6.15	6.18	6.16	0.13	0.11	0.12	2.14	1.96	2.05
	P4(Ghumarwii)	7.37	7.64	7.51	0.33	0.24	0.28	1.22	0.76	0.99
	P5(Daggar)	6.52	6.55	6.54	0.57	0.55	0.56	0.84	0.56	0.70
A2(800-1200m)	P6 (Kalanjri Devi)	7.12	7.15	7.14	1.15	1.12	1.14	1.09	0.87	0.98
	P7 (Sihunta)	6.72	6.74	6.73	0.80	0.75	0.78	2.65	0.96	1.81
	P8(Dodar)	5.21	6.10	5.66	0.56	0.42	0.49	1.20	0.46	0.83
	P9(Kuthar)	5.98	6.30	6.14	0.13	0.07	0.10	2.55	2.50	2.53
	P10(Kutuldi)	6.09	6.11	6.10	0.22	0.19	0.21	2.38	2.13	2.26
A3 (1200-1600m)	P11(Awah devi)	6.27	6.14	6.21	0.33	0.24	0.28	2.03	1.79	1.91
	P12 (Dharot)	6.50	6.90	6.70	0.19	0.15	0.17	2.26	1.12	1.69
	P13(Neri)	6.06	6.79	6.43	0.14	0.11	0.13	1.82	1.11	1.47
	P14(Basni)	6.25	6.65	6.45	0.32	0.28	0.30	2.17	1.08	1.63
	P15(Jagdhar)	5.95	6.50	6.22	0.44	0.39	0.42	2.41	1.98	2.20
A4 (1600-2000m)	P16 (Shogi)	7.02	7.09	7.06	0.35	0.30	0.33	2.09	1.77	1.93
	P17 (Sangrah)	6.25	6.31	6.28	0.22	0.19	0.21	2.38	1.80	2.09
	P18 (Ghanahatti)	6.10	6.21	6.16	0.21	0.17	0.19	1.79	1.32	1.56
	P19 (Garhkhal)	6.03	6.70	6.37	0.28	0.22	0.25	2.01	1.43	1.72
	P20 (Ranichauri)	5.35	5.60	5.48	0.41	0.38	0.40	2.58	2.01	2.30
Mean (Depth)		6.36	6.60		0.39	0.33		2.00	1.44	
		$CD_{0.05}$	SE(d)	SE(m)	$CD_{0.05}$	SE(d)	SE(m)	$CD_{0.05}$	SE(d)	SE(m)
Population		0.21	0.10	0.07	0.01	0.01	0.01	0.06	0.03	0.02
Soil Depth		0.07	0.03	0.02	0.01	0.01	0.01	0.02	0.01	0.01
Population x Soil Depth		0.29	0.15	0.10	0.02	0.01	0.01	0.08	0.04	0.03

An important analysis of the data shown in Table 4.24 revealed considerable differences between the populations. The population P4's soil had the highest pH reading (7.50), which was followed by the population P2. The pH of the soil was measured at its lowest (5.66) under the P8 population. At a depth of 15-30 cm, a high pH value (6.6) was measured. Regarding the interaction effects of population and soil depth, the maximum value for pH (7.38 at 0-15 cm, 7.44 at 15-30 cm soil depth) was recorded underneath population P2 (at both soil depths), whereas population P8 had the lowest pH at soil levels of 0-15 cm (5.21) and 15-30 cm (6.10).

An examination of Table 4.24 revealed that the electrical conductivity of the soil was at its highest under the P6 population (1.13 dSm^{-1}), while it was at its lowest below the P9 population (0.10 dSm^{-1}). Comparatively, the electrical conductivity of the soil at depths of 0-15 cm (0.39 dSm^{-1}) was significantly higher than that of the soil at depths of 15-30 cm (0.33 dSm^{-1}). The population and soil depth showed substantial interaction effects, which indicated considerable changes in electrical conductivity. The population P6 had the highest value at 0-15 cm soil depth (1.15 dSm^{-1}) and at 15–30 cm soil depth (1.11 dSm^{-1}), while the population P9 had the lowest pH at 0-15 cm soil depth (0.13 dSm^{-1}) and at 15-30 cm soil depth (0.07 dSm^{-1}).

A perusal of the data that is shown in Table 4.24 demonstrated that there was substantial variation found among populations, soil depth and the interaction between each other for soil organic carbon. The population P9 had the highest recorded percentage of soil organic carbon (2.53 %), while, the population P5 had the lowest (0.83 %). It was found that the organic carbon percentage dropped with increasing soil depth; hence, the highest value (2.00 %) for the organic percentage was recorded for 0-15 cm soil depth. Ascertainment of the interaction effects of population and soil depth: for population P7, the maximum percentage of soil organic carbon (2.65 %) was found at a soil depth of 0-15 cm soil depth, but for population P9, maximum value (2.50 %) was found at a depth of 15-30 cm. For population P8, the minimum percentage found in the soil was 0.84 % at a depth of 0-15 cm and 0.56 % at a depth of 15-30 cm. According to the overall state, it can be seen that the soils at various sites have varying amounts of organic carbon. It is reasonable to assume that the percentage of SOC present in the soil lessened with increasing soil depth, yet an abundance of SOC was discovered near the soil's surface (Table 4.24). It is because of the assimilation of leaf litter that there has been a larger deposit of soil organic carbon near the surface. The findings of this study were reinforced by the findings of other researchers (Minhas *et al.,* 1997; Arora *et al.,* 2013) who looked at land use systems involving agriculture and forests.

The results of the analysis of variance for available N, available P and available K are shown in Table 4.25. These results demonstrated that there was a significant amount of variation between populations, with soil depth, and in the interaction between populations and soil depth. It is clear from Table 4.25 that population P7 evinced the highest soil N value (426.13 kg ha^{-1}), while, minimum soil N was recorded beneath population P8 (251.45 kg ha^{-1}). With an increase in soil depth from 0-15 cm to 15-30 cm, soil N decreased. Therefore, a

high value of soil N was recorded at 0-15 cm depth, i.e., 371.33 kg ha^{-1}. While analysing the interaction between population and soil depth, the maximum soil N recorded for population P7 at both soil depths, i.e., at 0-15 cm depth, it was 454.66 kg ha^{-1} and at 15-30 cm soil depth, 397.59 kg ha^{-1}. In soil depth and population interaction, the least soil N was observed (298.00 kg ha^{-1}) at depths 0-15 cm and 204.00 kg ha^{-1} at 15-30 cm depth for population P8.

Table 4.25 Variations in Soil Nitrogen (kg ha^{-1}), Phosphorus (kg ha^{-1}) and Potassium (kg ha^{-1}) among different populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Soil Nitrogen (kg ha^{-1})		Mean (Population)	Soil P (kg ha^{-1})		Mean (Population)	Soil K (kg ha^{-1})		Mean (Population)
		Soil Depth			Soil Depth			Soil Depth		
		0-15 cm	15-30 cm		0-15 cm	15-30 cm		0-15 cm	15-30 cm	
A1(400-800m)	P1(Harsar)	363.47	359.70	361.59	42.04	40.21	41.13	250.43	217.32	233.88
	P2(SujanpurTihra)	395.43	360.08	377.76	38.14	35.11	36.63	235.65	225.89	230.77
	P3(Dramman)	372.97	317.35	345.16	36.03	31.96	34.00	304.80	275.30	290.05
	P4(Ghumarwii)	352.52	299.10	325.81	30.87	28.90	29.89	245.60	190.64	218.12
	P5(Daggar)	287.17	243.11	265.14	23.67	20.22	21.95	160.13	138.18	149.16
A2(800-1200m)	P6 (Kalanjri Devi)	300.67	267.50	284.08	29.43	27.22	28.33	149.44	125.32	137.38
	P7 (Sihunta)	454.66	397.59	426.13	50.07	42.69	46.38	220.89	198.11	209.50
	P8(Dodar)	298.00	204.89	251.45	23.20	20.54	21.87	173.39	150.29	161.84
	P9(Kuthar)	404.11	389.32	396.72	34.33	30.34	32.34	253.40	202.34	227.87
	P10(Kutuldi)	390.98	342.11	366.55	35.65	31.54	33.60	207.55	185.89	196.72
A3 (1200-1600m)	P11(Awah devi)	322.52	270.10	296.31	30.76	27.94	29.35	145.60	130.64	138.12
	P12 (Dharot)	380.92	368.21	374.57	32.69	29.56	31.12	210.67	190.90	200.79
	P13(Neri)	370.34	300.21	335.28	30.98	28.49	29.73	222.32	198.98	210.65
	P14(Basni)	395.36	299.62	347.49	33.89	29.44	31.67	170.57	184.28	177.43
	P15(Jagdhar)	427.52	395.69	411.61	44.42	38.89	41.66	188.22	166.23	177.23
A4 (1600-2000m)	P16 (Shogi)	365.23	348.34	356.79	30.43	26.34	28.39	153.56	130.45	142.00
	P17 (Sangrah)	410.35	386.18	398.27	45.02	39.54	42.28	144.00	127.65	135.82
	P18 (Ghanahatti)	379.89	359.27	369.58	27.98	21.65	24.82	136.43	120.59	128.51
	P19 (Garhkhal)	364.29	344.22	354.26	30.11	27.47	28.79	130.23	119.34	124.79
	P20 (Ranichauri)	390.15	350.03	370.09	28.50	22.56	25.53	118.56	100.90	109.73
Mean (Depth)		371.33	330.13		33.91	30.03		191.07	168.96	
		$CD_{0.05}$	SE(d)	SE(m)	$CD_{0.05}$	SE(d)	SE(m)	$CD_{0.05}$	SE(d)	SE(m)
Population		10.89	5.46	3.86	1.01	0.51	0.36	5.49	2.75	1.95
Soil Depth		3.44	1.73	1.22	0.32	0.16	0.11	1.74	0.87	0.62
Population x Soil Depth		15.40	7.72	5.46	1.44	0.72	0.51	7.77	3.90	2.75

The data illustrated in the Table 4.25 revealed that the highest value of soil P was recorded for population P7 (46.38 kg ha^{-1}), while, minimum value of soil P was recorded for population P5 (21.95 kg ha^{-1}). P in the soil was much higher at a depth of 0-15 cm (33.91 kg ha^{-1}) than at a depth of 15-30 cm (30.03 kg ha^{-1}). The research into the interaction effects of population and soil depth found that the population P7 had high levels of soil P at both 0-15 cm depth (50.07 kg ha^{-1}) and 15-30 cm soil depth (42.69 kg ha^{-1}). For population P8, the

minimum soil P reported at a depth of 0-15 cm was 23.20 kg ha^{-1}, while, for population P5, the minimum soil P observed at a depth of 15–30 cm was 20.22 kg ha^{-1}.

The data that are depicted in Table 4.25 demonstrated that population, soil depth, and the interaction between soil depth and population all had a significant impact on the amount of K that was found in the soil. According to the data that was presented in Table 4.25, the population with the highest soil K content was P3 (290.05 kg ha^{-1}), whereas the population with the lowest soil K content was P20 (109.73 kg ha^{-1}). As soil depth increases from 0-15 cm to 15-30 cm, soil K likewise decreased. The interaction effect between population and soil depth indicated significant differences in which the maximum value of K was reported in the soil of population P3, which was equivalent to 304.80 kg ha^{-1} at depth 0-15 cm and 275.30 kg ha^{-1} at depth 15-30 cm of soil. The P20 population exhibited the lowest K levels in the soil at a depth of 0-15 cm (118.56 kg ha^{-1}) and at a depth of 15-30 cm (100.90 kg ha^{-1}).

The above mentioned results on the physiochemical characteristics of soil were supported by Kaistha *et al*. (1990), Sahu and Patnaik (1990) and Walia and Rao (1996), who found that the pH values increased with depth, possibly due to the leaching of bases. Both Sarkar and Sahoo (2000) and Patil *et al.* (2008) came to the conclusion that the soil alkalinity increases with depth due to the deposition of basic salts by irrigation and eluviations, which causes the pH value to increase with depth. The findings made by Prajapati *et al*. (2021) during their investigation into the macro and micronutrients present in the soil of the Tehri Garhwal districts of Uttarakhand support these conclusions. In the Chamba block in Uttarakhand, they found a pH range of 4.5-8.06 and in the Tehri Garhwal district, they found a pH range of 4.5-8.17. Verma and Tripathi (2007) reported that the soils in the mid-Shivalik hills in Himachal Pradesh have very low levels of soluble salt concentration, with EC values ranging from 0.01 to 0.15 dSm^{-1}. As a result of the absence of soluble salts, these soils are receptive to the addition of fertiliser. The outcomes of current study are also consistent with the findings of Prajapati *et al*. (2021), who recorded a range of (EC) 0.099 to 0.574 dSm^{-1} in the Chamba block of Uttarakhand and 0.099 to 0.931 dSm^{-1} in the Tehri Garhwal district of UK. Within the scope of their research, Prajapati *et al*. (2021) also published ranges for bulk density, particle density, SOC, available N, P and K in the soils of the Tehri Garhwal area of Uttarakhand. The findings of the studies conducted by Athokpam *et al.* (2013), Chander *et al.* (2014), Singh *et al.,* 2018 Arya *et al.* (2019) and Bungla *et al.* (2019) also lend credence to the conclusions of the present investigation.

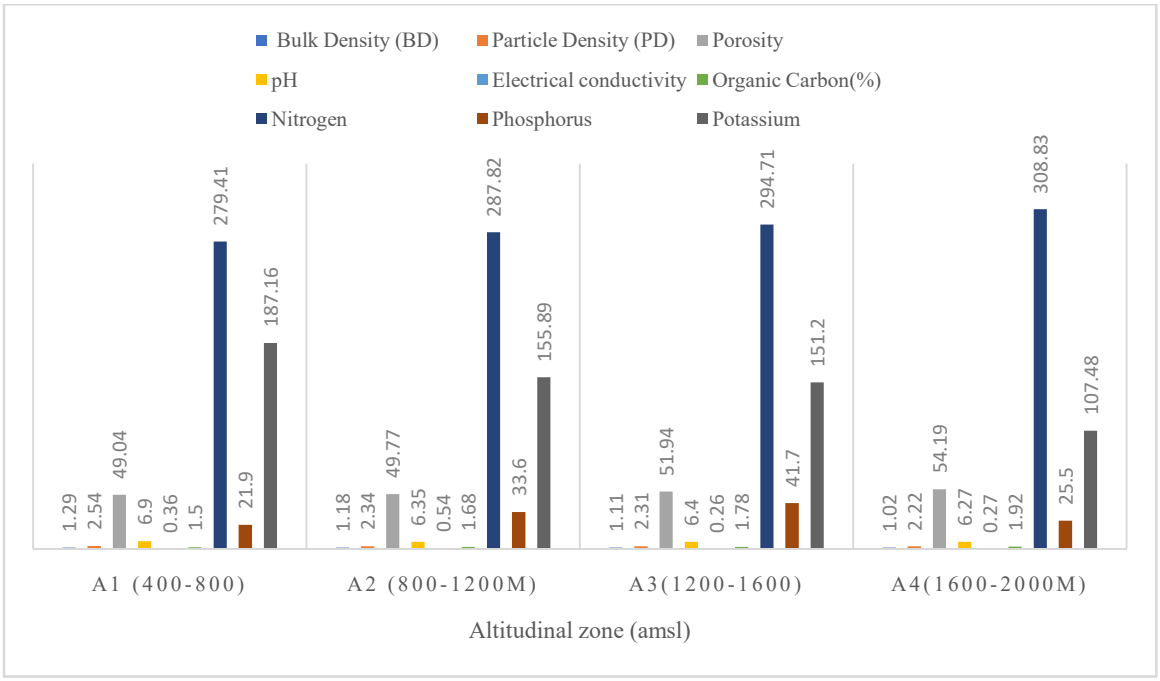


Fig 4.12 Altitudinal variation in (mean value) physiochemical characteristics of soil among populations of *Grewia optiva* Drummond







Plate 6. Drying of soil samples and recording observations on soil characteristics in the laboratory

B. Altitudinal variation

Altitudinal variation in (mean value) physiochemical characteristics of soil among populations of *Grewia optiva* Drummond

Altitudinal variation in soil physiochemical characteristics among different population also computed and presented in Table 4.26 and Fig 4.12. In the Table 4.26, each altitudinal zone displayed the population's average value for the soil physiochemical characteristics that are typical of that particular altitudinal zone. A critical observation of the mean data represented in Table 4.26 and Fig 4.12 showed that as we moved from the A1 to the A4 altitudinal zone, we saw a noticeable decrease in the bulk density, particle density, and potassium levels of the soil. However, when we proceed from the A1 zone to the A4 zone, the soil's porosity, organic carbon content and nitrogen content all rise. The soil beneath populations of the A1 altitudinal zone reported with highest soil pH value (6.90), while, the soil underneath population of A4 altitudinal zone reported the lowest soil pH value (6.27). The pH of the soil droped as we moved from A1 to A2, then rised again as we moved from A2 to A3, and finally droped again as we moved from A3 to A4. The soil under the population in the A2 altitudinal zone was reported to have the highest electrical conductivity (0.54), while the A3 altitudinal zone had the lowest (0.26) electrical conductivity.

Table 4.26 Altitudinal variation in (mean value) physiochemical characteristics of soil among populations of *Grewia optiva* Drummond.

Altitudinal Zone (a msl)	Bulk Density (BD) (g cm^{-3})	Particle Density (PD) (g cm^{-3})	Porosity	pH	Electrical conductivity (dSm^{-1})	Organic Carbon (%)	Nitrogen (kg ha^{-1})	Phosphorus (kg ha^{-1})	Potassium (kg ha^{-1})
A1 (400-800)	1.29	2.54	49.04	6.90	0.36	1.50	279.41	21.90	187.16
A2 (800-1200m)	1.18	2.34	49.77	6.35	0.54	1.68	287.82	33.60	155.89
A3(1200-1600)	1.11	2.31	51.94	6.40	0.26	1.78	294.71	41.70	151.20
A4(1600-2000m)	1.02	2.22	54.19	6.27	0.27	1.92	308.83	25.50	107.48

This study was supported by the findings of Singh *et al*. (2018), who demonstrated that soil potassium and soil pH decrease with an increase in altitudinal range, whereas soil N, P, soil porosity and SOC increase with an increase in altitudinal range from A1 (365–635 m a msl) to A2 (636–914 m a msl). However, Saeed *et. al*. (2014) found that as elevation increases, the amount of organic carbon in the soil also increases while the soil bulk density decreased. According to Bolstad *et.al.* (2001), this could be because of the texture of the soil,

a consistent intake of carbon with less loss, a drop in microbial and enzymatic activity due to the falling temperature at higher elevations. This study has been additionally supported by Jobbagy and Jackson (2000), Sevgi and Tecimen (2009), Kumar *et al*. (2019), Badia *et al.* (2016), Jeyakumar *et al*. (2020), and Mishra and Francaviglia (2021).

4.3 Variation in fodder quality parameters of populations (Mother trees) of *Grewia optiva* Drummond

A. Variation in fodder quality parameters among the different populations

Variation in fodder quality parameters among the different populations of *G. Optiva* was found significant and presented in Table 4.27. The data illustrated in Table 4.27 and Fig 4.13 revealed that the maximum value of fresh weight of 100 leaves (133.09 g) was recorded for population P9 which was followed by P7, while, population P20 recorded with minimum value of fresh weight of 100 leaves (76.93 g) which was statistically at par with P5, P12 and P19.

It is apparent from Table 4.27 and Fig 4.13 that the population P9 had the maximum dry weight of 100 leaves (66.46 g) which was followed by P7, P9 and P17, whereas, population P5 recorded with minimum dry weight of 100 leaves (40.50 g) which was statistically at par with P6 and P8.

A review of the information presented in Table 4.27 and Fig 4.13 revealed that the population P19 had the highest percentage of leaf dry matter content (65.84 %), while, the population P6 had the lowest percentage (48.91 %). The maximum value of leaf dry matter content was at par with P15 and minimum value was at par with population P7, P8 and P9.

An examination of data appended in Table 4.27 and Fig 4.13 showed that the six populations were found to have crude protein higher than 23.00 %. The population P7 had the highest value for crude protein (24.57 %) which was at par with P1, P2, P10, P15 and P17. The lowest value of crude protein was recorded for P8 (17.00 %) which was statistically at par with P4, P5, P18 and P20.

An appraisal of the data presented in Table 4.27 and Fig 4.13 elucidated that population P18 attained the maximum ether extract percentage (5.09 %), which was at par with P2, P4, P5, P9, P16 and P19. The population P7 recorded with the lowest ether extract content (3.15 %) which was statistically at par with P1, P10, P13 and P20.

Population P12 had the highest amount of crude fibre content (20.92 %) which was statistically at par with P2, P3, P4, P5, P6, P7, P9, P11, P13, P14 and P15. Minimum value of crude fibre was shown in P16 (17.10 %) which was statistically at par with P17 (Table 4.27 and Fig 4.13).

Table 4.27 Variations in fodder quality parameters (of mother trees) among populations of *Grewia optiva* Drummond.

Altitudinal Zone	Populations	Fresh weight of 100 leaves (gm)	Dry weight of 100 leaves (gm)	Leaf dry matter content (%)	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)
A1(400-800m)	P1(Harsar)	101.77	52.62	51.73	24.12	3.73	18.04	12.67	41.45
	P2(SujanpurTihra)	108.91	56.86	52.23	23.95	4.53	19.84	11.92	39.77
	P3(Dramman)	98.76	52.50	53.18	18.50	4.20	20.61	9.94	46.75
	P4(Ghumarwii)	92.50	50.05	52.10	17.76	4.48	19.68	9.65	48.43
	P5(Daggar)	80.64	40.50	50.27	17.02	4.52	19.46	9.74	49.27
A2(800-1200m)	P6 (Kalanjri Devi)	77.69	42.31	48.91	21.53	4.03	20.38	9.73	44.33
	P7 (Sihunta)	126.82	62.47	49.33	24.57	3.15	20.55	12.88	38.85
	P8(Dodar)	86.75	42.72	49.33	17.00	3.98	17.79	10.05	51.20
	P9(Kuthar)	133.09	66.46	49.97	20.05	4.80	20.02	10.06	45.08
	P10(Kutuldi)	112.53	53.37	52.83	23.66	3.69	20.50	12.01	40.14
A3 (1200-1600m)	P11(Awah devi)	102.80	53.00	55.07	20.71	4.00	19.49	11.33	44.47
	P12 (Dharot)	84.46	44.62	55.49	22.97	3.89	20.92	11.00	41.22
	P13(Neri)	99.91	53.22	53.28	21.37	3.72	19.59	11.20	44.13
	P14(Basni)	91.05	51.26	56.32	22.69	3.97	20.89	11.26	41.20
	P15(Jagdhar)	104.47	62.89	61.38	23.06	3.85	20.66	12.85	39.60
A4 (1600-2000m)	P16 (Shogi)	89.22	53.11	59.53	19.85	4.65	17.10	9.65	48.75
	P17 (Sangrah)	106.24	62.73	59.17	24.08	4.04	17.51	11.26	43.12
	P18 (Ghanahatti)	94.70	54.43	55.15	18.18	5.09	17.79	9.42	49.52
	P19 (Garhkhal)	84.75	55.49	65.84	18.75	4.38	19.26	9.67	47.94
	P20 (Ranichauri)	76.93	43.17	55.75	17.47	3.63	17.92	9.82	51.16
Mean		**97.70**	**52.62**	**54.34**	**20.86**	**4.12**	**19.40**	**10.80**	**44.82**
$CD_{0.05}$		**5.93**	**3.32**	**4.44**	**1.49**	**0.75**	**1.63**	**0.79**	**2.66**

A critical rummage of Table 4.27 and Fig 4.13 indicated the highest value of total ash content reported for P7 (12.88 %) which was statistically at par with P1 and P15 whereas, P18 exhibited the lowest value of total ash content (9.42 %) which was statistically at par with P3, P4, P5, P6, P16, P19 and P20. Nitrogen free extract (%) in P8 (51.20%) accounted for the highest value which showed parity with P5, P16, P19 and P20. However, the lowest value of nitrogen free extract was recorded for P7 (38.85 %) which found to be statistically at par with P2 and P15.

B. Altitudinal variations in (mean value) fodder quality parameters (of mother trees) among population of *Grewia optiva* Drummond

An appraisal of Table 4.28 and Fig 4.14 elucidated that populations in the A2 altitudinal zone had the highest mean fresh weight of 100 leaves (107.38 g), while,

populations in the A4 altitudinal zone had the lowest value (90.37 g). The maximum value for dry weight of 100 leaf was observed in the A4 altitudinal zone. These findings are supported by Yang *et al.,* 2022, who demonstrated that leaf fresh weight and dry weight increases considerably with increasing altitude up to 2500 metres above sea level and then decreases gradually. However in our study, the highest fresh weight of 100 leaves was observed in the A2 altitudinal range (800-1200 m a m s l). This may be due to variations in temperature and precipitation along the elevations. The maximum dry weight of 100 leaves was recorded for A4 altitudinal range this could be attributed to decreased soil water content at higher elevations, which could result in increased leaf thickness.

Table 4.28 Altitudinal variations in (mean value) fodder quality parameters (of mother trees) among population of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Fresh weight of 100 leaves (g)	Dry weight of 100 leaves (g)	Leaf dry matter content (%)	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)
A1 (400-800 m)	96.51	48.15	51.90	20.27	4.29	19.52	10.78	37.78
A2 (800-1200 m)	107.38	51.01	50.07	21.36	3.93	19.85	10.94	36.93
A3 (1200-1600 m)	96.54	50.62	56.31	22.06	3.88	20.31	11.53	35.60
A4 (1600-2000 m)	90.37	51.41	59.09	19.67	4.36	17.91	9.96	40.75

The percentage of leaf dry matter content decreased from A1 to A2 altitudinal zone, however, the percentage increased from A2 to A4 altitudinal zone. The populations found in A4 altitudinal zone (1600 to 2000 m a m s l) had the maximum leaf dry matter content (59.09 %), 100 leaf dry weight (59.09 g), ether extract (4.36 %) and nitrogen free extract (40.75 %), while, minimum mean value was reported for crude protein (19.67 %), crude fibre (17.91 %) and total ash (9.96 %). A3 altitudinal zone had the highest mean values for crude protein (22.06 %), crude fibre (20.31 %) and total ash (11.53 %), whereas, lowest mean value was recorded for ether extract (3.88 %) and nitrogen free extract (35.60 %).

