

**“AGRO-MORPHOLOGICAL CHARACTERIZATION
OF OAT (*Avena sativa* L.) ACCESSIONS FOR FORAGE
YIELD AND ITS CONTRIBUTING TRAITS”**

M.Sc. (Ag.) Thesis

by

Rashmi Toppo

DEPARTMENT OF GENETICS AND PLANT BREEDING

COLLEGE OF AGRICULTURE

INDIRA GANDHI KRISHI VISHWAVIDYALAYA

RAIPUR (Chhattisgarh)

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**“AGRO-MORPHOLOGICAL CHARACTERIZATION
OF OAT (*Avena sativa* L.) ACCESSIONS FOR FORAGE
YIELD AND ITS CONTRIBUTING TRAITS”**

Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.)

by

Rashmi Toppo

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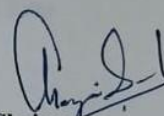
AUGUST, 2021

CERTIFICATE-I

This is to certify that the thesis entitled "**Agro-morphological characterization of Oat (*Avena sativa* L.) accessions for forage yield and its contributing traits**" submitted in partial fulfilment of requirements for the degree of **Master of Science in Agriculture** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Rashmi Toppo** under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Direction of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published/published part has been fully acknowledged. All the assistance and help received during the course of the investigation have been duly acknowledge by her.

Date: 13.08.21


Chairman

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

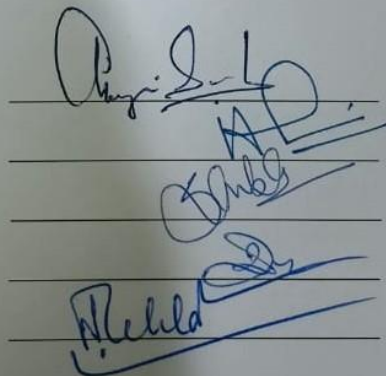
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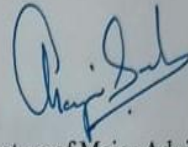
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**COLLEGE OF AGRICULTURE
RAIPUR (CHHATTISGARH)
CERTIFICATE**

This is to certify that the thesis Viva-voce in respect of **Miss Rashmi Toppo** student of **M.Sc. (Ag.) Genetics and Plant Breeding** has been conducted under the chairmanship of Head of the Department/Dean (In case of out campii) along with Advisory Committee on 30-10-2021. The necessary correction have also been made as per comments/suggestions made by the Advisory Committee and Head of the Department/Dean.

Date: 30-10-2021

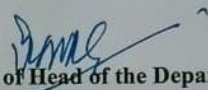


Signature of Major Advisor

Name: Dr. Mayuri Sahu

CERTIFICATE-II

This is to certify that the thesis entitled "**Agro-morphological characterization of Oat (*Avena sativa* L.) accessions for forage yield and its contributing traits**" submitted by **Rashmi Toppo** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur, in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture** in the **Department of Genetics and Plant Breeding** has been approved by the external evaluator and Student's Advisory Committee after oral examination, under the chairmanship of Head of Department/Dean (in case of out campii).


Signature of Head of the Department

Date: 30-10-2021

Major Advisor

Faculty Dean

Approved/Not approved

Director of Instructions

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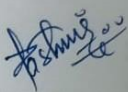

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LIST OF ABBREVIATIONS

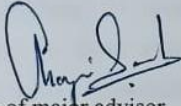
ABBREVIATIONS	DESCRIPTION
%	Per cent
DUS	Distinctiveness, uniformity and stability
°C	Degree Celsius
Cm	Centimeter
No.	Number
<i>viz.</i>	For example
<i>via</i>	Through
ANOVA	Analysis of variance
d.f.	Degree of freedom
<i>et al.</i>	Coworkers and others
G	Gram
Ha	Hectares
Qt	Quintal
Fig.	Figure
S. no	Serial number
SD	Standard deviation
CD	Critical difference
<i>i.e.</i>	that is
M	Meter
Mm	Millimeter
Approx.	Approximately
GCV	Genotypic coefficient of variation
PCV	Phenotypic coefficient of variation
r_g	Genotypic correlation coefficient
r_p	Phenotypic correlation coefficient
*	Significance at 5%
**	Significance at 1%
***	Significance at 0.1%

