GENETIC VARIABILITY AMONG THE OPEN POLLINATED PROGENIES OF BURMA DEK (*MELIA COMPOSITA* BENTH.) UNDER FIELD CONDITIONS

Thesis

Submitted to the Punjab Agricultural University
in partial fulfillment of the requirement
for the degree of

MASTER OF SCIENCE
in
FORESTRY
(Minor Subject: Plant Breeding and Genetics)

By

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2022

CERTIFICATE I

This is to certify that the thesis entitled, **"Genetic variability among the open pollinated progenies of Burma Dek (*Melia Composita* Benth.) under field conditions"** submitted for the degree of **M.Sc.** in the subject of **Forestry** (Minor subject: **Plant Breeding and Genetics**) of the Punjab Agricultural University, Ludhiana, is a bonafide research work carried out by **Karanpreet Kaur (L-2019-H-392-M)** under my supervision and that no part of this thesis has been submitted for any other degree.

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

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CERTIFICATE II

This is to certify that the thesis entitled, **"Genetic variability among the open pollinated progenies of Burma Dek (*Melia Composita* Benth.) under field conditions"** submitted by **Karanpreet Kaur (L-2019-H-392-M)** to the Punjab Agricultural University, Ludhiana, in partial fulfillment of the requirements for the degree of **M.Sc.** in the subject of **Forestry** (Minor subject: **Plant Breeding and Genetics**) has been approved by the Student's Advisory Committee along with External Examiner after an oral examination on the same.

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ACKNOWLEDGEMENT

First of all, I am ever grateful to ***God,*** *the Creator and Guardian, and to whom I owe my very existence. I praise God, the almighty, merciful and passionate, for providing me this opportunity and granting me the capability to proceed successfully. I am thankful to him whose strength has enabled me to complete various ventures in my life and also blessed me with potential thoughts, talented teachers, co-operative friends and opportunity to make some contribution to the already existing ocean of knowledge.*

At the outset, I would like to extend my profound regards and deep sense of gratitude to my esteemed Major advisor ***Dr. R.I.S Gill, Principal Scientist (Agroforestry)*** *Department of Forestry and Natural Resources, PAU, Ludhiana for his valuable guidance, your warm encouragement, insightful decision and keen interest rendered throughout my study. You are always a big inspiration and motivation for me.*

I express my deep sense of gratitude to members of my advisory Committee ***Dr. G. P. S. Dhillon (Senior Tree Breeder)*** *for offering valuable advice and support during whole period.* ***Dr. Inderjit Singh (Principal Pulse Breeder)*** *and* ***Dr. H.S Saralch (Professor of Forestry)*** *who guided me and has contributed to this thesis with a major impact. I am highly grateful to* ***Dr. S. K. Chauhan, Head Department of Forestry and Natural Resources*** *for providing me with the necessary facilities. I am also thankful to* ***Dr. Ashok Kumar Dhakad*** *for his valuable support and also for building my statistical concepts. I am also thankful to* ***Dr. Avtar Singh Principal Scientist (forestry)*** *for providing necessary support in accomplishing the research work.*

To my life-coach, my parents ***S. Saroop Singh*** *and* ***Sdn. Baljeet Kaur.*** *I am forever indebted to my parents for their understanding, endless patience and encouragement when it was most required and for providing me the means to learn and understand. I take great pleasure in thanking my best friend* **Nidhi** *for giving me moral support, ever-available cooperation and sharing the burden of my work thus making things much smoother. I also thank* ***Davinder, Amrita, Lakhwinder Kaur,*** *R****aziya, Ankita, Ramandeep, Amzed, Ravi Inder, Navjeet Singh*** *and* ***Raman*** *and many others which are not mentioned here for being just there and keeping it all pleasant and for all the unreturned favours. You have all been like a family. Thanks are also extended to the office and field staff of Department of Forestry and Natural Resources especially* ***Smt. Kuldeep Kaur, S. Gurpreet Singh*** *and* ***S. Gursewak Singh*** *for providing efficient support during research work and thesis submission.*

Last but not the least, I duly acknowledge my sincere thanks to all those who love and care for me. Every name may not be mentioned but none is forgotton.
Thanks everybody.

Dated:

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Title of the Thesis	:	Genetic variability among the open pollinated progenies of Burma Dek (*Melia Composita* Benth.) under field conditions
Name of the student and Admission No.	:	Karanpreet Kaur (L-2019-H-392-M)
Major Subject	:	Forestry
Minor Subject	:	Plant breeding and genetics
Name and Designation of Major Advisor	:	Dr. RIS Gill Principal Scientist Agroforestry
Degree to be awarded	:	M.Sc. (Forestry)
Year of award of degree	:	2022
Total pages in Thesis	:	60+ VITA
Name of the University	:	Punjab Agricultural University, Ludhiana

ABSTRACT

The present study entitled "Genetic variability among the open pollinated progenies of Burma dek (*Melia composita* Benth)" was carried out at Regional Research Station, Bathinda during 2020-22, to investigate variation among the progenies for different growth parameters, from an established replicated progeny trial at a spacing of 4×4 m, data was recorded on growth traits of twenty progenies. Progeny 1 exhibited outstanding performance for the growth parameters like Total height, DBH, straightness, clear bole height and crown length and followed by progeny 2, 19 & 6. Whereas, progeny 3 showed lowest values for these characters. The maximum mean value of number of branches was found in progeny 20. The difference between GCV and PCV was recorded for number of branches and crown length which ranged from 5.711 to 5.631% among the progenies. Majority of parameters studied were less influenced by the environment. In general, low to moderate heritability was observed for all the characters. The heritability varied from 20.950% (Crown Length) to 72.281% (Straightness). High Heritability with high genetic gain was observed for DBH and high heritability coupled with moderate genetic gain was observed for the characters like number of branches (55.862% with 1.591%) and total height (38.792% with 1.116%) among these characters. Path coefficient analysis revealed that the highest positive direct effect was observed in DBH followed by crown length and straightness at genotypic level, while at phenotypic level highest direct effect observed in DBH followed by straightness and number of branches. Highly significant and positive genotypic and phenotypic correlation was observed for majority of the characters. Genotypic correlation coefficient was higher than phenotypic correlation coefficient revealed that the less effect of the environment on the expression of these traits. All the progenies were clustered into five clusters, of which highest inter cluster distance was observed between cluster 2 and cluster 4 which showed as most divergent clusters. This study will help to identify the most distant accessions and most closely placed ones for breeding experiments to obtain hybrid vigour. Progeny 1 and 2 were promising one on the basis of Index score analysis.

Keywords: *Melia composita*, Genetic variability, heritability, path analysis

Signature of Major Advisor **Signature of the Student**

ਖੋਜ ਗ੍ਰੰਥ ਦਾ ਸਿਰਲੇਖ	:	ਬਰਮਾ ਡੇਕ (ਮੀਲੀਆ ਕੰਪੋਜਿਟਾ ਬੈਂਥ) ਦੇ ਖੁੱਲੇ ਪਰਾਗਿਤ ਪ੍ਰੋਜਨੀਆਂ ਵਿੱਚ ਜੈਨੇਟਿਕ ਪਰਿਵਰਤਨਸ਼ੀਲਤਾ
ਵਿਦਿਆਰਥੀ ਦਾ ਨਾਂ ਅਤੇ ਦਾਖ਼ਲਾ ਨੰਬਰ	:	ਕਰਨਪ੍ਰੀਤ ਕੌਰ (ਐੱਲ-2019-ਐੱਚ-392-ਐੱਮ)
ਪ੍ਰਮੁੱਖ ਵਿਸ਼ਾ	:	ਜੰਗਲਾਤ
ਸਹਿਯੋਗੀ ਵਿਸ਼ਾ	:	ਪਲਾਂਟ ਬ੍ਰੀਡਿੰਗ ਅਤੇ ਜੈਨੇਟਿਕਸ
ਮੁੱਖ ਸਲਾਹਕਾਰ ਦਾ ਨਾਂ ਅਤੇ ਅਹੁੱਦਾ	:	ਡਾ. ਆਰ.ਆਈ.ਐੱਸ ਗਿੱਲ ਪ੍ਰਿੰਸੀਪਲ ਸਾਇੰਟਿਸਟ (ਐਗਰੋਫੋਰੇਸਟਰੀ)
ਡਿਗਰੀ	:	ਐੱਮ. ਐੱਸ.ਸੀ
ਡਿਗਰੀ ਮਿਲਣ ਦਾ ਸਾਲ	:	2022
ਖੋਜ ਪੱਤਰ ਵਿੱਚ ਕੁੱਲ ਪੰਨੇ	:	60+ ਵੀਟਾ
ਯੂਨੀਵਰਸਿਟੀ ਦਾ ਨਾਮ	:	ਪੰਜਾਬ ਖੇਤੀਬਾੜੀ ਯੂਨੀਵਰਸਿਟੀ, ਲੁਧਿਆਣਾ-141004 ਪੰਜਾਬ, ਭਾਰਤ

ਸਾਰ ਅੰਸ਼

ਮੌਜੂਦਾ ਅਧਿਐਨ "ਬਰਮਾ ਡੇਕ (ਮੀਲੀਆ ਕੰਪੋਜਿਟਾ ਬੈਂਥ) ਦੇ ਖੁੱਲੇ ਪਰਾਗਿਤ ਪ੍ਰੋਜਨੀਆਂ ਵਿੱਚ ਜੈਨੇਟਿਕ ਪਰਿਵਰਤਨਸ਼ੀਲਤਾ" ਸਿਰਲੇਖ ਅਧੀਨ ਸਨ 2020-22 ਦੌਰਾਨ ਖੇਤਰੀ ਖੋਜ ਸਟੇਸ਼ਨ, ਬਠਿੰਡਾ ਵਿਖੇ ਵੱਖ-ਵੱਖ ਵਿਕਾਸ ਮਾਪਦੰਡਾਂ ਲਈ ਪ੍ਰੋਜਨੀਆਂ ਵਿੱਚ ਪਰਿਵਰਤਨ ਦੀ ਜਾਂਚ ਕਰਨ ਲਈ ਕੀਤਾ ਗਿਆ। 4×4 ਮੀਟਰ ਦੀ ਦੂਰੀ ਤੇ ਪ੍ਰੋਜਨੀਆਂ ਦਾ ਪਰੀਖਣ ਕੀਤਾ ਗਿਆ, ਅਤੇ ਵੀਹ ਪ੍ਰੋਜਨੀਆਂ ਦੇ ਵਿਕਾਸ ਗੁਣਾਂ ਦੇ ਅੰਕੜੇ ਦਰਜ ਕੀਤੇ ਗਏ। ਪ੍ਰੋਜਨੀ ਨੰਬਰ 1 ਨੇ ਕੁੱਲ ਉਚਾਈ, ਡੀ.ਬੀ.ਐੱਚ, ਸਿੱਧੇ ਪਣ, ਸਿੱਧੇ ਬੋਲ ਦੀ ਉਚਾਈ ਅਤੇ ਰੁੱਖ ਦੀ ਛੱਤਰੀ ਦੀ ਲੰਬਾਈ ਵਰਗੇ ਵਿਕਾਸ ਮਾਪਦੰਡਾਂ ਲਈ ਬਹੁਤ ਚੰਗੀ ਕਾਰਗੁਜਾਰੀ ਦਿਖਾਈ। ਇਸ ਤੋਂ ਬਾਅਦ ਪ੍ਰੋਜਨੀ ਨੰਬਰ 2,6 ਅਤੇ 19 ਵਿੱਚ ਵਿਕਾਸ ਦੇਖਿਆ ਗਿਆ। ਸ਼ਾਖਾਵਾਂ ਦੀ ਗਿਣਤੀ ਦਾ ਸਭ ਤੋਂ ਵੱਧ ਔਸਤ ਖੁੱਲ ਪ੍ਰੋਜਨੀ ਨੰਬਰ 20 ਵਿੱਚ ਪਾਇਆ ਗਿਆ। ਜੈਨੇਟਿਕ ਵਿਭਿੰਨਤਾ ਅਤੇ ਫੀਨੋਟੀਪਿਕ ਵਿਭਿੰਨਤਾ ਵਿੱਚ ਮਹੱਤਵਪੂਰਨ ਅੰਤ ਸ਼ਾਖਾਵਾਂ ਦੀ ਗਿਣਤੀ ਅਤੇ ਰੁੱਖ ਦੀ ਛੱਤਰੀ ਦੀ ਲੰਬਾਈ ਲਈ ਦਰਜ ਕੀਤਾ ਗਿਆ। ਜੋ ਕਿ ਪ੍ਰੋਜਨੀਆਂ ਵਿੱਚ 5.71 ਪ੍ਰਤੀਸ਼ਤ ਤੋਂ 5.63 ਪ੍ਰਤੀਸ਼ਤ ਤੱਕ ਸੀ। ਅਧਿਐਨ ਕੀਤੇ ਗਏ ਜਿਆਦਾਤਰ ਮਾਪਦੰਡ ਵਾਤਾਵਰਨ ਦੁਆਰਾ ਘੱਟ ਪ੍ਰਭਾਵਿਤ ਸਨ। ਆਮ ਤੌਰ ਤੇ ਸਾਰੇ ਗੁਣਾਂ ਲਈ ਵੱਧ ਅਨੁਵਾਸ਼ਿਕਤਾ ਦਰਜ ਕੀਤੀ ਗਈ। ਅਨੁਵਾਸ਼ਿਕਤਾ 21 ਪ੍ਰਤੀਸ਼ਤ (ਛੱਤਰੀ ਦੀ ਲੰਬਾਈ) ਤੋਂ 72 ਪ੍ਰਤੀਸ਼ਤ (ਸਿੱਧੇ ਪਣ) ਤੱਕ ਦਰਜ ਕੀਤੀ ਗਈ। ਡੀ.ਬੀ.ਐੱਚ ਲਈ ਉੱਚ ਜੈਨੇਟਿਕ ਲਾਭ ਦੇ ਨਾਲ ਵੱਧ ਅਨੁਵਾਸ਼ਿਕਤਾ ਦੇਖੀ ਗਈ। ਸ਼ਾਖਾਵਾਂ ਦੀ ਗਿਣਤੀ (55.86 ਪ੍ਰਤੀਸ਼ਤ, 1.59 ਪ੍ਰਤੀਸ਼ਤ) ਅਤੇ ਕੁੱਲ ਉਚਾਈ (38.79 ਪ੍ਰਤੀਸ਼ਤ, 1.11 ਪ੍ਰਤੀਸ਼ਤ) ਲਈ ਦਰਮਿਆਨੀ ਜੈਨੇਟਿਕ ਲਾਭ ਦੇ ਨਾਲ ਉੱਚ ਅਨੁਵਾਸ਼ਿਕਤਾ ਦੇਖੀ ਗਈ। ਪਾਥ ਕੋਫੀਸ਼ਿਐਂਟ ਵਿਸ਼ਲੇਸ਼ਣ ਤੋਂ ਪਤਾ ਲਗਦਾ ਹੈ ਕਿ ਸਭ ਤੋਂ ਵੱਧ ਸਿੱਧਾ ਅਸਰ ਕੁੱਲ ਉਚਾਈ ਵਿੱਚ ਦੇਖਿਆ ਗਿਆ, ਜਿਸ ਤੋਂ ਬਾਅਦ ਜੀਨੋਟੀਪਿਕ ਅਤੇ ਫੀਨੋਟੀਪਿਕ ਪੱਧਰ ਤੇ ਪ੍ਰਭਾਵ ਸ਼ਾਖਾਵਾਂ ਦੀ ਗਿਣਤੀ ਅਤੇ ਸਿੱਧੇ ਪਣ ਵਿੱਚ ਅਸਰ ਦੇਖਿਆ ਗਿਆ ਸੀ। ਬਹੁਤੇ ਗੁਣਾਂ ਲਈ ਬਹੁਤ ਮਹੱਤਵਪੂਰਨ ਅਤੇ ਸਕਾਰਾਤਮਕ ਜੀਨੋਟੀਪਿਕ ਕੋਰੀਲੇਸ਼ਣ ਫੀਨੋਟੀਪਿਕ ਕੋਰੀਲੇਸ਼ਣ ਨਾਲੋਂ ਵੱਧ ਪਾਇਆ ਗਿਆ ਜੋ ਕਿ ਇਹ ਦਰਸਾਉਂਦਾ ਹੈ ਕਿ ਇਹਨਾਂ ਗੁਣਾਂ ਦੇ ਪ੍ਰਗਟਾਵੇ ਤੇ ਵਾਤਾਵਰਨ ਦਾ ਘੱਟ ਪ੍ਰਭਾਵ ਹੈ। ਸਾਰੀਆਂ ਪ੍ਰੋਜਨੀਆਂ ਨੂੰ ਪੰਜ ਸਮੂਹ ਵਿੱਚ ਵੰਡਿਆ ਗਿਆ ਸੀ। ਜਿੰਨ੍ਹਾਂ ਵਿੱਚੋ ਸਭ ਤੋਂ ਵੱਧ ਅੰਤਰ ਸਮੂਹ 4 ਅਤੇ ਸਮੂਹ 2 ਵਿਚਾਕਰ ਦੇਖਿਆ ਗਿਆ ਸੀ ਜੋ ਕਿ ਸਭ ਤੋਂ ਵੱਖਰੇ ਸਮੂਹ ਦੇ ਰੂਪ ਵਿੱਚ ਦਿਖਾਇਆ ਗਿਆ । ਇਹ ਅਧਿਐਨ ਹਾਈਬ੍ਰਿਡ ਵਿਗਰ ਪ੍ਰਾਪਤ ਕਰਨ ਲਈ ਸਭ ਤੋਂ ਦੂਰ ਦੇ ਅਤੇ ਸਭ ਤੋਂ ਨਜਦੀਕੀ ਸਥਨਾਂ ਦੇ ਪਛਾਣ ਕਰਨ ਵਿੱਚ ਮਦਦ ਕਰੇਗਾ। ਸਕੋਰ ਵਿਸ਼ਲੇਸ਼ਣ ਦੇ ਆਧਾਰ ਤੇ ਪ੍ਰੋਜਨੀ ਨੰਬਰ 2 ਅਤੇ 1 ਵਧੀਆ ਪਾਏ ਗਏ।