A critical component of feeds and fodder is the percentage of leaf dry matter content, which is the fraction of feed that is devoid of water or free of water. To account for the wide range in moisture content of feeds that are frequently fed to cattle, feed values and nutrient requirements for ruminants are expressed on a dry matter or moisture-free basis to evaluate the chemical composition and nutritional value. The average dry matter value obtained in this research is in line with the value reported by Sharma and Negi (1969) in *Grewia oppositifolia*. Thakur *et al*. (2009) while studying on *B. variegata* found that leaf dry matter

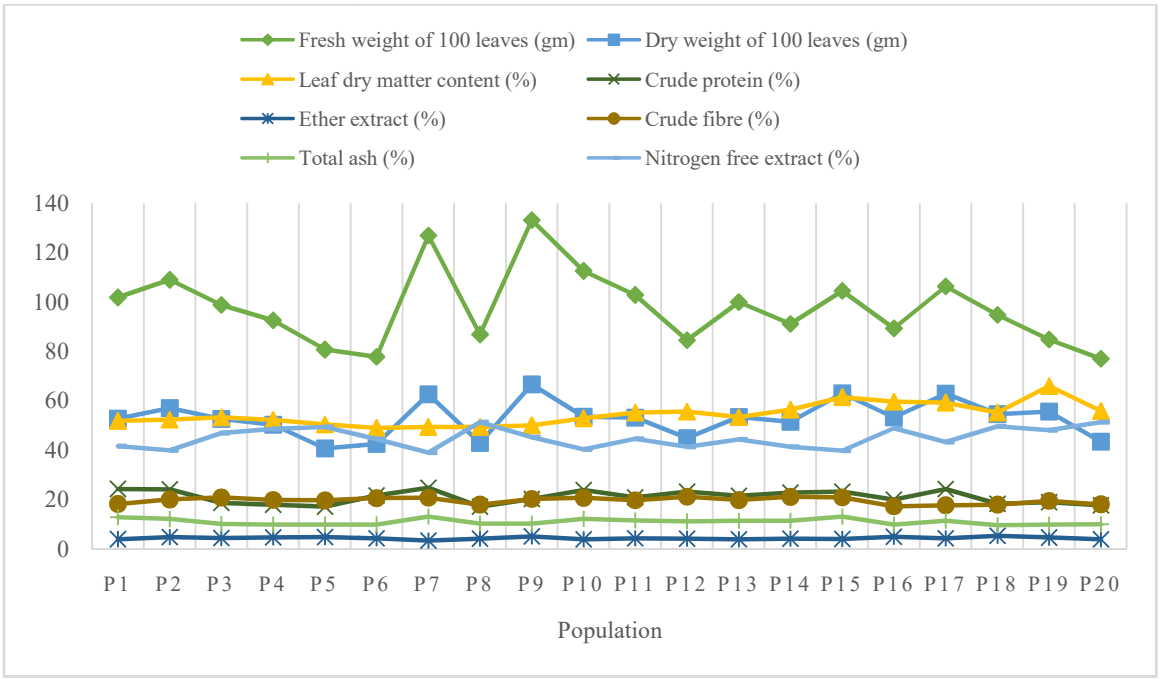


Fig 4.13 Variations in fodder quality parameters (of mother trees) among populations of *Grewia optiva* Drummond

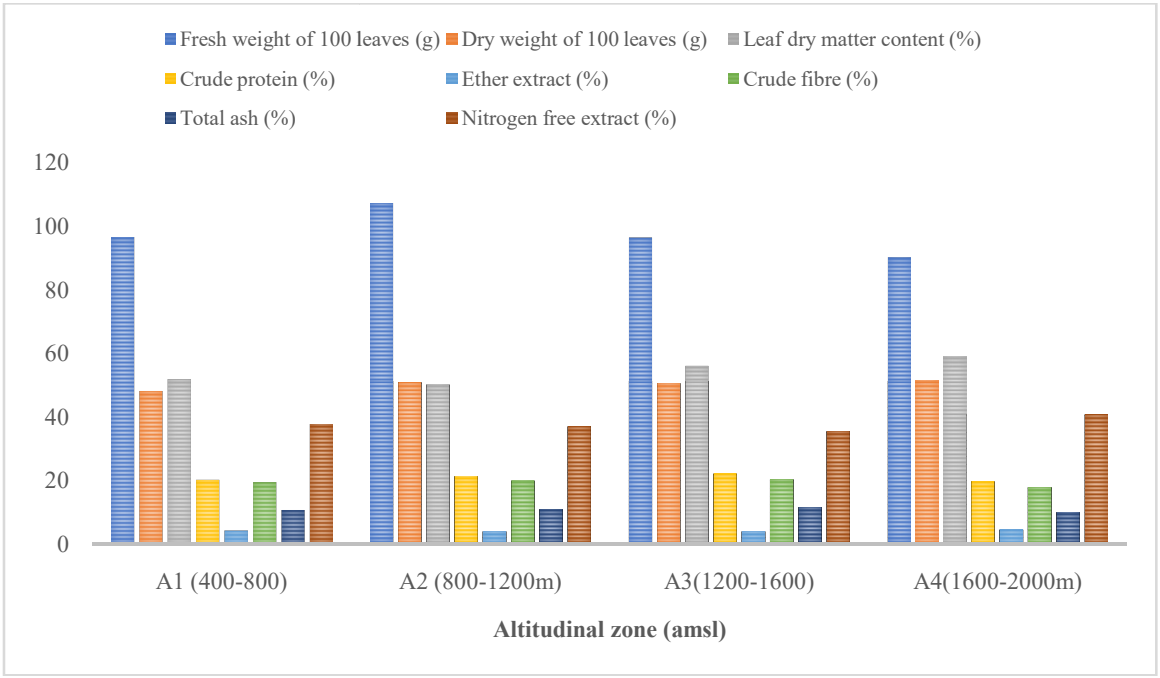


Fig 4.14 Altitudinal variations in (mean value) fodder quality parameters (of mother trees) among population of *Grewia optiva* Drummond

content ranged between 45.98 to 62.73 per cent. Sankhyan *et al.* (2008) conducted a similar study on variation in leaf dry matter content among diameter classes, sites and individual trees of *G. laevigata*. Crude protein value is important since protein contributes energy and provides essential amino acids for rumen microbes as well as the animal itself. The more protein that comes from forage, the less supplement is needed. The amount of crude protein found in the current study was equivalent to the values found by Sidhu *et al*. (1965), Bakshi and Wadhwa (2004), and Osti *et al.* (2006), all of which reported significant variation in *G. optiva* at different altitudes and locations. Gupta (2012) conducted variability experiments in *A. latifolia* and found that the crude protein concentration varied significantly among sites. The difference in crude protein mostly attributable to environmental conditions (Ljones and Landford, 1966; Jaswal, 1992), genetic factors or could be a result of the use of varied levels of nitrogen fertiliser during farming. Ether extract is a concentrated source of metabolizable energy primarily made up of oils, fats, waxes and other lipids. Gupta (2012) conducted a study on different sources of *A. latifolia* and found ether extract ranged between 2.26 (%) to 3.26 (%). The current study showed higher values for ether extract than reported by Singh and Todaria (2012) who showed range between 2.09 (%) to 3.29 (%) in *Q. Semicarpifolia* at various altitudal ranges. Most fodder crops contain cellulose, a complex carbohydrate polymer that is difficult for humans to digest but is a good source of energy for animals, particularly ruminants. The findings of Poonam *et al*. (2012), who observed variation in fibre content (%) during the evaluation of plus tree progenies of *B. variegata* for their forage qualities, lend support to the findings of the present study. In addition, Sankhya *et al*. (2013) investigated comparable outcomes in *A. latifolia.* Singh *et al.* (2010) and Singh and Todaria (2012) conducted studies on *Celtis australis* and *Q. semicarpifolia*, respectively, and discovered variation in crude fibre content between various sites and altitudes. The ash content of a leaf is the inorganic residue that measures the total mineral content of the leaf supply. Hashmi and Waqar (2014) found ash content in *G. optiva* ranging from 8.93% to 14.23%, which supports the current study's results. The present investigation was consistent with studies conducted by Saklani (1999) and Singh and Todaria (2012) on *Quercus leucotrichophora* and *Q. semicarpifolia*, respectively. Their research demonstrates a highly significant inverse relationship between ash concentration and altitude. According to Vitousek and Farrington, 1997; Brady and Weil, 2004 the low temperature may influence soil nutrient availability by reducing soil microbial activities and mineralization rate, which could explain the reduced leaf ash content at higher altitude. Nitrogen free extract (NFE) consist mainly of starch and most of hemi-cellulose. The result of present study on NFE was

comparable to the findings of Sidhu *et al.* (1965) in *G. optiva*, Sankhyan *et al.* (2009) in *G. laevigata* and Gupta (2012) in *A. latifolia.* Similarly to the current study findings, McCreary (1927) found that NFE increased with increasing altitudinal range.

4.4 Variations in mineral nutrients and biochemical estimates (amino acids) among different population of *Grewia optiva* Drummond

A. Variation among populations

Perusal of Table 4.29 showed that maximum value of P was recorded for P4 and P12 (0.32 gm/100 gm) which was statistically at par with P7. The minimum value of P was recorded for P5 (0.16 gm/100 gm) which was statistically at par with P19.

An examination of the data in Table 4.29 revealed that maximum Na content was observed for P5 (612.84 ppm), which was statistically at par with P4. The minimum value of Na was registered for P16 (262.25 ppm), which was statistically at par with P4 and P5.

Table 4.29 showed that P11 had maximum Ca level (4.05 gm/100 gm), which was statistically at par with P9. P14 had minimum Ca content (2.71 gm/100 gm), which was statistically at par with P6.

Table 4.29 Variations in mineral nutrients and amino acids (of mother trees) among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Populations	Phosphorus (gm/100 gm)	Sodium (ppm)	Calcium (gm/100 gm)	Potassium (gm/100 gm)	Total Amino acids (mg/gm)
A1 (400-800 m)	P1(Harsar)	0.25	566.19	3.19	2.54	33.73
	P2(SujanpurTihra)	0.29	468.39	3.38	2.47	31.55
	P3(Dramman)	0.18	518.68	3.08	2.71	25.45
	P4(Ghumarwii)	0.32	604.00	3.40	2.58	25.57
	P5(Daggar)	0.16	612.84	3.10	2.65	25.77
A2(800-1200 m)	P6 (Kalanjri Devi)	0.21	462.46	2.85	2.34	28.82
	P7 (Sihunta)	0.31	553.23	3.25	2.61	35.38
	P8(Dodar)	0.20	440.43	3.09	2.14	25.46
	P9(Kuthar)	0.25	588.62	3.94	2.40	29.99
	P10(Kutuldi)	0.27	508.19	3.24	2.81	32.10
A3 (1200-1600 m)	P11(Awah devi)	0.28	328.27	4.05	2.32	30.30
	P12 (Dharot)	0.32	466.11	3.46	2.38	33.31
	P13(Neri)	0.18	445.48	3.19	2.25	28.54
	P14(Basni)	0.24	522.54	2.71	2.41	31.02
	P15(Jagdhar)	0.29	476.22	3.34	2.21	34.59
A4 (1600-2000 m)	P16 (Shogi)	0.22	262.25	2.98	2.13	28.31
	P17 (Sangrah)	0.24	422.71	3.01	2.26	33.88
	P18 (Ghanahatti)	0.19	331.01	3.00	1.92	26.31
	P19 (Garhkhal)	0.17	439.21	2.93	2.21	27.26
	P20 (Ranichauri)	0.22	396.30	2.99	2.16	25.33
Mean		0.24	470.66	3.21	2.37	29.63
$CD_{0.05}$		0.01	40.85	0.17	0.09	3.26

Data pertaining to variation in K among population showed that the maximum value of K was registered for P10 (2.81 gm/100gm) which was followed by P3, while, minimum value of K was reported for P18 (1.92 gm/100 gm) which was followed by P16, P8 and P20.

The maximum value of amino acids was registered for P7 (35.38 mg/gm), while the lowest was reported in population P20 (25.33 mg/gm) (Table 4.29). Populations P1, P12, P14 and P17 were at par with the maximum value (35.38 mg/gm), while, populations P3, P4, P8, and P19 were at par with the minimum value (25.33 mg/gm) .

B. Altitudinal variations

Altitudinal variations in mineral nutrients (P, Na, K, Ca) and Amino acids among population of *Grewia optiva* Drummond

The observations depicted in Table 4.30 showed that the P, Ca and amino acid content of leaves follow the same trend along an altitudinal gradient. These components increased with an increase in altitude from A1 to A3, whereas, decreased from A3 to A4. Maximum mean values of P (0.26 gm/100 gm), Ca (3.35 gm/100 gm) and amino acids (31.55 mg/gm) were observed for A3 altitudinal zone, while, the minimum value was observed for A4 altitudinal zone. It was clear from Table 4.30 that leaf Na and K showed the same trend along the altitudinal gradient, i.e., both nutrients decreased with an increase in the altitudinal zone. Maximum values for both nutrients, i.e., leaf Na and K, were observed for A1 (554.02 ppm Na and 2.59 gm/100 gm K) and minimums for A4 altitudinal zones.

Table 4.30 Altitudinal variations in Mineral nutrients (P, Na, K, Ca) and Amino acids among populations of *Grewia optiva* Drummond

Altitudinal Zone (a msl)	Phosphorus (gm/100gm)	Sodium (ppm)	Potassium (gm/100gm)	Calcium (gm/100g)	Total Amino acids (mg/gm)
A1 (400-800 m)	0.24	554.02	2.59	3.23	28.41
A2 (800-1200 m)	0.25	510.59	2.46	3.27	30.35
A3 (1200-1600 m)	0.26	447.72	2.31	3.35	31.55
A4 (1600-2000 m)	0.21	370.30	2.14	2.98	28.22

The current research is corroborated by the results of Kaushal (1978), who examined variations in *G. optiva*'s proximate principles and mineral nutrients. The studies by Rathore (1997) in *G. optiva;* Gera *et al.* (2002) in *Dalbergia sissoo*; Wani *et al.* (2009) in *B. variegata,* Sankhyan *et al.* (2009) in *G. laevigata,* Bhat (2010) in *G. optiva* and Bhagta (2015) in *G. optiva* lend support to the present findings. The present study is in line with study conducted by Homeier *et al.,* 2021 who demonstrated variation in leaf P, K, and Ca

content along altitudinal gradients while studying leaf trait variation in species-rich tropical Andean forests.

4.5 Estimation of variability and genetic parameters

Significant differences in morphological growth parameters, leaf morphometric characteristics, seed and seedling parameters, fodder, mineral nutrients and biochemical estimations were reported among populations. As a result, data from several populations was pooled to calculate variability estimates and genetic parameters for various features.

Range, mean, coefficient of variation (standard deviation as a percentage of mean) and coefficients of variability (phenotypic and genotypic) were used to estimate variability, whereas, heritability (broad sense), genetic advance (at 5% selection intensity) and genetic gain (genetic advance as a percentage of the mean) were used to calculate genetic estimates. The results obtained for variability and genetic estimates of different growth parameters had been illustrated and summarised in Tables 4.31–4.37.

Table 4.31 Estimates of mean, range, Coefficient of variance for tree morphological characteristics among populations of *Grewia optiva* Drummond

Sr. No.	Parameters	Mean	Range	CV(%)
1	Tree Height(m)	7.63	5.50-10.50	15.76
2	Tree Diameter(cm)	25.27	20.09-29.82	8.97
3	Crown Spread (N-S)	4.03	2.78-5.52	18.69
4	Crown spread (E-W)	4.00	2.73-5.52	15.87
5	No. of Primary Branches	5.28	3.00-8.00	19.07
6	No. of secondary Branches	9.46	5.00-16.00	22.61
7.	Branch internodal length (cm)	6.25	5.25-7.08	8.61

Variability estimates for the morphological characteristics are provided in Table 4.31. Among different tree morphological characteristics, tree diameter showed the widest range (20.09-29.82 cm), with a mean value of 25.27 cm, followed by tree height (5.5-10.5 m, mean 7.63 m), no. of secondary branches (5-16, mean 9.46), branch nodal length (5.25-7.08 cm, mean 6.25 cm), no. of primary branches (3-8, 5.28), crown spread (N-S) (2.78-5.52 m, mean 4.03 m), crown spread (E-W) (2.73-5.52 m, mean 4 m). The number of secondary branches showed the highest coefficient of variation (22.61 %), but the branch nodal length showed the minimum value of coefficient of variation (8.61%).

Table 4.32 Estimates of mean, range, coefficient of variation, heritability, genetic advance and genetic gain for leaf morphometric and seed characteristics among populations of *Grewia optiva* Drummond

Parameters	Mean	Range	Coefficient of Variation		Heritability (%)	Genetic Advance	Genetic gain (%)
			Genotypic	Phenotypic			
Leaf length (cm)	12.40	10.10-17.44	18.37	21.59	72.33	3.99	32.18
Leaf width (cm)	9.01	5.98-10.87	13.91	16.17	73.96	2.22	24.64
Leaf area (cm^2)	87.52	60.52-128.15	24.41	25.18	94.00	42.68	48.76
Petiole length (cm)	0.99	0.90-1.14	6.89	11.55	35.63	0.08	8.48
Seed length (cm)	5.64	4.88-6.31	8.61	11.82	53.15	0.73	12.94
Seed width (mm)	4.61	3.92-5.11	8.73	11.53	57.34	0.63	13.62
Seed thickness (mm)	4.68	3.45-5.47	12.40	15.05	67.95	0.99	21.06
100 seed weight (gm)	10.84	6.96-14.07	21.96	23.36	88.43	4.61	42.54

Among all the leaf and seed parameters in Table 4.32, leaf area showed the widest range of values (60.52-128.15 cm^2, mean 12.40 cm^2), followed by leaf length (10.10-17.44 cm, mean 12.40 cm) and the narrowest range showed by petiole length (0.90-1.14 cm, mean 0.99 cm).

The study of genetic variability parameters (Table 4.32) revealed that the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all of the traits under consideration. In most characters, a small difference existed between PCV and GCV, indicating that they were very stable to environmental pressure, implying that environmental effect was very low and that phenotypic performance of traits might be utilised as a criteria for selection. Genetic parameters allow for the identification of the action nature of participating genes as well as the evaluation of the efficacy of various selection methods and strategies (Cruz *et al*., 2014).

The high value of phenotypic coefficient of variation (PCV) was recorded for leaf length (21.59 %), leaf width (16.17 %), leaf area (25.18 %), seed thickness (15.05 %), 100 seed weight (23.36 %), whereas moderate phenotypic coefficient of variation (PCV) was observed for petiole length (11.55 %), seed length (11.82 %), seed width (11.53 %) (Table 4.32).

The high Genotypic coefficient of variation (GCV) was observed for leaf length (18.37 %), leaf area (24.41 %) and 100 seed weight (21.96 %) while moderate genotypic coefficient of variation was noted for leaf width (13.91 %), seed thickness (12.40 %). Minimum genotypic coefficients of variation (GCV) observed for petiole length (6.89 %), seed length (8.61 %), seed width (8.73).

It is clear from Table 4.32 that the highest heritability with the highest genetic advance was observed for leaf area. The estimates of heritability (broad sense) varied from 35.63-94.00 per cent for different characters under study. The highest value of heritability was observed for leaf area (94.00 %) followed by 100 seed weight (88.43%), leaf width (73.96 %), leaf length (72.33 %), seed thickness (67.95), seed width (57.34 %), seed length (53.15 %). Minimum heritability was recorded for Petiole length (35.63 %). Maximum genetic advance (42.68) and genetic gain (48.76%) were recorded for leaf area, while the minimum genetic advance (0.084) and genetic gain (8.48%) were documented for petiole length. Genetic gain (expressed as a percentage of the mean) was observed with the range from low to high for the studied traits. High genetic gain was recorded for leaf area (48.76 %), leaf length (32.18 %), leaf width (24.64 %), 100 seed weight (42.54 %) and seed thickness (21.04 %). The moderate genetic gain was registered for seed length (12.94%) and seed width (13.62%), whereas, low genetic gain was registered for petiole length.

Table 4.33. Estimates of mean, range, coefficient of variation, heritability, genetic advance and genetic gain for seed germination characteristics among populations of *Grewia optiva* Drummond

Parameters	Mean	Range	Coefficient of Variation (%)		Heritability (h^2 bs) (%)	Genetic Advance	Genetic gain (%)
			Genotypic	Phenotypic			
Germination percentage (%)	66.04	41.67-84.17	22.97	24.70	86.46	29.06	44.00
Germination value	10.31	3.23-19.03	61.30	67.41	82.69	11.83	114.82
Germination Energy	47.63	25.00-73.33	37.67	41.21	83.54	33.78	70.93
Germination Index	43.30	25.25-57.08	21.94	27.44	63.92	15.65	36.13
Survival Percentage (%)	88.74	75.97-98.03	7.30	9.30	61.64	10.48	11.81

A careful analysis of Table 4.33 revealed that the survival percentage showed the largest range of values (75.97-98.03 %, with a mean of 88.74 %) This was followed by the germination percentage (41.67-84.17 %, with a mean of 66.04 %), the germination energy (25.00-73.33, with a mean of 47.63), the germination index (25.25-57.08 %, with a mean of 43 per cent.

According to the findings that were compiled in Table 4.33 and related to seed germination characteristics, the phenotypic coefficient of variation was found to be significantly larger than the genotypic coefficient of variation. Germination value showed the highest value of phenotypic coefficient of variation (PCV) (67.41 %) and genotypic

coefficient of variation (GCV) (61.30 %), while survival percentage showed the lowest values of both phenotypic coefficient of variation (PCV) (7.30 %) and genotypic coefficient of variation (GCV) (9.30 %).

Table 4.33 showed the estimates of heritability (broad sense) that varied from 61.64-86.46 per cent for different characters under study. It was found to be high for germination percentage (86.46 %) and minimum for survival percentage (61.64 %). Genetic advance varied from (10.48-33.78), with the maximum value observed for germination energy and the minimum for survival percentage. Genetic gain as per cent of mean varied from (11.81-114.82 %) for all germination characters under study. The highest value observed for germination value and minimum for survival percentage.

Estimates of mean, range, coefficient of variation, heritability, genetic advance, and genetic gain for growth characteristics of 18 months old seedlings are shown in Table 4.34. Critical analysis of Table 4.34 revealed that the highest range observed for seedling height was 58.43–107.37 cm with a mean value of 79.78 cm, followed by leaf area (52.90-67.03 cm^2, mean 59.61 cm^2), collar diameter (6.09–12.11 mm, mean 8.65 mm), internodal length (3.91-6.86 cm, mean 5.56 cm) and petiole length (0.72-1.1 cm, mean 0.83 cm).

Table 4.34 Estimates of mean, range, coefficient of variation, heritability, genetic advance and genetic gain for 18 months old seedling growth characteristics among populations of *Grewia optiva* Drummond

Parameters	Mean	Range	Coefficient of Variation (%)		Heritability (h^2 bs) (%)	Genetic Advance	Genetic gain (%)
			Genotypic (GCV)	Phenotypic (PCV)			
Seedling Height (cm)	79.78	58.43-107.37	21.84	23.62	85.54	33.20	41.61
Collar diameter (mm)	8.65	6.09-12.11	21.90	25.97	71.07	3.29	38.03
Internodal length (cm)	5.56	3.91-6.86	17.60	19.93	78.02	1.78	32.03
Petiole length (cm)	0.83	0.72-1.10	11.19	12.17	84.58	0.18	21.21
Leaf area (cm^2)	59.61	52.90-67.03	7.95	12.05	43.47	6.43	10.79

Persual of Table 4.34 showed that the phenotypic coefficient of variation (PCV) was found higher than the genotypic coefficient of variation for every seedling growth trait. High values of the phenotypic coefficient of variation (PCV) were observed for collar diameter (25.98 %), seedling height (23.62 %), and internodal length (19.93 %), while petiole length (12.17 %) and leaf area (112.05 %) exhibited moderate PCV. As far as the genotypic coefficient of variation (GCV) is concerned, collar diameter (21.90 %), seedling height

(21.84 %) and internodal length (17.60 %) were observed with high GCV. Petiole length exhibited a moderate GCV (11.19 %), while leaf area exhibited the lowest GCV (7.9 5%).

Table 4.34 demonstrated that among all seedling growth characteristics, height had the highest heritability and the highest genetic advance and gain. The observed heritability (in the broad sense) for various seedling growth traits varied between 43.47 and 85.54 per cent. High heritability (> 80%) was observed for seedling height (85.54 %) and petiole length (84.58 %), whereas moderate heritability was observed for collar diameter (71.07 %) and internodal length (78.02 %), and the lowest heritability range was observed for leaf area (43.47 cm^2).

It is evident from Table 4.34 that the highest genetic advance was recorded for seedling height (33.20), whereas, other seedling growth characteristics, including collar diameter (3.29), internodal length (1.78), petiole length (0.18) and leaf area (6.43) had low genetic advance. High genetic gain as a percentage of the mean was recorded for seedling height (41.61 %), collar diameter (38.03 %), and internodal length (21.20 %), while, it was moderate for leaf area (10.79 cm^2).

Table 4.35 Estimates of mean, range, coefficient of variation, heritability, genetic advance and genetic gain for 18 months old seedling's leaf fodder and mineral characteristics among populations of *Grewia optiva* Drummond

Parameters (Progeny	Mean	Range	Coefficient of Variation (%)		Heritability (h^2 bs) (%)	Genetic Advance	Genetic gain (%)
			Genotypic (GCV)	Phenotypic (PCV)			
Crude Protein (%)	21.04	18.20-23.40	6.84	8.78	60.63	2.31	10.97
Ether extract (%)	3.30	2.99-3.83	8.61	11.54	55.60	0.44	13.22
Crude fibre (%)	17.31	15.55-18.91	2.85	7.95	12.88	0.37	2.11
Total ash (%)	9.20	8.10-10.10	6.81	8.35	66.42	1.05	11.43
Nitrogen Free Extract (%)	49.18	46.23-54.46	4.04	5.92	46.58	2.79	5.68
Leaf P (g/100gm)	0.23	0.19-0.28	13.92	16.09	74.86	0.06	24.81
Leaf Na(ppm)	337.91	255.73-423.27	16.23	18.86	74.11	97.28	28.79
Leaf K(g/100gm)	2.08	1.86-2.14	5.40	5.96	82.17	0.21	10.09
Leaf Ca(g/100gm)	2.36	2.35-3.12	11.40	11.67	95.40	0.65	22.94

The assessment of Table 4.35 revealed that among the leaf fodder and mineral nutrient characteristics of 18 months old seedlings, a wide range was observed for leaf Na

(255.73-423.27 ppm, mean 337.91 ppm), followed by nitrogen-free extract (46.25-54.46 %, mean 49.18 %), crude protein (18.20-23.40 %, mean 21.04 %) and crude fibre (15.55-18.91 %, mean 17.31 %). Minimum range was observed for leaf P (0.19–0.28 %, mean 0.19 %).

Table 4.35 demonstrated that phenotypic coefficient of variation (PCV) values were higher than genotypic coefficient of variation (GCV). Both coefficients of variation, i.e., PCV and GCV, were recorded in the range of low to high for all of the documented characteristics. Leaf P (11.54 %) and leaf Na (18.86 %) had a high PCV. The phenotypic coefficient of variation was moderate for ether extract (11.54 %) and leaf Ca (11.67 %), whereas it was low for crude protein (8.78 %), crude fibre (7.95 %), total ash (8.35 %), nitrogen-free extract (5.92 %) and leaf K (5.96 %). High GCV observed for leaf Na (255.73-423.27 %), moderate GCV for leaf P (13.9 2%) and leaf Ca (11.40 %) and low GCV for crude protein (6.84 %), ether extract (8.61 %), crude fibre (2.85 %), total ash (6.81 %), nitrogen-free extract (4.04 %), and leaf K (5.40 %).

The heritability (broad sense) was observed in Table 4.35 ranged from 12.88 to 95.40 per cent. High heritability was observed for leaf K (82.17 %) and leaf Ca (95.40 %), whereas moderate heritability was observed for crude protein (60.63 %), ether extract (55.60 %), total ash (66.42 %), leaf P (74.86 %) and leaf Na (74.11 %). The heritability of crude fibre (12.88 %) and nitrogen-free extract (46.5%) was found to be low. In addition, leaf Na exhibited a high genetic advance (97.28) and a high genetic gain (28.79 %).

Critical examination of Table 4.36 showed that among leaf fodder and mineral nutrient characteristics of different populations (mother trees) of *G. optiva, a* wide range was observed for leaf fresh weight (76.93–133.09 g, mean 97.70), followed by leaf dry matter content (48.91–65.84 %, mean 54.34 %), leaf dry weight (40.50-66.46 g, mean 52.69 g), crude protein (17.00–24.57 %, mean 20.86 %), crude fibre (17.10–20.92 %, mean 19.40 %), and total ash (9.42–12.88 %, mean 10.80 %).

Table 4.36 illustrated that the recorded PCV values were higher than the GCV. For all the characters under examination, both PCV and GCV were recorded in the low to high range. Leaf fresh weight (18.22 %), leaf dry weight (16.62 %), crude protein (15.33 %), and ether extract (16.70 %) all showed high PCV. Low PCV was seen for crude fibre (8.98 %), while, moderate PCV was seen for leaf dry matter content (10.57 %), total ash (13.30 %), and nitrogen free extract (11.06 %). Leaf fresh weight (17.71 %) and leaf dry weight (16.00%)

both showed high GCV. Crude protein (14.47 %), ether extract (10.70 %), total ash (12.27 %) and nitrogen free extract (10.23 %) all displayed intermediate GCV values, however leaf dry matter content (8.86 %) and crude fibre (6.58 %) displayed low values.

Table 4.36 Estimates of mean, range, coefficient of variation, heritability, genetic advance and genetic gain for leaf fodder characteristics among different populations of *Grewia optiva* Drummond

Parameters	Mean	Range	Coefficient of Variation (%)		Heritability (%)	Genetic Advance	Genetic gain (%)
			Genotypic	Phenotypic			
Leaf fresh weight (g)	97.70	76.93-133.09	17.71	18.23	94.46	34.64	35.46
Leaf dry weight(g)	52.69	40.50-66.46	16.01	16.62	92.84	16.74	31.78
Leaf dry matter content (%)	54.34	48.91-65.84	8.86	10.57	70.26	8.31	15.30
Crude Protein (%)	20.86	17.00-24.57	14.47	15.33	89.11	5.87	28.14
Ether extract (%)	4.12	3.15-5.09	10.70	16.70	41.01	0.58	14.11
Crude fibre (%)	19.40	17.10-20.92	6.58	8.98	53.61	1.92	9.92
Total ash (%)	10.80	9.42-12.88	12.27	13.30	85.12	2.52	23.33
Nitrogen Free Extract (%)	44.82	38.85-51.2	10.23	11.06	85.60	8.74	19.50

Table 4.36 showed that for leaf fresh weight, leaf dry weight, crude protein and total ash, there was strong heritability (in the broad sense) and high genetic gain as per cent of mean. Heritability was found to range from 41.01 to 94.46%. Leaf fresh weight (94.46%), leaf dry weight (92.84%), crude protein (89.11%), total ash (85.11%), and nitrogen free extract (85.60%) all showed high heritability (>80%). Leaf dry matter content (70.26), crude fibre (53.61), and ether extract (41.04%) all showed moderate heritability.

Table 4.36 reported that high genetic advance was observed for leaf fresh weight (34.64) and moderate for leaf dry weight (16.74), while, another leaf dodder characteristics reported with low genetic advance. Genetic gain (as per cent of mean) reported high for leaf fresh weight (35.46 %), leaf dry weight (31.78 %), crude protein (28.14 %) and total ash (23.33 %). Minimum genetic gain was observed for crude fibre (9.921 %).

Probing analysis of Table 4.37 showed that among mineral nutrients and biochemical estimates (amino acids) of populations (mother trees) large range observed for leaf Na (262.25-612.84 ppm, with mean 470.66 ppm) followed by amino acids (25.33-35.38 mg/gm,

29.63 mg/gm), leaf Ca (2.71-4.05 gm/100 gm, mean 3.21 gm), leaf K (1.92-2.81 gm/100gm, mean 2.37 gm/100 gm), leaf P (0.16-0.32 gm/100 gm, mean 0.24 gm/100 gm).

All the mineral nutrients and amino acids showed high PCV values than GCV. High PCV and GCV examined for leaf P (PCV:24.17 %, GCV:24.00 %) and leaf Na (PCV:23.60 %, GCV:22.79 %) and moderate PCV recorded for leaf K (PCV:11.19 %, GCV:11.08), leaf Ca (PCV:12.29 %, GCV: 11.69%) and amino acids (PCV:14.79 %, GCV: 12.59%).