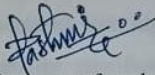
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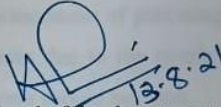
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THESIS ABSTRACT

- | | | | |
|----|---------------------------------------|---|--|
| a) | Title of the thesis | : | "Agro-morphological characterization of Oat (<i>Avena sativa</i> L.) accessions for forage yield and its contributing traits" |
| b) | Full name of the student | : | Rashmi Toppo |
| c) | Major subject | : | Genetics and Plant Breeding |
| d) | Name and address of the major advisor | : | Dr. Mayuri Sahu, Scientist,
Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur. |
| e) | Degree to be awarded | : | M.Sc. (Agriculture, Genetics and Plant Breeding) |


Signature of major advisor


Signature of student


Signature of head of the department

Date: 13.08.21

ABSTRACT

The experiment entitled “**Agro-morphological characterization of Oat (*Avena sativa* L.) accessions for forage yield and its contributing traits**” was carried out at Research Cum Farm Instructional, Department of Genetics and Plant Breeding, IGKV, Raipur, (C.G.). Experiment was conducted in *Rabi* 2019-20. Total 130 germplasm accession (including 5 checks) were kept under study. Experiment was done in augmented design with 5 blocks. Thirty two qualitative and quantitative traits were studied according to descriptor Indian grassland and Fodder Research Institute, Jhansi, India. (Roy *et al.*, 2017). The whole data calculated were for characterization of Oat and to estimate variability among the genotypes, association analysis and genetic diversity.

Data for randomly 5 plants were recorded for all the 19 quantitative traits and frequency was calculated for all 13 qualitative traits. Sufficient amount of variation found for qualitative and quantitative traits studied. Out of 13 qualitative traits 7

traits had high variation among the genotype whereas rest 5 traits showed no variation and are similar in morphological appearance.

The trait leaf: stem ratio and seed yield per plant had coupled high GCV and PCV value. This revealed that both traits had high genetic expressivity and by selecting these traits the chances of improvement of Oat will increase. From the study of GCV and PCV it was observed that there is PCV values was higher than the GCV values represents the environmental effect is more than the genetic effect. High value of heritability was recorded for 1000 seed weight and leaf: stem ratio. The trait 1000 seed weight and leaf: stem ratio was associated with high genetic advancement of percentage of mean and high heritability signifies the less environmental effect on these characters combined with high genetic gain. Association of high amount of heritability and genetic advancement of percentage of mean suggests that the characters mentioned above were due to the result of additive gene action. As a result, selection for these characters should be done.

Most of the traits studied had skewness value ranged from (-0.5 to 0.5) are normally distributed except traits days to 50% flowering, leaf : stem ratio, leaf dry weight per plant (g) and number of tillers per plant showed positive skewness means they showed dominant and complementary gene action and flag leaf length showed negative skewness *i.e.*, it exhibited dominant and duplicate gene action. Plant height (cm), flag leaf width (cm), culm diameter (cm), dry matter yield per plant (g), stem dry weight per plant (g) and seed yield per plant (g) exhibited negative kurtosis (platykurtic) indicates traits are controlled by large number of genes and rest of the traits showed positive kurtosis (leptokurtic) are governed by small number of genes.

In association analysis significant and positive correlation was detected for trait leaf dry weight per plant was followed by dry matter yield per plant, stem dry weight per plant and leaf width with green fodder yield. It indicated that selection for these traits can boost up the yield of green forage. Green fodder yield was found to have a negative significant relationship with the number of tillers per plant, the number of leaves per plant, and plant height. These traits were inversely related with the yield of green forage.

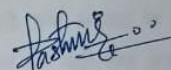
In path analysis green fodder yield was taken as dependent character. For green fodder yield, leaf dry weight per plant had the greatest significant positive correlation and positive direct effect, followed by dry matter yield per plant, stem dry weight per plant, culm diameter and leaf width. Due to direct effect and significant positive correlation of these characters the improvement in any of these traits will directly increase the production of green forage. Thus, these traits should be used in green forage yield improvement programme of Oat. Number of tillers per plant had the greatest negative significant correlation as well as direct and negative effect, followed by the number of leaves per plant, seed yield per plant and plant height which symbolizes that if the yield of these traits will increase then automatically the yield of green forage will decrease. That's why plants with lesser number of tillers per plant and leaves per plant, low seed yielder plant and short heighted plant should be used for selection.