ਮੁੱਖ ਸ਼ਬਦ:- ਮੀਲੀਆ ਕੰਪੋਜਿਟਾ, ਜੈਨੇਟਿਕ ਪਰਿਵਰਤਨਸ਼ੀਲਤਾ, ਵਿਸ਼ਲੇਸ਼ਣ, ਅਨੁਵਾਸ਼ਿਕਤਾ।

ਮੁੱਖ ਸਲਾਹਕਾਰ ਦੇ ਹਸਤਾਖਰ **ਵਿੱਦਿਆਰਥੀ ਦੇ ਹਸਤਾਖਰ**

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LIST OF ABBREVIATIONS AND SYMBOLS

Abbreviation	**Meaning**
%	Per cent
/	Per
Anon	Anonymous
CBH	Clear bole height
CL	Crown length
cm	Centimeter
CV	Coefficient of variance
DBH	Diameter at breast height
et al	and others
etc.	etcetera (and so on)
GCV	Genotypic Coefficient of variance
i.e.	That is
Kg	Kilogram
m	Meter
M.	*Melia*
No B	Number of branches
PCV	Phenotypic Coefficient of variance
spp	Species
ST	Straightness
TH	Total height
viz.,	Videlicet (Namely)
VoL	Volume
yr	Year

CHAPTER I

INTRODUCTION

There is a high demand for fuel and timber in emerging countries like India, which is provided by trees growing in forests and on farms. Forests are necessary for establishing ecological balance because they provide shelter for a diverse range of plants and wildlife. Forests play a vital role in climate change mitigation and adaptation by minimizing productive nutrient losses via erosion and leaching and increasing nutrient inputs through nitrogen fixation, as well as enhancing biological activity by supplying biomass and a suitable microclimate (Schroth and Sinclair 2003). Forest genetic resources serve as a storehouse for meeting future needs. They are means of survival of any civilization. The demand for food, shelter, and other products has increased as the human population has grown, which resulted in degradation of natural resources and climate change problems.

India is home to 17.5 percent of the world's population and 2.47 percent of its land area. But it has only one per cent of world's forests. In India, the total area covered by forests is 23.8 percent, compared to the national forest policy's requirement of 33 percent (Anonymous 2021). The gap between demand and supply of fuel wood, timber, and raw materials for wood-based businesses in India is expanding, putting additional strain on existing forest resources. To counteract this, fast-growing tree species such as poplar and eucalyptus are being planted for afforestation of agricultural and community lands through farm forestry and social forestry projects.

Punjab is an agriculture-intensive state where the rice-wheat cropping system has been widely adopted, ensuring the country's food security. Due to depletion of native nutrient supplies and shortages, lowering of the under-ground water table, and recurrence of insects and illnesses, the productivity of this system has stalled or even declined in certain regions. The necessity for diversification of the traditional rice-wheat cropping system has been pushed by the use of natural resources. Agroforestry has emerged as one of the potential solutions for diversification from the existing rice-wheat cropping system. Different tree species are traditionally grown in the Punjab state's distinct agro-climatic zones. Populus, Eucalyptus, and Melia are the most common tree species used by farmers as block and boundary plantations on their agricultural fields.

Agroforestry is an age-old land use practice, which has been practiced by farmers in various forms in different parts of country. It is a sustainable land management that combines food crops (annuals), tree crops (perennials), and livestock on the same unit of land, either alternately or simultaneously, using management practises that suit the social and cultural characteristics of the local people as well as the economic and ecological conditions of the area. In Punjab state, wheat and paddy crops occupy more than 80 percent cropped area but having only 6.8 percent area under forest (Anonymous 2019). The excessive use of agrochemicals in rice and wheat rotation has deteriorated soil health and water resources in the state. The situation demands some remedies which can augment the income of the farmers. The need of diversification has some alternative remunerative crops/cropping system. Farmers are willing to diversify the present cropping rotation provided the assured market of input and output of alternative crops are available. For its potential for carbon sequestration, soil erosion and runoff reduction, better nutrient and water cycling, as well as socio-economic benefits, a poplar-based agroforestry system is regarded one of the viable solutions. (Gill *et al* 2019).

A tree species is suitable for agroforestry if it has the following characteristics: rapid growth, straight trunk, clear bole, few branches, narrow crown, self-pruning nature, favourable effect of litter fall and early decomposition, good marketability, and so on. Fast growing and short rotation tree species are preferred for agroforestry plantations. Presently, poplar and eucalyptus are preferred agroforestry tree species. Though these are exotic tree species but these fit quite well in the traditional cropping system as block or boundary plantation. There is need to explore for more potential tree species which could be grown with agriculture crops. Recently, one such tree that seems to be suitable for agroforestry is *Melia composita* belonging to family Meliaceae. It has been reported at low and medium altitudes from India to tropical Africa, southern China, and tropical Australia via Malaya. *Melia composita* can be found at altitudes of 1,500-1800 metres in the tropical moist deciduous forests of the Sikkim Himalayas, North Bengal, and Upper Assam, the Khasi hills of Orissa, the Deccan, and Western Ghats.

In Punjab, a melia tree-based agroforestry system is gaining popularity. In the state's south-western region, the trees are planted on the edges of agricultural fields or as block plantations with or without agricultural crops. This plant has the potential to contribute significantly to crop diversity, which is a pressing need in the state.

Melia composita Benth. is potential fast-growing tree species which could be used for plantation due to its fast growth, multiple uses and ability to withstand a range of climatic and edaphic conditions. It can be grown under various agroforestry and silvicultural conditions. This tree provides industrial timber and raw material for plywood and pulp industries (Kumar *et al* 2018). This is commonly known as Burma dek, white cedar, Malabar neem, dhrek or dek. *Melia composita* tree attains a height of 20-25 meters, and a cylindrical bole upto 9 meters and 1.5 meter in girth. The tree is strong light demander. The tree is leaf less during winters and the new leaves appear in Feb – March. After all of the leaves have fallen off, leaf primordial appears. Within a week of the emergence of new leaf, the panicle with little projecting buds emerges. Floral buds bloom in 18-28 days, and over 80% of them open early in the morning (between 0800-0900 h). From panicle start to fruit maturity, the number of days required varies between 243-264. The whitish green flowers appear from March to May and they are replaced by bunches of ovoid drupes which cling on the tree till the next flowering season. The fruits of *Melia composita* are bitter and considered an anthelmintic. It belongs to mahogany group having about 550 species in the family Meliaceae under 50 genera, some commercially important tree species are *Azadirachta indica*, *Cedrela odorata*, *M. dubia*, *M. azedarach*, *Swietenia macrophylla*, *Toona ciliate* etc. This tree thrives well on variety of soils but optimum growth is observed under deep fertile sandy loam. This multipurpose tree is gaining popularity among agroforestry farmers as a suitable plywood and pulp tree that can be harvested at a young age of 6 to 8 years and cultivated for more than 10 to 12 years as a timber tree (Kumar *et al* 2017). *Melia composita* is identified as a potential alternate pulp wood species (Parthiban *et al* 2009). It is an important multipurpose tree species that is commercially farmed for fodder, timber, and industrial woods under various afforestation techniques. Because of its improved pulp yield and quality, it is suitable for the pulp and paper industries. Wood is moderately hard and can be used for packing cases, ceiling planks, building purposes, agriculture implements, pencils, match boxes, splints, musical instruments, and tea boxes. It is being cultivated in the arid and semi-arid as well as semi moist areas of the country. This species has potential for bio-energy uses, particularly biomass gasification to provide producer gas for use in lime kilns to replace fuel oil, as well as various wood product applications. It is well recognized as a wealthy and valuable source of bioactive limonoids which are especially oxygenated and changed terpenoids having, antibacterial, insecticidal, antifungal, anticancer, anti-malarial, and pharmaceutical properties. Oil is used in many industries for variety of purposes viz. soap industries, as lubricants, illuminants and medicinal uses. It can also be used as a source of biodiesel. Oil is utilised in a wide range of sectors for a number of reasons, including soap manufacturing, lubricants, illuminants and medical applications. It can also be utilised as a biodiesel fuel source. This species' oil extracts also operate as growth inhibitors, stomach poisons, moulting disorders, morphogenetic abnormalities and anti-feedants against a variety of insect pests.

Melia (*Melia azedarach* Linn.) is well known for its ornamental, wind break and reforestation projects, commonly known as bakain, Persian lilac, is a highly valuable species, also recognized as a species for social forestry and urban forestry (Khangia 1997). It is receiving worldwide recognition as an economic tree for its variety of uses i.e., leaves as fodder, juice of leaves as an antehelmitic and seed in curing rheumatism. Its roots improve soil aeration and utilize the nutrients leached below the root zone of annual crops. It is suitable for growing on a variety of sites ranging from light to heavy soil texture and from normal to problematic sites. Because of its quick growth and deciduous nature, as well as its small leaves, this species is ideal for growing alongside agricultural crops. Leaves are lopped and fed to livestock as a nutritious fodder in various parts of the country. The leaves of the tree were discovered to have 12.8% crude protein and 55.0 percent neutral detergent fibre. In agroforestry systems, roots serve as both a sink and a source of nutrients. On the other hand, roots of trees enrich the soil with organic matter and nutrients by rapid turnover, intercept the leached nutrients from sub surface soil layers and recycle them to the surface.

Melia dubia, also known as Gora neem or Malabar neem, is another fast-growing tree that can be used in a variety of agroforestry systems. *Melia dubia* is a deciduous tree that grows to be 25 metres tall. The leaves are bipinnate and dense, with a 30 to 90 cm tall stalk. Leaflets are oblong to ovate – lanceolate and 4 to 8 cm long, with 2 to 5 pairs. It's a promising tree with an 8 to 12-year life cycle that's ideal for agroforestry or farm forestry. In both domestic and international markets, it is increasing global influence. It is also becoming more popular among farmers due to traits such as rapid growth, stem straightness with fewer branches, resulting in less shade, and wood resistance to pest and insect attacks.

The breeding programme to study growth dynamics is less adopted in forest trees due to long rotation. Few studies on differential response of progenies of plus trees of forest trees have been reported. Thus, the present study was conducted to evaluate growth dynamics of *Melia composita* progenies. The Department of Forestry & Natural Resources, Punjab Agricultural University, Ludhiana had initiated genetic improvement of *Melia composita* with selection of plus trees following base line method. The seeds from the plus trees were used for establishing progeny trials to evaluate their genetic worth through G x E interactions and other genetic parameters. Genetic parameters were useful tools in predicting expected gains from a progeny trial. The differences between progenies were utilised to determine total genetic variation and calculate the degree of genetic control over a specific trait (Hood and Libby 1980). The current work screened open pollinated half-sib families for variability in order to short list the best progenies for use in future genetic enhancement programmes.

The information regarding genetic variation in growth and stem quality of *Melia composita* under Punjab conditions at rotation age is lacking. Keeping in view, the present study entitled, Variability among the open pollinated progenies of Burma dek (*Melia composita* Benth.) under field conditions was conducted with following objectives:

1. To evaluate the progenies for growth parameters.
2. To short list genetically superior progenies to use for mass multiplication of quality planting material.

CHAPTER II

REVIEW OF LITERATURE

The review of literature provides basis for the conceptualization of different ideas given by different researchers. In the present case, the relevant literature with particular focus on tree improvement aspects has been reviewed in this chapter.

Short rotation tree- based forestry is gaining importance to rejuvenate the degraded areas and to enhance productivity for meeting the increasing demand of fuel, fodder, timber etc. National and state governments are emphasizing to increase area under tree cover to achieve target set by National Forest Policy 1988. Public and private agencies are undertaking massive afforestation programmes. Rapid and uniform germination of seed is required to produce uniform and quality planting stock. The present study has been planned to evaluate growth dynamics of *Melia composita* progenies. In the present study, open pollinated half-sib families were screened for variability to short list best progenies for use in future genetic improvement programme.

2.1 Variation in growth characteristics and yield

2.2 Genetic variability parameters

2.3 Correlation between different traits

2.1 VARIATION IN GROWTH CHARACTERISTICS AND YIELD

Melia composita is a fast-growing tree. It is huge deciduous fast growing tree of the family Meliaceae. The leaves are long, bipinnate and usually crowded. They are long stalked with a length of 30 to 90 cm. Shape of leaflets varies from ellipsoid to lanceolate and the length varies from 4 to 8 cm. The flowers are panicles appearing in large numbers and are shorter than the leaves, usually seen on upper axils of the leaves. Flower colour varies from violet to white, fragrant, about 8mm in length, with pubescent petals. The fruit is a drupe, ellipsoid, about 1.5 cm long, yellow when ripe. The seed number varies from one to five and are pointed smooth and brown (Troup, 1921). In Kerala, it is distributed in semi evergreen and moist deciduous forests. It's a huge, fast-growing deciduous tree with wide spreading branches on a robust, straight, tall bole that's native to the Western Ghats of southern India and common in Kerala's moist deciduous woods (Gamble 1992). Trees have evolved over time and showed a wide range of growth patterns. This is due to exposure to different climatic, edaphic and topographic conditions. In addition, seasonal changes in abiotic and biotic factors may also alter the growth pattern. Lowman (1992) deliberated three major growth patterns such as a rapid synchronous annual spurt of growth (*Toona australis*), continuous growth (*Dendrocnide excelsa*) and an intermittent pattern of continuous growth in spring and summer, followed by winter (*Doryphora sassafras*). Deciduous species exhibit predictable annual changes in growth and development as compared to evergreen. Further, the trees have their own growth place and they respond to seasonal variations. It has been documented that there are two extremes in the growth allocation patterns of trees such as photosynthetic assimilates allocated more to plant height growth than to distribution of branches and foliage (height-growth type) and other are assimilates allocated more to lateral branches and foliage than to plant height growth (crown growth type) (Hara *et al* 1991). These two types of growth rate have their significant role in different types of trees such as height growth type in forest trees and crown growth type in fruit trees. It is emerging as a favourable tree for agroforestry in north Indian regions due to its rapid growth and many uses (Luna and Kumar 2006; Nuthan *et al* 2009). It can be found outside of India in China, Sri Lanka, Java, Malaysia and Australia. *Melia dubia*, with its several properties such as plywood, pulpwood, timber and fuel wood, could be a good choice for an agroforestry and farm forestry planting programme. The wood has been used as a timber, notably in the thalavadi region of Tamil Nadu, to suit domestic needs and is highly adaptable to plywood utility due to higher veneer recovery compared to standard plywood species such as Eucalyptus (Prathiban *et al* 2019).

In a provenance-cum-progeny trial involving 94 families of *E. tereticornis*, Ginwal *et al* (2004) reported that there was significant variation among the progenies for growth traits, at the age of 21 months. Growth (diameter and height) and wood density (pilodyn penetration) comparison of seedling and vegetative propagated cuttings from the related pedigrees of *E. globulus*. The significance of age, site and the interaction between propagation methods were also investigated. No significant differences between the two types of parent materials for the characters examined was observed in the study.

Kien *et al* (2009) reported the genetic parameters for growth and stem traits of *E. urophylla* based on two progeny trials studied at various ages. Heritability values for height and diameter ranged from 0.10 to 0.31. Genetic correlation between growth and stem straightness were weak to moderate.

Dhillon *et al* (2009) studied the performance of 11 progenies of *Melia azadirachta* plus trees under nursery and field conditions. The differences among progenies for collar diameter and plant height were significant at nursery stage. The plant height and diameter at age of 1, 3.5, 5 and 7 yrs. also varied significantly among progenies. The heritability was observed to be medium for diameter and height. The genetic gain and variation coefficients for diameter and height were higher under field conditions. The results indicated good potential for improvement for growth traits by seeds from plus trees or seed orchards.

Kumar and Bangarwa (2010) found significant variations for height, diameter at breast height (DBH) and clear bole height (CBH) in *E. tereticornis* (Sm.). The broad sense heritability was low to moderate for both height and CBH. The genetic gain for height and

CBH increased substantially per se with the increase in age of trees. The average genetic gain for three years was recorded maximum for height (159.60%) followed by DBH (110.97%) and CBH (70.34%). Clone 5 showed an upward trend for DBH and maintained its superiority for CBH as the age of the tree increased. Clones 6 and 10 performed poorly and clones 17, 14 and 5 were found to be the most promising clones for commercial development.

Melia composita coppices well and when the roots get injured enormous root suckers are produced. Pollarding ability is good and large number of new shoots emerges out from dormant buds (Kumar *et al* 2013). According to Saravan *et al* (2013) *Melia dubia cav*., a member of the Meliaceae family, is known as Malabar neem. The species is reported to be predominantly self fertilized (Johar *et al* 2015). *Melia dubia* Cav. synonym *Melia composita* generally known as Malabar Neem or Dreak or Gora Neem is a tree species indigenous to India and neighbouring countries like, Sri Lanka, Malaysia, Java, China and Australia (Kumar and Aiswarya 2017). It has tremendous adaptability to different climatic condition (Kumar *et al* 2017).