Table 4.37 Estimates of mean, range, coefficient of variation, heritability, genetic advance and genetic gain for leaf mineral nutrients and amino acids characteristics (of mother trees) among populations of *Grewia optiva* Drummond

Parameters	Mean	Range	Coefficient of Variation (%)		Heritability (%)	Genetic Advance	Genetic gain (%)
			Genotypic	Phenotypic			
Leaf P (gm/100 gm)	0.24	0.16-0.32	24.00	24.17	98.66	0.12	49.12
Leaf Na (ppm)	470.66	262.25-612.84	22.79	23.60	93.26	213.42	45.34
Leaf K(gm/100 gm)	2.37	1.92-2.81	11.08	11.19	94.51	0.52	21.79
Leaf Ca(gm/100 gm)	3.21	2.71-4.05	11.69	12.29	90.42	0.73	22.90
Amino acids (mg/gm)	29.632	25.33-35.38	12.59	14.79	72.48	6.54	22.09

A deep appraisal of Table 4.37 illustrated that High heritability with high genetic advance observed for leaf Na. Heritability (broad sense) observed in range between 72.48-98.66 %. High heritability recorded for leaf P (98.66 %), leaf Na (93.26 %), leaf K (94.51 %), leaf Ca (90.42 %), whereas, moderate observed for amino acids (72.48 %). High genetic advance noted for leaf Na (213.42) and other characters reported with low genetic advance. All the characters under study showed high genetic gain as per cent of mean i.e., leaf P (49.12 %), leaf Na (45.34 5), leaf K (21.79 %), leaf Ca (22.90 %) and amino acids (22.09 %).

Variations are the differences observed due to a particular trait. These differences are either genotypic or environmental and both factors combined reflect phenotypic effect (Jain, 1982). It is necessary to determine the extent of variation in a species and whether it is attributable to genetic or environmental factors in order to properly utilise observed variation. The knowledge of variation in the desirable characteristics and their correlation is critical for any breeding effort (Johnson *et al.,* 1955). As a result, a species with a large range of variability (in terms of parameter values and variance, coefficient of variation) provides

adequate opportunity for screening for the required features. Heritability and other genetic parameters signify the utility of variability in advanced breeding programmes. Heritability provides a measure of genetic variation, upon which all the possibilities of changing the genetic composition of the species depend. In other words, knowledge of its magnitude gives an idea about the scope for affecting genetic improvement, through selection, etc., while, genetic gain gives the relative measurements of change produced by selection in mean genetic level of the species. This is the mean genotypic value for a particular trait of the selected individuals in relation to the entire population. In the current investigation, the wide ranges (Tables 4.31-4.37) observed for different characteristics in variability estimation showed the presence of a significant amount of variation among the selected populations. The results are consistent with those reported by Jaswal (1992), Gupta (1993), Rathore (1997) in *G. optiva*, Kumar and Tokey (1996) in *Albizia lebbeck*, Bhat *et al.* (2018) in *G. optiva.* Johnson *et al.,* (1955) discovered that a high heritability estimate combined with a high genetic gain is usually more useful than a high heritability estimate alone in predicting the resultant effect of selecting the best individuals; thus, a high heritability estimate does not always imply a higher genetic advance. Kundal *et al.,* 2020 reported similar findings in their work on half-sib progeny evaluation of *Toona ciliata*. The relationship between a trait's heritability and genetic advance assists breeders in anticipating the performance of those traits in future generations, as well as their response to selection.

4.6 Correlation studies

4.6.1 Correlation between tree, leaf morphometeric characteristics and physiochemical characteristics of soil

Karl Pearson's correlation coefficients (at 5% level of significance) for tree and leaf morphometric characteristics (of different populations of *G. optiva*) and physiochemical characteristics of soil were worked out. It was evident from Table 4.38 and Fig 4.15 that leaf area showed a significant positive correlation with soil N (0.509), SOC (0.407), soil P (0.728), and soil K (0.577). Leaf length showed a highly significant correlation with SOC (0.401), soil N (0.509), soil P (0.710), and soil K (0.592). The tree height (0.385), tree diameter (0.602), crown spread (N-S) (0.629), crown spread (E-W) (0.334), branch nodal length (0.436) and leaf width (0.470) showed a significant positive correlation with soil P. Soil K showed a significant positive correlation with tree height (0.774), tree diameter (0.645), crown spread (N-S) (0.576), crown spread (E-W) (0.314), branch nodal length (0.737) and leaf width (0.592).

Table 4.38 Karl Pearson's correlation between tree and leaf morphometric characters and physiochemical characteristics of the soil

Parameters	TH	TD	CS(E-W)	CS(N-S)	NPB	NSB	BNL	LL	LW	LA	PL	BD	PD	Porosity	SoilpH	EC	OC	Soil N	Soil P	Soil K
TH	1																			
TD	0.747**	1																		
CS(E-W)	0.300	0.533**	1																	
CS(N-S)	0.602	0.728	0.588**	1																
NPB	0.362	0.445	0.396	0.512**	1															
NSB	-0.178	0.026	0.442	0.065	0.215	1														
BNL	0.851	0.816	0.460	0.628	0.452	-0.016	1													
LL	0.512	0.623	0.298	0.605	0.522	0.230	0.572	1												
LW	0.383	0.531	0.090	0.294	0.517	0.236	0.513	0.562	1											
LA	0.581	0.732	0.358	0.610	0.541	0.332	0.655	0.944	0.665	1										
PL	0.362	0.456	0.281	0.495	0.534	0.400	0.503	0.867	0.534	0.852	1									
BD	0.361	0.273	0.348	0.257	-0.079	-0.155	0.291	0.136	-0.232	0.138	0.084	1								
PD	0.508	0.328	0.119	0.123	-0.023	-0.357	0.476	0.237	0.024	0.246	0.221	0.669	1							
Porosity	-0.179	-0.165	-0.380	-0.268	0.080	-0.003	-0.103	-0.043	0.307	-0.038	0.013	-0.903	-0.286	1						
SoilpH	0.225	0.221	0.078	0.037	0.028	0.008	0.416	0.135	0.449	0.148	0.282	-0.067	0.229	0.214	1					
EC	0.038	-0.042	0.105	-0.009	0.294	-0.011	0.154	0.046	-0.069	0.003	0.359	0.201	0.229	-0.145	0.328	1				
OC	0.062	0.192	0.178	0.273	0.127	0.217	-0.017	0.401**	0.169	0.407**	0.260	-0.120	-0.310	-0.018	-0.312	-0.433	1			
Soil N	0.129	0.230	0.220	0.464**	0.226	0.291	0.147	0.525**	0.202	0.509**	0.434**	-0.297	-0.350**	0.182	0.018	-0.244	0.770	1		
Soil P	0.385**	0.602**	0.334**	0.629**	0.429**	0.049	0.436**	0.710**	0.470**	0.728**	0.607**	-0.064	0.088	0.130	0.236	0.010	0.522	0.738	1	
Soil K	0.774**	0.645**	0.314**	0.576**	0.289	-0.043	0.737**	0.458**	0.592**	0.577**	0.287	0.277	0.356**	-0.149	0.284	-0.232	0.174	0.229	0.437	1

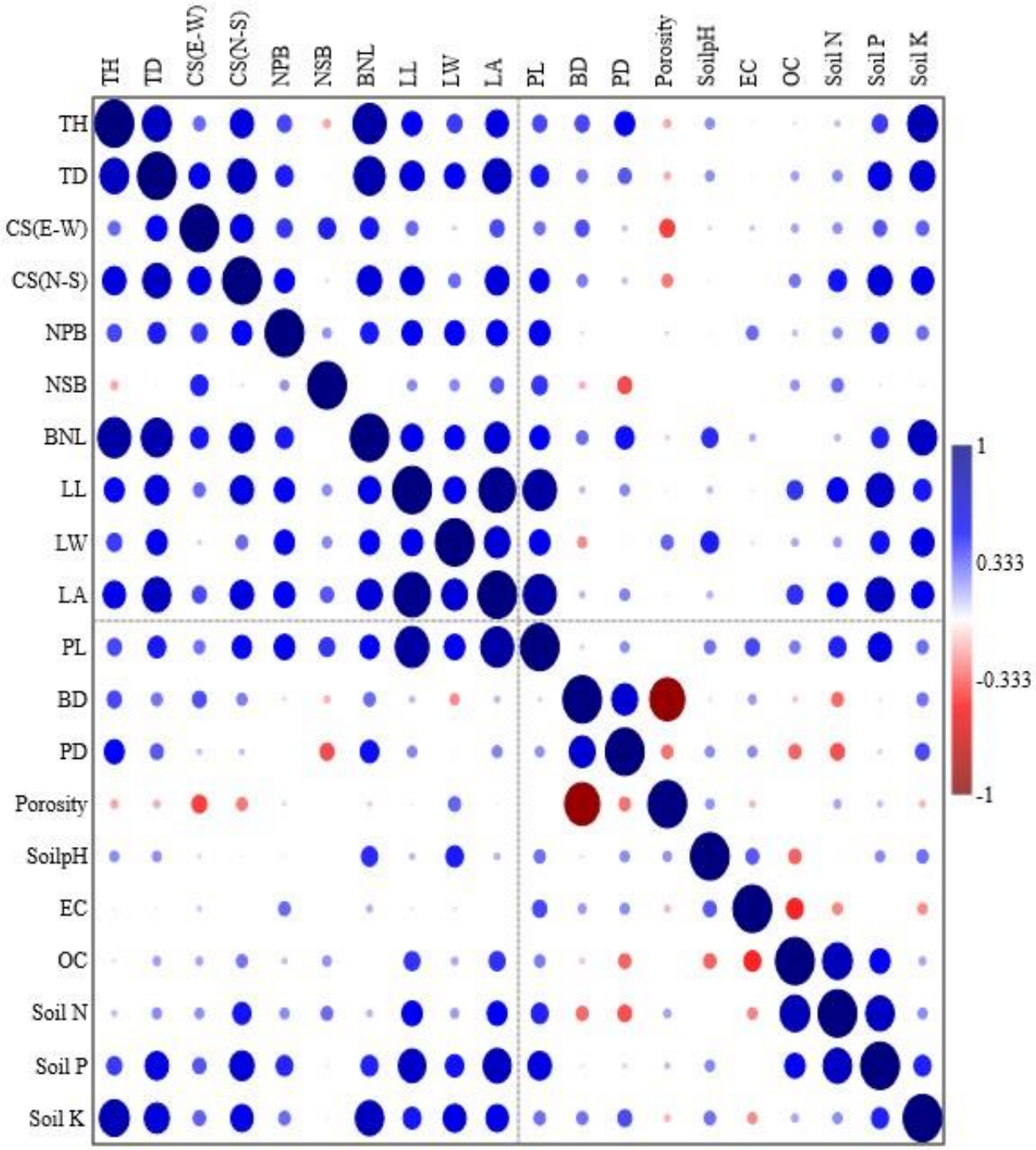
**5% level of Significance, where TH-tree height, TD-tree diameter, CS-crown spread, NPB-number of primary branches, NSB-number of secondary branches, BNL-branch nodal length, LL-leaf length, LW-leaf width, LA-leaf area, PL-petiole length, BD-bulk density, PD-particle density, EC-electrical conductivity, OC-organic carbon, N-nitrogen, P-phosphorus, K-potassium

4.6.2 Correlation between leaf fodder and mineral nutrients characters (of mother trees) with physiochemical characteristics of the soil.

Table 4.39 and Fig 4.16 demonstrated that a significant positive correlation developed between leaf dry matter (LDM) and SOC (0.361), leaf dry matter and soil N (0.341), and leaf dry matter and soil K (0.310), while leaf dry matter exhibited a negative correlation with bulk density (-0.351) and particle density (-0.556). Crude protein developed significant positive correlation with SOC (0.411), soil N (0.575) and soil P (0.821). Positive correlation observed between total ash and SOC (0.379), total ash and soil N (0.496), total ash and soil K (0.347). There was highly significant correlation observed between total ash and soil P (0.808). The nitrogen-free extract was significantly negatively correlated with soil pH (-0.315), soil organic carbon (-0.373), soil N (-0.541), soil P (-0.799) and soil K (-0.442).

It is clear from looking at Table 4.39 and Fig 4.16 that there was a correlation observed between the mineral and nutritional content of the leaf and the physiochemical properties of the soil. Phosphorus, one of the features of leaf minerals and nutrients, had a positive and substantial connection with SOC (0.458) and soil P (0.547). There was found to be a positive association between the K levels in the soil and those in the leaf (0.650). There was shown to be a positive correlation between the leaf amino acids and the soil N (0.627), as well as the leaf amino acids and the soil P (0.840).

To estimate soil nutrient status and prescribe fertilizers, soil physiochemical parameters including organic carbon, accessible N, P, K, pH, electrical conductivity and bulk density must be known (Sumithra, 2013). pH indicates the soil's nutrient balance, while, electrical conductivity indicates its quantity. (Smith, 1996). Trees respond to rising CO_2 levels by using soil nutrients (Schleppi *et al*., 2019). The C cycle and nutrient cycles, especially N and phosphorus P, will determine whether terrestrial ecosystems, forests, and cropland trees are CO_2 sources or sinks (Ellsworth *et al*., 2017). Nitrogen (N), a component of amino acids, proteins, genetic materials, pigments and other vital organic molecules, is one of the most important biological elements for plants, agricultural crops and forest trees (Chen *et al*., 2014; Ji *et al*., 2015; Liu *et al*., 2018). Plant organ construction, metabolism, fruit yield and fruit tree quality depend on N (Bai *et al*., 2016). K is needed for photosynthesis, fruit quality, flowering and disease prevention (Valente *et al*., 2012), it activates dozens of critical enzymes, including protein synthesis, sugar transport, N and C metabolism and photosynthesis.



**5% level of Significance, where TH-tree height, TD-tree diameter, CS-crown spread, NPB-number of primary branches, NSB-number of secondary branches, BNL-branch nodal length, LL-leaf length, LW-leaf width, LA-leaf area, PL-petiole length, BD-bulk density, PD-particle density, EC-electrical conductivity, OC-organic carbon, N-nitrogen, P-phosphorus, K-potassium

Fig 4.15 Correlation between tree, leaf morphometeric characteristics and physiochemical characteristics of soil

Table 4.39 Karl Pearson's Correlation between leaf fodder and mineral nutrients characters (of mother trees) with physiochemical characteristics of the soil

Parameters	LDM	CP	EE	CF	TA	NFE	Leaf P	Leaf Na	Leaf K	Leaf Ca	Amino acids	BD	PD	Porosity	SoilpH	EC	OC	Soil N	Soil P	Soil K
LDM	1																			
CP	0.030	1																		
EE	0.117	-0.491	1																	
CF	-0.186	0.335	-0.275	1																
TA	-0.024	0.853	-0.644	0.328	1															
NFE	0.031	-0.948	0.478	-0.590	-0.875	1														
Leaf P	-0.111	0.554	-0.308	0.371	0.581	-0.609	1													
Leaf Na	-0.478	0.107	-0.161	0.532	0.218	-0.278	0.192	1												
Leaf K	-0.445	0.274	-0.288	0.572	0.326	-0.417	0.271	0.733	1											
Leaf Ca	-0.218	0.103	0.070	0.233	0.234	-0.215	0.530	0.109	0.173	1										
Leaf AA	0.094	0.945	-0.487	0.307	0.874	-0.910	0.627	0.128	0.205	0.234	1									
BD	-0.351	-0.113	-0.235	0.198	0.203	-0.019	0.097	0.461	0.472	0.134	-0.106	1								
PD	-0.556	0.028	-0.018	0.087	0.251	-0.115	0.078	0.560	0.547	0.156	-0.018	0.671	1							
Porosity	0.133	0.159	0.301	-0.222	-0.117	-0.036	-0.091	-0.276	-0.295	-0.092	0.124	-0.902	-0.285	1						
SoilpH	-0.146	0.315	0.191	0.191	0.101	-0.315**	0.360**	0.213	0.290	0.009	0.205	-0.050	0.235	0.201	1					
EC	-0.367	0.103	-0.181	0.170	0.039	-0.110	0.056	0.061	0.049	-0.234	0.051	0.209	0.228	-0.145	0.349	1				
OC	0.361**	0.411**	-0.143	0.036	0.379**	-0.373**	0.277	-0.174	0.015	0.304	0.447**	-0.123	-0.307	-0.018	-0.312	-0.437	1			
Soil N	0.341**	0.575**	-0.159	0.127	0.496**	-0.541**	0.458**	0.018	-0.002	0.110	0.627**	-0.296	-0.349	0.182	0.020	-0.249	0.770	1		
Soil P	0.088	0.821**	-0.460**	0.261	0.808**	-0.799**	0.547**	0.264	0.335**	0.143	0.840**	-0.063	0.085	0.130	0.245	0.006	0.521	0.738	1	
Soil K	0.310**	0.281	-0.106	0.489**	0.347**	-0.423**	0.307**	0.587**	0.650**	0.293	0.202	0.273	0.351	-0.149	0.291	-0.231	0.174	0.229	0.437	1

**significant at 5% level of significance, where; LDM-Leaf dry matter, Cp-crude potein, EE-ether extract, CF-crude fiber, TA-total ash, NFE-nitrogen free extract, P-phosphorus, Na-sodium, K-potassium, Ca-calcium, AA-amino acids, BD-bulk density, PD-particle density, EC-electricle conductivity, N-nitrogen, P-phosphorus, K-potassium

Various tree growth functions require P (Jonard *et al*., 2015; Becquer *et al.,* 2014). The findings of the current study are corroborated by the results of Bhandari (1992) and Awasthi *et al*. (1998), in their study they reported a significant positive correlation between leaf and soil samples. In addition, Paoli *et al.* (2007), Muche *et al.* (2015) and Kumar *et al*. (2016) provide their support for this investigation.

4.6.3 Correlation between tree morphological and leaf morphometric characteristics of populations of *Grewia optiva* Drummond.

Table 4.40 and Fig 4.17 exhibited a positive and statistically significant correlation between tree height and tree diameter (0.618), tree height and crown spread (N-S) (0.441), tree height and number of primary branches (0.320). A highly positive and significant correlation was observed between tree height and branch nodal length (0.722). The number of secondary branches had a negative correlation with the tree height (-0.129). There was a significantly strong positive correlation between leaf area and leaf length (0.872), leaf area and leaf width (0.543). There was a positive correlation between tree diameter and crown spread (E-W) (0.375), tree diameter and crown spread (N-S) (0.414). There was also a positive correlation observed between tree diameter and the number of primary branches (0.375), between tree diameter and branch nodal length (0.625) and between tree diameter and leaf area (0.626).

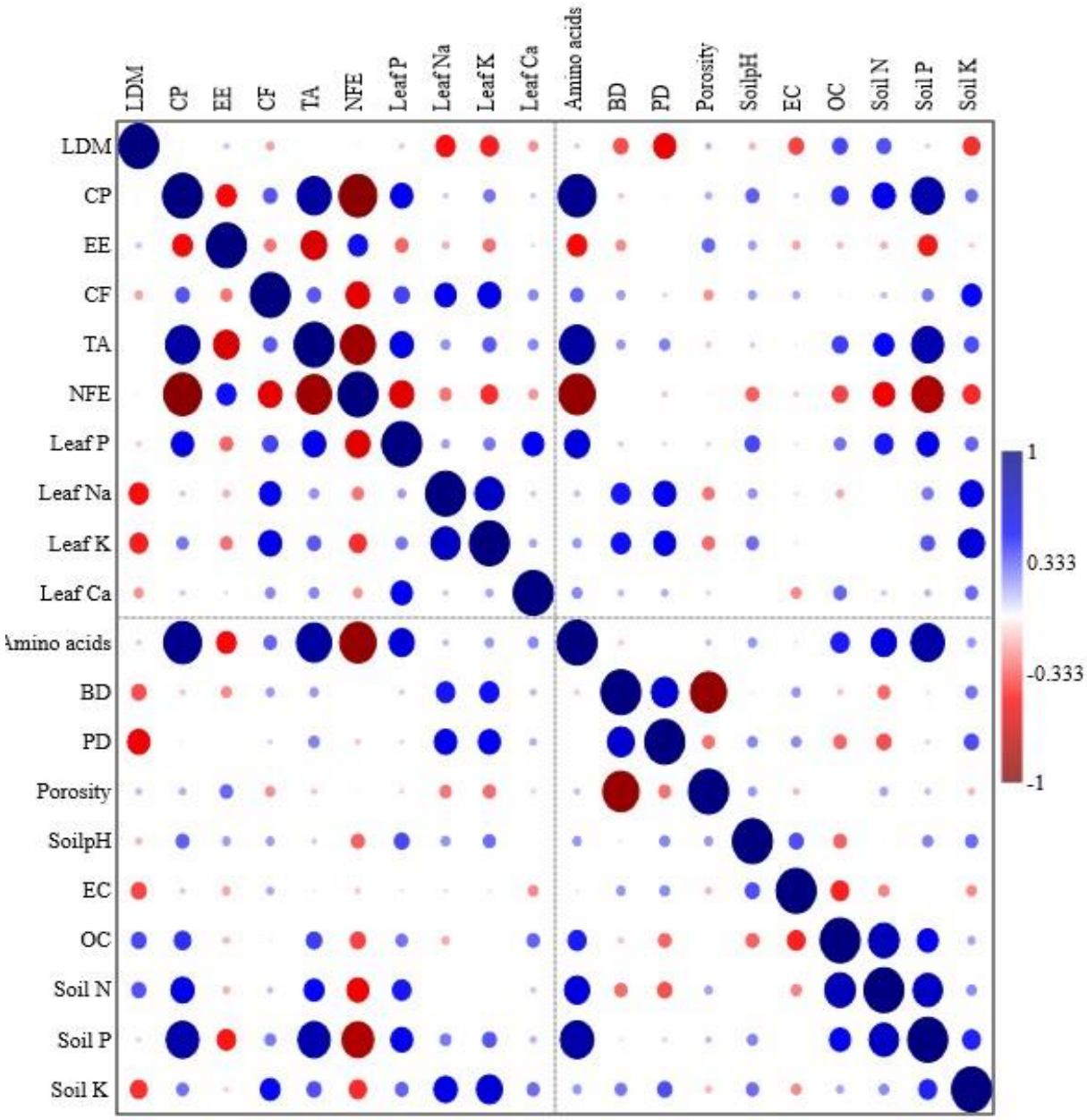
Table 4.40 Karl Pearson Correlation between tree morphological and leaf morphometric characteristics among populations of *Grewia optiva* Drummond

Parameters	TD	CS(E-W)	CS(N-S)	NPB	NSB	BNL	LL	LW	LA	PL	TH
TD	1										
CS(E-W)	0.327**	1									
CS(N-S)	0.414**	0.376**	1								
NPB	0.375**	0.264	0.329**	1							
NSB	0.069	0.348**	0.084	0.164	1						
BNL	0.625**	0.279	0.446**	0.317**	-0.006	1					
LL	0.460**	0.189	0.426**	0.435**	0.139	0.432**	1				
LW	0.373**	0.060	0.240	0.405**	0.165	0.325	0.384	1			
LA	0.626**	0.294	0.442**	0.491**	0.275	0.491**	0.872**	0.543**	1		
PL	0.289	0.147	0.297	0.374**	0.305	0.182	0.556**	0.325**	0.557**	1	
TH	0.618**	0.232	0.441**	0.320**	-0.129	0.722**	0.383**	0.342**	0.500**	0.211	1

** 5 % level of Significance

Where; TH-Tree height, TD-Tree diameter, CS(E-W)-Crown spread East-West, CS(N-S)- Crown spread North-South, NPB-No. of Primary branches, NSB-no. of Secondary branches, BNL-Branch nodal length, LL-Leaf length, LW-leaf width, LA-leaf area, PL-Petiole length

The correlation coefficient among the different characters was also worked out at phenotypic and genotypic levels (Table 4.41). In general, the genotypic correlation was



**significant at 5% level of significance, where; LDM-Leaf dry matter, Cp-crude potein, EE-ether extract, CF-crude fiber, TA-total ash, NFE-nitrogen free extract, P-phosphorus, Na-sodium, K-potassium, Ca-calcium, AA-amino acids, BD-bulk density, PD-particle density, EC-electricle conductivity, N-nitrogen, P-phosphorus, K-potassium

Fig 4.16 Correlation between leaf fodder and mineral nutrients characters (of mother trees) with physiochemical characteristics of the soil

higher in magnitude than phenotypic correlation coefficient. A perusal of the Table 4.41 revealed that tree height exhibited a highly significant and positive genotypic and phenotypic correlation with tree diameter (rg: 0.802, rp:0.625) and branch nodal length (rg: 939, rp:723). There was non-significant and negative correlation observed between tree height and number of secondary branches (rg:-0.193,rp:-0.141). Leaf length and leaf area exhibited a highly significant and positive genotypic and phenotypic correlation (rg: 0.978, rp: 0.873), whereas, leaf width demonstrated a highly significant and positive genotypic correlation and a significant positive correlation with leaf area (rg: 0.721, rp: 0.544). Leaf area expressed highly significant positive genotypic and significant positive phenotypic correlation with tree diameter (rg:0.779, rp:0.628). Tree diameter showed significant and positive phenotypic and genotypic correlation with crown spread (E-W) (rg: 0.637, rp:0.334). Tree diameter showed highly significant positive genotypic and significant positive phenotypic correlation with crown spread (N-S) (rg:0.927, rp:0.418). Crown spread (N-S) was shown to have a highly significant positive genotypic association and a significantly positive phenotypic connection with crown spread (E-W) (rg: 0.739, rp: 0.366).

Table 4.41 Genotypic and Phenotypic correlation between tree morphological and leaf morphometric characteristics among populations of *Grewia optiva* Drummond

		DBH	CS(E-W)	CS(N-S)	PB	SB	BNL	LL	LW	LA	PL	TH
DBH	g	**1**										
	p	**1**										
CS(E-W)	g	0.637**										
	p	0.334**										
CS(N-S)	g	0.927**	0.739**									
	p	0.418**	0.366**									
PB	g	0.476**	0.457**	0.619**								
	p	0.377**	0.277*	0.339**								
SB	g	0.005NS	0.490**	0.057NS	0.236*							
	p	0.072NS	0.355**	0.083NS	0.165NS							
BNL	g	0.940**	0.578**	0.764**	0.534**	-0.020NS						
	p	0.627**	0.284*	0.450**	0.317**	-0.014NS						
LL	g	0.704**	0.356**	0.723**	0.561**	0.270*	0.660**					
	p	0.461**	0.187NS	0.427**	0.438**	0.145NS	0.435**					
LW	g	0.604**	0.094NS	0.364**	0.582**	0.259*	0.647**	0.657**				
	p	0.374**	0.064NS	0.244*	0.404**	0.169NS	0.326**	0.384**				
LA	g	0.779**	0.387**	0.714**	0.560**	0.349**	0.754**	0.978**	0.721**			
	p	0.628**	0.296	0.446**	0.494**	0.288**	0.496**	0.873**	0.544**			
PL	g	0.589**	0.384**	0.683**	0.695**	0.487**	0.783**	0.624**	0.701**	0.681**		
	p	0.290**	0.172NS	0.316**	0.370**	0.308**	0.182NS	0.566**	0.326**	0.567**		
TH	g	0.802**	0.336**	0.704**	0.376**	-0.193NS	0.939**	0.570**	0.410**	0.608**	0.461**	
	p	0.625**	0.224*	0.439**	0.326**	-0.141NS	0.723**	0.385**	0.345**	0.506**	0.222*	

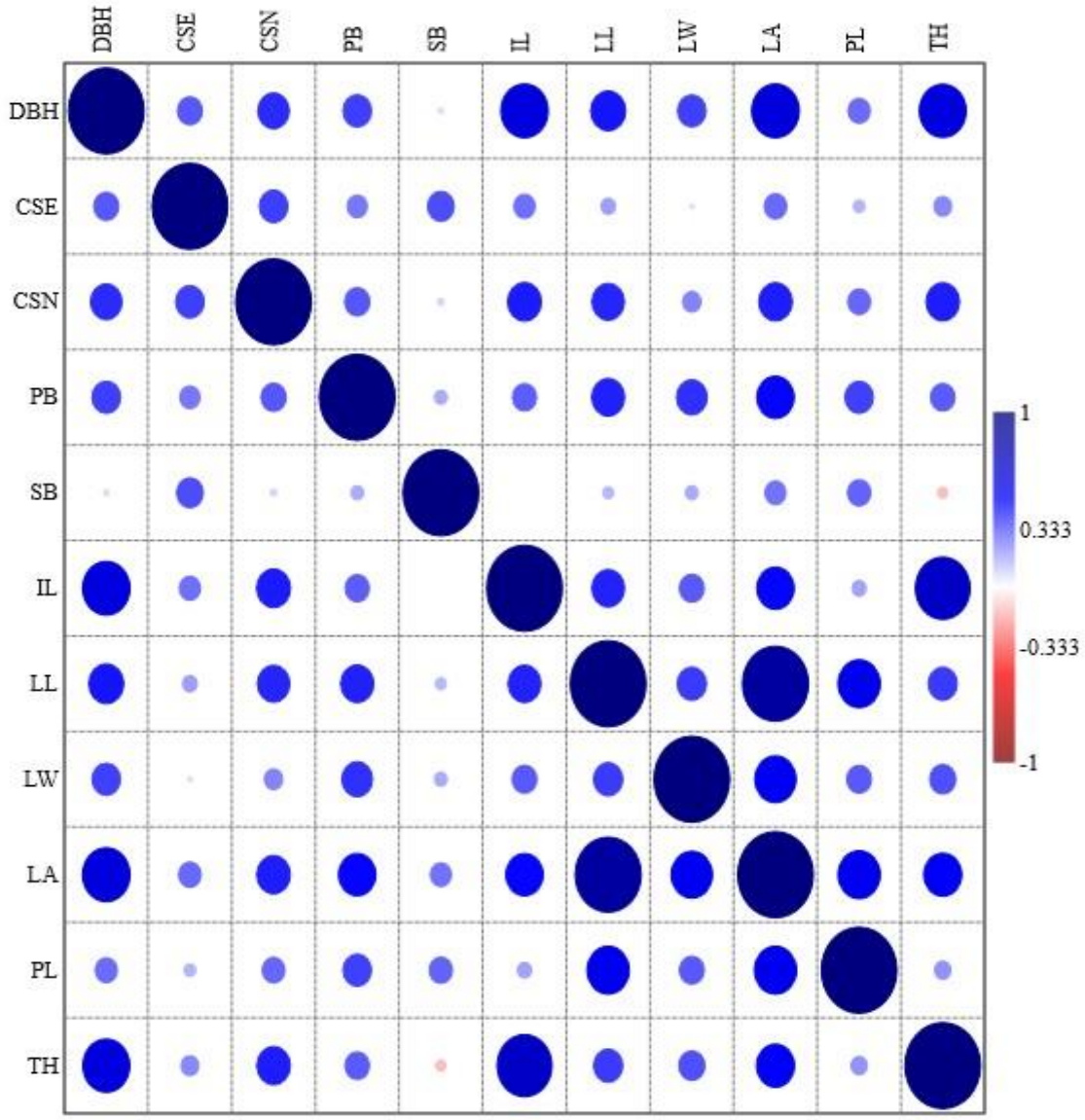
**5% level of Significance; Where, DBH-Tree diameter, CS-Crown spread, PB-Number of primary branches, SB-Number of secondary branches, BNL-Branch nodal length, LL-Leaf length, LW-Leaf width, LA-leaf area, PL-petiole length, TH-Tree height

4.6.4 Correlation between seed, germination and seedling growth characteristics

Table 4.42 and Fig 4.18 showed Karl Pearson's correlation coefficients for seed, germination and seedling growth characteristics. There was a substantial positive association between 100 seed weight and seed length (0.316), 100 seed weight and seed width (0.397), and 100 seed weight and seed thickness (0.449). 100 seed weight also showed significantly positive correlation with germination value (0.908), germination energy (0.644), germination percentage (0.652) and survival percentage (0.609). There was highly significant correlation between seedling height and collar diameter (0.929), seedling height and intermodal length (0.884). Seedling height correlated significantly positive with leaf area (0.718). A highly significant correlation reported between germination percentage and survival percentage (0.766), germination percentage and germination value (0.908), germination percentage and germination energy (0.870).