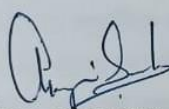
All the genotypes were clustered by using Tocher method and grouped into 12 clusters. Largest cluster group was found cluster I which comprised by 66 genotypes followed by cluster III (33), cluster V (14), cluster X (9), and cluster VI (4). Seven cluster II, IV, VII, VIII, IX, XI, XII had only 1 genotype. Distribution of genotypes between these clusters indicates the ample of diversity among genotypes. The intra cluster distance values ranged from 0 to 1506.42. The distance of inter clusters of genotypes were ranged from 429.41 to 23009.13. Result of this analysis indicated the presence of commendable amount of genetic divergence in the study material. Cluster X and XI had highest inter cluster value suggested that genotypes which fell under these both clusters had high genetic divergence. Genotypes belonging to cluster X and XI will give superior recombinants by using them in hybridization programme of Oat. According to the findings, high values of inter cluster distance were reported as compare to intra cluster distance, indicating that the genotypes had a lot of genetic divergence. Contribution for genetic divergence was highest by trait 1000 seed weight followed by green fodder yield, seed yield per plant and no. of nodes on the main culm while flag leaf length, leaf length and number of tillers per plant had lowest contribution.

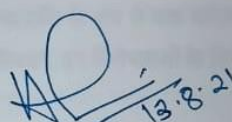
In principal component analysis total diversity was portioned into 6 PCs. PC I contributed majority of total variability present among the genotypes followed by subsequent PCs. Highest negative loading was contributed by green fodder yield and leaf dry weight per plant which fell under PC I followed by 1000 seed weight which fell under PC V. Positive loading was estimated highest for leaf: stem ratio followed by leaf length and stem dry weight per plant which comes under cluster VI, III and II respectively. These traits contributed most towards diversity.

थीसिस सार

a)	थीसिस का शीर्षक	:	"चारा उपज और इससे संबंधित लक्षणों के लिए जई (अवेना सटाइवा एल.) का सस्य आकारिकी लक्षणों का आकलन"
b)	छात्रा का पूरा नाम	:	रश्मि टोप्पो
c)	प्रमुख विषय	:	आनुवंशिकी और पादप प्रजनन
d)	प्रमुख सलाहकार का नाम और पता	:	डॉ. मयूरी साहू, वैज्ञानिक, आनुवंशिकी और पादप प्रजनन विभाग, कॉलेज ऑफ एग्रीकल्चर, इं. गां. कृ. वि., रायपुर।
e)	उपाधि प्रदान की जाएगी	:	एम.एस.सी. (कृषि, आनुवंशिकी और पादप प्रजनन)


छात्रा का हस्ताक्षर


प्रमुख सलाहकार के हस्ताक्षर


विभाग के प्रमुख का हस्ताक्षर

दिनांक : 18.08.21

शोध ग्रंथ सारांश

चारा उपज के लिए "चारा उपज और इससे संबंधित लक्षणों के लिए जई (अवेना सटाइवा एल.) का सस्य आकारिकी लक्षणों का आकलन" नामक प्रयोग अनुसंधान सह कृषि अनुदेशात्मक, आनुवंशिकी और पादप प्रजनन विभाग, इं. गां. कृ. वि., रायपुर, (छ.ग.) में किया गया था। प्रयोग रबी 2019-20 में किया गया था। कुल 130 जर्मप्लाज्म परिग्रहण (5 मानक चेक) को अध्ययन के तहत 5 ब्लॉकों के साथ संवर्धित डिजाइन में प्रयोग किया गया था। भारत के झांसी स्थित वर्णनकर्ता भारतीय चरागाह एवं चारा अनुसंधान संस्थान के अनुसार 32 गुणात्मक और मात्रात्मक लक्षणों का अध्ययन किया गया। (रॉय एट अल., 2017)। गणना किए गए पूरे डेटा जई के लक्षण वर्णन और जीनोटाइप, संघ विश्लेषण और आनुवंशिक विविधता के बीच परिवर्तनशीलता का अनुमान लगाने के लिए थे।