Anand *et al* (2012) investigated the influence of several seed treatments on *Melia dubia* germination and seedling growth characteristics at the Ponnampet Nursery, College of Forestry (Banglore). Seven pre-sowing treatments were applied to the seeds. The results demonstrated that a seven-day treatment with cow dung slurry resulted in significantly higher seedling germination and growth. In cow dung slurry, seed germination starts 32 days after seeding and sustained up to 66 days. The maximum germination percentage (31.5%) was observed with 100 ppm gibberlic acid for 24 hours. The control had the lowest germination percentage (18.7%). Cow dung slurry also had the greatest germination value (2.2) and germination energy (25). In comparison to control and other treatments, *Melia dubia* seeds treated in cow dung slurry for seven days and 100 ppm gibberlic acid for 24 hours showed faster germination, higher germination percentage, seedling growth, and biomass output. Shoot length, root length, collar diameter, and leaf number all increased in response to a 24 hour treatment with cow dung slurry and 100 ppm Gibberlic acid. A similar pattern was found in the dry weight of the shoot, root, and whole seedling. As a result, pre-sowing treatment with cow dung was more effective in improving germination and yielding high-quality *Melia dubia* seedlings in the nursery.

Swaminathan *et al* (2012) assessed variation in wood properties of *Melia dubia* trees grown under similar conditions however showed morphological variations in growth. The anatomical properties such as fibre length, fibre diameter, lumen diameter and double wall thickness vessel element length and vessel diameter were analysed. The fast grown timber showed higher numerical values for anatomical properties as compared to slow grown timber though the differences were not significant.

Sharma *et al* (2012) evaluated the wood quality parameters of 9-year-old *Melia dubia* trees grown in a seedling seed orchard at Yeshwanthpura Research Station, Karnataka. Trees were grouped into three classes based upon their girth at the breast height small (<40 cm), medium (40–60 cm) and big (>60 cm). Different anatomical, physical and mechanical properties of the wood were evaluated using standard testing procedures. The results showed that there was no significant difference in the heartwood percentage and specific gravity among the different girth classes.

Meena *et al* (2014) evaluated 54 progenies of *Melia azedarach* Linn. from eleven geographical locations for different growth parameters. Significant differences were found among and within progenies for all the characters at the age of 8 years and also observed that for all the traits progeny one shows superior growth except for number of branches and clear bole height. Narrow-sense heritability (progeny basis, within-progeny basis, and individual plant basis) was higher for mean annual increment for total height and diameter at breast height than other recorded growth parameters. Genetic gain within progeny selection was higher than progeny selection for all traits. Out of 54 progenies, progeny number 10 (Himachal Pradesh, Solan seed source) was found to be the best for the characters studied on the basis of adjusted treatment mean ranking for further multiplication.

They revealed that two pulp and paper mills in Tamil Nadu, use melia wood for pulp and paper production and have adopted this species for commercial plantation establishment. It is preferred in the paper industry because of increased pulp recovery, exceptional strength and anti termite property (Suresh and Devakumar 2017). The tree grows up to 25 m in height with a straight bole of about 5 to 12 m and nearly 1.5 m in girth at breast height (Rawat *et al* 2018). Though the tree grows well on variety of soils, it prefers deep fertile sandy soils.

Sharma *et al* (2017) studied on *Melia composita* plantation at Handesra, Mohali Village, district Hoshiarpur in Punjab with the spacing 2x2, 3x3, and 4x4. Height and diameter were regularly measured for three years. In 2016, maximum height and diameter was recorded in 3x3 m spacing, while minimum increase in height and diameter in 4x4 m spacing.

Ten cultivars of Melia were released for commercial cultivation in Northern India (Kumar *et al* 2017). The cultivars were not only productive but also have an excellent bole form which is one of the essential characteristics for plywood-based industries. The average productivity of released cultivars was 34.57 m ha yrs., while the maximum was 55.83 m ha yrs. for the cultivar SHARAD followed by 40.41 m ha yrs. for cultivar SHASHI. Such release of productive germplasm on commercial scale is expected to play an important role in bridging increasing gap between demand and supply for industrial wood. The varieties have been recommended under irrigated conditions for different growing regions of Haryana, Punjab, Uttar Pradesh and Uttarakhand.

Thakur *et al* (2017) analysed the allele-chemicals in leaf litter *Melia composita* Wild. and studied the allelopathic effect on germination, initial growth and biomass of chickpea (*Cicer arietinum* L.) through leaf aqueous extract in laboratory and leaf litter in pot culture under greenhouse condition. Gas chromatography mass-spectrometry (GC-MS) analysis of leaf litter detected compounds like phenolic acids and their derivatives, unsaturated fatty acid, alkaloids, methyl ketones (volatile allele-chemical), unsaturated fatty acids, aromatic ketone, chromene, etc. Laboratory and pot culture bioassays revealed that, the leaf aqueous extracts [0 (distilled water), 25, 50, 75 and 100 %)] and leaf -1 litter [0 (no litter application) 5, 10, 15 and 20 g pot] inhibited the germination and its attributes [germination, germination rate index (GRI), mean daily germination (MDG), peak value (PV) and germination value (GV)]. Similarly, inhibitory effect was studied on growth (shoot length, shoot length and vigour index) and initial biomass parameters (shoot, root and total biomass) of chickpea. Per cent reduction in germination and initial growth parameters increased with increasing aqueous extract concentration or litter amount. However, pot experiments, carried out till maturity of the test crop and revealed that growth and biomass were not affected due to leaf litter application.

Sathya and Parthiban (2018) conducted a systematic tree improvement program which included evaluation of 16 clones. The clones registered significant variation for growth attributes. Among the clones evaluated, the clone MD 26 witnessed increased height, basal diameter and volume index and could be adopted in agroforestry programme. The variability estimates indicated increased phenotypic coefficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCA) indicating the role environment in growth and development. Almost all the growth attributes exhibited higher heritability estimates and could play a better role in Melia improvement programme.

Green gram (*Vigna radiata* L.) is an important pulse crop and *Melia composita* is an emerging industrial agroforestry plantation in southern Gujarat (Bhusara 2018). To maximize the land utilization, an agroforestry trial was laid to investigate the performance of green gram varieties under different spatial arrangements of 2-year-old *Melia composita* plantation with three spacing of S1 (2 x 2m), S2 (2x 3 m) and S3 (2x 4 m) while S0 as open field, during winter season of 2015-16 and 2016-17. Green gram varieties such as GV1, GV2 and GM4 were intercropped with *M. composita* and reported lower growth parameters and yield than open condition. The results of pooled analysis of two years showed that in intercropping the growth and yield attributes were minimum reported in 2x 2 closer spacing while under wider spacing of S2 and S3 green gram responded significantly better, respectively. Thus, wider spacing of 2 x 4 m could be suggested for intercropping under *Melia composita* plantations in initial 2-4 years.

Parthiban *et al* (2019) studied the growth pattern of *Melia dubia* in Tamil Naidu at 13 plots over a 4-year period at three densities ranging from 2500/ha (distance 2–2 m) to 625 plants/ha (distance 4–4 m) and obtained results after 4 years, the highest density was recorded with an increase in height from 14.19 m to 2500 plants/ha, then from 13.25 m to 1100 trees/ha and 13.06 m at 625 trees/ha. Similarly, at 2500 plants/ha, the average diameter at breast height was 17.50 cm, followed by 21.94 cm at 1100 plants/ha, and a maximum of 25.75 cm diameter at breast height was observed at 625 plants/ha.

Prajapati *et al* (2020) evaluated *M. dubia* for growth and yield performance and observed significant variation in tree height (m), girth at breast height (GBH) (cm), standing volume (m^3 /tree) and biomass (kg/tree) at Sorghum Sudan Grass (SSG) intercropping (July) and final SSG forage harvest (November), among the silvi-pasture and sole plantation systems. At the SSG planting period, the height and GBH was higher under *M. dubia* (3 × 3 m)-SSG system than sole *M. dubia* plantation at 4×4 m. At the time of SSG planting, volume and biomass per tree were higher in trees from sole *M. dubia* plantation at 4 × 4 m spacing, though, at the final SSG harvest, *M. dubia* (4×2 m) SSG system was higher in volume, biomass and increment in per tree volume and per tree biomass. Overall, the results showed that intercropping of SSG under *M. dubia* plantation has positive effect on growth and yield attributes of *M. dubia*.

2.2 GENETIC VARIABILITY PARAMETERS

Simple measurements of variability, such as range, arithmetic mean, variance, standard deviation, coefficient of variation, and standard error, can be used to examine population variability. Heritability is a key metric for a population that determines how well a tree improvement programme is implemented. It refers to the proportion of phenotypic variation that is genetically determined. It refers to the proportion of phenotypic variation that is genetically determined. When variability is due to additive components, it is referred to as narrow sense, and when variability is due to additive and non-additive components, it is referred to as broad sense. In diverse tree species, heritability has been determined for a variety of traits. The second technique involves crossing many genotypes using one of the mating designs and analysing the progeny in repetitive trials to determine the components of total variance of a sample. However, this technique is expensive, time-consuming, and inconvenient. Clustering techniques are the third way, and they aid in determining the quantity of diversification as well as the proportional percentage of each component character to the overall divergence. Some of the studies that were based on this are listed below.

Kaushik *et al* (2007) conducted research to determine the genetic diversity in Jatropha seed characteristics and oil content (*Jatropha curcas* L.). The seed characteristics and oil content of 24 *Jatropha curcas* accessions obtained from different agroclimatic zones in Haryana, India, were evaluated. Seed size, 100-seed weight, and oil content differed significantly ($p>0.05$) amongst accessions. Seeds obtained from IC-520602 had the highest seed weight, whereas seeds collected from IC-520587 had the lowest. The phenotypic coefficient of variation was generally larger than the genotypic coefficient of variation, indicating that the environment was the most important factor. Seed weight had a high heritability and genetic gain (96 percent and 18 percent, respectively), indicating additive gene activity.

Callister and Collins (2008) investigated genetic parameter estimations in a *Tectona grandis* Linn clonally repeated progeny test. It has been extensively planned in the tropics for its highly valuable timber, and data from a 3.5-year-old teak progeny test with clonal replication in northern Australia was analysed. For economically significant features, additive and non-additive genetic variations were calculated. For growth attributes, no additive genetic variation accounted for 35-50 percent of total genetic variance, while for incidence of flowering, it represented for 63 percent of total genetic variance. The heritability of diameter was 0.22, 0.07 for stem straightness, 0.18 for height and volume, 0.03 for epicormic sprouts, 0.05 for insect defoliation and 0.30 for blooming incidence (estimated on an assumed underlying continuous scale). Broad sense heritability was 0.37 for diameter, 0.35 for volume, 0.28 for height, 0.12 for stem straightness, 0.12 for epicormic sprouts, 0.06 for insect defoliation and 0.71 for incidence of flowering.

Pongamia pinnata (L.) Pierre from the Konkan area of Maharashtra was investigated by Raut *et al* (2011) for seed and fruit variability. The differences between PCV and GCV were small, indicating that the environment has a little effect in the development of various characters. In general, the magnitude of PCV for all characters analysed was greater than the related GCV. In a general sense, heritability was characterised as extremely high (above 95%) for all features, ranging from 95.75 percent (seed thickness) to 99.55 percent (pod length).

Bush *et al* (2011) discussed their research on genetic diversity in natural durability features of juvenile *Eucalyptus cladocalyx*, a plant that thrives in temperate, low-rainfall environments. For all characteristics, the results indicated a significant variance among three regions of Provenance, with low-mode, narrow-sense heritability for growth traits and extractives content, and moderate-high heritability for basic density and decay resistance to two of the three fungus.

Twenty open pollinated *Melia dubia* families were chosen and analysed for growth characteristics and genetic divergence. The volume index was the most important factor in genetic divergence, followed by plant height. The population's genetic variability was found to be enough after a genomic examination of the families. Volume index was superior in the PVC and GCV calculations, followed by basal diameter and plant height. Plant height and volume index, on the other hand, showed considerable heritability. The volume index had the highest genetic advance, followed by plant height, indicating that these two criteria are reliable enough to be used in future improvement programmes (Kumar *et al* 2013).

Meena *et al* (2015) conducted research in Rajasthan to assess genetic characteristics in pods and seed attributes of *Tecomella undulata* (SM.) Sem candidate plus trees. All pod and seed characteristics, such as seed weight (0.6 to 1.3g), seed length (16.7 to 22.2 mm), seed width (8.3 to 9mm), number of seeds/pods (60 to 68), pod length (18.6 to 26.2 cm), and pod width (8.3 to 9mm), showed significant variation (9 to 1n). The phenotypic and genotypic coefficients of variation were found to be similar to one other for all the genetic parameters investigated, with 100- seed weight and pod length having the highest values. Broad sense heritability estimates varied from 55.4 percent (for seed length) to 78.26 percent (for pod length).Genetic advance as per cent of mean ranged between 3.78% and 17.7% with seed width giving the lowest value and 100- seed weight giving the highest value.

In Punjab, Singh *et al* (2016) conducted the experiment to evaluate the growth parameters of Melia tree under different levels of N and P. Nutrient concentration and accumulation in leaf and fine roots were recorded at intervals of three months (April, July, October and January). It was observed that N accumulation and highest root biomass were found during July and October months as compare to April and January. Highest leaf and root N were observed in April and lowest in January. From this study, it can be concluded that during summer higher root competition for nutrients and moisture was recorded between intercrop roots and tree.

Brandani *et al* (2017) studied the impact of *Acacia mangium* plantations on soil C and Al availability at depths of 0-5 and 5-10 cm. They discovered that introduction of *Acacia* enhanced the Al availability by about 13%. They also claimed that the C content of the soil had increased by about 10%.

Johar *et al* (2017) compared the chemical characteristics of soil under pre-established five-year-old plantations of kinnow alone and kinnow + Eucalyptus to the effect of a three-tier agroforestry system (Eucalyptus – kinnow – wheat) in comparison to control (devoid of trees). The data showed that soil organic carbon increased sharply and electrical conductivity dropped, but that soil pH remained unchanged. Similarly, in an agroforestry system, soil nutrient status N, P, and K were much higher than in a control system (sole crop).

Under *Melia azedarach* trees, Sarkar *et al* (2017) investigated soil characteristics. It showed a considerable rise in soil pH and electrical conductivity under a ten-year-old tree, showing its utility in acid soil reclamation. Furthermore, a considerable drop in available nitrogen and potassium in soil at 0-15 cm depth suggested that it is necessary for nutrient replenishment in topsoil to keep plants fertile.

Sirohi and Bangarwa (2017) conducted a study to observe how spacing of 5 × 4m, 10 × 2m, and 18 × 2 ×2m (paired row) of 7 and 8 year old poplar agroforestry systems affected soil chemical components. It was discovered that the nutritional quality of the poplar agroforestry system was superior to that of a single wheat crop. Further, discovered that the lowest soil pH value was under 5 × 4m spacing. Similarly, the lowest EC value was found at 5 × 4m spacing, followed by 10 × 2m, and 18 × 2 × 2 m spacing. They also discovered that soil organic carbon increased as tree spacing decreased, with the highest levels under 5 × 4m spacing, followed by 10 × 2m, 18 × 2 × 2 × 2m spacing, and control (sole crop). In comparison to a single crop, nutrient status is better in a poplar-based agroforestry system.

Sharma *et al* (2017) conducted the study at two sites Handesra, Mohali and Bhera Village, in the Hoshiarpur plain of Punjab. Two mature Melia fields have been selected with low and high quality. In each Melia case, fourteen soil samples were selected from both sites. Soil samples were taken from 0-30cm depth and the pH, Organic Carbon (OC), Available Nitrogen (N), Phosphorus (P) available and potassium (K) deposited were determined from each soil sample in the laboratory. The results showed that the high concentrations of carbon (2.89%), available nitrogen (0.037%), phosphorus (0.0011%) and potassium substitutes (0.027%) were detected in Handesra, Mohali and organic carbon (1.69%), available nitrogen (0.027%), phosphorus available (0.00068%) and potassium substitutes (0.021%) were identified in Bhera Village, Hoshiarpur. The results also show that low-lying fields have a negative impact on soil fertility and reduce their fertility. Reduced nutrient depletion has had a detrimental effect on the abundance and quality of Melia trees.

The genetic diversity can also be studied through biotechnological means. RAPD molecular markers were used to evaluate the genetic diversity in populations of *Melia azedarach* Linn. from different locations of Himachal Pradesh and Punjab (Thakur *et al* 2017). In the study, 17 primers were used where 13 yielded polymorphic banding patterns. In total, 97 different DNA bands were obtained which showed cent percent polymorphism. Cluster analysis based on Jaccard's similarity coefficient using UPGMA grouped all the 19 populations into three major groups. Similarity indices ranged from 0.24 to 0.92. High genetic diversity detected in the present study may be due to all prevalent background factors as populations of selected trees studied are widely distributed in different eco-geographic regions.

Bhagasara *et al* (2017) carried out a study to estimate the GCV, PCV, heritability and genetic gain for nine different characters of *Sorghum bicolour*. Analysis of variance revealed significant difference between genotypes for the different quantitative characters. Furthermore, the study revealed high GCV, PCV and genetic gain for grain yield per panicle, and high heritability for 100 - seed weight.