The correlation coefficient between the seed, germination and seedling growth characteristics was calculated at both the phenotypic and genotypic levels (Table 4.43). In general, the genotypic correlation coefficient was greater than the phenotypic correlation coefficient. It is clear from Table 4.43 that there was significant and positive phenotypic and genotypic correlation observed between seed thickness and seed length (rg: 0.690, rp:0.351), seed thickness and 100 seed weight (rg: 0.654, rp: 0.445), 100 seed weight and seed width (rg: 0.460, rp: 0.355), germination percentage and seed thickness (rg: 0.486, rp: 0.353), germination percentage and seed width (rg: 0.604, rp: 0.369), germination value and seed thickness (rg: 0.464, rp: 0.330), germination value and seed width (rg: 0.530, rp: 0.340), survival percentage and seed thickness (rg:0.484, rp: 0.333), seed length and survival percentage (rg: 0.556, rp: 0.426).

Critical analysis of Table 4.43 depicted that there was highly significant genotypic and significant phenotypic correlation observed between seed thickness and seed width (rg: 0.728, rp:0.392), seed width and seed length (rg: 0.777, rp: 0.464), seed length and 100 seed weight (rg: 0.958, rp: 0.592), germination percentage and seed length (rg: 0.876, rp: 0.655), 100 seed weight and germination percentage (rg: 0.842, rp: 0.670), germination value and seed length (rg: 0.964, rp: 0.653), germination value and 100 seed weight (rg: 0.853, rp: 0.671), germination value and germination percentage (rg: 0.943, rp: 0.907), germination energy and seed length (rg: 0.937, rp: 0.585), germination energy and 100 seed weight (rg: 0.817, rp: 653), germination energy and germination percentage (rg: 0.938, rp:0.873), germination energy and germination value (rg: 0.995, rp: 0.967), survival percentage and 100



**5% level of Significance; Where, DBH-Tree diameter, CS-Crown spread, PB-Number of primary branches, SB-Number of secondary branches, BNL-Branch nodal length, LL-Leaf length, LW-Leaf width, LA-leaf area, PL-petiole length, TH-Tree height

Fig 4.17 Correlation between tree morphological and leaf morphometric characteristics of populations of *Grewia optiva* Drummond.

Table 4.42 Karl Pearson's Correlation between seed, germination and seedling growth characteristics among populations of *Grewia optiva* Drummond

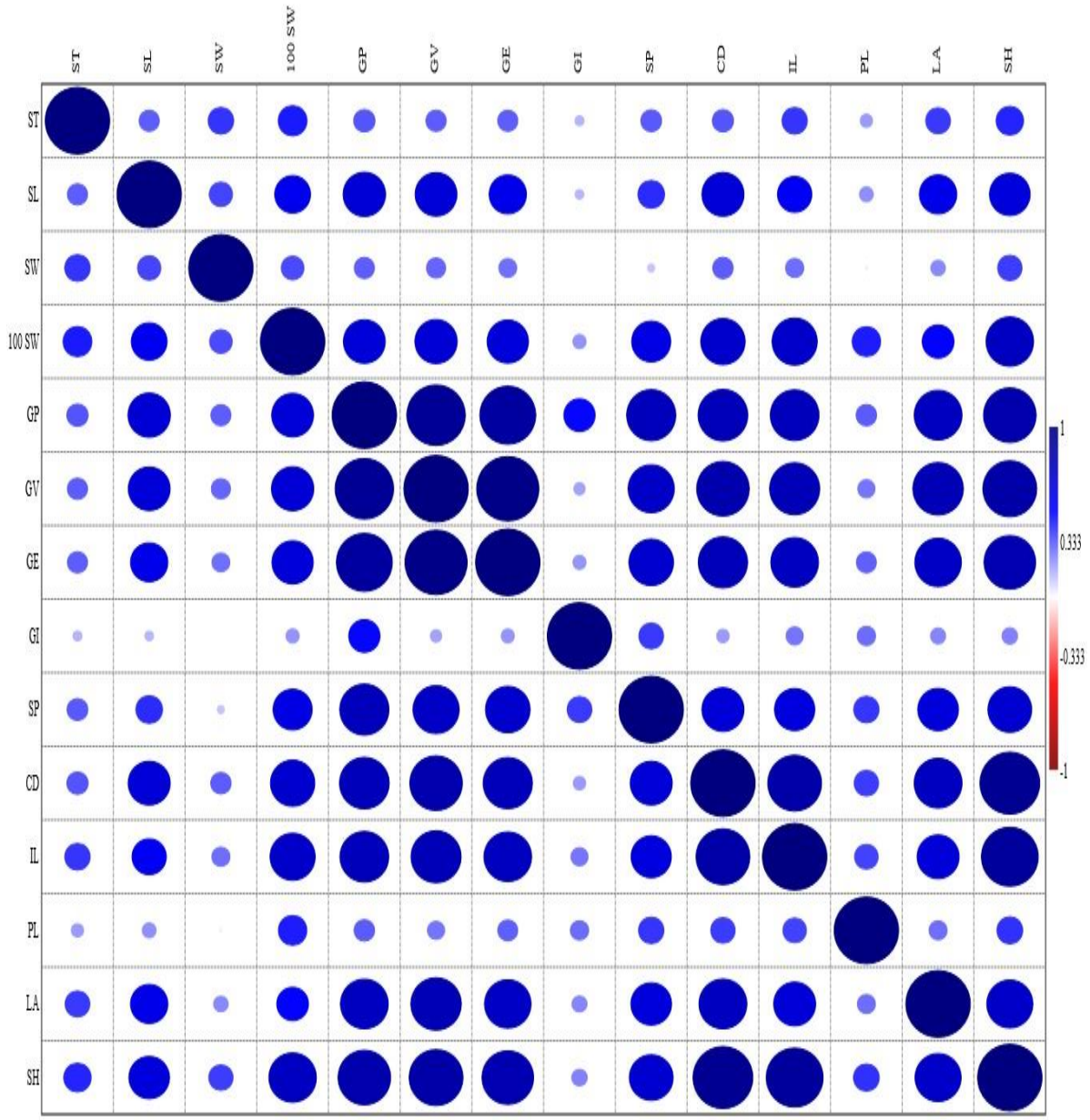
Parameters	Seed thickness (mm)	Seed length (mm)	Seed width (mm)	100 Seed weight (gm)	Germination Percentage (%)	Germination Value	Germination energy	Germination index	Survival percentage (%)	Collar Diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (Cm^2)	Seedling height (cm)
Seed thickness(mm)	1													
Seed length (mm)	0.316	1												
Seed width (mm)	0.397	0.364	1											
100 Seed weight (gm)	0.449**	0.558**	0.353	1										
Germination Percentage (%)	0.333	0.661*8	0.314	0.652**	1									
Germination Value	0.316	0.652**	0.300	0.659**	0.908	1								
Germination energy	0.315	0.581	0.280	0.644**	0.870	0.966**	1							
Germination index	0.145	0.139	0.004	0.210	0.488	0.180	0.207	1						
Survival percentage (%)	0.325	0.415	0.115	0.609**	0.766**	0.719	0.695	0.386	1					
Collar Diameter (mm)	0.332	0.655	0.318	0.691	0.773	0.818	0.767	0.198	0.655	1				
Internodal length (cm)	0.396	0.534	0.284	0.704	0.759	0.779	0.743	0.269	0.628	0.837	1			
Petiole length (cm)	0.195	0.219	0.036	0.444	0.320	0.270	0.312	0.287	0.395	0.381	0.368	1		
Leaf area (cm^2)	0.386	0.583	0.230	0.495	0.744	0.785	0.725	0.237	0.634	0.746	0.654	0.282	1	
Seedling height (cm)	0.428**	0.633**	0.379	0.740**	0.819	0.838	0.804	0.245	0.682	0.929**	0.884**	0.402	0.718**	1

**Significant at 5% level of Significance

Table 4.43 Genotypic and Phenotypic Correlation between seed and seedling growth characteristics among populations of *Grewia optiva* Drummond

		ST	SL	SW	100 SW	GP	GV	GE	GI	SP	CD	IL	PL	LA	SH
ST	**g**	1													
	p	1													
SL	**g**	0.690**	1												
	p	0.351**	1												
SW	**g**	0.728**	0.777**	1											
	p	0.392**	0.464**	1											
100 SW	**g**	0.654**	0.958**	0.460**	1										
	p	0.445**	0.592**	0.355**	1										
GP	**g**	0.486**	0.876**	0.604**	0.842**	1									
	p	0.353**	0.655**	0.369**	0.670**	1									
GV	**g**	0.464**	0.964**	0.530**	0.853**	0.943**	1								
	p	0.330**	0.653**	0.340**	0.671**	0.907**	1								
GE	**g**	0.462**	0.937**	0.522**	0.817**	0.938**	0.995**	1							
	p	0.328**	0.585**	0.312**	0.653**	0.873**	0.967**	1							
GI	**g**	0.315**	0.425**	0.212NS	0.373**	0.460**	0.183NS	0.241*	1						
	p	0.167NS	0.112NS	0.040NS	0.224*	0.475**	0.165NS	0.197NS	1						
SP	**g**	0.484**	0.556**	0.422**	0.942**	0.974**	0.960**	0.959**	0.490**	1					
	p	0.333**	0.426**	0.128NS	0.615**	0.769**	0.719**	0.696**	0.381**	1					
CD	**g**	0.561**	0.916**	0.610**	0.955**	0.843**	0.904**	0.907**	0.176NS	0.923**	1				
	p	0.342**	0.646**	0.373**	0.706**	0.777**	0.825**	0.777**	0.196NS	0.669**	1				
IL	**g**	0.600**	0.883**	0.416**	0.880**	0.834**	0.873**	0.868**	0.258*	0.938**	0.950**	1			
	p	0.398**	0.541**	0.307**	0.708**	0.773**	0.788**	0.750**	0.282*	0.638**	0.840**	1			
PL	**g**	0.240*	0.402**	0.029NS	0.525**	0.431**	0.399**	0.467**	0.473**	0.624**	0.498**	0.513**	1		
	p	0.177NS	0.272*	-0.000NS	0.444**	0.349**	0.291**	0.338**	0.323**	0.408**	0.404**	0.382**	1		
LA	**g**	0.670**	0.774**	0.596**	0.698**	0.994**	0.789**	0.820**	0.213NS	0.753**	0.969**	0.931**	0.465**	1	
	p	0.406**	0.573**	0.276*	0.508**	0.743**	0.785**	0.723**	0.224*	0.638**	0.749**	0.659**	0.319**	1	
SH	**g**	0.644**	0.915**	0.593**	0.901**	0.854**	0.898**	0.891**	0.217NS	0.920**	0.991**	0.956**	0.487**	0.985**	1
	p	0.436**	0.629**	0.425**	0.750**	0.823**	0.843**	0.811**	0.245*	0.691**	0.928**	0.886**	0.420**	0.721**	1

5% level of Significance, where, ST-Seed thickness, SL-Seed length, SW-Seed width, 100 SW-100 seed weight, GP-Germination percentage, GV-Germination value, GE-Germination energy, GI-Germination index, SP-Survival percentage, CD-Collar diameter, IL-Internodal length, PL-Petiole length, LA-Lefa area, SH-Seedling height.



5% level of Significance, where, ST-Seed thickness, SL-Seed length, SW-Seed width, 100 SW-100 seed weight, GP-Germination percentage, GV-Germination value, GE-Germination energy, GI-Germination index, SP-Survival percentage, CD-Collar diameter, IL-Internodal length, PL-Petiole length, LA-Lefa area, SH-Seedling height.

Fig 4.18 Correlation between seed, germination and seedling growth characteristics

seed weight (rg: 0.942, rp: 0.615), survival percentage and germination percentage (rg: 0.974, rp: 0.769), survival percentage and germination value (rg: 0.960, rp: 719), survival percentage and germination energy (rg: 0.959, rp: 696), collar diameter and survival percentage (rg: 0.923, rp: 0.669), collar diameter and germination percentage (rg: 0.843, rp: 0.777), leaf area and collar diameter (rg: 0.969, rp: 0.749), seedling height and 100 seed weight (rg: 0.901, rp: 0.750), seedling height and germination percentage (rg: 0.854, rp: 0.823), seedling height and survival percentage (rg: 0.920, rp: 0.691), seedling height and collar diameter (rg: 0.991, rp: 0.928), seedling height and leaf area (rg: 0.985, rp: 0.721). Similar studies on Karl Pearson correlation, genotypic and phenotypic correlation between different tree and seed growth characteristics were conducted by Srivastava (1995) in *B. variegata,* Gupta (1993) in *G. optiva,* Manga and Sen, (1998) in *Prosopis cineraria*, Neelannavar *et al.* (2009) in *Albizia lebbeck,* Bhatt (2010) and Bhagta (2015) in *G. optiva.*

Table 4.44 Karl Pearson correlation between leaf fodder and nutrient characteristics of 18 months old seedlings of twenty selected population of *Grewia optiva* Drummond

Parameters	Crude fibre (%)	Ether extract (%)	Total ash (%)	Nitrogen free extract (%)	Phasphorus (P) (gm/100gm)	Calcium (Ca) (gm/100gm	Sodium (Na) (gm/100gm	Pottasium (K) (gm/100gm)	Crude protein (%)
Crude fibre (%)	1								
Ether extract (%)	0.074	1							
Total ash (%)	0.110	-0.089	1						
Nitrogen free extract (%)	-0.523	0.035	-0.657	1					
Phasphorus (P) (gm/100gm)	0.148	-0.148	0.466**	-0.523	1				
Calcium (Ca) (gm/100gm	-0.027	0.107	0.136	-0.184	0.279	1			
Sodium (Na) (gm/100gm	0.268	-0.082	-0.001	0.010	-0.013	-0.239	1		
Pottasium (K)(gm/100gm)	0.075	-0.148	0.369**	-0.280	0.268	0.237	0.031	1	
Crude protein (%)	0.066	-0.045	0.692**	-0.863	0.566**	0.275	-0.203	0.262	1

A perusal of Table 4.44 and Fig 4.19, which showed Karl Pearson correlation between leaf fodder and nutrient characteristics of 18-month-old progeny of twenty selected populations of *G. optiva* revealed a significant and positive correlation between crude protein and leaf P (0.566). Total ash showed a significant and positive correlation with leaf P (0.466), leaf K (0.369) and crude protein (0.692).

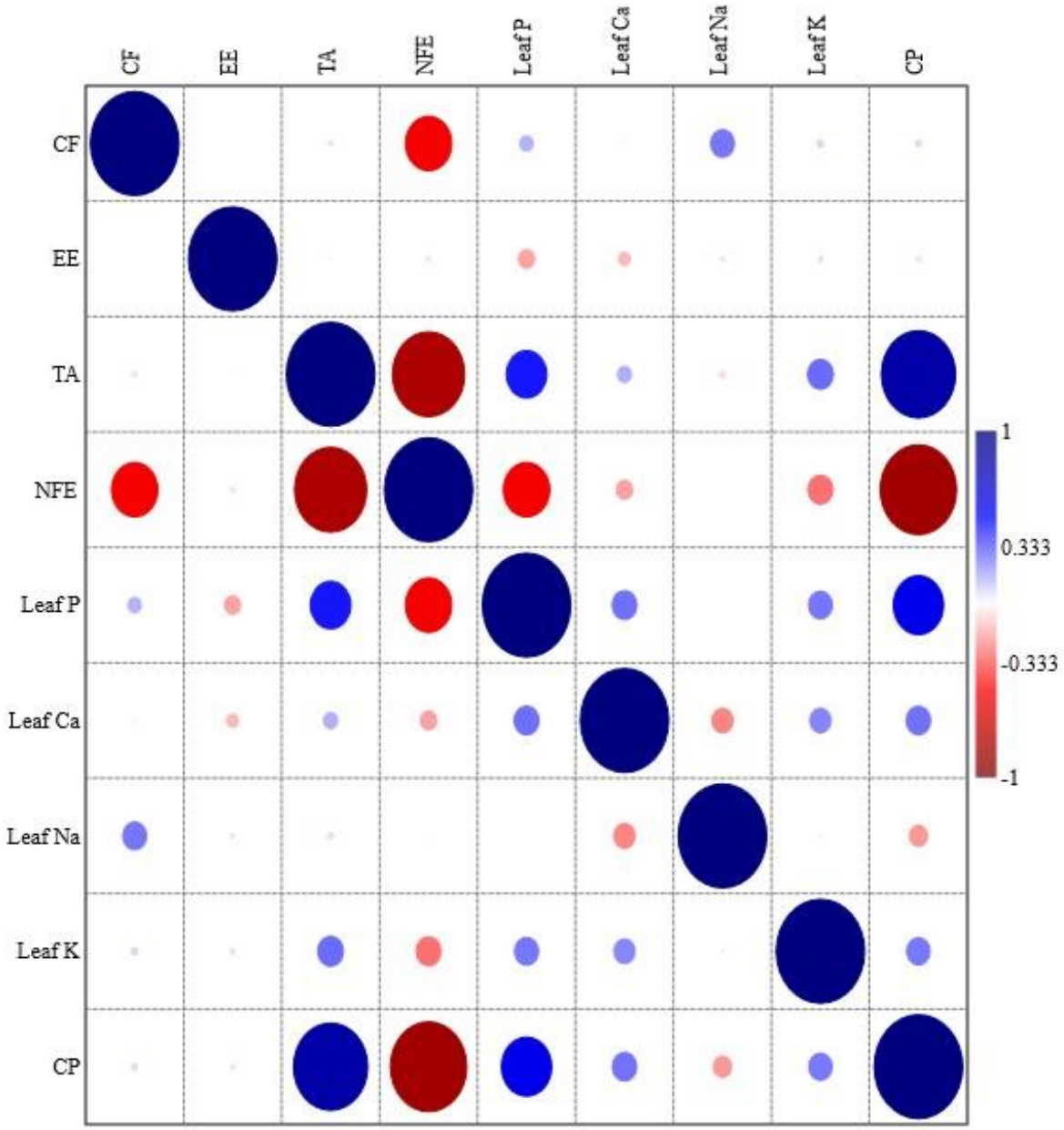
Table 4.45 Genotypic and Phenotypic Correlation between leaf fodder and nutrient characteristics of 18 months old seedlings of twenty selected population of *Grewia optiva* Drummond

Parameters		Crude fibre (%)	Ether extract (%)	Total ash (%)	Nitrogen free extract (%)	Phasphorus (P) (gm/100gm)	Calcium (Ca) (gm/100gm	Sodium (Na) (gm/100gm	Pottasium (K)(gm/100gm)	Crude protein (%)
Crude fibre (%)	g	1								
	p	1								
Ether extract (%)	g	-0.051NS	1							
	p	0.077NS	1							
Total ash (%)	g	0.049NS	-0.209NS	1						
	p	0.126NS	-0.093NS	1						
Nitrogen free extract (%)	g	-0.218NS	0.228*	-0.808**	1					
	p	-0.526**	0.039NS	-0.668**	1					
Phasphorus (P) (gm/100gm)	g	0.277*	-0.119NS	0.670**	-0.755**	1				
	p	0.149NS	-0.159NS	0.482**	-0.522**	1				
Calcium (Ca) (gm/100gm)	g	-0.068NS	0.024NS	0.166NS	-0.376**	0.354**	1			
	p	-0.028NS	0.105NS	0.142NS	-0.183NS	0.256*	1			
Sodium (Na) (gm/100gm)	g	0.284	-0.149NS	0.059NS	-0.092NS	-0.059NS	-0.505**	1		
	p	0.270*	-0.081NS	0.008NS	-0.001NS	-0.013NS	-0.248*	1		
Pottasium (K)(gm/100gm)	g	0.389**	-0.240*	0.547**	-0.493**	0.359**	0.353**	-0.040NS	1	
	p	0.068NS	-0.145NS	0.395**	-0.302**	0.290**	0.246*	0.021NS	1	
Crude protein (%)	g	-0.011NS	-0.169NS	0.798**	-0.963**	0.753**	0.453**	-0.225*	0.396**	1
	p	0.069NS	-0.051NS	0.695**	-0.863**	0.562**	0.271*	-0.196NS	0.290**	1

Phenotypic and genotypic correlation coefficient worked out between leaf fodder and nutrient characteristics of 18 months old progeny of twenty selected population of *G. optiva* and presented in Table 4.45. There was highly significant and positive genotypic and significant phenotypic correlation observed between crude protein and leaf P (rg: 0.753, rp: 0.562), total ash and crude protein (rg: 0.798, rp: 0.695). Total ash showed significant and positive genotypic and phenotypic correlation with leaf P (rg: 0.670, rp: 0.482).

Data presented in Table 4.46 and Fig 4.20 showed Karl Pearson correlation between leaf fodder, leaf mineral nutrients and biochemical estimates (of mother trees) among populations of *G. optiva*. It showed the highly significantly positive correlation between leaf fresh weight and leaf dry weight (0.804), crude protein and total ash (0.735), amino acids and crude protein (0.848).There was significant and positive correlation developed between crude protein and leaf dry weight (0.545), leaf phosphorus and crude protein (0.520), total ash and leaf P (0.531), total ash and leaf dry weight (0.388), leaf P and amino acids (0.529), leaf dry weight and amino acids (0.462), leaf Na and leaf K (0.677), leaf Ca and leaf P (0.302).

Genotypic and Phenotypic correlation between fodder, minerals and biochemical estimates (of mother trees) among populations of *G. optiva* are presented in Table 4.47. Leaf fresh weight showed highly significant and positive genotypic and phenotypic correlation



**significant at 5 %level of significance, where, LCP-leaf crude protein, LEE-leaf ether extract, LCF-leaf crude fiber, LTA-Total ash, NFE-nitrogen free extract, K-potassium, Na- sodium, P-phosphorus

Fig 4.19 Correlation between leaf fodder and nutrient characteristics of 18 months old progeny of population of *Grewia optiva* Drummond.

Table 4.46 Karl Pearson Correlation between Leaf fodder, leaf mineral nutrients and biochemical estimates (of mother trees) among populations of *Grewia optiva* Drummond

Parameters	Leaf fresh weight (gm)	Leaf Dry matter content (%)	Crude protein (%)	Ether extract (%)	Crude fibre (%)	Total ash (%)	Nitrogen free extract (%)	Amino acids (mg/gm)	Pottasium (K)(gm/100gm)	Calcium (Ca) (gm/100gm)	Sodium (Na) (gm/100gm)	Phasphorus (P) (gm/100gm)	Leaf dry weight (gm)
Leaf Fresh weight (gm)	1												
Leaf Dry matter content (%)	-0.213	1											
Crude protein (%)	0.466	0.040	1										
Ether extract (%)	-0.067	0.106	-0.296	1									
Crude fibre (%)	0.203	-0.191	0.241	-0.099	1								
Total ash (%)	0.496	-0.036	0.735	-0.411	0.283	1							
Nitrogen free extract (%)	-0.508	0.040	-0.901	0.199	-0.590	-0.806	1						
Amino acids(mg/gm)	0.466	0.091	0.848**	-0.203	0.208	0.728	-0.803	1					
Pottasium (K) (gm/100gm)	0.292	-0.393	0.260	-0.203	0.436	0.283	-0.380	0.163	1				
Calcium (Ca) (gm/100gm)	0.505	-0.171	0.072	0.036	0.142	0.170	-0.153	0.164	0.150	1			
Sodium (Na) (gm/100gm)	0.264	-0.374	0.114	-0.113	0.392	0.223	-0.265	0.141	0.677	0.101	1		
Phosphorus (P) (gm/100gm)	0.416	-0.080	0.520**	-0.245	0.277	0.531	-0.554	0.529**	0.262	0.500	0.188	1	
Leaf dry weight (gm)	0.804**	0.325**	0.545**	0.055	0.043	0.388	-0.423	0.462	-0.022	0.324	0.045	0.302	1

**Significant at 5 % level of significance.

with leaf dry weight (rg: 0.857, rp: 805), whereas, leaf fresh weight showed significant positive genotypic and phenotypic association with crude protein (rg: 0.529, rp: 0.472), total ash (rg: 0.577, rp: 0.511), amino acids (rg: 0.603, rp: 0.469), leaf calcium (rg: 0.574, rp: 0.505), leaf phosphorus (rg: 0.436, rp: 0.416).

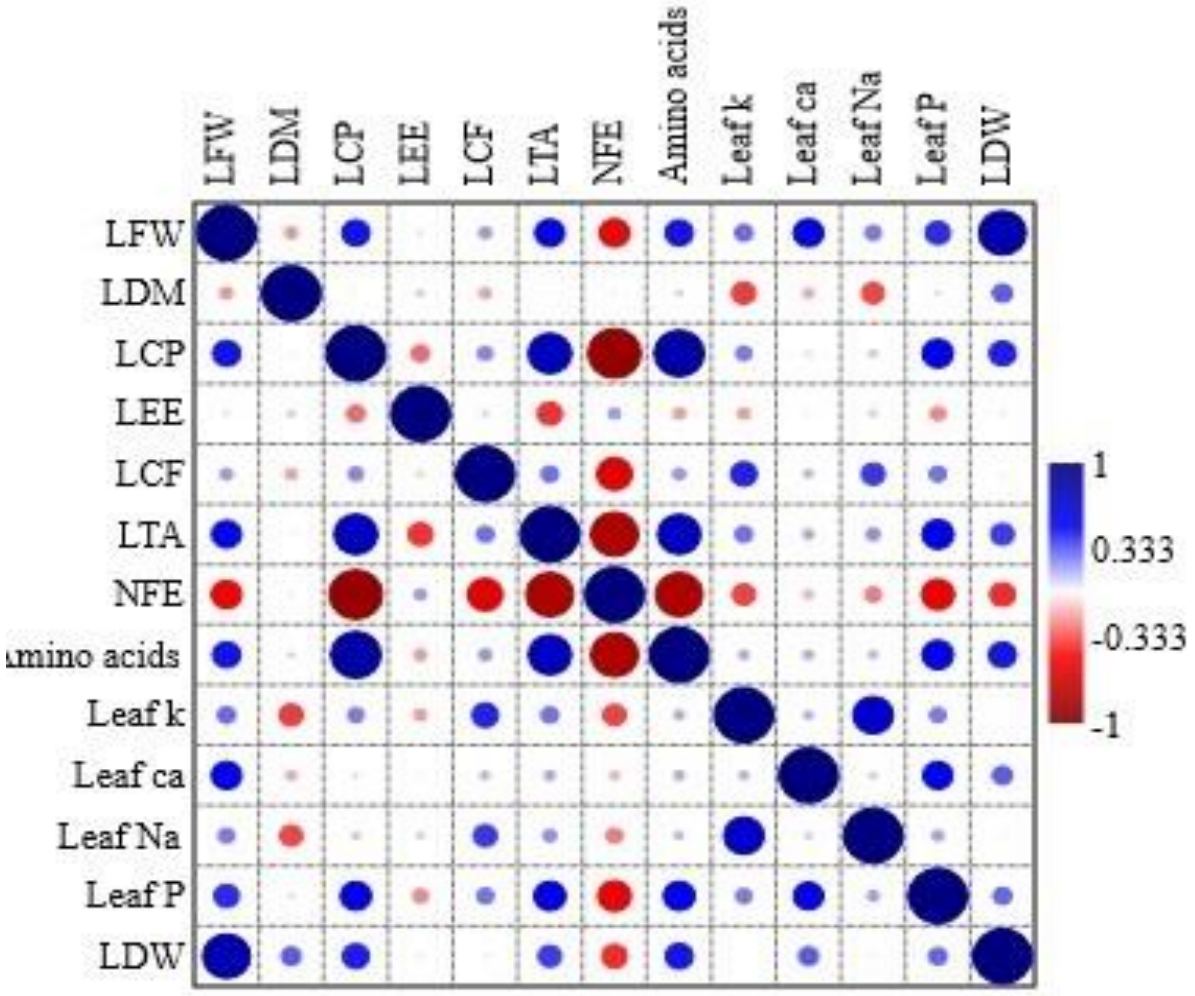
Table 4.47 illustrated that crude protein showed highly significant positive genotypic and phenotypic association with total ash (rg: 0.898, rp: 0.740) and amino acids (rg: 0.988, rp: 0.852), whereas, significant positive correlation with leaf P (rg: 0.572, rp: 0.525) and leaf dry weight (rg: 0.504, rp: 0.449). Crude protein showed significant negative correlation with ether extract (rg: -0.628, rp: -0.300), nitrogen free extract (rg: -0.967, -0.901).