बेतरतीब ढंग से 5 पौधों के लिए डेटा सभी 19 मात्रात्मक लक्षण के लिए दर्ज किया गया था और आवृत्ति सभी 13 गुणात्मक लक्षण के लिए गणना की गई थी। गुणात्मक और मात्रात्मक लक्षणों के लिए पर्याप्त मात्रा में भिन्नता का अध्ययन किया गया। 13 गुणात्मक लक्षणों में से 7 लक्षण जीनोटाइप के बीच

उच्च भिन्नता थी जबकि बाकी 5 लक्षणों में कोई भिन्नता नहीं दिखाई दी और रूपात्मक उपस्थिति में समान हैं।

विशेषता पत्ती: तना अनुपात और प्रति पौधा बीज उपज उच्च जीसीवी और पीसीवी मूल्य युग्मित था। इससे पता चला कि दोनों लक्षणों में उच्च आनुवंशिक अभिव्यक्ति थी और इन लक्षणों का चयन करके जई में सुधार की संभावना बढ़ जाएगी। जीसीवी और पीसीवी के अध्ययन से यह देखा गया कि जीसीवी मूल्यों की तुलना में पीसीवी मूल्य उच्च है जो पर्यावरणीय प्रभाव का प्रतिनिधित्व करता है और जो आनुवंशिक प्रभाव से अधिक है। लक्षण 1000 बीज वजन और पत्ती: तना अनुपात के लिए वंशागतिका का उच्च मूल्य दर्ज किया गया था। विशेषता 1000 बीज वजन और पत्ती: तना अनुपात आनुवंशिक उत्तति की उच्च आनुवंशिक अग्रिम उत्तति के साथ जुड़े थे और उच्च आनुवंशिकता उच्च आनुवंशिक लाभ के साथ संयुक्त इन पात्रों पर कम पर्यावरणीय प्रभाव का प्रतीक है। आनुवंशिकता और आनुवंशिक उत्तति मतलब की आनुवंशिक उत्तति की उच्च राशि के संघ से पता चलता है कि ऊपर वर्ण पर योजक जीन क्रिया के परिणाम के कारण थे। नतीजतन, इन विशेषताओं के लिए चयन किया जाना चाहिए।

लक्षण 50% फूल आने के दिनों, पत्ती: तना अनुपात, पत्ती का शुष्क भार प्रति पौधा (ग्रा.) और प्रति पौधे टिलर की संख्या ने सकारात्मक विषमता दिखाया जिसका अर्थ है कि वे प्रमुख और पूरक जीन क्रिया दिखाते हैं को छोड़कर अध्ययन किए गए अधिकांश लक्षणों में विषमता मान (-0.5 से 0.5) के बीच सामान्य रूप से वितरित था। ध्वज पत्ती की लंबाई ने नकारात्मक विषमता दिखाया यानी, इसने प्रमुख और डुप्लिकेट जीन क्रिया का प्रदर्शन किया। पौधे की ऊंचाई (से.मी.), पत्ती की चौड़ाई (से.मी.), तना व्यास (से.मी.), शुष्क पदार्थ उपज प्रति पौधा (ग्रा.), तना शुष्क भार प्रति पौधा (ग्रा.) और प्रति पौधा बीज उपज (ग्रा.) नकारात्मक कुटोसिस (प्लैटिकर्टिक) प्रदर्शित करता है जो इंगित करता है कि लक्षण बड़ी संख्या में जीनों द्वारा नियंत्रित होते हैं और शेष लक्षण सकारात्मक कुटोसिस (लेटोकोर्टिक) दिखाते हैं जो कम संख्या में जीन द्वारा नियंत्रित होते हैं।

सहयोग विश्लेषण में लक्षण प्रति पौधे शुष्क पत्ती वजन के लिए हरे चारे की उपज के साथ महत्वपूर्ण और सकारात्मक सहसंबंध का पता चला था, इसके बाद प्रति पौधे शुष्क पदार्थ उपज, प्रति पौधे के लिए तना शुष्क वजन और पत्ती की चौड़ाई थी। यह संकेत दिया है कि इन लक्षणों के लिए चयन हरे चारे की उपज को बढ़ा सकते हैं। हरे चारे की उपज प्रति पौधा टिलर की संख्या, प्रति पौधे पत्तियों की संख्या, और पौधे की ऊंचाई के साथ एक महत्वपूर्ण नकारात्मक संबंध पाया गया था। ये लक्षण हरे चारे की उपज के साथ विपरीत संबंधित थे।