According to Chaturvedi *et al* (2017), spacing of 5 m × 5 m is good for *Melia dubia,* whereas spacing of 8 m × 8 m is suitable for *Melia dubia*. However, farmers generally plant at 3 m × 3 m or 3 m × 4 m. The spacing used varies depending on the size of the farm, the type of intercropping used, the availability of water, and the farmer's needs. Pruning every 6 months controls branching in *Melia dubia* and is done annually to obtain straight cylindrical boles.

During the kharif season of 2014, Patel *et al* (2017) did a study at the department of Forestry, college of agriculture, and Jabalpur (M.P) to assess the impact of pruning and agronomical management on wood production and yield of paddy under *Dalbergia sissoo*. The experiment includes four pruning intensities, one open plot (without tree), and three agronomical management approaches in the main plot. As a result, different pruning methods had a major effect on the diameter of the tree at breast height. The higher dbh (23.98 cm) was greatly influenced by 25% trimming. Different pruning treatments had a major effect on the cylindrical volume and stand biomass of trees, 25% pruning produced substantially higher cylindrical volume and stand biomass than 75 percent pruning and was comparable to no pruning and 50 percent pruning. The study found that tree shade has a negative impact on crop growth and yield, while reduce tree canopy, facilitated entry of sunlight, pruning is one of them.

Naugraiya *et al* (2018) investigated biomass, nutrient accumulation, and soil improvement in an eighteen-year-old *Azadirachta indica* plantation with 3 × 3 m spacing at a research farm in Chattisgarh. The experiment yielded 62.07 kg of aboveground biomass per tree.

Roshanzada *et al* (2018) investigated the growth and carbon storage potential of some of the most important agroforestry trees in the north western Himalaya. The study included seven tree species and 210 trees in total. The above-ground biomass and carbon storage in *Melia composita* were found to be 950 kg/tree and 475 kg/tree, respectively.

Kumar (2018) conducted an experiment at the Division of Agroforestry of Sher-e-Kashmir University of Agriculture Sciences and Technology, Jammu to evaluate tree crop interaction in a *Melia composita*-*Tagetes erecta* based agroforestry system. The presence of crop had no effect on the growth characteristics of *Melia composita* in pure plantation, such as dbh, height, crown width, above ground biomass and volume, both at the start of the trial and at the end. At the end of the trial, the trees had a dbh of 13.41 centimetres, height of 8.62 metres, an aboveground wood biomass of 102.61 kg and a crown width of 7.25 metres, per tree.

Kumar *et al* (2018) carried out an experiment to determine the effect of pruning intensity on *Dalbergia sissoo* tree biomass production and fresh turmeric yield at the research farm (M.P). Four pruning intensities were used in the experiment, as well as an open condition. The canopy spread in both north-south and east-west directions was highest in no pruning (9.88 m and 9.95 m), and lowest in 75 percent pruning (6.41 m and 6.46 m). Heavy pruning, i.e., 75 percent pruning, resulted in the greatest pruned biomass (1085 kg ha^{-1}), compared to 50 percent pruning (932 kg ha^{-1}) and 25% pruning (701 kg ha^{-1}). The data also demonstrated that 25% pruning resulted in a higher yield (27.3 q ha^{-1}) than 50% pruning (25.3 q ha^{-1}) which significantly lowered yield.

Singh and Kishori (2018) carried out a study to estimate the heritability, variability and genetic advance based on twelve morphological characters of Ocimum. The results showed the PCV for all the characters to be higher than the corresponding GCV. The broad sense heritability was observed to be high for all studied characters, with maximum being days to maturity (99.46%). Genetic advance was also recorded as maximum for eugenol content (96.65).

Yadav *et al* (2019) studied the genetic divergence of 20 phenotypically superior trees of *Melia dubia* in the natural distribution zones of Uttar Pradesh. Based on the relative magnitude of D^2 values, progenies were grouped into eight clusters on the basis of morphological and biomass traits. Cluster V exhibited the highest number of five superior tree progenies. Cluster V exhibited maximum intra cluster distance (4.79) indicating that progenies in this cluster were more diverse than the other clusters. The maximum inter cluster D^2 value was obtained between cluster VI and VII (9.21). The clustering pattern in this study revealed that superior tree progenies from different geographic region were grouped together in a cluster and vice-versa suggesting that geographical diversity did not necessarily represent the genetic diversity. The study also showed that the PCV was higher than the corresponding GCV for all the morphological and biomass traits which revealed that the traits were sensitive to environmental fluctuations. The traits with low genetic gain and high heritability indicate that the expression is possibly controlled by intra and inter allelic interactions. The hybridization between the more diverse genotypes of *Melia dubia* can produce genotypes with high heterotic vigour.

Sharma *et al* (2019) established trial of 17 improved genotypes of *Melia dubia* procured from Division of Genetics and Tree propagation, FRI, Dehradun at village Lethwin, District Bilaspur, Himachal Pradesh. Data on growth parameters such as height and diameter were recorded after one year of plantation and genetic parameters viz. phenotypic variance, genotypic variance, heritability, genetic gain and genetic advance were worked out. Significant variation for diameter, height and genetic parameters was observed among the evaluated genotypes. Genetic parameters recorded high values for heritability and genetic advance for diameter as well as height growth in all evaluated genotypes indicating scope of early selection for these traits. The maximum values for height and diameter growth were recorded for genotypes 241 and 231 which indicated their suitability for the cultivation in the area under study.

Chauhan *et al* (2019) studied tree biomass and carbon sequestration in four short rotation tree plantations at the university seed farm, Ladhowal, Ludhiana, Punjab (*Acacia* *catechu*, *Dalbergia sissoo*, *Melia azedarach* and *Terminalia arjuna*). *Terminalia arjuna* had the highest aboveground biomass of 261.40 t ha^{-1}, while *Melia azedarach* had the lowest at 96.58 t ha^{-1}.

Das *et al* (2019) studied the performance and characterize soil fertility status, plant growth behaviour and light profile of multipurpose tree species in Ranchi, Jharkhand and resulted that biomass production and higher photosynthetically active radiation potential of *Dalbergia sisso, Leucaena leuocephala* and *Gmelia arborea,* was higher. Also, a significant increase in pH and decrease in EC of trees were observed and indicated that a need for replenishment of nutrients in soil for maintaining soil fertility in agroforestry systems.

Dilla *et al* (2019) investigated agroforestry parklands in Ethopia and other parts of the tropics, as well as a number of *Faidherbia albida* trees and adulala soil. A watershed was sampled to offer a preliminary evaluation of these systems' carbon sequestration capacity. Selected albida trees in a 79-hectare area had been clipped 2-4 years prior, and their canopies had since regrown, and their height and diameter had been measured. Although the study found that albida trees store about 2 t C ha^{-1} in aboveground biomass, other studies have found that albida tree parkland systems can store more C in their aboveground biomass.

Beadle *et al* (2019) studied the effects of pruning on stem form and the incidence of heart rot in an 18-month-old acacia mangium plantation in south Sumatra to see if pruning is linked to an increase in the incidence of heart rot and improved stem form. They found that pruning compared to lift pruning reduced the incidence of heart rot and improved stem form. By eliminating huge branches and those that subtending a small angle with the stem up to 3 m height, form pruning removed 25% of leaf area, while lift pruning removed 25% of crown length from below. Before trimming, the trees in these treatments were singled out. The third treatment, a control, was utilised to determine the basal degree of heart rot. There was no clear differentiation in diameter increment between the two pruning methods. The findings indicated that form pruning is likely to improve stem straightness and is likely to be beneficial at any pruning height. A later lift pruning is, however, still regarded necessary.

2.3 CORRELATION BETWEEN DIFFERENT TRAITS

Along with heritability, correlation between different traits is another important parameter that greatly influence the gain obtained in a tree improvement programme. When the economically important traits are positively correlated gain achieved in one trait automatically brings about improvement in the other. Tree crops generally have long rotation periods. Thus, proper conclusions on the improvement made in a programme can be drawn only at the harvestable age. Obtaining juvenile- mature correlations will be helpful in predicting the gain based on the performance in the juvenile stages. These correlations may vary with species and prevailing growth conditions.

At the population level, Loha *et al* (2006) discovered patterns of genetic variation in *Cordia aftricana*, a tropical wood species. Bulk seed samples were obtained from six Ethiopian natural populations and analysed for differences in seed morphometric characteristics, seed germination, and seedling development at the nursery stage. Seed weight had a substantial positive association with altitude and a negative correlation with mean annual temperature of seed origin, according to the findings. Longitude and mean yearly rainfall were shown to be significantly correlated with germination energy. Seedling characteristics and seed origin geoclimatic factors were fairly correlated.. Between seed length and seed weight, root collar diameter at 4 months and seed length and weight, and seedling after 4 and 8 months of growth, there was a significant inter character correlation. The observed patterns of variation will have significance for genetic resource conservation and tree enhancement, it might be concluded.

Luna *et al* (2006) investigated *Albizia lebbeck* pod, seed, and germination traits across 20 seed sources. A statistically significant correlation between seed, pod, and germination properties was discovered using the correlation matrix.

In order to investigate the regional variation in tree development and wood density of *Guazuma crinita* Mart. in the Peruvian Amazon, Weber and Montes (2007) established a trial of 11 Peruvian provenances in three planting zones. The development of trees at 6, 12, 18, and 30 months, as well as the density of their wood at 32 months, were studied across and within zones. Larger trees exhibited lower density and considerable density differences between the lower and upper stems, according to the correlations, although the strength of these correlations varied depending on provenances and zones. The study was carried to the key finding that fast-growing provenances might be chosen at an early age without reducing wood density significantly.

Lune *et al* (2008) evaluated forty-nine exotic and indigenous clones of poplar for eight morphological traits. Plant height showed positive and significant correlation with diameter.

Wani *et al* (2008) assessed genotypic and phenotypic correlation between several variables using 32 distinct seed sources of *Bauhinia variegate* and discovered that correlation studies provide improved understanding during selection programmes. They discovered that phenotypic correlation coefficients were lower than genotypic correlation coefficients, possibly due to the modifying influence of the high inherent character association at the genetic level.

Kumaran *et al* (2010) investigated correlation and path coefficients in fifteen *Simarouba glauca* seed sources. For height and diameter, there was a highly significant positive correlation. Height and basal diameter had a favourable direct effect on volume index, according to path analysis.

In south-east Australia, Gapare *et al* (2012) investigated at provenance variation and genetic characteristics for wood qualities in mature radiata pine (*Pinus radiata* D. Don). The current study results genetic correlations between breast height diameter and wood qualities were smaller (less negative) than the mean calculated from the current radiata pine breeding population generation. The strongest negative genetic connections with growth were seen in density (mean rA0-0.23± 0.09).

In introduced Salix species, Gupta *et al* (2012) found the highest positive and significant correlation coefficient (0.959) for basal diameter with volume index. Three out of eight components provided 85.03 percent of the overall variation, with the first principle component (λ= 3.086) explaining 38.57 percent of the variance weighted maximum (0.937) by volume index, according to principal component analysis via correlation matrix.

The study's goals were to establish the level of genetic variation in stem deviations from straightness in *Eucalyptus globulus* and to assess the utility of a six-point subjective scoring technique as a stem straightness selection criteria, according to Blackburn *et al* (2013). There was a lot of additive genetic variability. Between the stem straightness evaluations and DBH at ages five and nine years, there were strong, positive, and substantial additive genetic correlations. At ages 5 and 9 there were significant positive genetic correlations between subjectively scored stem straightness and DBH.

Changrong *et al* (2017) studied the heritability and trait-trait correlations for growth, volume, diameter at breast height and wood mechanical traits including green density and basic density of *Eucalyptus cloeziana* F. Muell. For growth across ages 0.5-9.5 years the narrow heritability ranges was 0.04 to 0.35 and at the age of 9.5 years the heritability ranges from 0.06-0.24 for wood mechanical properties thus indicating low to average magnitude of additive genetic control of such traits. At the final age 9.5 years, genetic and phenotypic correlations were consistently positive between growth traits and significantly positive between mechanical traits.

Sharma *et al* (2017) conducted a correlation study on morphological characters viz. Diameter at breast height, total height clear bole height, crown spread and straightness among forty- five plus trees of shisham which were selected from three agro- ecological regions. Seed sources from dry sub humid region were found more promising than other two. Significant variations were observed among morphological traits and significantly positive correlation was found among the traits.

Chhetri *et al* (2019) conducted a study on 40 genotypes of jackfruit (*Artocarpus heterophyllus* Lam.) selected from six north – eastern states of India (Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram and Tripura) and reported yield per plant to have positive and significant correlation with fruit diameter, rachis diameter, petiole length, fruit weight, fruit length and flake length.

CHAPTER III

MATERIALS AND METHODS

Experimental details, procedures and methodology used in the current study entitled "Genetic variability among the open pollinated progenies of burma dek (*Melia composita* Benth.) under field conditions" is described under this chapter as follows:

Experiment No. 3.1

3.1.1 Name of Experiment

Genetic variability among the open pollinated progenies of burma dek (*Melia composita* Benth.) under field conditions.

3.1.2 Location

The experiment was carried out at experimental area of the Regional Research Station, Bathinda. The area is located in the southern part of the Punjab State, and it lies in between 29^{o} 33` and $30^{o}$ 36` North latitude and 74^{o} 38` and $75^{o}$ 46` East longitude at an elevation of about 202 m above mean sea level.

3.1.3 Climate

The area falls in the south west plain agro-climatic zone of Punjab. The region is categorized by semi-arid environmental conditions. In May to June and December to January, the region has exceptionally hot summer and severe winter. The coldest temperature fall up to 4°C or even below, and in the summer time the maximum temperature rise to more than 45°C. It is not usual to get frost. The land is deep, well drained, granular, low humus textured loam. The soil's pH is neutral. The area receives an average rainfall of about 421 mm per annum and ~75% of total amount of rainfall is predictable during July with an average of about 31 rainy days.

3.1.4 Methodology

The study was conducted on 9.5-year-old progenies of *Melia composita.* The open pollinated progenies seed source collected from roadside and boundary plantations of farmers field were (Table 3.1) already established at Experimental Area of the Regional Research Station, Bathinda with 4 x 4 m spacing under complete randomized block design with four replications. The observation on various growth parameters was collected at 6-months interval. In February month first observations was taken.

3.1.4 Observations recorded on morphological characters

3.1.4.1 Tree height (m)

The tree height of *Melia composita* was measured from the base to the tip of the highest branch of the tree with the help of Ravi's altimeter in meters and height of the observer was added. Measurements of 9.5 and 10 yr old plantation was taken.

3.1.4.2 Diameter at breast height (cm)

Girth at breast height of progenies at height of 1.37 m above the ground level was measured by using measuring tape. It was measured with the help of measuring tape in cm. Diameter was estimated by following formula.

$$D = G/\pi$$

Where, D- Diameter at breast height

G- Girth at breast height

The data was recorded in February and September month.

Table 3.1: Geographical details of progenies of *Melia composita*

Code	Progeny name	Locality*	Height (m)	Girth (cm)
1	MCS 1	Morinda - Chamkaur sahib road	14.5	76
2	CSN – 2	Chamkaur Sahib - Neelon road	14.8	91
3	CSN – 1	Chamkaur Sahib - Neelon road	14	86
4	NK – 1	Neelon - Khuhara road	13.5	65
5	Hedon – 2	Village Hedon	13.5	106
6	Jodhan – 1	Village Jodhan	15	100
7	Hedon – 3	Village Hedon	14	71
8	D Hoor Brg - 2	Village Dadhahur	18	81
9	GSS - 1 SBS Ngr	SBS Nagar Ludhiana	13	99
10	D Hoor Canal LS 3	Village Dadhahur	15	104
11	D Hoor Brg - 1	Village Dadhahur	16	94
12	D Farmer Dhanaula	Village Dadhahur	14	85
13	Brick Kiln R1	Village Raikot	16	97
14	D Hoor Girls school (DHSG)	Village Dadhahur	15	82
15	Teaching area(TA)	PAU Ludhiana	13	95
16	GSS - 3 SBS Ngr	SBS Nagar Ludhiana	14	95
17	RRS – 3	RRS Bathinda	13	102
18	CIPHET L10 P9	PAU Ludhiana	15	95
19	RRS- 7	RRS Bathinda	12	105
20	Jodhan – 8	Village Jodhan	14.2	78

*Locality – roadside plantations or superior trees on farmers field.