Table 4.47 depicted that crude fiber showed positive genotypic and phenotypic correlation with leaf potassium (rg: 0.651, rp: 0.439), crude protein (rg: 0.391 and positive genotypic correlation with total ash (rg: 0.358), crude protein (rg: 0.391) and amino acids (rg : 0.370). Present study is in line with the studies conducted by Negi *et al.* (1980) who obtained a positive correlation between crude protein and crude fibre content in *Dendrocalamus hamiltonii.* However, the crude fibre and NFE content followed the general trend of results established with other tree fodders. This trend may be due to the association of protein with acid detergent fibre (ADF).

A thorough examination of Table 4.47 revealed the amino acids had a significant positive correlation with leaf P (rg: 0.678, rp: 0.529), as well as leaf dry weight (rg: 0.598, rp: 0.464). Leaf Na was found to have a significant positive genotypic and phenotypic connection with leaf K (rg: 0.752, rp: 0.680), but not with leaf Ca or leaf dry weight. Leaf P had a significant positive connection with leaf dry weight (rg: 0.312, rp: 0.302).

Correlation is a useful biometrical technique for determining the degree and amount of correlation between distinct features. A comprehensive understanding of the link between distinct features is critical in tree improvement programmes because it shows whether the selection of one character confirms the appearance or disappearance of the other. The traits that are highly connected with the required traits may be used for undertaking selection for the desired characters in the species.

Many substantial and positive correlations, as well as significant and negative correlations, reported in the current investigations among various growth and nutrient characteristics point to the importance of using such correlations in indirect selection for desirable traits in the species.



*significant at 1 % level of significance; **significant at 5 %level of significance, where, LFW-leaf fresh weight, LDM-leaf dry matter content, LCP-leaf crude protein, LEE-leaf ether extract, LCF-leaf crude fiber, LTA-Total ash, NFE-nitrogen free extract, K-potassium, Na-sodium, P-phosphorus, LDW-leaf dry weight.

Fig 4.20 Correlation between Leaf fodder, leaf mineral nutrients and biochemical estimates (of mother trees) among populations of *Grewia optiva*Drummond

Table 4.47 Genotypic and Phenotypic Correlation between fodder, minerals and biochemical estimates (of mother trees) among populations of *Grewia optiva* Drummond

Parameters		LFW	LDM	LCP	LEE	LCF	LTA	NFE	Amino acids	Leaf k	Leaf ca	Leaf Na	Leaf P	LDW
LFW	g	1												
	p	1												
LDM	g	-0.221*	1											
	p	-0.207NS	1											
LCP	g	0.529**	0.024NS	1										
	p	0.472**	0.043NS	1										
LEE	g	-0.124NS	0.128NS	-0.628**	1									
	p	-0.067NS	0.106NS	-0.300**	1									
LCF	g	0.269*	-0.183NS	0.391**	-0.422**	1								
	p	0.204NS	-0.193NS	0.240*	-0.100NS	1								
LTA	g	0.577**	-0.013NS	0.898**	-0.810**	0.358**	1							
	p	0.511**	-0.049NS	0.740**	-0.417**	0.282*	1							
NFE	g	-0.578**	0.026NS	-0.967**	0.669**	-0.599**	-0.902**	1						
	p	-0.517**	0.042NS	-0.901**	0.202NS	-0.590**	-0.807**	1						
Amino acids	g	0.603**	0.096NS	0.988**	-0.695**	0.370**	0.941**	-0.959**	1					
	p	0.469**	0.091NS	0.852**	-0.205NS	0.205NS	0.730**	-0.804**	1					
Leaf K	g	0.330**	-0.467**	0.276*	-0.351**	0.651**	0.341**	-0.428**	0.223*	1				
	p	0.294**	-0.398**	0.268*	-0.203NS	0.439**	0.287**	-0.387**	0.165NS	1				
Leaf Ca	g	0.574**	-0.240*	0.111NS	0.093NS	0.282*	0.256*	-0.235*	0.264*	0.182NS	1			
	p	0.505**	-0.172NS	0.082NS	0.037NS	0.145NS	0.180NS	-0.164NS	0.168NS	0.148NS	1			
Leaf Na	g	0.287**	-0.522**	0.106NS	-0.197NS	0.614**	0.218NS	-0.285*	0.124NS	0.752**	0.110NS	1		
	p	0.269*	-0.382**	0.110NS	-0.114NS	0.392**	0.216NS	-0.261*	0.138NS	0.680**	0.106NS	1		
Leaf P	g	0.436**	-0.129NS	0.572**	-0.366**	0.417**	0.609**	-0.634**	0.678**	0.279*	0.540**	0.200NS	1	
	p	0.416**	-0.081NS	0.525**	-0.246*	0.277*	0.537**	-0.559**	0.529**	0.262*	0.501**	0.188NS	1	
LDW	g	0.857**	0.255*	0.504**	0.051NS	0.117NS	0.491**	-0.512**	0.598**	-0.002NS	0.353**	0.035NS	0.312**	1
	p	0.805**	0.330**	0.449**	0.056NS	0.044NS	0.396**	-0.427**	0.464**	-0.022NS	0.325**	0.046NS	0.302**	1

*significant at 1 % level of significance; **significant at 5 %level of significance, where, LFW-leaf fresh weight, LDM-leaf dry matter content, LCP-leaf crude protein, LEE-leaf ether extract, LCF-leaf crude fiber, LTA-Total ash, NFE-nitrogen free extract, K-potassium, Na- sodium, P-phosphorus, LDW-leaf dry weight.

4.7 Path coefficient analysis

Path coefficient analysis demonstrates the impact of independent characters on the expression of dependent characters, both separately and in combination with other characters. Dewey and Lu (1959) developed path coefficient analysis which gives a realistic basis for allocating proper weightage to various variables. The perusal of data depicting path coefficient analysis at the genotypic level for direct and indirect impacts of important characters over dependent characters is presented in tables 4.48-4.51.

The direct and indirect impacts of tree morphological and leaf morphometric features on tree height are presented in Table 4.48. A review of the genotypic path coefficient analysis presented in Table 4.48 revealed that intermodal length (0.499) had the greatest direct positive effect on tree height, followed by leaf area (0.410), tree diameter (0.131), crown spread (E-W) (0.020), crown spread (N-S) (0.100), number of primary branches (0.021) and leaf width (0.015), whereas, number of secondary branches (-0.243) and leaf length (-0.309) had negative direct effects.

Table 4.48 Estimation of direct and indirect effects of tree and leaf morphometric characteristics on tree height using Path analysis

Parameters	Tee diameter (cm)	Crown Spread (E-W) (m)	Crown Spread (N-S)(m)	No. of Primary Branches	No. of Secondary Branches	Internodal Length (cm)	Leaf Length (cm)	Leaf width (cm)	Leaf area (cm^2)
Tee diameter(cm)	**0.131**	0.006	0.042	0.008	-0.017	0.312	-0.142	0.005	0.257
Crown Spread (E-W)(m)	0.042	**0.020**	0.038	0.006	-0.084	0.139	-0.058	0.001	0.121
Crown Spread (N-S)(m)	0.054	0.007	**0.100**	0.007	-0.020	0.222	-0.131	0.004	0.181
No. of Primary Branches	0.049	0.005	0.033	**0.021**	-0.040	0.158	-0.134	0.006	0.201
No. of Secondary Branches	0.009	0.007	0.008	0.003	**-0.243**	-0.003	-0.04	0.003	0.113
Internodal Length (cm)	0.081	0.005	0.045	0.007	0.001	**0.499**	-0.133	0.005	0.201
Leaf Length (cm)	0.060	0.003	0.043	0.009	-0.034	0.215	**-0.309**	0.006	0.357
Leaf width (cm)	0.049	0.001	0.024	0.009	-0.040	0.162	-0.119	**0.015**	0.223
Leaf area (cm^2)	0.082	0.006	0.045	0.010	-0.067	0.245	-0.269	0.008	**0.410**
Residual effect= 0.36786 **Diagonal figure represent the direct effect**									

Table 4.49 revealed the direct and indirect effects of seed, germination and seedling growth characteristics on seedling height. A perusal of the genotypic path coefficient analysis presented in Table 4.49 indicated that the maximum direct positive effect on seedling height was imposed by germination percentage (0.536), followed by germination energy (0.521),

Table 4.49 Estimation of direct and indirect effects of seed, germination and seedling growth characteristics on seedling height using Path analysis

Parameters	Seed thickness (mm)	Seed length (mm)	Seed width (mm)	100 Seed weight (gm)	Germination Percentage (%)	Germination Value	Germination energy	Germination index	Survival percentage (%)	Collar Diameter (mm)	Internodal length (cm)	Petiole length (cm)	Leaf area (Cm^2)
Seed thickness(mm)	**0.037**	-0.137	0.064	0.222	0.637	-0.826	0.524	-0.157	-0.362	0.352	0.531	0.048	0.065
Seed length (mm)	0.032	**-0.094**	0.046	0.145	0.310	-0.383	0.242	-0.049	-0.175	0.197	0.318	0.011	0.044
Seed width (mm)	0.022	-0.137	**0.050**	0.213	0.641	-0.796	0.491	-0.067	-0.382	0.322	0.468	0.019	0.070
100 Seed weight (gm)	0.023	-0.106	0.064	**0.102**	0.385	-0.438	0.273	-0.033	-0.153	0.215	0.220	0.001	0.039
GerminationPercentage(%)	0.021	-0.131	0.029	0.222	**0.536**	-0.705	0.428	-0.059	-0.341	0.336	0.467	0.025	0.072
Germination Value	0.016	-0.137	0.039	0.187	0.637	**-0.779**	0.491	-0.072	-0.352	0.297	0.443	0.021	0.065
Germination energy	0.014	-0.132	0.034	0.189	0.600	-0.826	**0.521**	-0.029	-0.347	0.318	0.463	0.019	0.071
Germination index	0.015	-0.128	0.033	0.181	0.598	-0.822	0.524	**-0.038**	-0.347	0.319	0.460	0.023	0.073
Survival percentage (%)	0.010	-0.058	0.013	0.083	0.293	-0.151	0.126	-0.157	**-0.177**	0.062	0.137	0.023	0.014
Collar Diameter (mm)	0.016	-0.144	0.027	0.209	0.621	-0.794	0.502	-0.077	-0.362	**0.325**	0.498	0.030	0.069
Internodal length (cm)	0.018	-0.125	0.039	0.212	0.537	-0.747	0.475	-0.028	-0.334	0.352	**0.504**	0.024	0.063
Petiole length (cm)	0.019	-0.121	0.027	0.195	0.532	-0.721	0.454	-0.041	-0.339	0.335	0.530	**0.025**	0.060
Leaf area (Cm^2)	0.008	-0.055	0.001	0.116	0.274	-0.329	0.244	-0.074	-0.226	0.176	0.272	0.048	**0.030**

Residual effect= 0.01973

Diagonal figure represent the direct effect

intermodal length (0.504), collar diameter (0.325), 100 seed weight (0.102), seed length (0.094), seed thickness (0.037), and leaf area (0.030). Germination value (-0.779), germination index (-0.038), and survival percentage (-0.177) showed negative direct effects on seedling height.

Table 4.50 demonstrated the direct and indirect effects of leaf fodder and mineral nutrients on crude protein in 18 months old seedlings. Critical probing of genotypic path coefficient analysis, as shown in Table 52, revealed that P (0.130), Ca (0.048), ether extract (0.042), Na (0.019) and K (0.004) had the highest direct positive effect on crude protein, while crude fibre (-0.267), total ash (-0.040) and nitrogen-free extract (-0.944) had the highest direct negative effect.

Table 4.50 Estimation of direct and indirect effects of leaf fodder and mineral nutrients (of 18 months old seedling) on leaf crude protein using Path analysis

Parameters	Crude fibre (%)	Ether extract (%)	Total ash (%)	Nitrogen free extract (%)	Phasphorus (P) (gm/100gm)	Calcium (Ca) (gm/100gm	Sodium (Na) (gm/100gm	Potassium (K)(gm/100gm)
Crude fibre (%)	**-0.267**	-0.002	-0.001	0.206	0.035	-0.003	0.020	0.002
Ether extract (%)	0.013	**0.042**	0.008	-0.216	-0.015	0.001	-0.002	-0.001
Total ash (%)	-0.012	-0.009	**-0.040**	0.763	0.087	0.008	0.001	0.002
Nitrogen free extract (%)	0.058	0.010	0.033	**-0.944**	-0.097	-0.018	-0.002	-0.002
Phasphorus (P) (gm/100gm)	-0.074	-0.005	-0.027	0.713	**0.130**	0.017	-0.001	0.001
Calcium (Ca) (gm/100gm	0.018	0.001	-0.007	0.355	0.046	**0.048**	-0.010	0.001
Sodium (Na) (gm/100gm	-0.290	-0.006	-0.002	0.086	-0.008	-0.024	**0.019**	-0.001
Potassium (K)(gm/100gm)	-0.104	-0.010	-0.022	0.465	0.047	0.017	-0.001	**0.004**

Table 4.51 demonstrated the direct and indirect effects of leaf fodder, amino acids, and mineral nutrients (of mother trees) on leaf dry weight (LDW). Maximum direct positive effects on leaf dry weight were imposed by leaf fresh weight (0.937), leaf dry matter content (0.414), crude protein (0.367), ether extract (0.140), sodium (0.132), phosphorus (0.092), and total ash (0.044), whereas K (-0.312), amino acids (-0.564), crude fibre (-0.198), Ca (-0.181) and crude fibre (-0.198) exhibited negative direct effects on leaf dry weight. The values displayed below and above the diagonal exhibited an indirect effect on leaf dry weight.

Table 4.51. Estimation of direct and indirect effects of leaf fodder, Amino acids and mineral nutrients (of mother trees) on leaf dry weight (LDW) among populations of *Grewia optiva* Drummond

Parameters	**Leaf fresh weight (gm)**	**Leaf Dry matter content (%)**	**Crude protein (%)**	**Ether extract (%)**	**Crude fibre (%)**	**Total ash (%)**	**Nitrogen free extract (%)**	**Amino acids(mg/gm)**	**Pottasium (K)(gm/100gm)**	**Calcium (Ca) (gm/100gm)**	**Sodium (Na) (gm/100gm)**	**Phasphorus (P) (gm/100gm)**
Leaf Fresh weight (gm)	**0.937**	-0.091	-0.194	-0.017	-0.053	0.025	0.619	-0.340	-0.103	-0.103	0.038	0.040
Leaf Dry matter content (%)	-0.229	**0.414**	-0.009	0.017	0.036	-0.001	-0.028	-0.054	0.146	0.043	-0.069	-0.011
Crude protein (%)	0.549	0.009	**0.367**	-0.088	-0.077	0.039	0.035	-0.558	-0.086	-0.020	0.014	0.053
Ether extract (%)	-0.129	0.053	0.230	**0.140**	0.083	-0.035	-0.716	0.392	0.110	-0.016	-0.026	-0.034
Crude fibre (%)	0.279	-0.076	-0.143	-0.059	**-0.198**	0.016	0.641	-0.209	-0.203	-0.051	0.081	0.039
Total ash (%)	0.598	-0.005	-0.330	-0.113	-0.070	**0.044**	0.966	-0.531	-0.107	-0.046	0.029	0.056
Nitrogen free extract (%)	-0.600	0.011	0.355	0.094	0.118	-0.039	**-0.073**	0.541	0.134	0.042	-0.038	-0.059
Amino acids(mg/gm)	0.626	0.040	-0.363	-0.097	-0.073	0.041	0.027	**-0.564**	-0.070	-0.047	0.016	0.063
Pottasium (K)(gm/100gm)	0.343	-0.193	-0.101	-0.049	-0.128	0.014	0.458	-0.126	**-0.312**	-0.033	0.100	0.026
Calcium (Ca) (gm/100gm)	0.596	-0.099	-0.041	0.012	-0.056	0.011	0.251	-0.149	-0.057	**-0.181**	0.014	0.050
Sodium (Na) (gm/100gm)	0.298	-0.216	-0.039	-0.027	-0.121	0.009	0.305	-0.070	-0.235	-0.019	**0.132**	0.019
Phasphorus (P) (gm/100gm)	0.452	-0.053	-0.210	-0.051	-0.082	0.027	0.679	-0.383	-0.0871	-0.098	0.027	**0.092**
Residual effect= 0.00532 **Diagonal figure represent the direct effect**												

Similarly, Thakur (2014) conducted path coefficient analysis in *Acacia catechu* and *Toona ciliata*, while, Dogra *et al*. (2018) performed path coefficient analysis in *Juglans regia* for fruit-yield.

4.8 Principal Component Analysis

Principal component analysis is done with the purpose of viewing data more realistically. Through this analysis, the number of variables is reduced to a few linear variable combinations that can be easily interpreted. The principal component analysis (PCA) is one of the powerful statistical methods widely applied to classify phenotypic traits in tree germplasm into groups based on similarities. PCA guides the choice of parents for genetic improvement (Afuape *et al.,* 2011; Beheshtizadeh *et al.,* 2013). PCA reduces the original variables into a new set of uncorrelated variables known as principal components (PCs). These PCs clarify the connections between traits and divide the total variance of the original traits into a small number of uncorrelated new variables (Wiley and Lieberman 2011).

Table 4.52 Principal Component Analysis for tree morphometric and leaf morphometric characteristics

Parameters	PC 1	PC 2	PC 3
Tree diameter (cm)	0.35	-0.22	0.08
Crown Spread (E-W)	0.20	0.13	0.72
Crown Spread (N-S)	0.29	-0.10	0.26
No. of Primary Branches	0.29	0.14	-0.07
No. of Secondary Branches	0.11	0.60	0.34
Branch internodal length (cm)	0.39	-0.38	0.12
Leaf length (cm)	0.36	0.14	-0.26
Leaf width (cm)	0.27	0.09	-0.34
Leaf area (cm^2)	0.41	0.15	-0.17
Petiole length (cm)	0.27	0.39	-0.23
Tree height (m)	0.32	-0.44	0.03
Eigenvalue	4.72	1.49	1.16
% variance	42.93	13.58	10.52

Table 4.52 showed the principal component analysis for tree and leaf morphometric features, while Fig. 4.21 showed the relationship between principal components and eigen value (%). Table 4.52 and Fig. 4.21 revealed that the principal components I (PC I), II (PC II)

and III (PC III) all had eigen values greater than 1.0. For PC1 having eigen value (λ_1=4.72) comprising 42.93 per cent variation, leaf area had the maximum loading value (0.41), followed by leaf length (0.36), tree diameter (0.35), branch nodal length (0.33), tree height (0.32), crown spread (N-S) (0.29), no. of primary branches (0.29), leaf width (0.27), petiole length (0.27), crown spread (E-W) (0.20), number of secondary branches (0.110). For PC2 (λ_2=1.49), which accounted for 13.58 per cent of the variation, the number of secondary branches had the highest loading value (0.60), followed by petiole length (0.39), while other parameters exhibited no meaningful association with this component. Crown spread (E-W) had the highest loading value (0.72) for PC3 (λ_3=1.16) with 10.52 per cent variance, followed by the number of secondary branches.

Therefore, for tree morphometric and leaf morphometric characteristics, leaf area should be given the highest preference, followed by tree height and tree diameter, as these components showed the highest loading value in PCI. The number of secondary branches and crown spread (E-W) (both of which showed the maximum loading value under components II and PCIII, respectively) can be weighted in conjunction with PCI components to select the best genotypes of *G. optiva*. The use of these traits will save a significant amount of time when identifying and selecting the most desirable genotypes of *G. optiva.*

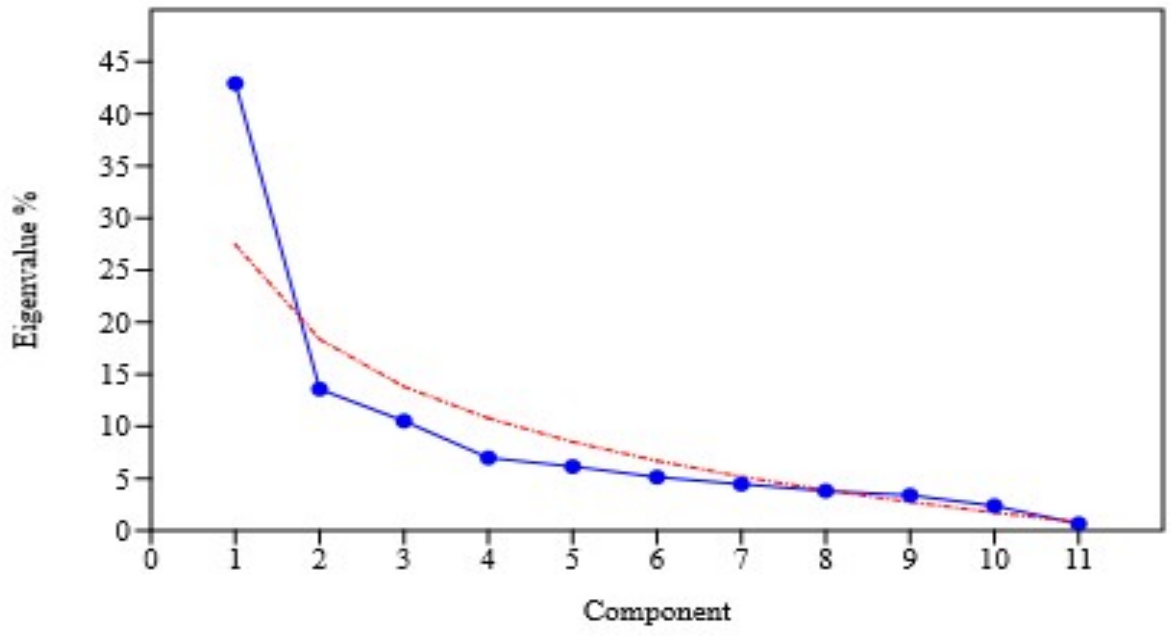


Fig 4.21. Screeplot between Principal components and Eigenvalue (%) for tree and leaf morphometric characteristics

A biplot (Fig. 4.22) was also drawn using the values of PCA I and PCA II from Table 4.52. The PCA allows visual differentiation among enteries and identifies possible

associations by providing a two-dimensional scatter plot consisting of individual enteries. The geometric distance among individuals in this plot reveals the genetic distance among them. The amalgamation of individuals in a similar quadrant of the plot may indicate a group of genetically related individuals. (Warburton *et al*., 2002). The higher the coefficients of a particular character, the more it is related to the respective principal component axis. Two groupings of tree characteristics (Fig 4.22) were observed in the biplot and some overlapping occurred within groups, demonstrating the relatedness of the tree and leaf morphometric characteristics of different seed sources. A PCA biplot shows both PC scores of samples (dots) and loadings of variables (vectors). The further away these vectors were from a PC's origin, the more influence they have on that PC. Loading plots also hint at how variables correlate with one another: a small angle implies positive correlation; a large one suggested negative correlation and a 90° angle indicated no correlation between two characteristics. A scree plot displayed how much variation each principal component captures from the data. If the first two or three PCs are sufficient to describe the essence of the data, the scree plot is a steep curve that bends quickly and flattens out.

In the biplot graph (Fig 4.22) of PCA, the quadrant I consisting of 23 different genotypes formed cluster 1, which was highly influenced by leaf area (LA), leaf length (LL), leaf width (LW), petiole length (PL), number of primary branches (NB), number of secondary branches (SB) and crown spread (E-W). The tree and leaf morphometric characters presented in cluster I, *viz.,* leaf area (LA), leaf length (LL), leaf width (LW), petiole length (PL), number of primary branches (NB), number of secondary branches (SB), and crown spread (E-W) were highly related. Among these characters, leaf length (LL), leaf width (LW), and leaf area (LA) overlapped, as did the number of secondary branches (SB) and crown spread (E-W) that depicted their highly relatedness with each other. The cluster II, corresponding to the quadrant II contained 19 different genotypes and was highly influenced by crown spread (N-S), tree diameter (DBH), branch nodal length (BNL) and tree height (TH). Similarly, cluster III corresponding to quadrant III consisted of 17 different genotypes of *G. optiva,* and cluster IV corresponding to quadrant IV consisted of 21 genotypes. The quadrants III and IV were least influenced by the tree and leaf morphometric characteristics under study.

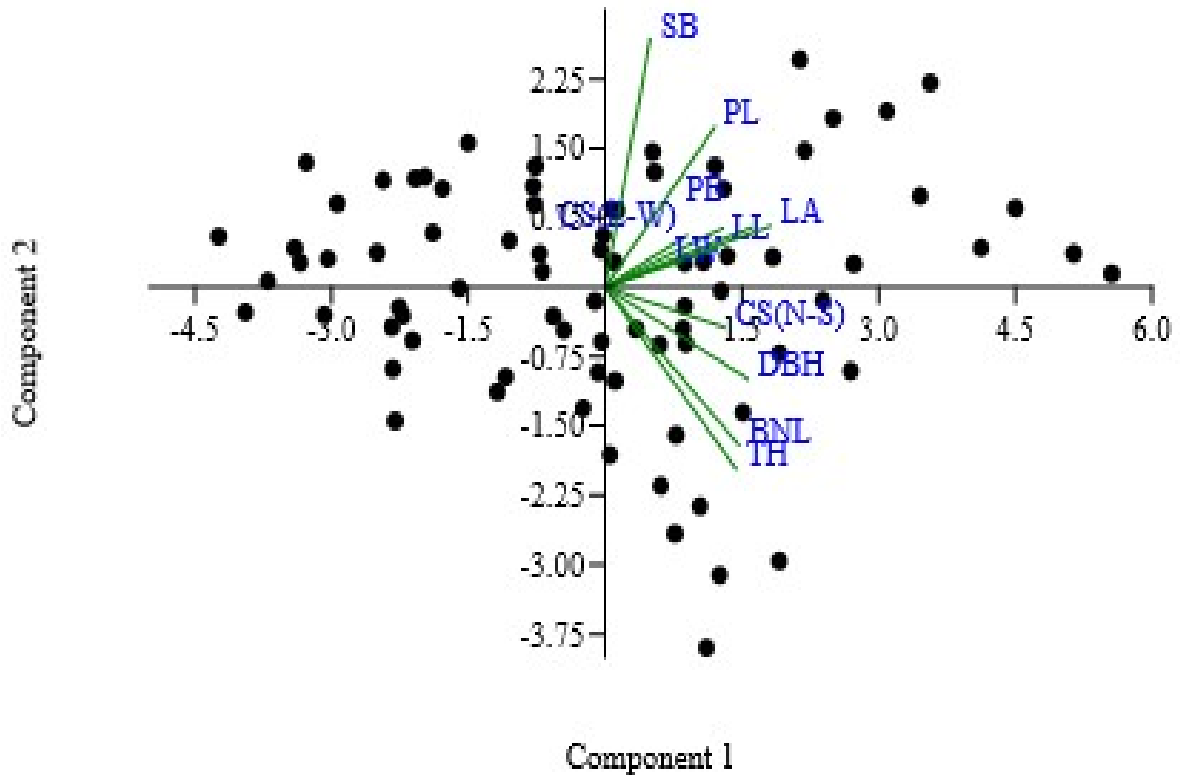


Fig 4.22 Biplot between PCI and PCII of tree and leaf morphometric characteristics

Table 4.53 exhibited the principal component analysis for seed, germination and seedling growth characteristics and Fig. 4.23 represented the relation between principal components and eigen value (%). Table 4.53 and Fig 4.23 revealed that the principal components I (PC I), principal component II (PC II) and principal component (PC III) all had eigen values >1.0. For PC1 having eigen value (λ_1=8.08) comprising 57.72 per cent variation, seedling height had the maximum loading value (0.33), followed by germination value (0.33), germination percentage (0.32), collar diameter (0.32), germination energy (0.31), intermodal length (0.31), leaf area (0.29), survival percentage (0.29), seed width (0.25) and other remaining characters showed less than 250 loading value. PC II gave eigen value > 1.29, comprising 9.25 per cent variation. Germination index had maximum loading value (0.54) followed by survival percentage and petiole length under PCII. PCIII (λ_3=1.06) comprising 7.55 per cent variation, seed thickness showed maximum loading value (0.57) followed by petiole length (0.42), seed width (0.34), germination index (0.39) and 100 seed weight (0.21). Characters with high loading values in PC II and PCIII should be prioritised in conjunction with PCI characters for further selection and enhancement of superior *G. optiva* strains.

Table 4.53: Principal Component Analysis for seed, germination and seedling growth (at the age of 18 months) characteristics.