पथ विश्लेषण में हरे चारे की उपज को आश्रित चरित्र के रूप में लिया गया था। हरे चारे की उपज के लिए, प्रति पौधे पत्तियों के सूखे वजन का सबसे बड़ा महत्वपूर्ण सकारात्मक संबंध और सकारात्मक प्रत्यक्ष प्रभाव था, जिसके बाद प्रति पौधे शुष्क पदार्थ उपज, प्रति पौधा तना का सूखा वजन, तना व्यास और पत्ती की चौड़ाई थी। प्रत्यक्ष प्रभाव और इन पात्रों के महत्वपूर्ण सकारात्मक संबंध के कारण इन लक्षणों में से किसी में सुधार से सीधे हरे चारा के उत्पादन में वृद्धि होगी। इस प्रकार, इन लक्षणों का उपयोग जई के हरे चारा उपज सुधार कार्यक्रम में किया जाना चाहिए। प्रति पौधे टिलर्स की संख्या का सबसे बड़ा नकारात्मक महत्वपूर्ण संबंध और प्रत्यक्ष नकारात्मक प्रभाव था और साथ ही था, इसके बाद प्रति पौधे पत्तियों की संख्या, प्रति पौधे बीज उपज और पौधों की ऊंचाई जो इस बात का प्रतीक है कि यदि इन लक्षणों की उपज में वृद्धि होगी तो स्वचालित रूप से हरे चारे की उपज कम हो जाएगी। यही कारण है कि प्रति पौधे कम बीज यील्डर, पत्तियों की कम संख्या वाले पौधे और कम ऊंचाई वाले पौधे का उपयोग चयन के लिए किया जाना चाहिए।

सभी जीनोटाइप को टोचर विधि का उपयोग करके 12 क्लस्टर में बांटा गया था। सबसे बड़ा क्लस्टर समूह क्लस्टर I पाया गया जिसमें 66 जीनोटाइप उसके पश्चात क्लस्टर III (33), क्लस्टर V (14), क्लस्टर X (9), और क्लस्टर VI (4) शामिल थे। सात क्लस्टर द्वितीय, चतुर्थ, सातवीं, आठवीं, नौवीं, ग्यारहवीं, बारहवीं में मात्र 1 जीनोटाइप था। इन क्लस्टर के बीच जीनोटाइप का वितरण जीनोटाइप के बीच विविधता के पर्याप्त इंगित करता है। इंटर क्लस्टर दूरी मूल्य 0 से लेकर 1506.42 तक थे। जीनोटाइप के इंटर क्लस्टर की दूरी 429.41 से 23009.13 तक थी। इस विश्लेषण के परिणाम ने अध्ययन सामग्री में आनुवंशिक विचलन की सराहनीय मात्रा की उपस्थिति का संकेत दिया। क्लस्टर X और XI उच्चतम इंटर क्लस्टर मूल्य का सुझाव दिया था कि जीनोटाइप जो इन दोनों क्लस्टर के तहत गिर गया उच्च आनुवंशिक विचलन है। क्लस्टर X और XI से संबंधित जीनोटाइप जई के संकरण कार्यक्रम में उनका उपयोग करके बेहतर पुनर्संयोजन देंगे। निष्कर्षों के अनुसार, इंटर क्लस्टर दूरी के उच्च मूल्यों को इंटर क्लस्टर दूरी की तुलना के रूप में सूचित किया गया था, अतः जीनोटाइप में बहुत आनुवंशिक विचलन है। आनुवंशिक विचलन के लिए योगदान विशेषतया 1000 बीज वजन के बाद हरे चारे की उपज, बीज उपज और मुख्य तने पर नोड्स की संख्या द्वारा उच्चतम था। मुख्य तने पर नोड्स की, जबकि ध्वज पत्ती की लंबाई, पत्ती की लंबाई और प्रति पौधे टिलर्स की संख्या का योगदान सबसे कम था।

सैद्धांतिक घटक विश्लेषण में कुल विविधता को 6 सैद्धांतिक घटकों में विभाजित किया गया था। सैद्धांतिक घटक प्रथम के बाद अन्य सैद्धांतिक घटकों के बीच मौजूद कुल परिवर्तनशीलता का अधिकांश योगदान दिया। उच्चतम ऋणात्मक लोडिंग का योगदान हरे चारे की उपज और पत्तियों के सूखे वजन प्रति पौधे द्वारा किया गया था जो सैद्धांतिक घटक I के तहत गिर गया था जिसके बाद