Table 3.2: Layout of the experiment

	Extra # 22				Extra # 21		# 22		Extra # 23		
SB1	1	1	1	1	1	2	2	2	2	2	R1
	3	3	3	3	3	4	4	4	4	4	
SB2	5	5	5	5	5	6	6	6	6	6	
# 21	7	7	7	7	7	8	8	8	8	8	
SB3	9	9	9	9	9	10	10	10	10	10	# 21
	11	11	11	11	11	12	12	12	12	12	
SB4	13	13	13	13	13	14	14	14	14	14	
	15	15	15	15	15	16	16	16	16	16	
SB5	17	17	17	17	17	18	18	18	18	18	
	19	19	19	19	19	20	20	20	20	20	
SB2	8	8	8	8	8	7	7	7	7	7	R2
	6	6	6	6	6	5	5	5	5	5	
SB4	16	16	16	16	16	15	15	15	15	15	
# 21	14	14	14	14	14	13	13	13	13	13	# 21
SB1	4	4	4	4	4	3	3	3	3	3	
	2	2	2	2	2	1	1	1	1	1	
SB5	20	20	20	20	20	19	19	19	19	19	
	18	18	18	18	18	17	17	17	17	17	
SB3	10	10	10	10	10	12	12	12	12	12	
	9	9	9	9	9	11	11	11	11	11	
SB5	19	19	19	19	19	17	17	17	17	17	R3
	20	20	20	20	20	18	18	18	18	18	
SB1	3	3	3	3	3	1	1	1	1	1	
# 21	4	4	4	4	4	2	2	2	2	2	
SB4	15	15	15	15	15	13	13	13	13	13	# 21
	16	16	16	16	16	14	14	14	14	14	
SB3	12	12	12	12	12	11	11	11	11	11	
	10	10	10	10	10	9	9	9	9	9	
SB2	7	7	7	7	7	5	5	5	5	5	
	8	8	8	8	8	6	6	6	6	6	
SB3	11	11	11	11	11	9	9	9	9	9	R4
	12	12	12	12	12	10	10	10	10	10	
SB4	14	14	14	14	14	16	16	16	16	16	
# 21	13	13	13	13	13	15	15	15	15	15	
SB5	18	18	18	18	18	20	20	20	20	20	# 21
	17	17	17	17	17	19	19	19	19	19	
SB2	6	6	6	6	6	8	8	8	8	8	
	5	5	5	5	5	7	7	7	7	7	
SB1	2	2	2	2	2	4	4	4	4	4	
	1	1	1	1	1	3	3	3	3	3	
					# 23						

In the layout of the experiment 20 progenies with 5 trees of each are present in one replication. Trees are present at a spacing of 4×4 m. In this, block design 5 blocks are present/ replication with 4 progenies in each block.

3.1.4.3 Volume (m^3)

Volume is one of the most important calculated tree growth parameter and volume of the trees was calculated by using single-entry model.

Volume = $0.000137 * D^{2.48}$

3.1.4.4 Straightness (score 1-5)

The straightness of the bole was recorded based on visual observation. They were subjectively scored from 1 to 5, with the number of points allotted according on the individual's relative straightness. Thus, a tree with a little bit of spiral and a little bend in one place receives a score of one, but a totally straight individual with no spiral receives a score of five.

Table 3.3: Scores given to *Melia* progenies for stem straightness

Score	Categorization
1	Crooked, serious bends in main stem
2	Slightly crooked, less bends in main stem
3	Mostly straight, 1-2 small bends
4	Straight but small bends
5	Perfectly straight

3.1.4.5 Clear bole height (m)

The distance between ground level and the crown point of the tree is known as the clear bole height. The position of the first crown-forming branch, whether alive or dead, is known as the crown point. Ravi's altimeter was used to record the clear bole height of the trees. It was taken at a six-month interval and measured in metres.

3.1.4.6 Branching behaviour

Branching behaviour is the patterns created by main branches of the tree.

3.1.4.7 Number of branches/m Crown length

The number of branches per meter crown length was recorded by counting branches.

3.1.4.8 Crown length (m)

Crown length was measured along with the main axis from the base of the crown to the tip of the tree. This length was usually calculated by excluding the clear bole height from the total height of the tree. It was expressed in meter.

3.1.5 Statistical analysis

Statistical analysis was done as per the procedure laid down for Complete

Randomized Block Design (CRBD). Analysis of variance, critical difference (CD) and variance components was calculated for the interpretation of research of the study following Panse and Sukhatme (1989) method. The statistical analysis was carried out by using CPCS1 and OPSTAT software.

3.2 Estimation of Genetic parameters

3.2.1 ANOVA studies

The analysis of variance (ANOVA) was estimated by Panse and Sukhatme (1989) methods. The variability parameters i.e., GCV, PCV and Environment coefficients of variability were estimated by using OPSTAT software.

3.2.1.1 Mean

The mean for each character in all the populations was computed as follows**.**

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$$

Where,

$\bar{x}$ = Sample mean

x= Individual values;

n= Number of observation

3.2.1.2 Range

The range for a particular trait was determined by calculating the minimum and maximum values based on individual plant observations.

3.2.1.3 Variance

Variance was calculated for all of the characteristics as follows.

$$\text{Variance} = \frac{1}{n}\Sigma(Y_i - \bar{Y})^2$$

Where,

Y_i = Individual value

$\bar{Y}$ = Population mean

n = Number of observation

3.2.1.4 Standard deviation

(SD) = $\sqrt{\text{variance}}$

Standard error (SE) = $\frac{sd}{\sqrt{n}}$

Where,

d = Deviation of individual value from population mean

n = Number of observation

3.2.1.5 Critical difference (CD)

To compare the treatment means, the critical difference (CD) for all characters was determined. The critical difference was determined using the standard error for the difference of two means and the tabulated value 't' at a 5% level of significance for error degree of freedom .

$$CD = SE_d \times t_{0.05} \text{ error degree of freedom}$$

Where,

SE_d=Standard error of difference of the treatment means to be compared

$$SE_d = \frac{\sqrt{2}Me}{e}$$

$t_{0.05}$ error degree of freedom = t value at 5% level of significance for error degree of freedom.

3.3 Variability studies

The data was recorded at the age of 9.5 and 10 year.

3.3.1 Genotypic coefficient of variability

The formula proposed by Johnson *et al* (1955) was used to estimate the Genotypic coefficient of variability.

$$GCV = \frac{\sigma^2 g \times 100}{\overline{x}}$$

Where,

$\overline{x}$ = population mean,

$\sigma^2 g$= Genotypic standard deviation.

The genotypic and phenotypic coefficient of variation was categorized as.

S. No.	Range	GCV (category)
1.	0-10%	Low
2.	10-20%	Moderate
3.	>20%	High

3.3.2 Phenotypic coefficient of variability

The formula proposed by Johnson *et al* (1955) was used to estimate the Genotypic coefficient of variability. Burton and De-vane (1953) suggested the formula for calculating the Coefficient of variability.

$$PCV = \frac{\sigma^2 p \times 100}{\overline{x}}$$

Where,

$\overline{x}$ = Population mean,

$\sigma^2 p$ = Phenotypic standard deviation.

3.3.3 Heritability (Broad sense)

Burton and De-vane (1953) and Johnson *et al* (1955) suggested the formula for calculating the Broad sense heritability. It was calculated as the ratio of genotypic variance to the phenotypic variance and expressed in percent.

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

Where,

H^2= Heritability

Vp= Phenotypic variance

Vg= Genetic variance

The heritability classified into three groups as:

S. No.	Range	Heritability (classes)
1.	0-30%	Low
2.	30-60%	Moderate
3.	>60%	High

3.3.4 Genetic advance

Johnson *et al* (1955) suggested the formula for calculating the genetic advance

$$\text{Genetic advance} = \frac{(Vg)}{(Vp)} \times (\sqrt{V_p}) \times K$$

Where,

K = Selection differential at 5% selection intensity.

The value K = 2.06 (Allard 1960)

3.3.5 Genetic advance as %age of mean

Johnson *et al* (1955) suggested the formula for calculating the Genetic advance as per cent of mean as under.

$$\text{Genetic gain (\%)} = \frac{GA}{\bar{x}} \times 100$$

Where,

$\bar{x}$ = Population mean

GA= Genetic advance

Genetic advance as per cent of mean was classified into three groups as follows.

S. No.	Range	Category
1.	0-10%	Low
2.	10-20%	Moderate
3.	>20%	High

3.4 Association studies

The data recorded at the age of 9.5 and 10 year was used for association studies. The calculations related to GCC and PCC were done following the method suggested by Goulden (1952). Correlation parameters and path analysis parameters were statistically analyzed using OPSTAT software. The simple correlation coefficients (Pearson 1901) were found by using the formula proposed by Panse and Sukhatme (1989).

3.4.1Genotypic and Phenotypic correlation coefficient

$$r(XY) = \frac{cov.XY}{\sqrt{V(x), V(y)}} \times 100$$

Where,

r (XY) = Simple correlation between X and Y

V (X) =Variance of X character

V (Y) = Variance of Y character

The significance of V values was tested against (n-2) degree of freedom by using Fisher and Yates tables. For testing simple correlation, the 'f' value was calculated by the following formula.

$$t = \frac{r}{\sqrt{1-r^2}} \times \sqrt{n-2}$$

Where,

r = Simple correlation

n = Number of observations in the sample

Analysis of covariance was worked out as per the procedure suggested by Panse and Sukhatme (1989).

3.4.2 Path coefficients

Path analysis was carried out using the correlation coefficient. This was done to analyze the direct and indirect effects of the components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). The following set of simultaneous equations was used for estimating the direct and indirect effects.

$r_1y = a + r_{12}b + r_{13}c + \ldots\ldots. + r_{11}i$

$r_2y = r_{21}ab + r_{23}c + \ldots\ldots\ldots. + r_{21}i$

$r_3y = r_{31}ab + r_{23}c + \ldots\ldots\ldots. + r_{31}i$

$r_ny = r_{n1}ab + r_{12}c + \ldots\ldots\ldots. + i$

Where, r_1y to r_ny = correlation coefficient between causal factors 1 to n and dependent character y.

$r_{12}, r_{21}, r_{31,}$ ... . . .… r_n1 = coefficient of correlation between causal factors 1 to n.

a, b, c, ... i = direct effects of characters 'a' to 'i' on the dependent character 'y'.

3.5 Genetic divergence analysis

Genetic divergence D^2 analysis as detailed by Rao (1952) and was used to assess the genetic divergence among the *Melia composita* progenies. The linear functions of the mean squares and mean products were used to estimate the variance and covariance of the components. Pivotal condensation method was used to calculate divergence using error, variance, covariance and determinants of error. Test of significance for p characters were performed by calculating V-statistics which in turn utilized Wilk's criterion as described by Rao (1948).

$$\text{Wilk's } \wedge = \left|\frac{W}{W+Q}\right| = \frac{\text{Determination of ferror matrix}}{\text{Determination of ferror} + \text{Variety matrix}}$$

V-statistics was calculated using Wilk's criterion as follows:

$$V(\text{stat}) = -m \log_e \wedge = -(n - \frac{p+q+1}{2}) \log_e \wedge$$

Where,

$$m = (n - \frac{p+q+1}{2})$$

p = number of characters;

n = d.f. for error

q = number of seed sources – 1 d.f.

V(stat) is distributed as X^2 with pq degrees of freedom. Significance of V (stat) indicated the significance of the differences between the means in respect of pooled effect of p characters and allows us to analyze further to estimate the D^2 values.

For the computation of D^2 values, the original variables (X's) that were correlated were transformed into a set of uncorrelated variables (Y's) by pivotal condensation method. The transformed coefficients were obtained by dividing reduced matrix rows by square root of corresponding pivotal condensation elements. D^2 between genotypes results from the sum of differences between the Y's:

$$D^2 = \Sigma (Yi1 - Yi2)^2$$

D^2 values between all possible $\left| g\frac{(g-1)}{2} \right|$ pairs of 'g'

3.5.1 Determination of Genetic Diversity

9.5 year and 10 year old trees were used in evaluation trial for diversity analysis. Fisher Linear Discriminant Function Analysis (DISCRIM Procedure) was used for assessing the genetic divergence among the tested clones.

3.5.1.1 Clustering of D^2 values

Cluster is not a well-defined term (Rao 1952) so that there are no formal rules for their construction. The conclusion is that two progenies belonging to the same cluster have a lower D^2 value as compare to different clusters. The method used was given by Rao (1952).

3.5.1.2 Overall scoring of cluster means

The ranking provided to each cluster was calculated based on performance across all characters, with the cluster with the least score being ranked first and the cluster with the greatest score being ranked last.

3.6 Index score analysis

Data on growth and yield characteristics was used to carry out the index score analysis (Anderson 1957). The class intervals used for different characters were prepared by classifying the range of variability into four equal groups as given in Table 3.4. For volume scores of 2, 4, 6 and 8 were allotted, whereas, score 1, 2, 3, and 4 were given for the remaining parameters.

Table 3.4: Class intervals for index scoring for 20 progenies of *Melia composita* based on growth and yield characteristics

Characters	Score			
	1(2)*	**2(4)***	**3(6)***	**4(8)***
Tree height (m)	<18.51	18.51 - 19.54	19.55 - 20.56	>20.56
DBH (cm)	<25.25	25.25 - 28.74	28.75 - 32.27	>32.27
Straightness	<3.24	3.24 - 3.57	3.58 - 3.89	>3.89
CBH (m)	<6.91	6.91 - 7.29	7.30 - 7.66	>7.66
Number of branches	<4.48	4.48 - 5.37	5.38 - 6.27	>6.27
Crown length (m)	<11.77	11.77 - 12.48	12.49 - 13.18	>13.18
Volume (m^3)*	<0.402	0.402 - 0.561	0.562 - 0.719	>0.719

***Values in parenthesis were given more weightage to the volume only.

CHAPTER IV

RESULTS AND DISCUSSION

The results of the present study entitled "Genetic variability among the open pollinated progenies of Burma dek (*Melia composita* Benth) under field conditions" was conducted on 10 year old plantations established at Regional research station, Bathinda during 2020-2022. The observations were recorded on already established trial. The results obtained were discussed under following headings are discussed in this chapter in the light of appropriate reasoning and available literature. The relevant data have been presented in Tables (4.1 to 4.11) and Figure (4.1).

4.1 Morphological characters

4.1.1 Tree height (m)

4.1.2 Diameter at breast height (DBH, cm)

4.1.3 Straightness (score 1 to 5)

4.1.4 Clear bole height (m)

4.1.5 Branching behaviour

4.1.6 Number of branches/m crown length

4.1.7 Crown length (m)

4.2 Genetic parameters

4.2.1 Genotypic coefficient of variability (PCV),

4.2.2 Phenotypic coefficient of variability (GCV),

4.2.3 Heritability

4.2.4 Genetic gain of progeny selection (G),

4.2.5 Genotypic correlation coefficients (GCC),

4.2.6 Phenotypic correlation coefficients (PCC),

4.3 Genetic divergence analysis

4.4 Index score analysis

4.1 Morphological characters

The superior genotypes were selected from the progeny trial of *Melia composita* established at Regional Research Station, Bathinda at a spacing of 4 x 4 m. The data on morphology traits viz. total height, diameter at breast height (DBH), crown length (m), clear bole height (CBH), number of branches, straightness, and branching behaviour of selected different progenies are given in Table 4.1. It is clearly evident from the data that total height was maximum in progeny 1 (21.58 m) and minimum in progeny 3 (17.49 m). The maximum DBH was found in progeny 1 (32.19 cm) and minimum in progeny 15 (19.34 cm). The maximum Clear bole height was found in progeny 1 (9.5 m) and minimum in progeny 9 and 10 (7.2 m). The maximum crown length was found in progeny 20 (12.55 m) and minimum was in progeny 15 (9.66 m).The number of branches varied from 7.54 (progeny 20) to 3.65 (progeny 9).

Analysis of Variance

Tables 4.3 and 4.4 show the ANOVA studies for growth characteristics of twenty progenies in *Melia composita* from four replications at the age of ten years old plantation. For all parameters studied, including total height, diameter at breast height, straightness, clear bole height, number of branches, and crown length, the mean sum of squares due to progenies was very significant, indicating that there was a lot of genetic diversity. Because the computed F values and the tabulated F values were compared. Because the computed F value was more than the tabulated value, it was considered significant. All of the features that indicated significant differences across progenies were subjected to further genetic parameter analysis.

Mean performance of progenies

Tables 4.1 and 4.2 show the mean performance of all twenty progenies from four replications at 9.5 and 10 years old for various traits, as well as the critical difference and general mean observed in different months.

4.1.1 Total height (m)

The height of trees ranged from 17.49-21.58 m with mean value of 19.48 m. The maximum and minimum average height was observed in progeny1 (MCS 1) and progeny 3 (CSN 1). The coefficient of variation (CV) was found to be 6.88 per cent.

4.1.2 Diameter (cm)

The diameter of trees ranged from 19.34-32.91cm with mean value of 24.85 cm and the minimum average diameter was observed in progeny 15 (TA) . The maximum average diameter was observed in progeny1 (MCS 1) followed by progeny 2 (CSN 2), when data was observed at the age of 9.5 year with coefficient of variation (CV) was found to be 8.14 per cent.

The diameter of trees ranged from 21.69-33.60cm with mean value of 26.57 cm. The minimum average diameter was observed in progeny 15 (TA). The maximum average diameter was observed in progeny 1(MCS 1) followed by progeny 2(CSN 2) when observed at the age of 10 year with coefficient of variation (CV) 9.34.

4.1.3 Straightness (score 1-5)

In terms of stem straightness, wide range of variation was observed among the progenies. Tree straightness ranged from 1 (mostly crooked) to 5 (totally straight), with a maximum 6.37 coefficient of variation (CV). The mean values of straightness was 3.43 and range of straightness was 4.21- 2.92. The highest value of straightness was observed in progeny 1(MCS 1) and followed by progeny 2(CSN 2) and a lowest value of straightness was observed in progeny 14(DHGS).