Parameters	PC 1	PC 2	PC 3
Seed thickness(mm)	0.17	-0.30	0.57
Seed length (mm)	0.25	-0.22	-0.09
Seed width (mm)	0.14	-0.58	0.34
100 Seed weight (gm)	0.28	-0.06	0.21
Germination Percentage (%)	0.33	0.12	-0.08
Germination Value	0.33	-0.03	-0.28
Germination energy	0.31	0.01	-0.24
Germination index	0.12	0.54	0.39
Survival percentage (%)	0.28	0.27	-0.01
Collar Diameter (mm)	0.32	-0.04	-0.12
Internodal length (cm)	0.31	0.01	-0.02
Petiole length (cm)	0.16	0.37	0.42
Leaf area (cm^2)	0.29	0.01	-0.16
Seedling height (cm)	0.33	-0.05	-0.02
Eigen value	8.08	1.29	1.06
% variance	57.72	9.25	7.55

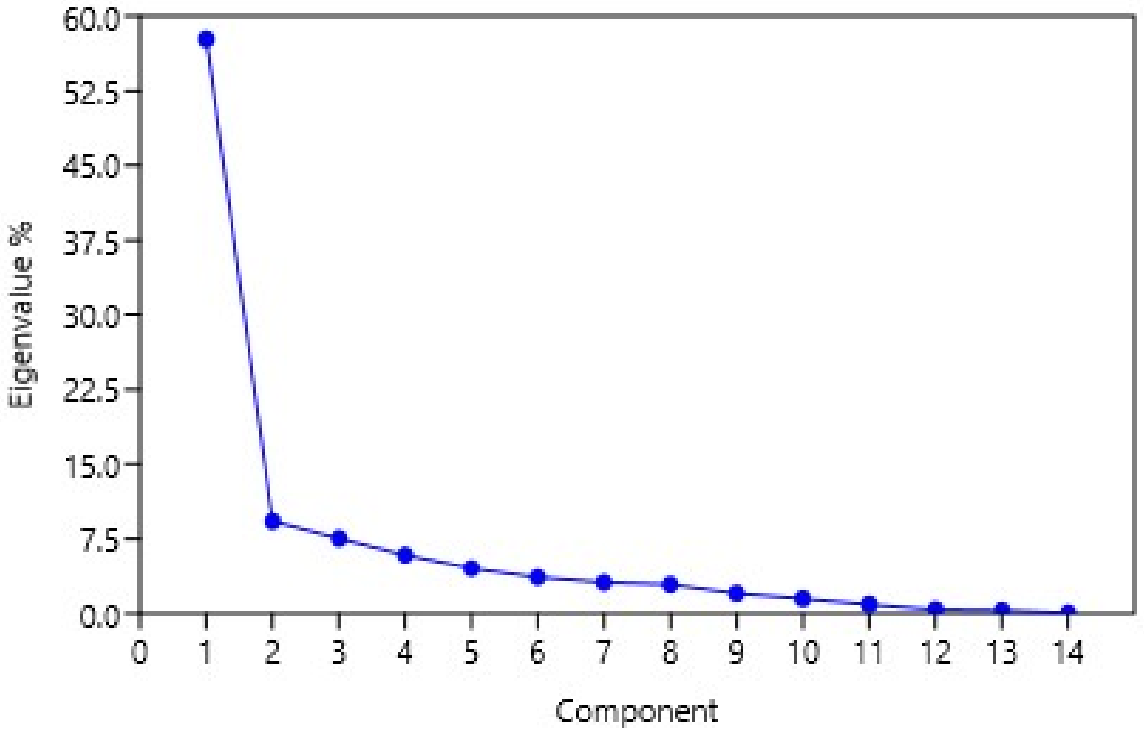


Fig. 4.23 Screeplot between Principal components and Eigenvalue (%) for seed, germination and seedling growth characteristics

In the biplot graph (Fig 4.24) of the PCA, the characteristics of the seed, seed germination and seedling growth that were being studied were divided into two groups. Characters that were present in the same cluster (group) were linked to one another, while overlapping characters within the same group demonstrated a strong genetic relationship with one another**.** The biplot graph of PCA demonstrates that the quadrant I, which included 23 different genotypes, formed cluster 1. Germination index (GI), petiole length (PL), survival percentage (SP), germination percentage (GP), leaf area (LA), germination value (GV) and germination energy (GE) were all significant influencing factors. Cluster II, which corresponded to quadrant II had 18 genotypes that were heavily influenced by associated features such as 100 seed weight (100 SW), seedling height (SH), collar diameter (CD), intermodal length (IL), seed length (SL), seed thickness (ST) and seed width (SW). Seedling height, 100 seed weight, collar diameter and intermodal length were overlapped among these parameters, indicating their tight connection. Similarly, cluster III, which corresponded to quadrant III, included 18 different genotypes of *G. optiva* whereas, cluster IV, which corresponded to quadrant IV, contained 21 genotypes. The seed, germination, and seedling growth characteristics observed had the least influence on quadrants III and IV.

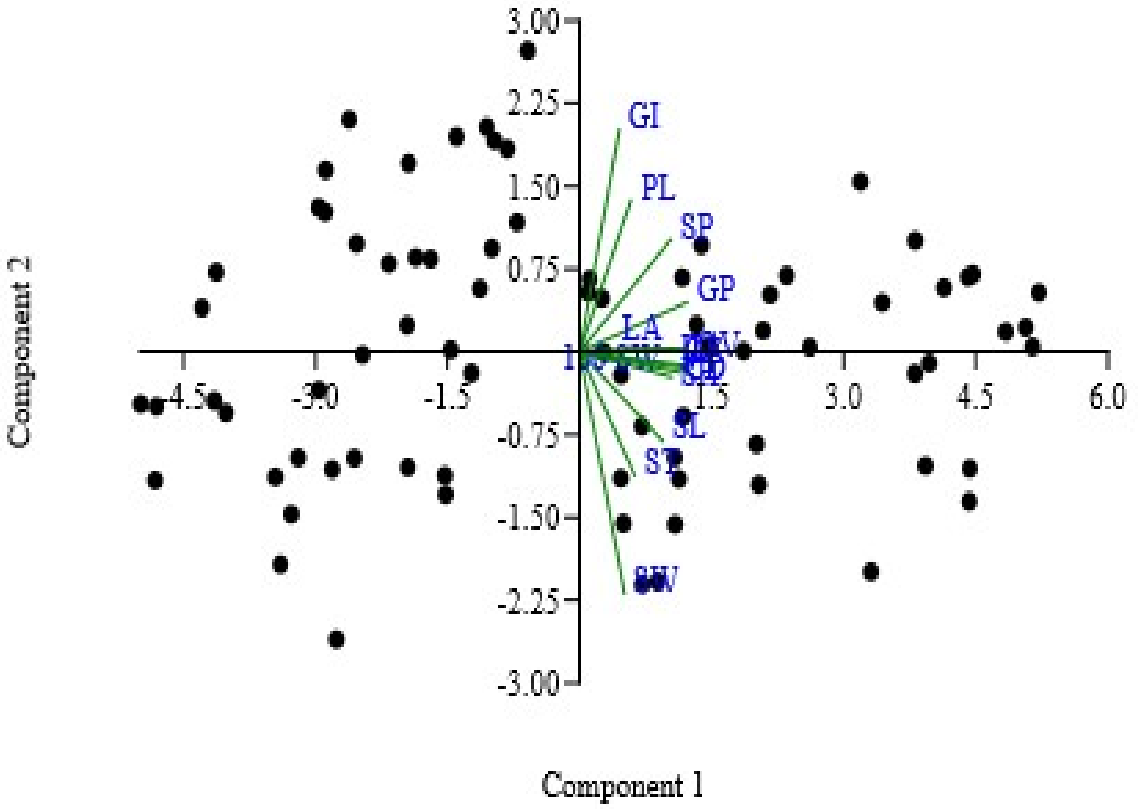


Fig. 4.24 Biplot between PCI and PCII of seed, germination and seedling growth characteristics.

Data appended to Table 4.54 and Fig. 4.25 revealed the principal component analysis (PCA) for fodder quality and mineral nutrient characteristics of 18 months old seedlings of *G. optiva*. Table 4.54 and Fig 4.26 depicted that the principal components I (PC I), principal component II (PC II) and principal component (PC III) gave eigen value>1.0. For PC1 (λ_1= 3.27) comprising 36.32 per cent variation, the maximum loading value was recorded for crude protein (0.49), followed by total ash (0.44), P (0.40), K (0.27) while remaining characters had low loading values and showed negative association with PCI. PC2 (λ_2=1.45) comprising 16.15 per cent variation, Na presented highest loading value (0.65) followed by crude fibre (0.57) whereas, remaining characters were not strongly associated with the respective component (PCII). PC3 (λ_3=1.16) comprising 12.91 per cent variation, ether extract had maximum loading value (0.79), followed by crude fibre (0.40). For the selection of superior strains of *G. optiva*, the fodder quality and mineral nutritional features that displayed a high loading value in PCI, PCII, and PCIII should be assessed.

Table 4.54 Principal Component Analysis for fodder and mineral nutrient characteristics of 18 months old seedlings of *Grewia optiva* Drummond

Parameters	PC 1	PC 2	PC 3
CF	0.18	0.57	0.40
EE	-0.06	-0.11	0.79
TA	0.44	0.02	-0.11
NFE	-0.50	-0.18	-0.19
Leaf P	0.40	-0.03	-0.11
Leaf Ca	0.20	-0.44	0.19
Leaf Na	-0.04	0.65	-0.14
Leaf K	0.27	-0.03	-0.33
CP	0.49	-0.14	0.05
Eigen value	3.27	1.45	1.16
% variance	36.32	16.15	12.91

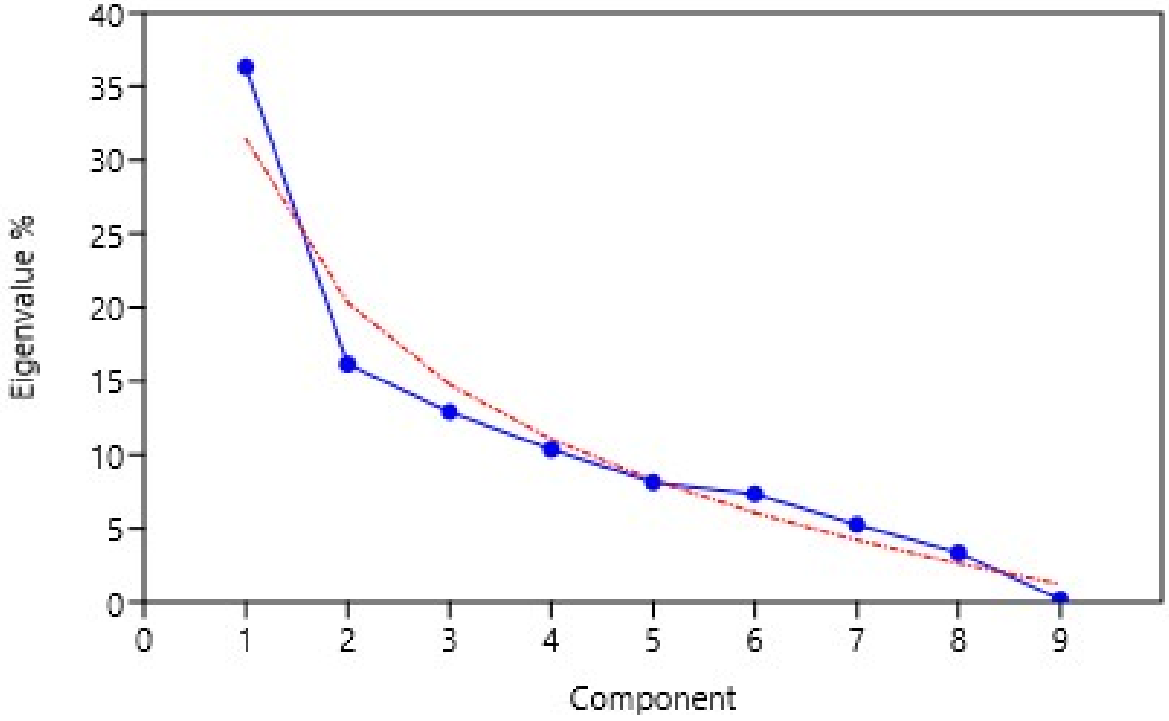


Fig 4.25 Screeplot between Principal components and Eigen value (%) for fodder and mineral nutrient characteristics of 18 months old seedlings of *Grewia optiva* Drummond

The Fig. 4.26 displayed a biplot graph concerning PCI and PCII. It showed four grouping of fodder quality and mineral nutrient characteristics of 18 months old seedlings of *G. optiva*. There were crude fibre, total ash and leaf K in cluster (group) 1. Leaf P, crude protein (CP) and leaf Ca were discovered in cluster 2, while, nitrogen free extract and ether extract were located in cluster III and leaf Na was found in cluster IV. It is depicted from biplot graph (Fig 4.26) of PCA that the quadrant I comprised of 18 different genotypes of *G. optiva* which were highly influenced by crude fiber, total ash and leaf (K). The cluster II, corresponding to the quadrant II, it contained 22 different genotypes were highly influenced by associated characters *viz.,* Leaf (P), crude protein (CP), leaf (Ca). Similarly, the cluster III corresponding to quadrant III consisted of 21 different genotypes of *G. optiva* were highly influenced by nitrogen free extract and ether extract. Cluster IV corresponding to quadrant IV consisted of 19 genotypes were highly influenced by leaf Na. Among four quadrants characters which were present at distant angle ($>90^0$) showed no correlation with each other. However, characters which were present at close angle or overlapped showed high correlation with each other.

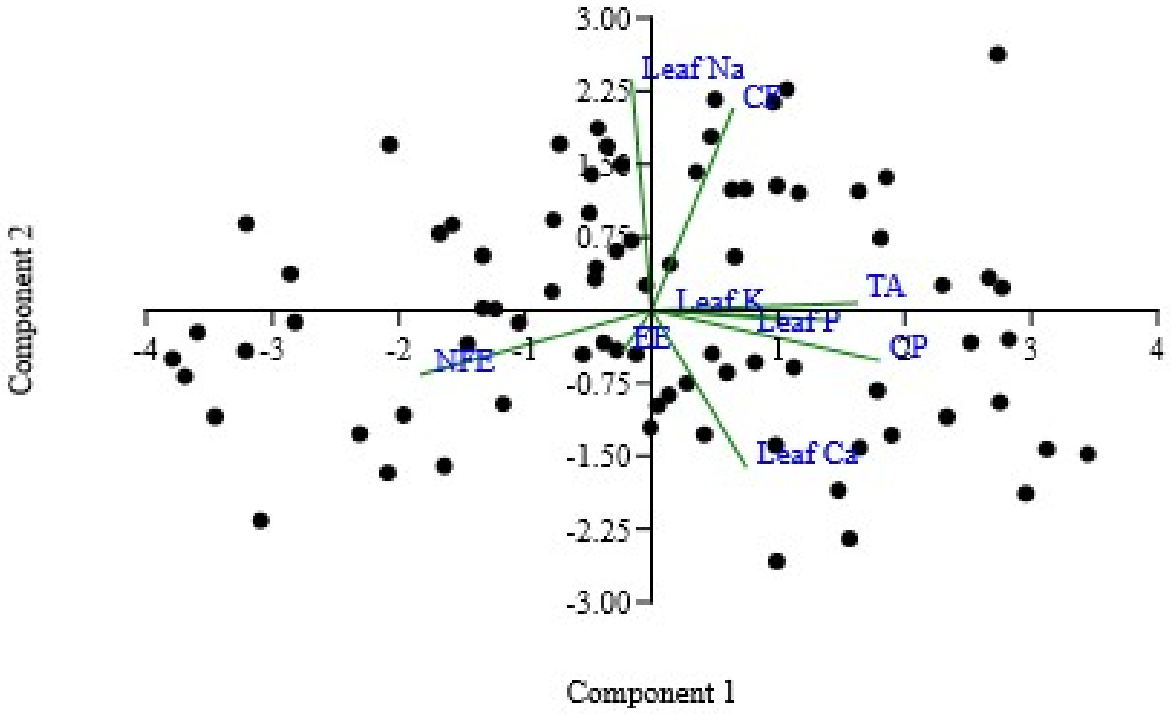


Fig. 4.26 Biplot between PCI and PCII of fodder and mineral nutrient characteristics of 18 months old seedlings of *Grewia optiva* Drummond

Data appended in Table 4.55 and Fig. 4.27 revealed the principal component analysis (PCA) for fodder quality and mineral nutrient characteristics of mother trees. Table 4.55 and Fig 4.27 depicted that the principal components I (PC I), principal component II (PC II), principal component III (PC III) and principal component IV (PC IV) gave eigen value>1.0 and all the four components accounted for 75.65 per cent variation. For PC1 (λ_1= 5.13) comprising 39.49 per cent variation, the highest loading value observed for crude protein (0.37), followed by total ash (0.37), amino acids (0.36), leaf fresh weight (0.32), P (0.31), leaf dry weight (0.25), whereas, the characters viz., crude fibre, K, Ca and Na exhibited less than 250 loading value and other remaining characters showed negative association with PCI. PC2 (λ_2=2.14), which accounts for 16.42 per cent of variation had the highest loading value for leaf dry matter content (0.49), followed by leaf dry weight (0.35), while, the remaining characters had low loading values. PC3 (λ_3=1.54) containing 11.83 per cent variation, leaf Ca had greatest loading value (0.58), followed by leaf fresh weight (0.43), ether extract (0.38), leaf dry weight (0.36) and other characters reported with low loading values. In PC4 (λ_4=1.03) component 7.91 per cent variation was reported, ether extract had loading value (0.60) followed by crude fibre (0.35) and leaf dry matter (0.28).

Among fodder quality and mineral nutrient characteristics which showed high loading value in PCI should be considered with high loaded components of PCII and PCIII for selection of superior strains of *G. optiva*.

Table 4.55 Principal Component Analysis for leaf fodder, mineral nutrients and biochemical (amino acids) characteristics of populations (mother trees) of *Grewia optiva* Drummond

Parameters	PC 1	PC 2	PC 3	PC4
Leaf fresh weight	0.32	0.06	0.43	0.02
Leaf dry matter (%)	-0.05	0.49	-0.13	0.28
Crude fibre (%)	0.21	-0.30	-0.07	0.35
Ether extract (%)	-0.14	0.10	0.38	0.60
Nitrogen free extract (%)	-0.40	-0.03	0.19	-0.21
Crude protein (%)	0.37	0.17	-0.25	0.03
Amino acids	0.36	0.21	-0.17	0.04
Potassium (K)	0.21	-0.48	0.01	0.14
Calcium (Ca)	0.17	-0.02	0.58	-0.36
Sodium (Na)	0.17	-0.47	0.07	0.25
Phosphorus (P)	0.31	0.01	0.10	-0.36
Total ash (%)	0.37	0.08	-0.21	-0.12
Leaf dry weight (g)	0.25	0.35	0.36	0.22
Eigen value	5.13	2.14	1.54	1.03
% Variance	39.49	16.42	11.83	7.91

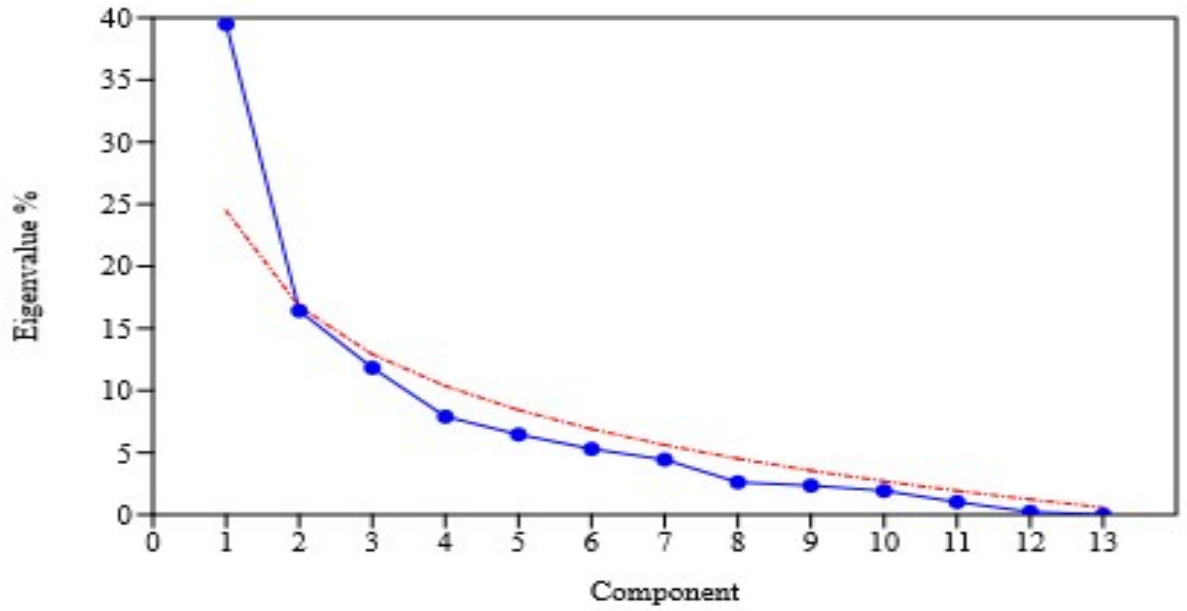


Fig 4.27 Screeplot between Principal components and Eigen value (%) for fodder quality and mineral nutrient characteristics of mother trees

Fig. 4.28 showed biplot graph between PCI and PCII (from Table 57). It showed four grouping of fodder quality and mineral nutrient characteristics of populations (mother trees) of *G. optiva*. Leaf dry weight (LDW), leaf crude protein (LCP), leaf fresh weight (LFW), total ash (LTA), leaf (Ca), amino acids were present in cluster (group) 1. Leaf (P), leaf crude fibre (LCF), leaf (K), leaf (Na) was found in cluster 2, nitrogen free extract (NFE) in cluster III, and ether extract (EE) and leaf dry matter (LDM) content were present in group IV.

It is depicted from biplot graph Fig. 4.28 of PCA that the quadrant I consisting of 19 different genotypes formed the cluster 1, which were highly influenced by leaf dry weight (LDW), leaf crude protein (LCP), leaf fresh weight (LFW), total ash (LTA), leaf (Ca), Amino acids. The cluster II, corresponding to the quadrant II contained 21 different genotypes and were highly influenced by associated characters, *viz.,* leaf (P), leaf crude fibre (LCF), leaf (K) and leaf (Na). Similarly, the cluster III corresponding to quadrant III consisted of 23 different genotypes of *G. optiva* and was highly influenced by nitrogen free extract (NFE). Cluster IV corresponding to quadrant IV consisted of 17 genotypes were highly influenced by ether extract (EE) and leaf dry matter (LDM). Between the four quadrants, characters that were present at a distant angle (>90^0) had no correlation, whereas, characters that were present at a close angle or overlapped had a strong correlation.

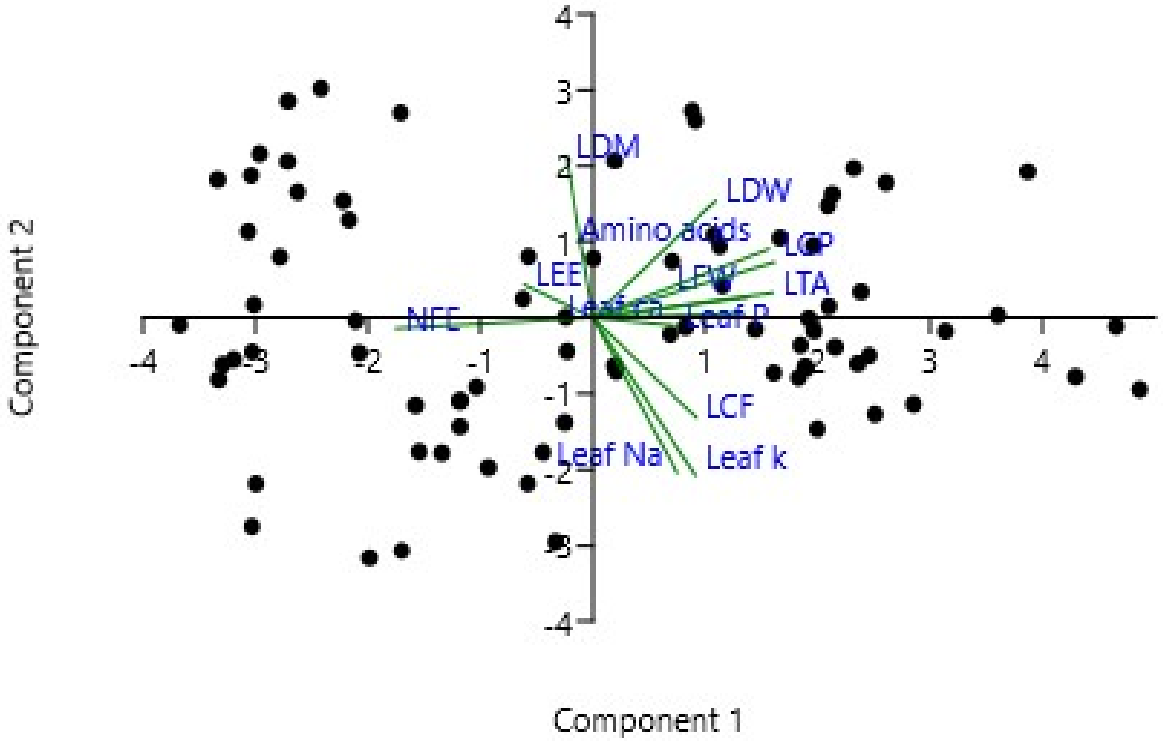


Fig. 4.28 Biplot between PCI and PCII of fodder quality and mineral nutrient characteristics of mother trees

Principal component analysis (PCA) was performed in order to summarize the information in a data set of multiple variables and to data containing large number of variables into smaller sets. For PCA initial variables were transformed into a new small set of variables without losing the most important information in the original data set. These new variables corresponded to a linear combination of the originals and were called principal components. PCA method is particularly useful when the variables within the data set were highly correlated. Correlation indicated that there was redundancy in the data. Due to this redundancy, PCA was used to reduce the original variables into a smaller number of new variables (principal components) explaining most of the variance in the original variables. The findings in this investigation can be related to similar findings of Singh and Huse (2004) and Singh *et al*. (2012b) on *Salix* clones.

4.9 Cluster Analysis

The analysis of variance revealed highly significant differences between the genotypes and populations of *G. optiva* for the examined growth characteristics. This indicated the existence of substantial variation among genotypes and it was reasonable to analyse genetic divergence further (Bhat, 2010).

Cluster analysis (genetic divergence analysis) classified eighty genotypes of twenty populations of *G. optiva* into two major clusters and four sub-clusters based on analysis of tree and leaf morphometric characteristics under consideration and presented as a dendrogram (Fig 4.29) using Ward's method (Ward, 1963). Cluster I and Cluster II comprised of 44 (DR1, DR2, GH4, DR4, GH2, GH3, DA3, KD3, DA4, NR1, DA2, AD2, KD4, NR2, DO2, GR1, NR4, AD4, NR3, DH3, RA3, GT2, GT3, RA4, GT4, GT1, GR4, BA2, KD1,KD2, BA3, BA4, SH1, SH3, SH2, DO1, DO4, BA1, DO 3, SH 4, GR2, GR3, RA1, RA2) and 36 (ST2, ST1, ST3, SN2, HR2, AD1, AD3, JG1, KU3, JG3, KU2, DH1, DH2, JG2, ST4, JG4, DH4, SN3, GH1, SN1, DR3, DA1, SN4, HR1, HR3, HR4, KU4, KU1, SI1, SI2, SI3, SI4, KT3, KT4, KT1, KT2) different genotypes, respectively. The maximum inter-cluster distance was reported between genotype DR1 and KT2. However, the maximum intra-cluster distance was recorded between genotype DR1 and RA2 in cluster I, and genotype ST2 and KT2 in cluster II.

Dendrogram of eighty genotypes (based on seedling growth and fodder Quality characteristics of 18 months old seedlings) of twenty populations of *G. optiva* (Fig 4.30) demonstrated that eighty genotypes were separated into two main clusters and four sub-clusters. Cluster I consisted of 26 (DH 1, DH2, DH4, GT2, KD3, GR4, GH2, JG3, NR2, JG1, JG2, SN3, GR1, SN4, GR3,GH1,GT3,GH3,AD3, AD1, KD1 AD4, AD2, KD2,BA4, GR2) and cluster II comprised of 54 genotypes i.e., SH4, SH3, SH1, SH2, DA4, SI4, SI2, SI3,DR2, SI1, ST4, DA2, ST2, ST1, KU1, BA2, KU2, DR4, NR3, HR4, DH3, KU3, HR3, NR1, HR1, BA3, DR1, KT1, KT2, NR4, BA1, DR3, ST3, KT4, DA3, KT3, DA1, HR2, KU4, RA3, RA2, RA4, GH4, RA1, DO 1, DO4, DO2, DO3, KD4, JG4, SN2, GT4, SN1, GT1. The greatest distance between clusters was observed between genotype DH1 and GT. In Cluster I, the greatest intra-cluster distance was observed between genotype DH1 and GR2, whereas, in Cluster II, the greatest intra-cluster distance was observed between genotype SH4 and GT1.

The cluster diagram (Fig 4.31) of 80 genotypes (based on leaf fodder and mineral nutrient properties of mother trees) from twenty populations of *G. optiva* revealed two major clusters and four sub-clusters. Cluster I contained 49 genotypes, including GH4, DO4, DA4, D01, DO2, DA2, DO3, RA1, DA3, RA3, RA4, KD4, DH1, DH2, DH3, KD1, KD2, KD3, DA1, GT1, GT4, GH3, GR1, AD2, NR2. NR1, AD4, GH2, DR4, DR2, GT3, DR3, DR1, NR3, GR4, GR2, GR3, BA3, DH4, BA4, BA1, BA2, SH4, RA2, GH1, GT2, SH1, SH2, SH3 while, 31 genotypes (SI2, SI1, SI4, KT1, KT4, KT2, KT3, ST1, ST3, ST4, KU1, KU2, AD3, HR4, NR4, HR2, HR3, AD1, ST2, HR1, KU4, SN1, SN2, SI3, KU 3, JG1, JG3, SN4, JG2, JG4, SN3) were found in cluster II. The maximum inter-cluster distance was observed between genotype GH4 and SN3. The maximum intra-cluster distance in Cluster I was observed between genotypes GH4 and SH3, while, in cluster II maximum intra cluster distance observed between genotypes SI2 and SN3. Therefore, hybridization between distant genotypes of *G. optiva* may result in increased hybrid vigour. Similar studies on cluster analysis were reported by Kundal *et al*., 2020 in *Toona ciliata*, Behera *et al*., 2017 in *Eucalyptus,* Kumar *et al*., 2016 in *Dalbergia sissoo* and Mohanraj *et al*., 2022 in *T. ciliata*.