सैद्धांतिक घटक वी के तहत सकारात्मक लोडिंग का अनुमान लगाया गया था: पत्तियों की लंबाई और तना शुष्क भार प्रति पौधे जो क्रमशः छठी, III और II के तहत आता है। इन लक्षणों ने विविधता की दिशा में सबसे अधिक योगदान दिया।

CHAPTER 1

INTRODUCTION

The plant Oat (*Avena sativa* L.) is dual purpose crop which can be grown as grain and also as a forage crop. Oat is self-pollinated hexaploid crop ($2n = 6x = 42$) with basic chromosome number ($x = 7$) having genomic constitution of AACCCDD (Rines *et al.*, 2006). Oat is thought to be originated in Asia Minor (Gibson and Benson, 2002). The plant Oat belongs to the grass family Poaceae. *A. sativa*, *A. byzantine* and *A. nuda* are the most commonly cultivated species. Its presence found first in the reference of literature of a Greek physician, Dienes, in the 400 B.C. Oat has become a major forage crop in the Himalayan Hindu Kush (HHK) which ranges from Afghanistan to Myanmar since the 1950s (Stevens *et al.*, 2003). In world, Oat ranks sixth in cereal production next to wheat, rice, maize, barley and sorghum (Oliver *et al.*, 2011). Oat is used more for a forage purpose than human consumption. More than 90% of the total produce is used for forage purpose. Irrespective of it is an important forage crop it is also a good multipurpose crop which is grown for grain and pasture also. It can be considered as a one of the best dual purpose cereal crops that work well for the platter of cattle and human as well as. It contains high amount of antioxidants, α -tocopherol, α -tocotrienol and avenanthramides, as well as total dietary fiber including the soluble fiber β -glucan (Oliver *et al.*, 2011).

Health of human and animal are associated. Whatever nutrition provided to the animal through fodder will go to the human through animal products. It is difficult for a dairy man to feed their animals a concentrate-based ration due to selling price of milk and other livestock products are lower than the cost of animal feed. So, it is necessary to increase the production of good quality fodder. Green fodder production is important for animals to provide balanced nutrition (Anonymous, 2002). Therefore, it increases the necessity to grow green fodder crops along with other crops in cropping system with good quality fodder for economical livestock production. As per research carried out by Indian Grassland and Fodder

Research Institute (IGFRI), Jhansi, it indicated that cultivation of fodder crop is profitable.

The average yield of Oat for green fodder varies from 45 to 55 tons per hectare. Sandy loam soil is known as best for Oat although it can be grown on various type of soils. Mostly fertile and well drained soil is suitable for crop Oat. Addition of lime brings the soil pH up to the range of 5.3-5.7 which can provide high yield of Oat. Oat can tolerate acid soils with a pH of 4.5. Oat is a *Rabi* crop which is usually grown from the month of October to the end of December. Early sowing provides the good cutting and high production.

Oat shows quick regeneration ability and excellent growth habit after its cutting. It has good quality fodder. Oat provide succulent, palatable and highly nutritious fodder. During *Rabi* season it is grown as a forage crop in central parts of the country and western region and now its cultivation also increases to the eastern region of India. In India, Oat occupies 5,00,000 ha area for its cultivation. It cultivated maximum in UP (34%), followed by Punjab (20%), Bihar (16%), Haryana (9%) and Madhya Pradesh (6%). Rest of the area is shared by other states viz., Orissa, Gujarat, Uttaranchal, Maharashtra *etc.* (Anonymous, 2012).

With minimum Irrigation Oat crop produce high green fodder yield per unit area per unit time (Solanki, 1977). Oat contains protein content (8-10%), dry matter content (18-23%) and *in vitro* dry matter digestibility (IVDMD (60-70%)) (Phogat *et al.*, 2003). In comparison to other green fodder crops of *Rabi* season, it contains relatively high dry matter content and more disease resistance ability. It is also used for making silage and its straw can be used to feed animals. In Oat crop, multi-cut system is followed and after taking one cut grain production can also be obtained. There is the requirement of 761.5 MT of green fodder in the country and present the shortage of 24.7% of green fodder (Solanki, 2003). Therefore, Oat is an important green fodder crop which can decrease the shortage of green fodder in the country.