Table 4.1: Variation in morphological characters of selected progenies of *Melia composita* (9.5 year old age)

Progeny	TH(m)	Rank	DBH (cm)	Rank	Straightness	Rank	CBH (m)	Rank	No B	Rank	CL (m)	Rank	Vol.	Rank
1	21.58*	**1**	32.19*	**1**	4.21*	**1**	9.5*	**1**	5.43	**5**	11.93	**2**	0.755	**1**
2	21.43*	**2**	30.95*	**2**	4.15*	**2**	9.2*	**2**	4.93	**11**	11.86	**4**	0.683	**2**
3	17.49	**20**	23.24	**16**	3.58	**7**	7.6	**18**	5.08	**7**	11.32	**13**	0.348	**15**
4	18.68	**18**	22.04	**17**	3.09	**18**	8.2	**6**	4.83	**16**	10.55	**18**	0.305	**17**
5	19.95	**6**	25.80	**7**	3.53	**8**	8.2	**6**	4.89	**13**	11.88	**3**	0.440	**7**
6	20.16	**4**	26.23	**5**	3.77*	**5**	8.8	**4**	4.90	**12**	11.01	**15**	0.453	**5**
7	19.14	**13**	27.89*	**3**	3.81*	**3**	7.8	**14**	4.89	**13**	11.06	**14**	0.530	**3**
8	19.15	**12**	23.38	**14**	3.03	**18**	7.9	**10**	5.00	**8**	11.85	**6**	0.345	**16**
9	19.31	**10**	25.37	**9**	3.21	**16**	7.2	**19**	3.65	**20**	11.73	**7**	0.425	**8**
10	19.14	**13**	26.00	**6**	3.30	**13**	7.2	**19**	4.58	**17**	11.48	**10**	0.448	**6**
11	19.28	**11**	21.67	**18**	3.37	**11**	7.8	**14**	4.94	**9**	11.33	**12**	0.288	**18**
12	19.44	**9**	23.61	**13**	3.23	**14**	7.9	**10**	5.23	**6**	11.59	**8**	0.353	**14**
13	18.79	**17**	25.48	**8**	3.60	**6**	8.8	**4**	4.46	**18**	10.22	**19**	0.423	**9**
14	18.99	**15**	24.26	**11**	2.92	**20**	7.8	**14**	4.88	**15**	10.77	**17**	0.380	**10**
15	17.65	**19**	19.34	**20**	3.33	**12**	7.8	**14**	4.05	**19**	9.66	**20**	0.215	**20**
16	20.08	**5**	24.30	**10**	3.38	**10**	7.9	**10**	5.95	**4**	11.42	**11**	0.375	**11**
17	18.96	**16**	20.29	**19**	3.21	**16**	8.0	**9**	4.94	**9**	10.93	**16**	0.248	**19**
18	19.90	**7**	23.72	**12**	3.23	**14**	8.1	**8**	6.94	**2**	11.51	**9**	0.360	**12**
19	20.56	**3**	27.50	**4**	3.80*	**4**	8.9	**3**	6.64	**3**	11.86	**4**	0.513	**4**
20	19.87	**8**	23.37	**15**	2.97	**19**	7.9	**10**	7.54	**1**	12.55	**1**	0.355	**13**
MEAN±SE	19.48±0.773		24.85±1.43		3.43±0.150		8.1±0.462		5.18±0.802		11.32±0.878		0.755±0.053	
RANGE	17.49-21.58		19.34-32.91		2.92-4.21		7.2-9.5		3.65-7.54		9.66-12.55		0.75-0.22	
CD at 5%	1.54		2.86		0.30		0.92		1.60		1.81		0.10	
C.V. %	6.88		8.14		6.37		12.47		17.96		8.50		7.56	

Note- TH: Total height, DBH: Diameter at breast height, St : Straightness, CBH: Clear bole height, No B: Number of branches, CL: Crown length, Vol: Volume

Table 4.2: Variation in morphological characters of selected progenies of *Melia composita* from progeny trial (10 year old age)

Progeny	TH (m)	Rank	DBH (cm)	Rank	ST	Rank	CBH (m)	Rank	No B	Rank	CL(m)	Rank	Vol.	Rank
1	21.58*	**1**	33.60*	**1**	4.21*	**1**	7.99*	**2**	6.96	**4**	13.55*	**3**	0.840	**2**
2	21.43*	**2**	31.79*	**2**	4.15*	**2**	7.73*	**3**	8.42	**2**	13.88*	**1**	0.877	**1**
3	17.49	**20**	24.57	**15**	3.58	**7**	7.00	**12**	4.72	**19**	11.06	**20**	0.368	**16**
4	18.68	**18**	22.36	**19**	3.09	**18**	7.27	**8**	5.59	**12**	11.07	**19**	0.331	**17**
5	19.95	**6**	26.80	**9**	3.53	**8**	7.34	**6**	5.56	**13**	12.75	**8**	0.474	**9**
6	20.16	**4**	28.11	**5**	3.77*	**5**	8.03*	**1**	5.54	**14**	11.90	**15**	0.509	**5**
7	19.14	**13**	29.23	**3**	3.81*	**3**	7.20	**9**	5.85	**11**	11.94	**14**	0.596	**3**
8	19.15	**12**	25.40	**13**	3.03	**18**	6.89	**17**	6.71	**8**	12.93	**5**	0.400	**13**
9	19.31	**10**	27.37	**7**	3.21	**16**	6.54	**20**	6.88	**5**	12.84	**6**	0.483	**7**
10	19.14	**13**	27.44	**6**	3.30	**13**	6.60	**19**	4.91	**17**	12.49	**10**	0.490	**6**
11	19.28	**11**	24.02	**17**	3.37	**11**	6.99	**13**	5.20	**16**	11.87	**16**	0.325	**18**
12	19.44	**9**	25.57	**12**	3.23	**14**	6.93	**16**	5.31	**15**	12.43	**12**	0.391	**14**
13	18.79	**17**	26.96	**8**	3.60	**6**	7.63	**4**	4.80	**18**	11.60	**17**	0.475	**8**
14	18.99	**15**	25.32	**14**	2.92	**20**	6.97	**14**	6.10	**9**	12.46	**11**	0.420	**10**
15	17.65	**19**	21.69	**20**	3.33	**12**	6.83	**18**	4.48	**20**	11.14	**18**	0.244	**20**
16	20.08	**5**	24.56	**16**	3.38	**10**	6.94	**15**	7.08	**3**	13.01	**4**	0.406	**11**
17	18.96	**16**	22.74	**18**	3.21	**16**	7.13	**10**	6.00	**10**	12.25	**13**	0.273	**19**
18	19.90	**7**	25.77	**11**	3.23	**14**	7.34	**6**	6.79	**6**	12.51	**9**	0.389	**15**
19	20.56	**3**	28.30	**4**	3.80*	**4**	7.63	**4**	6.77	**7**	12.82	**7**	0.549	**4**
20	19.87	**8**	25.86	**10**	2.97	**19**	7.03	**11**	8.48	**1**	13.67*	**2**	0.405	**12**
MEAN±SE	19.48±0.773		26.57±1.84		3.43±0.15		7.2±0.336		6.11±0.807		12.49±0.834		0.4621± **0** .080	
RANGE	17.49-21.58		21.69-33.60		2.92-4.21		6.54-8.03		4.48-8.48		11.06-13.88		0.24-0.87	
CD at 5%	1.54		3.51		0.31		0.67		1.31		1.62		0.15	
C.V.%	6.88		9.34		6.37		12.27		19.72		8.50		8.76	

Note- TH: Total height, DBH: Diameter at breast height, St: Straightness, CBH: Clear bole height, No B: Number of branches, CL: Crown length, Vol: Volume

Plate 1: Overview performance of progenies of Melia under field condition

Plate 2: Morphological view of Progeny 1

Plate 3: Morphological view of Progeny 19

4.1.4 Clear bole height (m)

The clear bole height (m) of different progenies ranged from 7.2-9.5m with mean value of 8.1 m and the minimum average clear bole height (m) was observed in progeny 9(GSS1) and 10 (DHC L53) and the maximum average clear bole height (m) was observed in progeny 1(MCS1) followed by progeny 2(CSN2) when data was recorded at the age of 9.5 year with coefficient of variation (CV) of 12.74 per cent.

The clear bole height (m) of different progenies ranged from 6.54-8.03 m at 10 year age with mean value of 7.2 m and the minimum average clear bole height (m) was observed in progeny 9(GSS1) (7.20 m). The maximum average clear bole height (m) was observed in progeny 6 (8.03m) followed by progeny 1(MCS1) (7.99 m) and 2(CSN2) (7.73 m) when data was recorded at the age of 10 year with coefficient of variation (CV) 12.27 per cent.

4.1.5 Number of branches

The Number of branches of different progenies ranged from 3.65-7.54 with mean value of 5.18. The number of branches observed in progeny 9 (GSS1) were minimum. The maximum average number of branches was observed in progeny 20 (Jodhan8) followed by progeny 18(CIPHET L10P9) observed from the data recorded at the age of 9.5 year with coefficient of variation (CV) of 17.96 %.

The Number of branches of different progenies ranged from 4.48-8.48 m at 10 year age with mean value of 6.11 m. The number of branches observed in progeny 15(TA) were minimum. The maximum average number of branches was observed in progeny 20 (Jodhan8) followed by progeny 2(CSN 2) when the data recorded at the age of 10 year with coefficient of variation (CV) 19.72 %.

4.1.6 Crown length (m)

The Crown length (m) of different progenies ranged from 9.66-12.55 m with mean value of 11.32 m. The minimum average Crown length (m) was observed in progeny 15(TA). The maximum average Crown length (m) was observed in progeny 20 (Jodhan8) followed by progeny 19 (RRS 7) observed from the data recorded at the age of 9.5 year with coefficient of variation (CV) of 9.99 %.

The Crown length (m) of different progenies ranged from 11.07-13.88 m at 10 year age with mean value of 12.49 m. The minimum average Crown length (m) was observed in progeny 3 (CSN 1). The maximum average Crown length (m) was observed in progeny 1(MCS 1) followed by progeny 20 (Jodhan8) when the data recorded at the age of 10 year with coefficient of variation (CV) 8.50 per cent.

The variation in height and diameter was significant in the current investigation, according to the analysis of variance. Overall, eight progenies, namely progenies 1, 2, 3, 5, 6, 16, 18, and 20 showed higher value than the population mean (19.48m). Progeny 1 showed the maximum height (21.58m) and followed by progeny 2 (21.43m) among all the progenies (Table 4.1 and 4.2). Nine progenies, namely progenies 1, 2, 5, 6, 7, 9, 10, 13, and 19, showed higher value than the population mean in terms of diameter. However, among the twenty progenies, progeny 1 had the largest diameter (32.19 cm), followed by progeny 2 (30.95cm). The present study revealed substantial variability among the progenies. Progeny 15, 4 and 17 were found very poor for height and DBH. The total score of all selections were presented in Table 4.1 and 4.2. These progenies will be used for future breeding programme and for development of new progenies. Meena *et al* (2014) did a similar analysis for growth and yield parameters in *Melia azedarach*, in which all variables exhibited considerable variations between progenies with respect to all traits, demonstrating a high level of morphological and genetic diversity. The highest level of variation was observed in the number of branches (35.63%), followed by DBH (26.89 %) and total height (16.01%) had the lowest amount of variance across progenies.

Table 4.3 Analysis of variance for growth characters of twenty progenies of *Melia composita* (9.5 year old age)

Mean sum of squares								
Source	**d.f**	**Total height (m)**	**Diameter at breast height (cm)**	**Straightness (score 1to 5)**	**Clear bole height (m)**	**Number of branches**	**Crown length (m)**	**Volume (m^3)**
Blocks	3	10.766	40.156	1.849	3.813	1.803	6.595	0.056
Treatment	19	4.221*	39.965*	0.517*	1.525*	3.504*	1.797	0.070
Error	57	1.194	4.090	0.045	0.427	1.285	1.542	0.006
(10 year old age)								
Blocks	3	10.766	21.021	1.849	0.402	1.735	8.525	0.039
Treatment	19	4.221*	48.863*	0.517*	0.709*	5.118*	2.704*	0.104
Error	57	1.194	6.828	0.045	0.226	0.844	1.313	0.013

In another study conducted by Kumar *et al* (2013) on Genetic Variations among Open Pollinated varieties of *Melia dubia*, a significant difference was observed for growth parameters. Likewise, results were observed in *Melia azedarach* by Dhillon *et al* (2009). Similar study for index scoring analysis has been done by Dhillon (1992) in *Acacia nilotica*, Kumar *et al* (2007) in *Eucalyptus* clones. A logical method to perform any breeding effort is to conduct a survey of the variation existing in the germplasm (Pandey, 2002). According to Lone and Tewari (2008), efficient phenotypic selection for major economic qualities and their interrelationships is highly dependent on the quantity of genetic diversity present in the population. A descriptive analysis of economically significant growth factors such as height, clear bole height, girth at breast height, collar girth, crown diameter, straightness, and branching was carried out in the current study. *Melia dubia* plus trees were also chosen by Chauhan and Gera (2012) in Punjab based on economic characteristics such as total tree height, girth at breast height, crown spread, and self-pruning ability.

4.2 Genetic variability studies

The degree and amount of variation contained in a species germplasm is essential for development in tree improvement and breeding. The estimate of genetic diversity is important in the planning of strategies for improving and breeding any species (Zobel 1981). As a result, assessing genetic differences in *Melia composita* progenies is critical for choosing prospective *Melia composita* seed sources. The components of variance in variability traits are additive and non-additive. Heritability and genetic advance provide data on overall differences in planting material as well as environmental impacts on the variables being studied. The heritable additive component of variance is the set of factors with the highest genetic gain and heritability that may be used in future development efforts.

4.2.1 Coefficient of variability, heritability and genetic advance

Table 4.4 shows results on PCV, GCV, mean, heritability estimates, and genetic advance as a percentage of mean. Volume had the highest phenotypic coefficient of variation (40.79%), followed by number of branches (22.60%). For all of the traits, the phenotypic coefficient of variation was found to be greater than 7.17 percent. The highest genotypic coefficient of variation (GCV) of 32.70 percent was recorded for volume, followed by 16.89 percent for number of branches. The magnitude of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all traits which shows that the variation present among the traits is due to environmental factor.

Broad sense heritability is important for different growth traits like total height (38.79), DBH (60.61), straightness (72.28), clear bole height (34.76), number of branches (55.86), crown length (20.95) and volume (64.29). For all of the traits studied, heritability estimates are more than 20.95 percent. Characters with a high heritability were less affected by the environment. The genetic advance as % of mean was determined to be low to moderate, ranging from 4.48 for crown length to 54.02 for volume. Simultaneous consideration of all variability factors revealed that high heritability recorded in straightness, volume and DBH showed that these traits were least affected by environment and low heritability recorded in crown length showed that this trait was more affected by environment.

Variation in Bark colour and texture

It was visually observed that progenies varied in bark colour and texture (Plate 4). Progeny 15 had smooth bark texture with greyish colour but progeny 1and 2 had brownish bark colour with rough bark texture. The progeny 5 showed dark brown colour with rough fissured texture.

Variation in drupe size and shape

It was visually observed that progenies varied in drupe size and shape. In progenies, namely progeny 1 and 13 round drupe were noted but there was differences in drupe size. The drupes of progeny 1 were bigger than the drupes of progeny 13.

Total height (m)

The overall population mean recorded for total height was 19.48 m. The coefficient of variance for genotypic and phenotypic were 4.46 and 7.17 %, respectively. The heritability was 38.79 %, and the genetic advance value (percent of mean) was 5.73, indicating that genetic components were responsible for variations among progenies.

Diameter at breast height (cm)

The overall population mean recorded for DBH was 26.57 cm. The coefficient of variation for genotypic and phenotypic were 12.48 and 16.03 per cent, respectively. The heritability was 60.616 % and value of genetic advance (percent of mean) was 20.01.

Straightness (score 1to 5)

The overall population mean for Straightness was 3.43 cm. The coefficient of variation for genotypic and phenotypic were 10.01 and 11.77 per cent, respectively. The heritability was 72.28 % and value of genetic advance (percent of mean) was 17.53 observed from the recorded data.

Clear bole height (m)

The overall population mean recorded for clear bole height was 7.2 m. The genotypic and phenotypic coefficient of variation was 4.82 and 8.18 per cent, respectively. The heritability was 34.76 % and value of genetic advance (% of mean) was 5.85.

Number of branches

The overall population mean recorded for number of branches was 6.11. The genotypic and phenotypic coefficient of variation were 16.89 and 22.60 per cent, respectively. The heritability was 55.86 % and value of genetic advance (% of mean) was 26.01 observed from the recorded data.