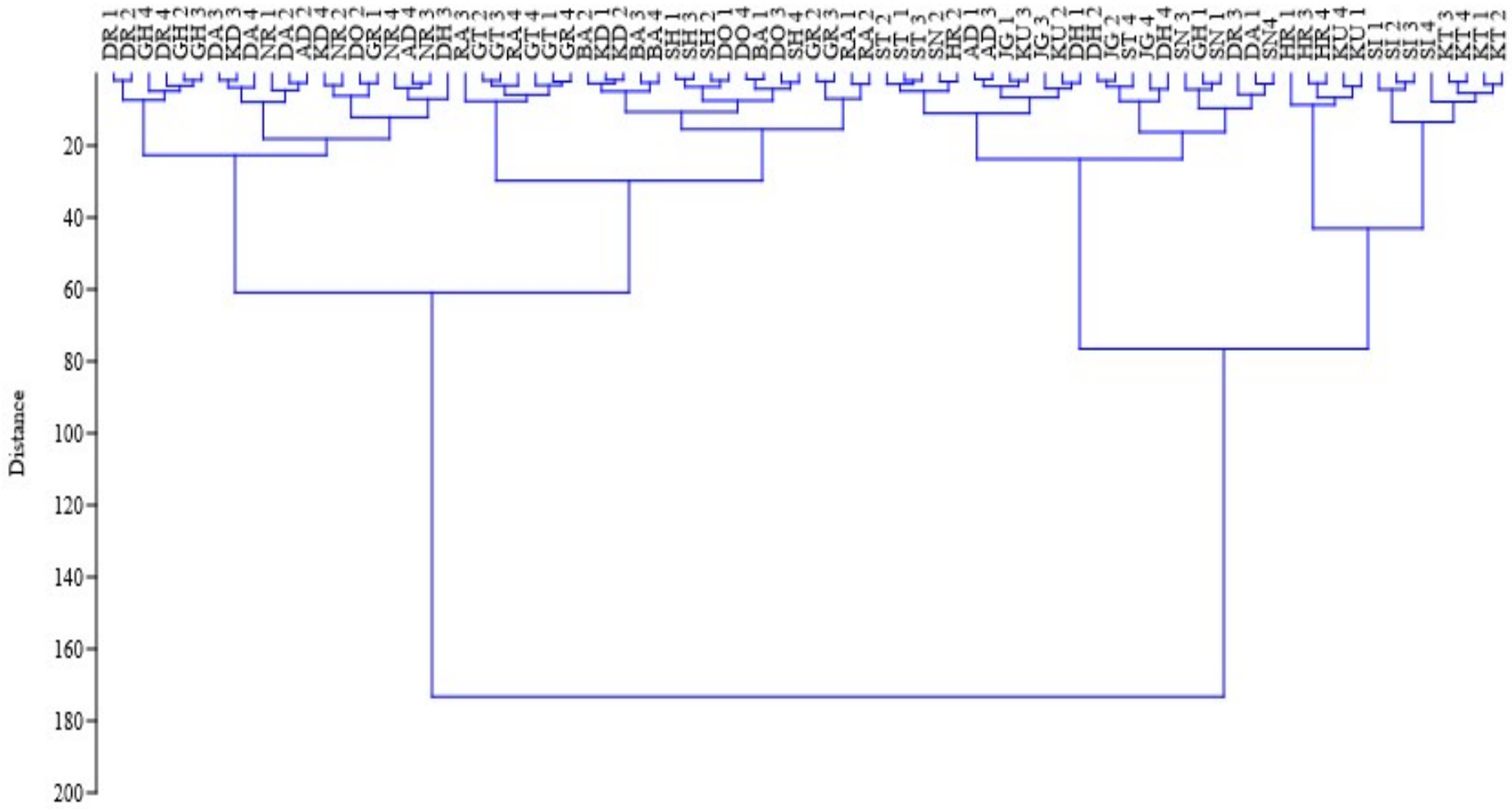


Fig 4.29 Cluster diagram of 80 genotypes (on the basis of tree and leaf morphometric characters) of twenty populations of *Grewia optiva* Drummond

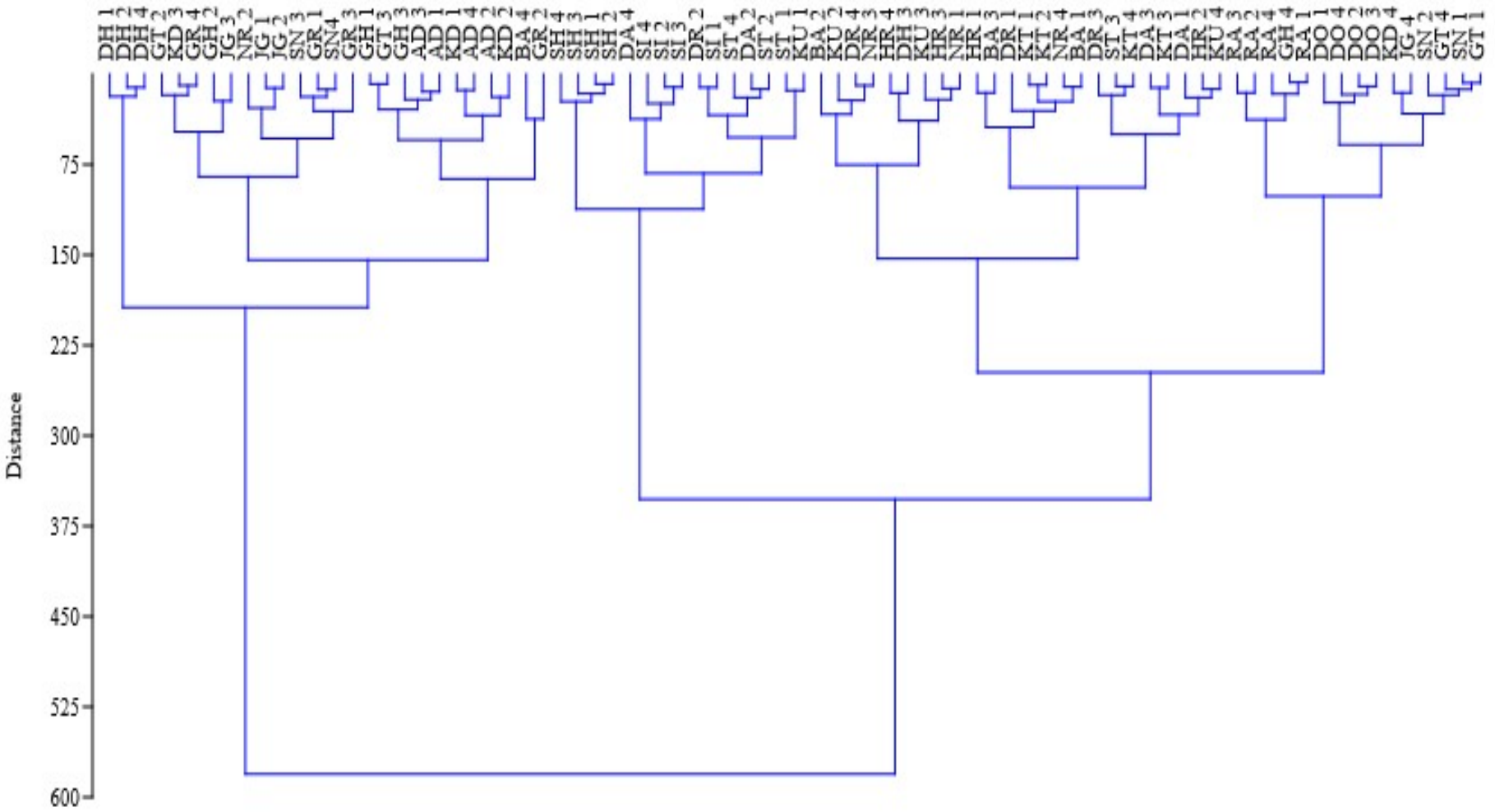


Fig 4.30. Cluster diagram of 80 genotypes (on the basis of seedling growth and fodder quality characteristics of 18 months old seedlings) of twenty populations of *Grewia optiva* Drummond

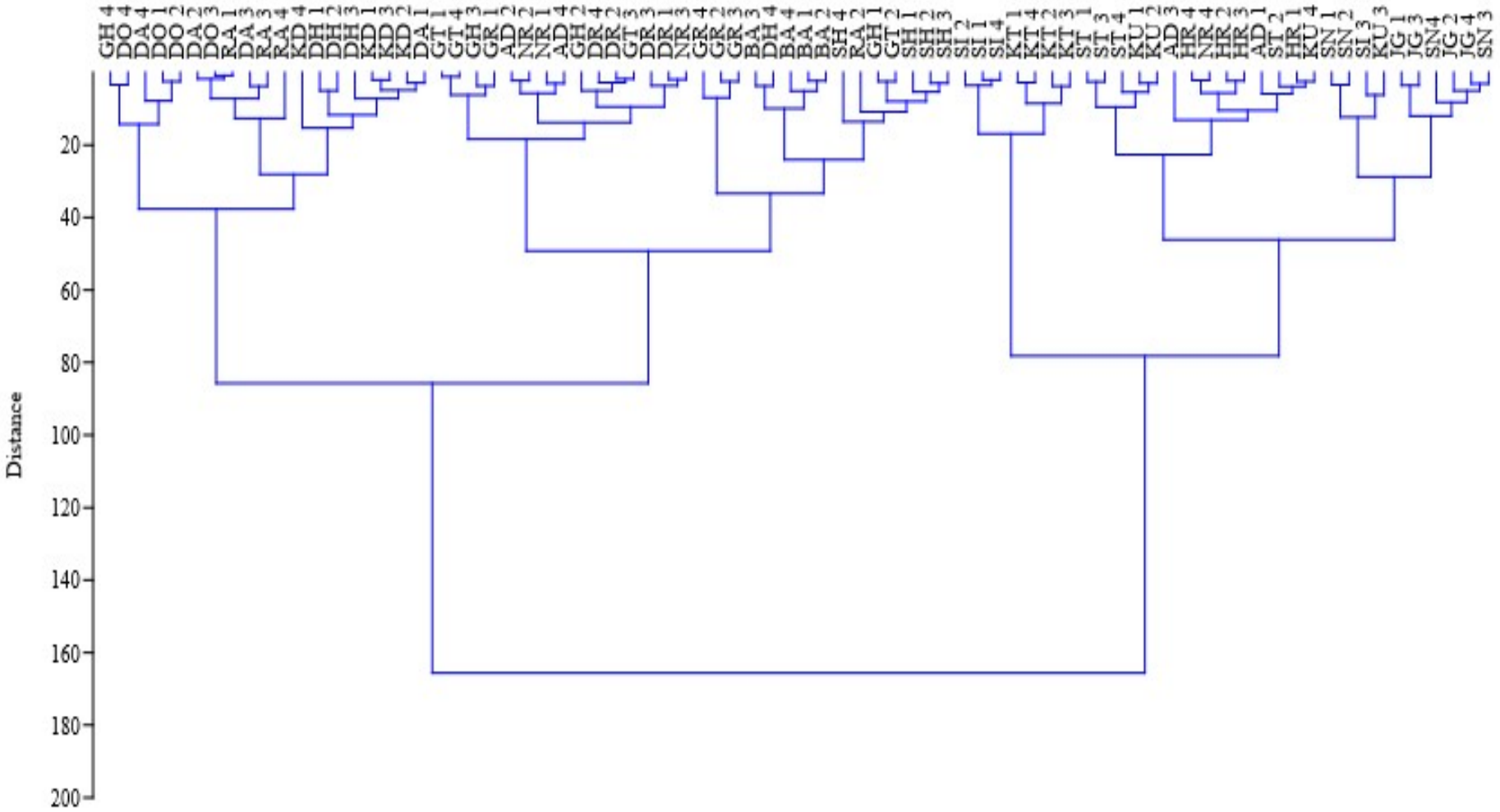


Fig 4.31 Cluster diagram of 80 genotypes (on the basis of leaf fodder and mineral nutrient characteristics of mother trees) of twenty populations of *Grewia optiva* Drummond

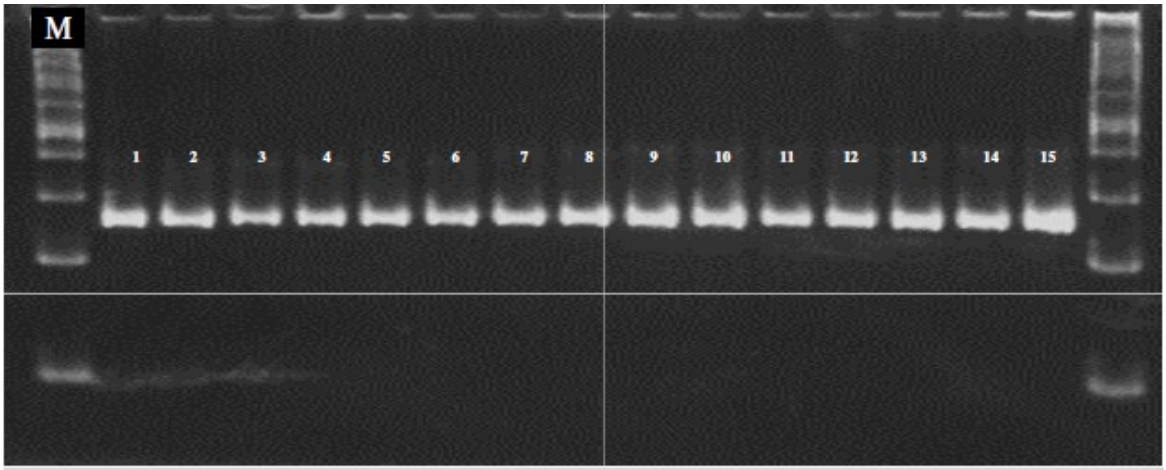
4.10 Molecular markers based analsysis of best studied material

The best-growing half-sib progeny of 15 of the best-identified genotypes, including DH1, DH2, DH4, HR1, ST1, DR1, DR2, NR4, DA4, BA3, KU1, SI2, SI3, KT1 and KT2, of *G. optiva*, were used for molecular marker-based analysis. These genotypes were selected based on 18 months seedling growth and their fodder characteristics. ISSR (Inter Simple Sequence Repeat) markers, which are expected to have higher repeatability than RAPD markers, had been used for the identification and assessment of varietal genetic relationships in several plant species (Ajibade *et al*., 2000).

Out of a total of ten ISSR primers used in this investigation, only two of them (UBC 809 and UBC 820) amplified and produced a banding pattern (Table 4.56). Primers UBC 809 and UBC 820 produced different types of bands, with the former producing monomorphic bands and the latter producing polymorphic bands. The maximum variations were observed between the half sib progeny of DA3 and DH2 genotypes and the same results were recorded in the cluster diagram of 80 genotypes, which was developed based on seedling growth and fodder quality characteristics of 18 months old seedlings (Fig 4.30). Similarly, ISSR molecular markers were used by Verma *et al*., 2015 to characterise *G. optiva* and found that primer UBC 820 produced polymorphic bands. Sharma *et al.,* 2022 used ISSR markers to assess genetic diversity in *Salix tetrasperma* and Saresh (2013) employed 14 RAPD and 11 ISSR markers for paternity analysis in *Grewia optiva* hybrids.

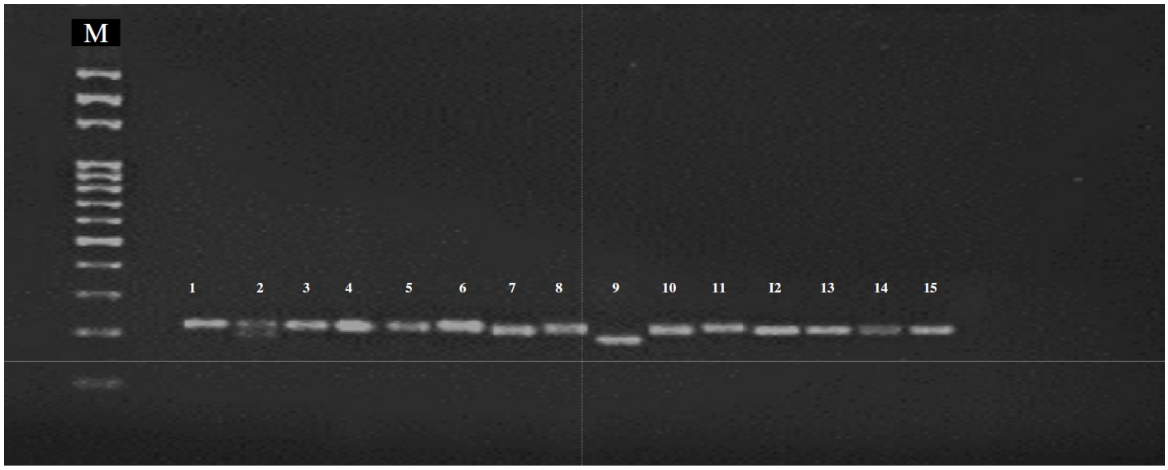
Table 4.56 Total number of amplified and polymorphic fragments generated by PCR using ISSR primers in *Grewia optiva*

Primer name (ISSR)	Base sequence (5'-3')	Total number of scorable bands	No. of polymorphic bands	No. of monomorphic bands	Band size range	Percentage of monomorphism	Percentage of polymorphism
UBC - 809	AGAGAGAGAGAGAGAGG	1	-	1	250-300bp	100%	-
UBC - 820	GAGAGAGAGAGAGAGAT	2	2	-	200bp, 200-250bp	-	100%



Where, M: 100 bp ladder
1- DH1 , 2- DH2, 3- DH3, 1-HR1, 5-ST1 , 6- DR1 , 7- DR2, 8- NR4, 9- DA4, 10-BA3, 11- KU 2, 12- SI2, 13- SI3, 14- KT1, 15 – KT2

UBC 809



Where, M: 100 bp ladder
1- DH1 , 2- DH2, 3- DH3, 1-HR1, 5-ST1 , 6- DR1 , 7- DR2, 8- NR4, 9- DA4, 10-BA3, 11- KU 2, 12- SI2, 13- SI3, 14- KT1, 15 – KT2

UBC 820

Plate 7. ISSR fingerprints of half sib progeny of 15 genotypes generated by UBC-820 and UBC-809

Chapter-5

SUMMARY AND CONCLUSION

The current study, titled **"Morphogenetic variation for leaf fodder quality parameters in populations of *Grewia optiva* Drummond,"** was conducted in the research field and laboratory of the Department of Tree Improvement and Genetic Resources, College of Forestry, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan (H.P.) between the years 2020 and 2023 to study variations in morphological, seed and germination parameters, fodder quality and mineral nutrients characteristics of different selected populations of *G. optiva*. The physiochemical characteristics of the soil samples collected underneath different populations of *G. optiva* were analysed to determine their correlation with the leaf, fodder and morphometric characteristics. Half-sib progenies of *G. optiva* were also evaluated for 18 months under Shilli nursery conditions and the top performing progeny of 15 best selected genotypes were further examined using ISSR genetic markers. This study's key results are summarized below:

5.1 Selection of genotypes of *G. optiva* Drummond from populations on the basis of morphometric characters.

5.2 Nursery evaluation for the selection of best genotypes of *G. optiva* Drummond.

5.3 Physiochemical properties of soil of different populations.

5.4 Variations in fodder quality parameters among different population.

5.5 Molecular markers-based analysis of best studied material.

5.1 Selection of genotypes of *G. optiva* Drummond from populations on the basis of morphometric characters.

5.1.1 Tree Morphological characteristics

The analysis of variance revealed highly significant differences between genotypes and populations for all tree morphological characteristics, including height, diameter, crown spread (east-west), crown spread (north-south), number of primary branches, number of secondary branches and branch nodal length. This facilitates the selection of a genetically diverse population, preserving genetic diversity in long-term improvement programmes. There were three types of leaf shapes observed among populations *i.e.,* narrowly ovate, ovate and broadly ovate. The leaf apex was narrowly acuminate and broadly acuminate. It indicates

that a great deal of variation existed in the extant material chosen for the study and demonstrates its suitability for future tree breeding programmes. On the basis of tree morphological characteristics, it was determined that four populations (Dramman, Sihunta, Kutuldi and Dharot) and eight genotypes (DR1, SI1, SI3, SI4, KU1, DH3, DH4 and NR2) are superior.

According to the altitudinal differences (mean value) among *G. optiva* populations, tree height, diameter, crown spread, number of primary branches and branch nodal length were observed to decrease from A1 (400–800 m a msl) to A4 (1600–2000 m) altitudinal ranges.

The coefficient of variation for the number of secondary branches was the highest (22.61 %), while the coefficient of variation for branch nodal length was the lowest (8.61 %). In accordance with the correlation studies, there was a strong correlation between tree height and tree diameter (0.618). Tree height and crown spread (N-S) (0.441) and tree height and number of primary branches (0.320). A highly positive and statistically significant correlation (0.722) between tree height and branch nodal length was observed. The number of secondary branches correlated negatively (-0.129) with the height of the tree. In general, the magnitude of the genotypic correlation coefficient was greater than the phenotypic correlation coefficient.

Path analysis determined the direct and indirect effects of tree morphological and leaf morphometric characteristics on tree height. Internodal length had the greatest direct positive effect on tree height (0.499), followed by leaf area (0.410), tree diameter (0.131), crown spread (E-W) (0.020), crown spread (N-S) (0.100), number of primary branches (0.021), and leaf width (0.015), while, number of secondary branches (-0.243) and leaf length (-0.309) had negative direct effects.

5.1.2 Leaf morphometric Characteristics.

For all leaf morphometric characteristics, namely leaf area, leaf length, leaf width and petiole length, analysis of variance exhibited highly significant variations between genotypes and populations. In terms of leaf morphometric characteristics, the two populations (Sihunta and Kuthar) and three genotypes (SI1, KT2, and KT4) were reported to be the best.

With regard to altitudinal variation in leaf morphometric traits among populations, traits including leaf area, leaf length and leaf width were observed to rise from the A1 (400–800 m) to A2 (800–1200 m a msl) altitudinal zone. However, as the altitudinal range grew from A2 to A4, these observable features further decreased. Maximum values for average leaf area, length, width and petiole length were discovered for A2 (800–1200 m a msl altitudinal range).

The analysis of the genetic variability parameters showed that for all of the traits under examination, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). It suggested how the environment affects the expression of characters. Among leaf characters the high heritability (94.00 %) with high genetic gain (48.76%) was recorded for Leaf area. It indicated the presence of additive genes in the trait and selection of these traits very much reliable for tree improvement programmes. There was a significant positive correlation reported between leaf area and leaf length (0.87) and leaf area and leaf width (0.53).

PCA principal components analysis indicated that the eigen values of the first three components, PC I, PC II and PC III, were all greater than 1.0. All three variables accounted for 67.03 (%) of the total variation. The leaf area should be given the highest priority (as it had the highest loading value in PCI), along with the highest loaded components of PCI, PCII, and PCIII.

Cluster analysis (genetic divergence analysis) was utilised to classify eighty genotypes of twenty populations of *G. optiva* into two main clusters and four subclusters based on tree and leaf morphometric characteristics. The maximum inter cluster distance observed between DR1 and KT2 genotypes. Crossing between distant genotypes found in Clusters I (DR1 and RA2) and II (ST2 and KT2) may result in hybrid vigour with better tree and leaf features.

Experiment 1b: Nursery evaluation for the selection of best genotypes of *G. optiva.*

Seed characteristics including seed length, seed width, seed thickness and 100 seed weight, as well as, germination characteristics, including germination percentage, germination value, germination energy, germination index and survival percentage varied significantly among genotypes and populations of *G. optiva*.

The populations from the altitudinal range A1 (400-800m a m s l) have the highest average germination and survival percentage. Populations from the A3 (1200-1600m) altitudinal zone showed the greatest growth in terms of seedling height and collar diameter (at the age of 18 months).

The 15 best genotypes of *G. optiva i.e.,* DH1, DH2, DH4, HR1, ST1, DR1, DR2, NR4, DA3, BA3, KU1, SI2, SI3, KT1 and KT2 were identified after 18 months of nursery evaluations. These genotypes were chosen based on seedling height (>95 cm), crude protein (>22.50 %) and leaf area (>63 cm^2) in addition to other grouping characteristics.

Germination value demonstrated the highest phenotypic coefficient of variation (67.41 %) and genotypic coefficient of variation (61.30 %), whereas, survival percentage showed the lowest phenotypic coefficient of variation (7.30 %) and genotypic coefficient of variation (9.30 %). High PCV and GCV values were recorded for collar diameter (PCV: 25.98 %, GCV: 21.90 %) and seedling height (PCV: 23.62 %, GCV: 21.84 %) among seedling growth characteristics. High heritability (85.54 %) with high genetic advance (33.20) was recorded for seedling height.

The correlation between seedling height and collar diameter (0.929) and seedling height and internodal length (0.884) was found to be highly significant. Leaf area correlated significantly and positively with seedling height (0.718). There is a highly significant correlation observed between germination percentage and survival percentage (0.760), germination percentage and germination value (0.908) and germination rate and germination energy (0.870).

The path coefficient analysis revealed both direct and indirect effects of seed, germination and seedling growth characteristics on seedling height. A perusal of the genotypic path coefficient analysis indicated that germination percentage had the greatest direct positive effect on seedling height (0.54), followed by germination energy (0.52), intermodal length (0.50), collar diameter (0.33), 100 seed weight (0.11), seed length (0.09), seed thickness (0.04), and leaf area (0.01). Germination value (-0.78), germination index (-0.04) and survival percentage (-0.18) all had direct negative effects on seedling height.

Genotypic path coefficient analysis between leaf fodder and mineral nutrients of 18 months old seedlings, revealed that P (0.13), Ca (0.05), ether extract (0.04), Na (0.02) and K

(0.01) had the direct positive effect on crude protein, whereas, crude fibre (-0.27), total ash (-0.04) and nitrogen-free extract (-0.94) had the direct negative effect.

Principal component I, principal component II and principal component III all had eigen values greater than 1.0 and collectively accounted for 74.52 per cent of the total variation. Height of seedlings was the greatest loaded value component in PC I. For the further selection and improvement of superior strains of *G. optiva*, it is necessary to prioritise seedling height in conjunction with highly loaded components of PCII and PCIII.

Eighty genotypes (based on seedling growth and forage quality characteristics of 18 months old seedlings) of twenty populations of *G. optiva* were separated into two main clusters and four sub-clusters, according to cluster analysis. The largest distance between clusters was observed between the DH1 and GT1 genotypes. In Cluster I, the genotypes with the greatest intra-cluster distance were DH1 and GR2, whereas, in Cluster II, SH4 and GT1 exhibited the greatest intra-cluster distance.

5.3 Physiochemical properties of soil of different populations.

With the exception of bulk density and particle density, all physiochemical soil characteristics decreased as soil depth increased from 0 to 15 cm to 15 to 30 cm.

As we moved from A1 (400-800 m a msl) to A4 (1600-2000 m a msl), altitudinal zone the proportions of soil organic carbon, soil nitrogen and soil porosity increased, whereas, proportion of soil bulk density (BD), particle density (PD) and available potassium decreased.

A Significant positive correlations were observed between leaf area and soil N (0.509), leaf area and SOC (0.407), leaf area and soil P (0.728) and leaf area and soil K (0.577). There was a highly significant correlation examined between leaf length and SOC (0.401), leaf length and soil N (0.509), leaf length and P (0.710) and leaf length and soil K (0.592). Soil P showed significant positive correlations with tree height (0.385), tree diameter (0.602), crown spread (N-S) (0.629), crown spread (E-W) (0.334), branch nodal length (0.436) and leaf width (0.470). Significant positive correlations were observed between soil K and tree height (0.774), soil K and tree diameter (0.645), soil K and crown spread (N-S) (0.576), soil K and crown spread (E-W) (0.314), soil K and branch nodal length (0.73), and soil K and leaf width (0.55).

Correlation between leaf fodder and soil physiochemical characteristics reveals a significant positive correlation between leaf dry matter (LDM) and SOC (0.361), leaf dry matter and soil N (0.341) and leaf dry matter and soil K (0.310), whereas, leaf dry matter demonstrated a negative correlation with bulk density (-0.351) and particle density (-0.556). Crude protein showed a significant positive correlation with SOC (0.411), soil N (0.575) and soil P (0.80). Significantly negative correlations were observed between the nitrogen-free extract and soil pH (-0.315), nitrogen free extract SOC (-0.0373), nitrogen free extract and soil N (-0.541), nitrogen free extract and soil P (-0.799), and nitrogen free extract and soil K (-0.445).

5.4 Variations in fodder quality parameters among different population.

There were significant variations observed between populations (mother trees) of *G. optiva* with regard to leaf fodder quality and mineral nutrient characteristics. The ranges for leaf fresh weight (76.93-133.09 gm, mean 97.70gm), leaf dry matter content (48.91–65.84 %, mean 54.34 %), leaf dry weight (40.50-66.46 g, mean 52.69 g), crude protein (17.00–24.57 %, mean 20.86 %), crude fibre (17.10–20.92 %, mean 19.40 %) and total ash (9.42–12.88 %, mean 10.80 %) were all noted. It was discovered that six populations *i.e.,* Harsar, Sujanpur Tihra, Sihunta, Kutuldi, Jagdhar and Sangrah contained more than 23 per cent crude protein. Sihunta had the greatest level of crude protein among these populations.

The populations of mid-altitudinal zone A3 (1200–1600 m a msl) had the highest average concentration of crude protein. P, Ca and total amino acid levels were at their maximum and lowest points in the populations of A3 (1200–1600 m a msl) and A4 (1600–2000 m a msl) altitudinal zones, respectively.

For all of the investigated fodder quality characteristics, PCV and GCV values fell within the low and high ranges. Leaf fresh weight (PCV: 18.22 %, GCV: 17.71 %) and leaf dry weight (PCV: 16.62 %, GCV: 16.00 %) reported high PCV and GCV. High PCV and GCV were recorded for leaf P (PCV: 24.17 %, GCV: 24.00 %) and leaf Na (PCV: 23.60 %, GCV: 22.79 %) among mineral nutrient characteristics.