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(a) Greyish smooth (b) Brownish rough (c) Dark brown fissured

Plate 4: Variability for bark colour and bark texture among the progenies

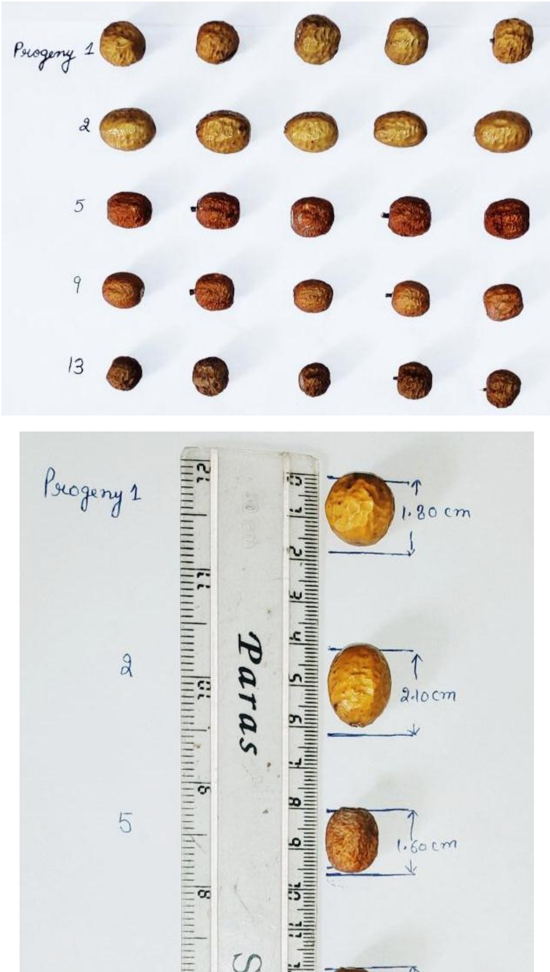

Plate 5: Variability for drupe size and drupe shape among the progenies of *Melia composita*

Table 4.4 Variability, heritability and genetic advance in the progenies of *Melia composita* (10 year record)

Parameters	Mean	Range	Coefficient of variation		Heritability (%)	Genetic advance	Genetic gain (% of mean)
			Genotypic (%)	Phenotypic (%)			
TH	19.477	17.49-21.58	4.46	7.17	38.79	1.11	5.73
DBH	26.573	21.69-35.79	12.48	16.03	60.61	5.19	20.01
ST	3.435	2.92-4.21	10.01	11.77	72.28	0.60	17.53
CBH	7.202	6.54-8.03	4.82	8.18	34.76	0.42	5.85
NO B	6.117	3.58-7.17	16.89	22.60	55.86	1.59	26.01
CL	12.495	11.07-13.88	4.75	10.38	20.95	0.55	4.48
Vol.	0.462	0.24-0.87	32.70	40.79	64.29	0.25	54.02

Note, TH: Total height, DBH: Diameter at breast height, ST: Straightness, CBH: Clear bole height, NoB: Number of branches, CL: Crown length,VOL:volume

Crown length (m)

The overall population mean recorded for crown length was 12.49 m. The coefficient of variation for genotypic and phenotypic were 4.75 and 10.38 per cent, respectively. The heritability was 20.95 % and value of genetic advance (percent of mean) was4.48 observed from the recorded data.

Genetic diversity in tree species is a gift to the world, since it serves as the basis for species selection and enhancement. The genetic structure and diversity connection of a prospective plus tree offer a foundation for future effective genetic resource usage in order to maximise growth and yield potential. The findings showed that there is plenty of potential for improvement in *Melia composita* for the vast majority of parameters. Variations among progenies are often used to determine overall genetic variation and the degree of genetic control for a certain characteristic. The PCV was found to be higher than the GCV for all features in this investigation.

Maximum heritability recorded in straightness (72.28%) followed by volume (64.29%) and diameter at breast height (60.61%) showed that the variation occur in these traits is purely genetic in origin, moderate heritability recorded in number of branches (55.86%) followed by total height (38.79%) and clear bole height (34.76%) which means that the traits were under the strong influence of additive gene action and selection would be quite effective, whereas lowest heritability percentage was recorded for crown length (20.95%) which shows that the character was strong influenced by the environment.

The estimates of genetic advance was also recorded higher for DBH followed by number of branches and very low for clear bole height. In fact, the maximum genetic gain (54.02 %) was recorded for volume followed by number of branches (26.01 %) straightness (17.53 %) and lowest crown length (4.48 %). In the current study, the trend of genetic advance as per cent of mean (Table 4.4) shows a huge scope for genetic improvement in the species. Similar study was also carried out by Apiolaza *et al* (2005) on *E. globules* to report low heritability for number of branches. Kumar *et al* (2013) also found that the trend of genetic advance as percentage of mean was highest in volume (15.21) and followed by plant height (6.21), indicating that the species has a lot of scope for genetic improvement. They also discovered that volume had the highest genetic advance, followed by plant height, indicating that these two traits were reliable enough to be included in future development programmes.

The variance component analysis revealed that genetic variation was higher than environmental variance for both characteristics, which was represented in heritability value, where both the character showed higher heritability value. The expected genetic advance (GA) for diameter was slightly higher than tree height. Because high heritability does not always signify high genetic gain, it is a good idea to combine heritability with genetic advance to evaluate the final impact of selecting superior kinds (Ali *et al* 2002).

High heritability shows the effectiveness of phenotypic performance-based selection, but it does not ensure high genetic gain for a specific trait. Therefore, selection encompassing heritability and expected genetic gain gives more realistic results (Johnson *et al* 1955) as they reflect the additive type of gene action.

One of the first procedures in a tree improvement programme for large-scale production of genetically improved species is the selection of excellent quality phenotypes based on essential characteristics (Clark and Wilson, 2005). The selection of plus trees, according to Hazel *et al* (2016), is a significant and most important technique for the genetic improvement of tree species. For key economic qualities and their interrelationships, successful phenotypic selection is heavily dependent on the fraction of genetic diversity present in the population (Lone and Tewari, 2008). The genetic variety in the population, the heritability of the characteristics, and the genetic and environmental correlation of each trait with the others must all be given high priority in order to make selection efficient.

The Heritability and genetic advance as % of mean for plant height, collar diameter recorded in present study provided evidences for existence of adequate genotypic variations (Kumar *et al* 2010) and thus lend support for exploitation of genetic variability for further improvement in this species. Kumar *et al* (2013) found low to moderate heritability for height (0.51), volume index (0.43), and basal diameter (0.30) in his study on Genetic variations among open pollinated varieties in *Melia dubia*, in which broad sense heritability was identified for many characters .

Similar finding were also reported in *Melia* by Meena *et al* (2014), and Dhillon *et al* (2009). Vishwakarm and Vimal (1998), El-Bawab (2003), Wang *et al* (2006), Singh (2011) and Al-Tabbal and Al-Fraihat (2012) also revealed high heritability for different traits in barley.

4.2.2 Association studies

Correlation provides an insight to the deep complexity and the amount of inter-relationship existing among the traits. Few characters are strongly inter-linked with each other therefore knowledge of association of these characters is most important during the selection of one or more characters. It serves as a suitable baseline for indirect selection, particularly for below-ground or biomass traits that require destructive sampling. When defining selection criteria in any tree improvement programme, the amount of genetic gain obtained by indirect selection, i.e. correlated response, provides a better knowledge of the degree and magnitude of genetic association and must be given proper weightage.

4.2.1.1 Correlation analysis

The purpose of breeding is to achieve high expression of all or most desirable features in a single genotype. In this context, understanding the correlation between quantitative traits is beneficial in two ways. Firstly, it helps in predicting the responses of other characters when we choose one. Positive, negative, or no correlation can help in the selection of eligible parents or individuals for the formulation of an appropriate selection procedure for simultaneous improvement of many characters. Second, selection based on highly correlated compound character is more successful than direct selection for complex compounds like yield and timber. Tables 4.5 and 4.6 shows the phenotypic and genotypic correlations for all possible combinations of the characteristics under investigation. All correlations were positive with each others.

In general, Genotypic correlation coefficient were higher than corresponding phenotypic correlation coefficients for most of the traits, thus indicating the less effect of environment true representation of genotype by phenotype. Majority of growth traits had positive significant correlation. However, some have negative significant correlation with number of branches. Total height was found significantly correlated with all the characters viz., diameter at breast height, straightness, clear bole height, number of branches, crown length and volume. At Genotypic level, number of branches had highly positive correlation with crown length and at phenotypic level, total height had high correlation with crown length.

Tree height, DBH and volume showed positive correlation with all the characters under study both at genotypic and at phenotypic level. At genotypic level, straightness exhibited significantly positive correlation with total height, DBH, clear bole height, crown length and volume. While at phenotypic level no correlation found with number of branches and crown length. Clear bole height had positive significant correlation with all the characters under study at genotypic and found no correlation with number of branches and crown length at phenotypic level. Number of branches had highly significant positive correlation with all characters and found no correlation with straightness both at genotypic and phenotypic level.

Total height showed significant genotypic correlation with DBH (0.962), straightness (0.641), clear bole height (0.760), number of branches (0.940), crown length (0.904) and again high significant with volume (0.918). The data revealed that DBH registered highly significant genotypic correlation with volume (0.995), straightness (0.822), clear bole height (0.770), low with number of branches (0.554) and again high significant with crown length (0.931). Straightness exhibited very low genotypic correlation with number of branches (0.102) and high significant with clear bole height (0.959). Whereas, number of branches was found to be very high correlation with crown length (0.979).

Genotypic correlation were found to be higher than phenotypic correlation showed that the variation occur in the traits among the different progenies is due to genetic factor. Total height showed highly significant phenotypic correlation with crown length (0.757), clear bole height (0.434), DBH (0.429), straightness (0.404), volume (0.426) and low with number of branches (0.388). The data revealed that DBH registered highly significant genotypic correlation with volume (0.985), clear bole height (0.770), number of branches (0.329) and low with crown length (0.300) and again high significant with straightness (0.666). Straightness exhibited high significant with volume (0.682) and very low phenotypic correlation with number of branches (0.094) Whereas, clear bole height was found to be negative correlation with crown length (-0.043).

Table 4.5: Genotypic Correlation Coefficient among different characters of *Melia composita* progenies

Parameters	TH	DBH	St	CBH	No B	CL
DBH	0.962					
St	0.641	0.822				
CBH	0.760	0.770	0.959			
No B	0.940	0.554	0.102	0.260		
CL	0.904	0.931	0.241	0.403	0.979	
Vol.	0.918	0.995	0.844	0.767	0.566	0.945

Note, TH: Total height, DBH: Diameter at breast height, St : Straightness, CBH: Clear bole height, No B: Number of branches, CL: Crown length, Vol: Volume.

Table 4.6 Phenotypic Correlation Coefficient among different characters of *Melia composita* progenies

Parameters	TH	DBH	St	CBH	No B	Cl
DBH	0.429*					
St	0.404*	0.666*				
CBH	0.434*	0.353*	0.398*			
No B	0.388*	0.329*	0.094	0.107		
CL	0.757*	0.300*	0.142	-0.043	0.429*	
Vol.	0.426*	0.985*	0.682*	0.366*	0.344*	0.284*

Note: TH: Total height, DBH: Diameter at breast height, St: Straightness, CBH: Clear bole height, No B: Number of branches, CL: Crown length, Vol: volume.

***** Significant at 5 % level

According to Choudhary *et al* (2017), character correlation information is important in any improvement programme because improving one character causes changes in other characters that are correlated to it. The economically important variables, such as fruit diameter, fruit length, seed diameter, seed length, and seed weight of 100 seeds (g), were shown to have positive and significant relationships (P=0.00) with other characters in the current study. Further positive and negative correlations (P>0.00) exist between these four features and pulp thickness and the number of seeds per 100g, indicating that genetic improvement in these three characters is likely to enhance all of the positively linked characters.

In Sclerocarya birrea, Mkwezalamba *et al* (2015) found significant (P<0.05) and positive associations between fruit weight and pulp weight, as well as fruit length and diameter. Okello *et al* (2018) conducted a study on *Tamarindus indica* L. genotypes from various agroecological zones in Uganda and found that Pearson's correlation coefficient was highest between seed mass and seed number (0.78), fruit length and total fruit mass (0.73), total fruit mass and pulp mass (0.72), and total fruit mass and seed mass (0.72). Naghmouchi *et al* (2009) also found the highest positive correlation coefficient (0.91) between pod weight and width, as well as the highest negative correlation between pod length and the number of aborted kernels, and between the number of viable kernels and the number of aborted kernels, in *Ceratonia siliqua* L.

4.2.1.2 Path analysis

Correlation analysis evaluates the relation between dependent and independent characters, but does not provide precise estimates of how much a character contributes to the overall influence of other characters. Path coefficient analysis is useful in resolving correlation into components of direct and indirect effects in such cases (Wright 1921). As a result, each component has two modes of action direct and indirect impacts via components that aren't exposed in correlation analyses. In the present study, genotypic and phenotypic path coefficient analysis was carried out considering volume as dependent character and tree height, diameter at breast height, straightness, clear bole height, number of branches and crown length as independent characters.

Path coefficient analysis revealed that the highest positive direct effect contributing to volume was observed due to DBH (0.98) followed by crown length (0.61) and straightness (0.60) at genotypic level, while DBH (0.94), straightness (0.051) and number of branches (0.03) at phenotypic level. As a result, direct selection for certain features may be beneficial. At Genotypic level, total height exhibited negative indirect effect. Straightness contributing to volume was observed due to direct effect of straightness (0.60) and indirect effect by clear bole height (0.58) followed by DBH (0.49) and tree height (0.388). Number of branches contributing indirectly with clear bole height (0.62) followed by crown length (0.32) and tree height (0.22) at genotypic level. While at phenotypic level indirect effect found between DBH with straightness (0.62) followed by tree height (0.40), clear bole height (0.33), Number of branches (0.30) and crown length (0.28). Straightness showed positive indirect effect contributing to volume was observed due to clear bole height (0.051) followed by diameter at breast height (0.034) and tree height (0.020) showed in table 4.7 and 4.8.

Correlation studies were carried out on *Moringa oleifera* to determine the significant results between the parameters. At the genotypic and phenotypic level, the yield per plant had the strongest significant positive correlation with the number of leaves per rachis (r = 0.949, 0.674), followed by number of branches per plant (r = 0.935, 0.776), number of pods per plant (r = 0.909, 0.756), and stem girth (r = 0.668, 0.397). According to the path coefficient analysis, number of branches per plant has the biggest positive direct influence on yields per plant (r = 5.444), followed by length of pod (r = 1.938), and leaf length (r = 1.751) (Verma *et al* 2019), which supports our findings. The conclusions of this study were also influenced by a wide variety of research findings in other tree species, such as *Simarouba glauca* (Kumaran *et al* 2010), Bixa orrelina (Kala 2009), and *Tectona grandis* (Parthiban 2001). As a result, path analysis can only explore the correlation and dependence of variables, not the influence of genotypes/provenances on the dependent variable.

Table 4.7 Path using genotypic correlation among different characters of *Melia composita* progenies

Parameters	TH	DBH	St	CBH	No B	CL
TH	**-1.17252**	1.01370	0.38855	0.00438	0.22786	0.55650
DBH	-1.20297	**0.98805**	0.49792	0.00444	0.13432	0.57329
St	-0.75213	0.81221	**0.60572**	0.00553	0.02469	0.14827
CBH	-0.89113	0.76080	0.58061	**0.00577**	0.06296	0.24830
No B	-1.10171	0.54726	0.06168	0.00150	**0.24251**	0.81482
CL	-1.05960	0.91982	0.14584	0.00233	0.32088	**0.61581**

Note: TH: Total height, DBH: Diameter at breast height, St: straightness, CBH: Clear bole height, No B: Number of branches, CL: Crown length,
Residual error -0.026.

Table 4.8 Path using phenotypic correlation among different characters of *Melia composita* progenies

Parameters	TH	DBH	St	CBH	No B	CL
TH	**-0.00718**	0.40459	0.02076	0.00477	0.01472	-0.01177
DBH	-0.00308	**0.94260**	0.03426	0.00388	0.01246	-0.00466
St	-0.00290	0.62812	**0.05142**	0.00438	0.00356	-0.00220
CBH	-0.00311	0.33248	0.02045	**0.01101**	0.00405	0.00066
No B	-0.00279	0.30969	0.00483	0.00117	**0.03793**	-0.00667
CL	-0.00544	0.28237	0.00729	-0.00047	0.01627	**-0.01554**

Note: TH: Total height, DBH: Diameter at breast height, St: straightness, CBH: Clear bole height, No B: Number of branches, CL: Crown length,
Residual error -0.026

4.3 Genetic divergence studies

Any breeder is most interested in genetic variety and genetic variability because they are critical in identifying genotypic responses as groupings and framing a successful breeding programme. The genetic distance between genotypes has been measured via genetic divergence. In a breeding programme, the use of heterosis and success in obtaining advantageous segregates is largely determined by how divergent a trait is in that population; additionally, the more diverse the parents, the greater the chances of increased heterotic effects and a wide range of variability in segregating generations. The genetically distinct parents should have genetic divergence that is consistent throughout environments (Paramathma and Surendran 2000). The Euclidean clustering method divides a group of observations into two or more homogeneous clusters. The genetic diversity within and between clusters is indicated by intra and inter cluster distances.

Geographic diversity was not always associated to genetic diversity, according to the clustering pattern found in this study. Different adoption procedures, selection criteria, natural selection pressure, or environmental variables might all contribute to genetic diversity (Vivekananda and Subramanian, 1993). This meant that genetic drift created more variety than geographic variation (Singh *et al* 1996). The trees that originated in the same place were divided into different clusters, indicating that plants with the same geographic origin may have experienced diverse selection for various traits. Cluster formation observations indicated that progenies within a cluster group together due to the presence of similar growth traits, such as total height, DBH, straightness, clear bole height, number of branches, and crown length, rather than geographical affinities. Clustering patterns, on the other hand, revealed no relationship between genetic diversity and geographic distribution (Kaushik *et al* 2007). On the basis of genetic divergence, the clustering pattern of all the progenies possessed in each cluster has been given in Table 4.9. All the progenies were clustered into five separate groups (Figure 4.1; Table 4.9). Cluster V was the biggest and consisted of six progenies namely P8, P12, P14, P16, P18, P20 followed by Cluster I which accommodated five progenies *viz* P3, P4, P11, P15, P17 and Cluster III which accommodated four progenies *viz*., P5, P9, P10, P13. Three progenies each namely P7, P19, P6 were contained by cluster IV and cluster II contained only two progenies P1, P2 respectively.

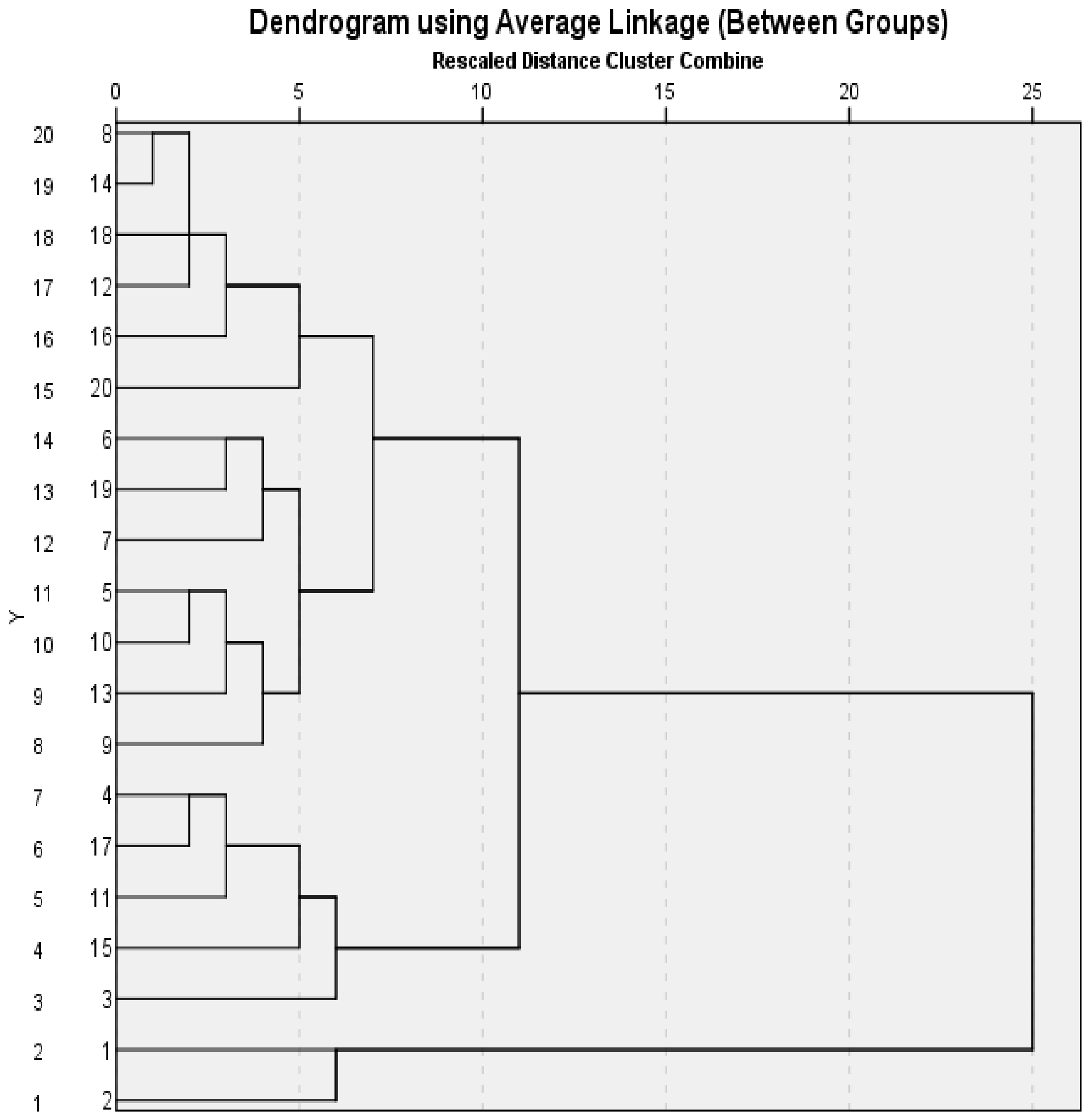

Figure 4.1: Dendrogram depicting genetic divergence of *M. Composita* progenies

(Note: 1=P1, 2=P2, 3=P3, 4=P4, 5=P5, 6=P6, 7=P7, 8=P8, 9=P9, 10=P10, 11=P11, 12=P12, 13=P13, 14=P14, 15=P15, 16=P16, 17=P17, 18=P18, 19=P19, 20=P20)

Table 4.9: Grouping of progenies into different clusters

Clusters	Number of progenies	Code of progenies
1	5	P3, P4, P11, P15, P17
2	2	P1, P2
3	4	P5, P9, P10, P13
4	3	P7, P19, P6
5	6	P8, P12, P14, P16, P18, P20

The inter-cluster distances among all the clusters are detailed in Table 4.10. It was observed that the average inter-cluster distance ranged from 2.47 to 13.27. The highest inter-cluster distance was observed between cluster 2 and 4 reflecting that the progenies present in these clusters were highly diverse, following by cluster 3 and 2, while lowest inter cluster distance was recorded between cluster 1 and 3 indicating the minimum diversity among the progenies. This showed that a wider genetic distance existed between *Melia composita* trees. Such inter and intra cluster divergence was also observed in the studies done for the species such as *Pinus gerardina* (Kant 2006), *Pinus wallichiana* (Aslam *et al* 2011), *Melia dubia* (Kumar 2013). This present study will help to identify the most distant accessions and most closely placed ones for breeding experiments to obtain hybrid vigour

Table 4.10: Distances between different Cluster

Cluster	1	2	3	4
2	9.246			
3	2.475	10.693		
4	4.430	13.278	2.679	
5	2.768	7.632	3.128	5.755

In a study done to estimate the genetic variation among the different progenies of Melia tree, high genetic divergence was reported for the trees of *Melia composita*. Here, the twenty progenies of *Melia dubia* resolved into five clusters. In earlier study among the six clusters, the cluster I and cluster II were biggest with 10 and 5 members, respectively (Kumar *et al* 2013). In *Tectona grandis,* the clustering of eighty batches of teak was grouped into eight clusters, of which group A formed the largest cluster containing 46 batches

(Subramanian *et al* 1994). In *Acacia nilotica,* clustering technique was used to group the 27 seed sources. The result showed that five clusters were formed after the analysis, in which group A was the largest and it possessed 21 seed sources. Group B and C included two seed sources each and Group D and E included only one seed source each (Bagchi 1992). Similarly, In *Prunus armeniaca* Cluster I, cluster II, and cluster III were developed from a diverse group of 50 germplasms based on their genetic similarity at 0.614 distance. Cluster II had the most genotypes (39), Cluster I had the most unusual genotypes (ten), and Cluster III had only one genotype (G28). (Singh and Chaudhiri 1992) which supports to the results of our findings. Thus, the pattern of divergence is dependent on genetic characters and the grouping could be due to difference in the genetic constituent of the co-occurring genotypes (Bhaumik *et al* 1971; Chauhan and Sehgal 2001). The same results were recorded by Kumar (2013) for *Eucalyptus* clones, Meena *et al* (2014) for *Melia azedarach* half-sib progenies and Vishnu *et al* (2018) for the *Causarina equisetifolia* clone.

Yadav *et al* (2019) used D^2 clustering to arrange twenty superior trees of *Melia dubia* into eight groups based on morphological features. Similarly, Kumar *et al* (2013) used D^2 clustering to organise the twenty genotypes in *Melia dubia* genetic resources into six groups. Bagchi (2000) did a similar research in which 80 batches of teak were divided into eight groups. Similarly, Algabal (2012) reported a dendrogram based on the morphological features of 36 tamarind genotypes being divided into two major clusters, each of which had two sub-clusters. In a hierarchical cluster analysis of morphological features of *Ceratonia siliqua* (L.) fruits and seeds, Sidina (2009) observed the establishment of two main groupings.

4.4 General performance of progenies

Index score analysis was carried out to assess the general performance of progenies of *Melia composita*. Data presented in Table 4.11 showed the classification of progenies for growth traits and yield among 20 progenies on the basis of comparative scores assigned according to the observations variability. Scores for growth traits ranged from 12 to 32. The maximum score (32) was assigned to progeny 1 and progeny 2 source followed by progeny (16) and progeny (19). Minimum index score (12) was recorded in progeny 3 and progeny 4. Therefore, on the basis of superiority for growth traits, progeny 1 and progeny 2 may be used in future improvement programmes.

The present study revealed substantial variability among the progenies. An examination of data revealed that progeny 1, 2, 16, 19 and 7 ranked better growth for total height, whereas progeny 1, 2 and 7 showed higher growth for DBH. Progeny 3 and 15 was found very poor height and DBH.

For straightness the highest score observed in the progeny 1, 2, 3, 6, 7, 13 and 19 and lowest score was observed in the progeny 4, 8, 9, 12, 14, 17, 18 and 20. The data revealed that the progeny 1, 2 and 6 found maximum score for clear bole height. The minimum score observed in progeny 8, 9, 10 and 15. The maximum score index recorded for number of branches in the progeny 1, 2, 8, 9, 16, 18, 19 and 20. For crown length the maximum index score was found in the clone 1, 2 and 20.

Table 4.11: Index scores recorded for growth traits and yield in 20 progenies of *Melia composita*

Progenies	TH	DBH	ST	CBH	NoB	CL	Vol.	Total
1	4	4	4	4	4	4	8	32
2	4	4	4	4	4	4	8	32
3	1	1	3	2	2	1	2	12
4	2	1	1	2	3	1	2	12
5	3	2	2	3	3	3	4	20
6	3	2	3	4	3	2	4	18
7	2	3	3	2	3	2	6	21
8	2	2	1	1	4	3	2	15
9	2	2	1	1	4	3	4	17
10	2	2	2	1	2	3	4	16
11	2	1	2	2	2	2	2	13
12	2	2	1	2	2	2	2	13
13	2	2	3	3	2	1	4	17
14	2	2	1	2	3	2	4	16
15	1	1	2	1	2	1	2	10
16	3	1	2	2	4	3	4	24
17	2	1	1	2	3	2	2	13
18	3	2	1	3	4	3	2	18
19	3	2	3	3	4	3	4	22
20	3	2	1	2	4	4	4	20

The present study found that progeny 1, 2, 6 and 19 may be used for field planting programmes. These progenies may be used for future breeding programme, mass multiplications and for development of new progenies. Similar study for index scoring analysis has been conducted by Dhillon (1992) in *Acacia nilotica*, Kumar *et al* (2007) in *Eucalyptus* clones.

The index selection method is the most efficient plus tree selection approach. This approach combines data from many qualities into index values, allowing all of the trees to be scored and ranked independently for overall height, clear bole height, diameter at breast height and other factors. (Kumar and Gurumurthi, 2000; Kumar *et al* 2003). Johar *et al* (2018) selected 24 candidate plus trees of *Melia dubia* in 2018 based on clear bole height, pruning ability, and disease resistance. Kumar *et al* (2018) identified and tested 230 candidate plus *Melia composita* trees using the index technique of selection in 2013. Different factors like as height, clear bole height, diameter at breast height, straightness, and crown diameter were used to make the decision.

CHAPTER V

SUMMARY

India is an agriculture- based country, about 70% of population depend on agriculture directly or indirectly. Punjab is an agriculture intensive state where the rice-wheat cropping system has been widely adopted, ensuring the country's food security. Agroforestry has emerged as one of the feasible alternatives to the present rice-wheat cropping system for diversification. Varied tree species are usually cultivated in Punjab's various agroclimatic zones. *Populus*, *Eucalyptus*, and *Melia* are the most common tree species planted by farmers as block and border plantations on their agricultural fields.

Melia composita (Burma dek) is a fast growing tree-species that can be adopted as one of tree species to meet the ever- increasing demands for timber, pulp and paper industry. Its straight growing nature results in long clear bole which adds to commercial value. It is one of the fast- growing tree species among timber species in India. This is commonly known as Burma dek or dhrek or dek. Because of its improved pulp production and quality, it is suitable for the pulp and paper industries. It is a multifunctional tree species that is commercially grown for timber, fodder and industrial woods under various afforestation programmes. Wood is a moderately hard material that may be utilised for a variety of purposes. *Melia composita* is a deciduous tree native to Indian sub-continental, due to its nature of wider adaptability it has been spread to wider parts of the Asian continent and other places on the globe having favorable environments for its growth (Murugesan *et al* 2013). *Melia composita* is a deciduous tree which remains leafless in winter season and bears new leaves in spring season which makes it as one of the good short rotation agroforestry tree species in Indo-gangatic plains of India for inter-cultivation (Chauhan *et al* 2008). As the species is of immense importance, a study to select and analyze potential open-pollinated progenies by assessing the existing variability was conducted so that the same could be used in future tree improvement and plantation programs. It is being cultivated in the arid and semi arid as well as semi moist areas of the country. This tree produces abundant seeds every year and usually nursery is raised from seedlings. Being open pollinated nature of most forest trees the plantations raised from seeds are quite variable. Keeping in view the present investigation entitled Variability among the open pollinated progenies of Burma dek (*Melia composita* Benth.) under field conditions was carried out in the Department of Forestry & Natural Resources, Punjab Agricultural University, Ludhiana, Punjab during 2020 to 2022. The present study is a step towards screening the open pollinated half-sib families for genetic variability in order to short list the best progenies for agroforestry plantations, which can be multiplied to produce quality planting material that will be further available to farmers on selection, with following objectives:

1. To evaluate the progenies for growth parameters.
2. To short list genetically superior progenies to use for mass multiplication of quality planting material.

To meet these objectives, the present investigations were conducted on 10-year-old progeny testing trial, established at Experimental Area of the Regional Research Station, Bathinda at a spacing of 4 x 4 m. From all progenies in a plantation the observation on various growth parameters were collected at 6-month interval at 9.5 yr and 10 yr. The results of the present study are summarized as under.

The observations for growth traits i.e. total height, diameter at breast height, straightness, number of branches, clear bole height and crown length of trees were recorded after 6 months intervals. All morphological characteristics were subjected to their ANOVA, genetic variability and association studies, genetic divergence analysis.

Among progenies, maximum mean values for plant height 21.58 m and diameter at breast height 32.91cm were observed for progeny 1 at the age of 9.5 year. Whereas, the DBH 33.60 cm was recorded for progeny 1 at 10 year age. However, straightness varied from 1 to 5 and maximum values were 4.21. The clear bole height was observed maximum (9.5m) in progeny 1 and 8.03m in progeny 6 at 9.5 and 10 year old plantation and number of branches showed maximum values for progeny 20 (7.54) and (8.48) for both 9.5 and 10 year old plantation Whereas at the age of 9.5, year crown length (14.53m) showed maximum values for progeny 20 and 13.88 was observed for progeny 1of 10 year plantation.

The variability and genetic estimates were computed for different traits of progenies under study. The difference between the PCV and GCV in number of branches, crown length and volume indicated the influence of the environment on the expression of these characters. All of the parameters under investigation have high degree of heritability estimations, suggesting that the environment has little or no impact on the expression of these traits. The GCV (%) ranged from 4.466-32.706, PCV (%) ranged from 40.790-7.171 and heritability (%) ranged from 20.950–72.281. The genetic gain ranged from 4.481– 54.021 among the traits. The maximum GCV was found in volume (32.706 %) followed by number of branches (16.898 %) whereas maximum PCV was found in volume (40.790%) followed by number of branches (22.609 %). Straightness (72.281 %), Volume (64.290 %) and diameter at breast height (60.616 %) were found to have high heritability. The genetic gain was found maximum in volume (54.021 %).

Genotypic correlation coefficient was found greater than the phenotypic characters for most of the growth characters. Highly significant and positive genotypic and phenotypic correlation were observed for crown length (G=0.945, P=0.284), total height (G=0.918, P=0.426), diameter at breast height (G=0.995, P=0.985), straightness (G=0.844, P= 0.682), clear bole height (G=0.767, P=0.366) and number of branches(G=0.566, P= 0.344) with volume and also highly significant and positive genotypic and phenotypic correlation were observed for total height and DBH.

On the basis of genetic divergence, all the progenies were clustered into five clusters. Cluster means revealed significant variation among the clusters for vegetative, morphological and biomass traits. In dendogram cluster I comprises of five progenies *viz*., P3, P4, P11, P15, P17. Cluster II comprises of only two progenies P1, P2. Cluster III comprises offour progenies *viz*., P5, P9, P10, P13. Cluster IV comprises of three progenies *viz* P6, P7, P19. Cluster V was the biggest cluster and comprises ofsix progenies namely P8, P12, P14, P16, P18, P20 respectively. The highest inter-cluster distance was observed between cluster 2 and 4 reflecting that the progenies present in these clusters were highly diverse.

Index score analysis of 20 progenies exhibited that highest index score of 32 was observed in progeny 1 and 2 which indicated its overall superiority in growth as well as in yield, followed by progeny 16 and 19. Progeny 5, 6, 7, 9, 10, 13, 14, 16, 18, and 19 had got score more than 20. Minimum index score of 12 was found in progeny 3 and 4.

Significant variation among all genotypes was found for height as well diameter growth. The high heritability (h_2) and genetic advance (GA) for DBH growth in evaluated genotypes suggest that early selection can be made for these traits in *Melia composita.* The best results was obtained for progeny 1(MCS 1) which exhibited best performance for all the growth parameters such as tree height, DBH, straightness, clear bole height and volume and followed by progeny 2(CSN 2). The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) in general, showing the influence of the environment in character expression. The coefficient of variability showed that phenotypic selection of Melia might result in satisfactory genetic gains. The genotypic correlation coefficients between the various features suggested that the parameters under investigation were purely genetic in origin.

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