The traits with highest genetic gain and heritability were found to be leaf fresh weight, leaf dry weight, crude protein and total ash. It anticipated that choosing these features is optimal for tree improvement programs. Among leaf nutrient characteristics, high

heritability was reported for leaf P (98.66 %), leaf Na (93.26 %), leaf K (94.51 %) and leaf Ca (90.42 %), whereas, high heritability with high genetic advance was observed for leaf Na.

Studies of correlation found numerous significant positive and negative values among various attributes, suggesting and emphasising the use of such correlations in indirect selection for desired traits of the species.

The long-distance reported genotypes, *i.e.,* SN3 and SI2 in cluster II and GH4 and SH3 in cluster I, It is anticipated that the hybridization between these genotypes will produce heterotic hybrids and the desired segregation for quantitative and qualitative traits.

Path coefficient analysis, demonstrated the direct and indirect effects of leaf fodder, amino acids and mineral nutrients (of mother trees) on leaf dry weight (LDW). Maximum direct positive effects on leaf dry weight were imposed by leaf fresh weight (0.937), followed by leaf dry matter content (0.414), crude protein (0.367), ether extract (0.140), Na (0.132), P (0.092) and total ash (0.044).

Principal Component Analysis, it evident that principal components I (PC I), principal component II (PC II), principal component III (PC III) and principal component IV (PC IV) gave eigen value>1.0 and all the four components accounted for 75.649 per cent variation. Highest loading value recorded for crude protein (0.372) in PCI, leaf dry matter content, leaf dry weight in PCII, leaf calcium, leaf fresh weight, leaf dry weight in PCIII. Ether extract, crude fibre and leaf dry matter content in PCIV.

The cluster diagram of 80 genotypes (based on leaf fodder and mineral nutrient properties of mother trees) of *G. optiva* Drummond revealed two major clusters and four sub-clusters. The maximum inter cluster distance was observed between genotypes GH4 and SN3. In Cluster I, the maximum intra cluster distance was observed between genotypes GH4 and SH3, while in Cluster II, the maximum intra cluster distance was observed between genotypes SI2 and SN3.

5.5 Molecular markers-based analysis of best studied material

The best growing half sib progeny from 15 best-identified genotypes *viz.,* DH1, DH2, DH4, HR1, ST1, DR1, DR2, NR4, DA4, BA3, SI2, SI3, KT1 and KT2 were employed for molecular markers based analysis using 10 ISSR markers. Only two of the 10 ISSR primers,

i.e., UBC 809 and UBC 820 were amplified and generated a banded pattern. Monomorphic bands were created by primer UBC 809. A polymorphic band was formed by UBC 820 and the half-sibling progeny of the DA3 and DH2 genotypes showed the most variation. These genotypes, DA3 and DH2, also had the greatest variation in a cluster diagram made up of 80 genotypes (based on seedling growth and fodder quality characteristics of 18 months old seedlings).

Conclusion:

- The altitudinal range between 1200 and 1600 m (a msl) was found best, as populations from this zone had the highest average crude protein content. Six nutritionally superior populations, including Harsar, Sujanpur Tihra, Sihunta, Kutuldi, Jagdhar and Sangrah, have been screened with more than 23 per cent crude protein and desired morphological characteristics. These screened nutritive selections of *G. optiva* can be used for further selection, hybridization, mass multiplication and the production of high quality planting material.
- By providing livestock access to superior and ample feed, the breeding of superior nutritive selection will contribute to improving the quality of livestock and easing the concerning strain that livestock have on the Western Himalayas' forest resources, especially during the harsh winter months.
- The studied characteristics, *viz.,* leaf area, seedling height, fresh weight of 100 leaves and dry weight of 100 leaves, were shown to have high heritability with high genetic advance suggested that there is a high level of genetic (additive gene) control, which would make the selection of these characteristics for tree improvement programmes more reliable.
- Except for soil bulk density and particle density, all physiochemical characteristics of the soil decreased as soil depth increased from 0-15 cm to 15-30 cm. The percentages of soil organic carbon, available soil nitrogen, and soil porosity increased as we moved from A1 (400-800 m a msl) to A4 (1600-2000 m a msl). Whereas, soil bulk density (BD), particle density (PD) and available potassium decreased from A1 (400-800 m a msl) to A4 (1600-2000 m a msl) altitudinal zone.
- It became apparent that there were significant variations among the different populations and genotypes for morphometric, seed, seedling growth and fodder quality characteristics which show their suitability for further tree breeding

programmes. In order to retain genetic diversity during long-term tree improvement programmes, it is easier to select a population with a broad genetic base as an outcome. Through selection and breeding strategies, this variability may be leveraged in tree development programmes to produce more advance generations.

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ANOVA of genotypes and population of *Grewia optiva* for different parameters under study

APPENDIX-I

ANOVA for Leaf Morphometric characteristics

Analysis of variance for leaf length (cm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.133476	0.066738	0.724482
Replication	79	1342.343	16.99168	184.4544
Error	158	14.55474	0.092119	

Analysis of variance for length (cm) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.991575	0.330525	0.166595
Replication	19	333.3677	17.54567	8.843562
Error	57	113.0883	1.984005	

Analysis of variance for leaf width (cm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.027209	0.013605	0.239829
Replication	79	391.248	4.952506	87.30541
Error	158	8.962744	0.056726	

Analysis of variance for leaf width (cm) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.141175	0.047058	0.085083
Replication	19	100.0718	5.266937	9.52278
Error	57	31.52603	0.553088	

Analysis of Variance for leaf area (cm^2) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	4.695257	2.347629	0.527979
Replication	79	85190.58	1078.362	242.5221
Error	158	702.5386	4.446447	

Analysis of Variance for leaf area (cm^2) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	159.0325	53.01084	1.819911
Replication	19	26577.52	1398.817	48.02267
Error	57	1660.311	29.12826	

Analysis of Variance for petiole length (cm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.000847	0.000424	0.60047
Replication	79	2.758646	0.03492	49.48907
Error	158	0.111485	0.000706	

Analysis of Variance for petiole length (cm) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.016594	0.005531	0.658783
Replication	19	0.424374	0.022335	2.660199
Error	57	0.478581	0.008396	

APPENDIX-II

ANOVA for Seed characteristics

Analysis of Variance for seed length (mm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.00697	0.003485	0.150463
Replication	79	95.33106	1.206722	52.09882
Error	158	3.659624	0.023162	

Analysis of Variance for seed length (mm) among populations of *Grewia optiva* Drummond

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	2.52215	0.840717	4.042095
Replication	19	17.39942	0.915759	4.402891
Error	57	11.85545	0.20799	

Analysis of Variance for seed width (mm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.027247	0.013624	0.939072
Replication	79	58.68282	0.74282	51.20233
Error	158	2.292193	0.014508	

Analysis of Variance for seed width (mm) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	1.174144	0.391381	3.24827
Replication	19	11.51891	0.606259	5.031645
Error	57	6.867881	0.120489	

Analysis of Variance for seed thickness (mm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.053208	0.026604	0.404496
Replication	79	95.20074	1.205073	18.32246
Error	158	10.3917	0.06577	

Analysis of Variance for seed thickness (mm) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.45004	0.150013	0.943854
Replication	19	22.22413	1.169691	7.359463
Error	57	9.05941	0.158937	

Analysis of Variance for 100 seed weight (gm) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.352105	0.176053	1.824971
Replication	79	1142.774	14.4655	149.9501
Error	158	15.24205	0.096469	

Analysis of Variance for 100 seed weight (gm) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	1.77897	0.59299	0.80073
Replication	19	336.9337	17.73335	23.94581
Error	57	42.21203	0.740562	

APPENDIX-III

ANOVA for Germination and Seedling growth characteristics

Analysis of Variance for germination percentage among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	275.8333	137.9167	2.922002
Replication	79	49006.25	620.3323	13.14281
Error	158	7457.5	47.19937	

Analysis of Variance for germination percentage among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	482.6389	160.8796	4.465675
Replication	19	13799.31	726.2792	20.15996
Error	57	2053.472	36.02583	

Analysis of Variance for germination value among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	27.37041	13.68521	2.318804
Replication	79	8854.795	112.086	18.99171
Error	158	932.4903	5.901837	

Analysis of Variance for germination value among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	41.863	13.95433	1.670323
Replication	19	2433.542	128.0811	15.33121
Error	57	476.1936	8.354273	

Analysis of Variance for germination energy among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	47.5	23.75	0.445709
Replication	79	70079.58	887.0833	16.64763
Error	158	8419.167	53.28586	

Analysis of Variance for germination energy among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	193.75	64.58333	1.018444
Replication	19	19551.53	1029.028	16.2272
Error	57	3614.583	63.41374	

Analysis of Variance for germination index among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	551.3083	275.6542	1.429728
Replication	79	27970.8	354.0607	1.836397
Error	158	30462.69	192.8018	

Analysis of Variance for germination index among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	306.0153	102.0051	2.002004
Replication	19	6113.349	321.7552	6.314932
Error	57	2904.235	50.95149	

Analysis of Variance for survival percentage among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	3243.711	1621.855	12.25962
Replication	79	13203.22	167.1293	1.263333
Error	158	20902.2	132.2924	

Analysis of Variance for survival percentage among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	23.32228	7.774094	0.297627
Replication	19	2888.896	152.0471	5.821045
Error	57	1488.854	26.12025	

Analysis of Variance for seedling height (at the age of 6 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	285.5218	142.7609	22.75133
Replication	79	22984.05	290.9374	46.36571
Error	158	991.4244	6.274838	

Analysis of Variance for seedling height (at the age of 6 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	101.4404	33.81348	1.435781
Replication	19	6124.148	322.3236	13.68644
Error	57	1342.383	23.55059	

Analysis of Variance for seedling height (at the age of 12 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2.00	18.71566	9.357831	3.406333
Replication	79.00	45731.4	578.8785	210.7169
Error	158.00	434.0554	2.747186	

Analysis of Variance for seedling height (at the age of 12 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	790.1602	263.3867	3.514702
Replication	19	10182.14	535.9021	7.151219
Error	57	4271.499	74.93857	

Analysis of Variance for seedling height (at the age of 18 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	4.952538	2.476269	0.559565
Replication	79	65339.46	827.0818	186.8967
Error	158	699.2041	4.425343	

Analysis of Variance for seedling height (at the age of 18 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	569.6283	189.8761	3.697887
Replication	19	18283.4	962.2843	18.74074
Error	57	2926.79	51.34719	

Analysis of Variance for collar diameter (at the age of 6 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.308262	0.154131	1.893974
Replication	79	293.891	3.720139	45.71333
Error	158	12.858	0.08138	

Analysis of Variance for collar diameter (at the age of 6 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	3.2089	1.069633	1.96299
Replication	19	64.38038	3.388441	6.218464
Error	57	31.0593	0.5449	

Analysis of Variance for collar diameter (at the age of 12 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	1.02592	0.51296	2.833154
Replication	79	416.9298	5.277592	29.14892
Error	158	28.60687	0.181056	

Analysis of Variance for collar diameter (at the age of 12 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	5.701285	1.900428	2.833265
Replication	19	95.04225	5.002223	7.457596
Error	57	38.23306	0.670756	

Analysis of Variance for collar diameter (at the age of 18 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	2.192276	1.096138	3.962964
Replication	79	984.7914	12.46571	45.06839
Error	158	43.70209	0.276595	

Analysis of Variance for collar diameter (at the age of 18 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	12.85186	4.283955	2.934501
Replication	19	232.2	12.22105	8.371399
Error	57	83.21191	1.459858	

Analysis of Variance for internodal length (at the age of 6 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.196119	0.098059	1.357051
Replication	79	190.2299	2.407974	33.32417
Error	158	11.41693	0.072259	

Analysis of Variance for internodal length (at the age of 6 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.231624	0.077208	0.500996
Replication	19	18.63621	0.980853	6.364681
Error	57	8.784201	0.154109	

Analysis of Variance for internodal length (at the age of 12 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.147214	0.073607	1.313428
Replication	79	190.2299	2.407974	42.9673
Error	158	8.854639	0.056042	

Analysis of Variance for internodal length (at the age of 12 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	1.42399	0.474663	1.486835
Replication	19	43.78908	2.304688	7.219206
Error	57	18.19691	0.319244	

Analysis of Variance for internodal length (at the age of 18 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.009977	0.004989	0.062254
Replication	79	228.7389	2.895429	36.13252
Error	158	12.66111	0.080134	

Analysis of Variance for internodal length (at the age of 18 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	1.132064	0.377355	1.398095
Replication	19	59.72956	3.143661	11.64723
Error	57	15.38466	0.269906	

Analysis of Variance for petiole length (at the age of 6 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.001748	0.000874	4.611256
Replication	79	1.101978	0.013949	73.58343
Error	158	0.029952	0.00019	

Analysis of Variance for petiole length (at the age of 6 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.000324	0.000108	0.067632
Replication	19	0.275324	0.014491	9.081472
Error	57	0.090951	0.001596	

Analysis of Variance for petiole length (at the age of 12 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.002888	0.001444	1.744961
Replication	79	1.570597	0.019881	24.02344
Error	158	0.130755	0.000828	

Analysis of Variance for petiole length (at the age of 12 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.021664	0.007221	2.478671
Replication	19	0.330794	0.01741	5.975995
Error	57	0.166061	0.002913	

Analysis of Variance for petiole length (at the age of 18 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.00027	0.000135	0.303681
Replication	79	1.932116	0.024457	55.10209
Error	158	0.070129	0.000444	

Analysis of Variance for petiole length (at the age of 18 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.033584	0.011195	7.126227
Replication	19	0.520914	0.027417	17.45275
Error	57	0.089541	0.001571	

Analysis of Variance for leaf area (at the age of 6 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	9.067881	4.53394	1.275659
Replication	79	8938.332	113.1434	31.83377
Error	158	561.563	3.554196	

Analysis of Variance for leaf area (at the age of 6 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	10.3197	3.439901	0.173124
Replication	19	1824.176	96.00924	4.831977
Error	57	1132.565	19.86955	

Analysis of Variance for leaf area (at the age of 12 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	2.92	1.457838	0.453207
Replication	79	5071.84	64.20046	19.95837
Error	158	508.24	3.216718	

Analysis of Variance for leaf area (at the age of 12 month) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	2.92	1.457838	0.453207
Replication	79	5071.84	64.20046	19.95837
Error	158	508.24	3.216718	

Analysis of Variance for leaf area (at the age of 18 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	4.979307	2.489654	0.984543
Replication	79	10712.12	135.5965	53.62216
Error	158	399.5408	2.528739	

Analysis of Variance for leaf area (at the age of 18 month) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	4.979307	2.489654	0.984543
Replication	79	10712.12	135.5965	53.62216
Error	158	399.5408	2.528739	

APPENDIX IV

ANOVA for fodder quality characteristics of 18 months old seedling of different genotypes of populations of *Grewia optiva* Drummond.

Analysis of Variance for crude protein (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.012562	0.006281	0.021041
Replication	79	683.7021	8.654457	28.99141
Error	158	47.16584	0.298518	

Analysis of Variance for crude protein (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	7.899254	2.633085	0.297627
Replication	19	143.442	7.54958	5.821045
Error	57	76.55942	1.343148	

Analysis of Variance for crude fiber (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.148503	0.074251	0.437989
Replication	79	424.9277	5.378832	31.72822
Error	158	26.78547	0.169528	

Analysis of Variance for crude fiber (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	2.182754	0.727585	0.440453
Replication	19	45.30139	2.384284	1.443357
Error	57	94.15842	1.651902	

Analysis of Variance for ether extract (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.018212	0.009106	1.270034
Replication	79	28.50105	0.360773	50.31715
Error	158	1.132856	0.00717	

Analysis of Variance for ether extract (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.013234	0.004411	0.068528
Replication	19	5.817924	0.306207	4.756844
Error	57	3.669191	0.064372	

Analysis of Variance for nitrogen free extract (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.117494	0.058747	0.037964
Replication	79	1733.636	21.94476	14.18146
Error	158	244.4933	1.547426	

Analysis of Variance for nitrogen free extract (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	9.098304	3.032768	0.670281
Replication	19	310.8771	16.36195	3.616205
Error	57	257.9033	4.524619	

Analysis of Variance for leaf phosphorus (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	1.58E-05	7.89E-06	0.226469
Replication	79	0.257793	0.003263	93.62943
Error	158	0.005507	3.49E-05	

Analysis of Variance for leaf phosphorus (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.00413	0.001377	4.134605
Replication	19	0.062825	0.003307	9.931853
Error	57	0.018977	0.000333	

Analysis of Variance for leaf calcium (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.005578	0.002789	0.559517
Replication	79	24.90478	0.31525	63.24823
Error	158	0.787525	0.004984	

Analysis of Variance for leaf calcium (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.203785	0.067928	1.563074
Replication	19	5.620695	0.295826	6.807147
Error	57	2.477115	0.043458	

Analysis of Variance for leaf sodium (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	10.65675	5.328377	0.073579
Replication	79	760746.5	9629.703	132.9747
Error	158	11441.97	72.41756	

Analysis of Variance for leaf sodium (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	2150.188	716.7292	0.681749
Replication	19	191507.4	10079.34	9.587416
Error	57	59924.61	1051.309	

Analysis of Variance for total ash (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	2	0.217626	0.108813
Replication	79	79	114.545	1.449937
Error	158	158	9.207859	0.058278

Analysis of Variance for leaf sodium (of 18 months old seedlings) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.772184	0.257395	1.298765
Replication	19	26.11299	1.374368	6.934807
Error	57	11.29649	0.198184	

Analysis of Variance for total ash (of 18 months old seedlings) among genotypes of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	2	0.217626	0.108813	1.86715
Replication	79	114.545	1.449937	24.87983
Error	158	9.207859	0.058278	

APPENDIX V

ANOVA for Physiochemical characteristics of Soil

Analysis of Variance for soil bulk density (BD) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	0.002		
Factot A	19	2.868	0.151	161.185
Factor B	1	0.466	0.466	497.814
Interaction	19	0.236	0.012	13.254
Error	78	0.073	0.001	

Analysis of Variance for soil pH among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	0.057		
Factot A	19	31.813	1.674	52.379
Factor B	1	1.746	1.746	54.609
Interaction	19	2.281	0.12	3.755
Error	78	2.493	0.032	

Analysis of Variance for soil particle density(PD) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	0.002		
Factot A	19	2.327	0.122	37.756
Factor B	1	0.12	0.12	37.012
Interaction	19	0.038	0.002	0.623
Error	78	0.253	0.003	

Analysis of Variance for soil porosity among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	5.492		
Factot A	19	3,203.59	168.61	90.128
Factor B	1	495.965	495.965	265.112
Interaction	19	474.603	24.979	13.352
Error	78	145.921	1.871	

Analysis of Variance for soil porosity among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	5.492		
Factot A	19	3,203.59	168.61	90.128
Factor B	1	495.965	495.965	265.112
Interaction	19	474.603	24.979	13.352
Error	78	145.921	1.871	

Analysis of Variance for soil organic carbon (OC) among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	0.003		
Factot A	19	29.393	1.547	599.684
Factor B	1	9.241	9.241	3,582.09
Interaction	19	4.434	0.233	90.457
Error	78	0.201	0.003	

Analysis of Variance for Soil Nitrogen among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	118.556		
Factot A	19	2,50,176.66	13,167.19	147.211
Factor B	1	50,904.03	50,904.03	569.113
Interaction	19	18,245.81	960.306	10.736
Error	78	6,976.68	89.445	

Analysis of Variance for Soil Phosphorus among populationsof *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	0.331		
Factot A	19	5,210.50	274.237	349.956
Factor B	1	451.656	451.656	576.362
Interaction	19	69.578	3.662	4.673
Error	78	61.123	0.784	

Analysis of Variance for Soil Potassium among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Replication	2	0.331		
Factot A	19	5,210.50	274.237	349.956
Factor B	1	451.656	451.656	576.362
Interaction	19	69.578	3.662	4.673
Error	78	61.123	0.784	

APPENDIX VI

ANOVA for fodder quality and mineral nutrient characteristics of populations (Mother trees) of *Grewia optiva* Drummond.

Analysis of Variance for leaf fresh weight among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	102.4024	34.13412	1.943056
Replication	19	17403.82	915.9905	52.14198
Error	57	1001.333	17.56724	

Analysis of Variance for leaf dry weight among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	4.597104	1.532368	0.279103
Replication	19	4159.98	218.9463	39.87849
Error	57	312.9492	5.490336	

Analysis of Variance for crude protein among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	10.09965	3.366552	3.022489
Replication	19	540.6889	28.45731	25.54897
Error	57	63.48855	1.113834	

Analysis of Variance for crude fiber among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.96265	0.320883	0.22771
Replication	19	119.5831	6.293846	4.466327
Error	57	80.3231	1.409177	

Analysis of Variance for ether extract among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.01107	0.00369	0.013237
Replication	19	16.34452	0.860238	3.085904
Error	57	15.88953	0.278764	

Analysis of Variance for total ash among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	2.390125	0.796708	2.590955
Replication	19	106.0946	5.583924	18.15934
Error	57	17.52727	0.307496	

Analysis of Variance for nitrogen free extractamong populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	23.19994	7.733313	2.186778
Replication	19	1265.473	66.60384	18.83382
Error	57	201.5746	3.536396	

Analysis of Variance for leaf phosphorus among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	7.4E-05	2.47E-05	0.551836
Replication	19	0.188711	0.009932	222.2887
Error	57	0.002547	4.47E-05	

Analysis of Variance for leaf sodium among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	3128.628	1042.876	1.253299
Replication	19	671825.3	35359.23	42.49371
Error	57	47429.98	832.1049	

Analysis of Variance for leaf calcium among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.059305	0.019768	1.32721
Replication	19	8.294495	0.436552	29.30934
Error	57	0.848995	0.014895	

Analysis of Variance for leaf potassium among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	0.009142	0.003047	0.78687
Replication	19	3.873848	0.203887	52.64394
Error	57	0.220758	0.003873	

Analysis of Variance for leaf potassium among populations of *Grewia optiva* Drummond.

Source of Variations	d.f.	Sum of Square (SS)	Mean Sum of Square (MSS)	Fcal
Treatment	3	4.327245	1.442415	0.272771
Replication	19	894.2288	47.06468	8.900252
Error	57	301.4169	5.288016	

APPENDIX VII

BUFFERS 50 X TAE buffer

Sr. No	Constituents	Quantity
1.	Tris Base	242 gm
2.	Glacial acetic acid	57.1ml
3.	0.5 M EDTA (Ph 8.0)	100ml

APPENDIX VIII

6 X LOADING DYE

Sr. No	Constituents	Quantity
1.	Bromophenole blue	0.25%
2.	Sucrose	40%

Added autoclaved Distilled water to make the final volume 100 ml.

APPENDIX IX

GEL ELECTROPHORESIS

Agarose gel 2%
4 gm agarose was added to 200 ml 1 X TAE buffer and dissolved. The molten gel was cooled to 40^{o}C and 5ul of Ethidium bromide solution was added and mixed well. The molten gel was casted in a gel tray with comb containing 26 teeth to produce wells.

APPENDIX-X

Variance Covariance Matrix of fodder quality characteristics of 18 months old seedlings of *Grewia optiva* Drummond.

Characters	Crude fiber	Ether extract	Total ash	Nitrogen free extract	Phosphorus	Calcium	Sodium	Potassium	Crude protein
Crude fiber	45.301	0.393	2.91	-48.614	0.31	-0.655	1,655.42	1.074	2.666
Ether extract	0.393	5.818	-2.027	6.648	-0.081	0.315	-130.602	-0.423	-3.495
Total ash	2.91	-2.027	26.113	-71.593	0.776	1.906	92.905	2.167	46.037
Nitrogen free extract	-48.614	6.648	-71.593	350.248	-3.099	-13.179	-461.769	-6.681	-204.16
Phosphorus	0.31	-0.081	0.776	-3.099	0.063	0.19	-4.851	0.072	2.034
Calcium	-0.655	0.315	1.906	-13.179	0.19	5.621	-432.032	0.642	10.823
Sodium	1,655.42	-130.602	92.905	-461.769	-4.851	-432.032	1,91,507.39	-7.333	-1,111.19
Potassium	1.074	-0.423	2.167	-6.681	0.072	0.642	-7.333	0.741	3.637
Crude protein	2.666	-3.495	46.037	-204.16	2.034	10.823	-1,111.19	3.637	140.676

APPENDIX XI

Variance Covariance Matrix of fodder quality characteristics mineral nutrient characteristics of populations (mother trees) of *Grewia optiva* Drummond.

Characters	Leaf fresh weight	Leaf dry matter	Crude protein	Ether extract	Crude fiber	Total ash	Nitrogen free Extract	Amino acids	Potassium	Calcium	Sodium	Phosphorus	Leaf dry weight
Leaf fresh Weight	17,403.82	-1,106.08	1,575.45	-53.262	352.018	758.613	-2,632.82	2,214.53	83.292	211.141	30,503.78	24.731	7,173.99
Leaf dry matter	-1,106.08	1,507.88	27.047	18.426	-78.983	-9.632	43.141	109.295	-33.99	-24.417	-15203.472	-1.93	694.144
Crude protein	1,575.45	27.047	540.689	-46.144	85.258	204.273	-784.076	656.962	12.53	6.907	2,045.05	5.658	733.503
Ether extract	-53.262	18.426	-46.144	16.345	-12.139	-26.81	68.749	-58.836	-2.289	0.814	-534.274	-0.549	13.337
Crude fiber	352.018	-78.983	85.258	-12.139	119.583	36.943	-229.645	100.369	12.313	7.324	4,766.58	1.737	64.3
Total ash	758.613	-9.632	204.273	-26.81	36.943	106.095	-320.5	269.294	6.61	6.942	1,836.46	2.639	308.419
Nitrogen free extract	-2,632.82	43.141	-784.076	68.749	-229.645	-320.5	1,265.47	-967.789	-29.164	-21.988	-8,113.82	-9.486	-1,119.56
Amino acids	2,214.53	109.295	656.962	-58.836	100.369	269.294	-967.789	894.229	12.055	20.192	3,137.85	8.224	1,073.39
Potassium	83.292	-33.99	12.53	-2.289	12.313	6.61	-29.164	12.055	3.874	0.979	1,181.94	0.235	-0.923
Calcium	211.141	-24.417	6.907	0.814	7.324	6.942	-21.988	20.192	0.979	8.294	257.342	0.663	64.169
Sodium	30,503.78	-15,203.47	2,045.05	-534.274	4,766.58	1,836.46	-8,113.82	3,137.85	1,181.94	257.342	671825.304	70.232	2,010.81
Phosphorus	24.731	-1.93	5.658	-0.549	1.737	2.639	-9.486	8.224	0.235	0.663	70.232	0.189	8.691
Leaf dry weight	7,173.99	694.144	733.503	13.337	64.3	308.419	-1,119.56	1,073.39	-0.923	64.169	2,010.81	8.691	4,159.98

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Title of Thesis	:	**Morphogenetic variation for leaf fodder quality parameters in populations of *Grewia optiva* Drummond**
Name of the Student	:	Jyoti Dhiman
Admission Number	:	F-2019-11-D
Major Advisor	:	Dr. Hari Paul Sankhyan
Major Discipline	:	Forestry
Minor Discipline	:	Forest Genetic Resources
Date of Thesis Submission	:	
No. of pages in Thesis	:	193+xxiv

ABSTRACT

The present investigation, entitled **"Morphogenetic variation for leaf fodder quality parameters in populations of** *Grewia optiva* **Drummond"** was conducted during 2020–2023 in the Department of Tree Improvement and Genetic Resources, College of Forestry, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan (H.P.). This investigation was conducted in the four altitudinal ranges (400 to 800 m (A1), 801–1200 m (A2), 1201–1600 m (A3), and 1601-2000 m (A4) above mean sea level (a msl)) of Himachal Pradesh and Uttarakhand. Four major experiments were conducted viz., morphological and genetic diversity of *Grewia optiva* Drummond**,** physiochemical properties of soil, variation in fodder quality characteristics and molecular marker-based analysis of the best studied material of this species. All physiochemical soil properties declined as soil depth increased from 0 to 15 cm to 15 to 30 cm, with the exception of bulk density and particle density. The proportions of soil organic carbon, soil nitrogen and soil porosity increased from A1 to A4 altitudinal zone. Based on useful and desired characteristics of both morphometric and fodder quality parameters six populations, *i.e.,* Harsar, Sujanpur Tihra, Sihunta, Kutuldi, Jagdhar and Sangrah and altitudinal zone A4 (1600-2000m) reported as best for further selection and tree breeding program. These populations reported with more than 23 per cent crude protein. Variability estimates, genetic parameters, correlation and divergence studies exhibited high variability between and among populations. 15 genotypes DH1 (Dharot 1), DH2 (Dharot 2), DH4 (Dharot 4), HR1 (Harasar 1), ST1 (Sujanpur Tihra 1), DR1 (Dramman 1), DR2 (Dramman 2), NR4 (Neri 4), DA3 (Daggar 4), BA3 (Basal 3), KU1 (Kutuldi), SI2 (Sihunta 2), SI3 (Sihunta 3), KT1 (Kuthar 1) and KT2 (Kuthar 2)) were identified based on seedling growth and fodder quality characteristics at 18 months old seedlings. Only two of the 10 ISSR primers, *i.e.,* UBC 809 and UBC 820 were amplified and generated a banded pattern. Maximum variation was observed in the progeny of the DA3 (Daggar) and DH2 (Dharot) genotypes. Morphological and genetic variation can be used to select suitable genotypes in accordance with the domestication process of this important multipurpose species, to develop further hybridization work and for mass multiplication of selected superior nutritive selections.

Signature of the Student **Signature of the Major Advisor**

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