Livestock is vital subsector of agriculture in India, it includes 155.3 million cattle and 108.7 million buffaloes (National Dairy Development Board, 2016). Livestock provides milk, butter and other products of animal origin for human nutrition. Despite this large population of livestock, milk production and

productivity is far below the world's average. At present, India faces a net deficit of 63% green fodder, 24% dry crop residues and 64% feeds (Kumar *et al.*, 2016). Availability of good quality and sufficient quantity of forage is essential to maintain high level of milk and meat production. Oats forms an exceptional fodder crop because of its excellent growth habit, quick regeneration ability, succulence, high palatability and high nutritive value for both milch and draft animals. Due to its multi-cut nature and quick generation ability it provides regular supply of green fodder over a period of time. It has dry matter digestibility in excess of 75% (Burgess *et al.*, 1972). Oat has adequate carbohydrate to make good silage. Oat straw is soft and is used as bedding material due to its dust free and absorbent nature. In dairy farms, Oat is well adopted as a fodder, as it can be used to feed animals in green and silage and hay can also be made from it.

Characterization is the description of plant germplasm. It helps in determining the expression of highly heritable characters like morphological or agronomical features, seed proteins or molecular markers. It provides information about the traits of accession which helps to maximize utilization of the germplasm collection to the final users. Characterization of any crop based on its DUS descriptors proposed by IGFRI for forage Oat. (Roy *et al.*, 2017). In present study such marker descriptors were used to identify the various germplasm lines uniqueness. Yield is influenced by many other important yield contributing traits which is controlled by polygene and environmental factors. The overall effect of plant breeding on genetic diversity has been a long standing concern in the evolutionary biology of crop plants. Thus, the present study will be carried out to assess the variability with the help of genetic parameters and diversity at genetic level.

Objectives

1. To characterize Oat germplasm accessions for forage yield and its contributing traits.
2. To estimate the genetic parameter for forage yield and its contributing traits.
3. Genetic diversity and association analysis for fodder yield and its contributing traits.

REVIEW OF LITERATURE

Characterization is the description of plant germplasm. Characterization of an accessions on important characteristics enables to distinction among different phenotypes. Morphological characterization enables to assess genetic variability, heritability, character association and genetic diversity of any crop. The crop Oat is studied for various characters.

The previous years published research papers are reviewed in order to understand the subject under the following headings:

- 2.1 Morphological characterization
- 2.2 Genetic variability parameters (*Avena sativa* L.)
- 2.3 Heritability and genetic advance
- 2.4 Association analysis in various yield contributing traits
- 2.5 Genetic diversity in oats (*Avena sativa* L.)

2.1 Morphological characterization

From very long time plant morphology is in use (Dhananjaya *et al.*, 2012). Cultivated varieties can be identify by morphological descriptors (Molona-Cano and Elena-Rossello, 1978). Plant characters are the basis for selection of plant material for breeders. Morphological traits are mainly used for varietal identification. These descriptors not only reflect the genetic constitution of the varieties, but also the genotype and environmental interaction expressed by (G x E) (Lin and Bias, 1984).

Sharapova *et al.*, (1997) evaluated genetic relationship among 72 oat varieties. They studied morphological characters like lemma color, awn presence and panicle shape for variety descriptions.

Diederichsen *et al.*, (2001) found the genetic diversity based on morphological traits like, plant height, panicle erectness, panicle type, lemma color, dorsal awn of lemma, ligules, green fodder yield, dry matter yield and flag leaf length.

Kumar *et al.*, (2002) found that the morphological characters like stem solidness, color of stem, plant growth habit, flag leaf angle, color of leaf sheath, leaf type, shape of panicle, color of node, presence of hair above or below the node and hairiness of lowest joint of panicle are important characters for identification of a variety in oat.

Arora (2013) evaluated oat germplasm for various morphological and yield contributing traits like plant stature, growth habit, panicle shape, presence or absence of awn and color of foliage. He observed that most of the genotypes he studied had semi-erect growth habit, green foliage, semi- dwarf, equilateral panicle shape and most had awn present.

Chakraborty *et al.*, (2014) characterized the oat genotype on the basis of growth habit, leaf color, color of panicle, stem girth, panicle length, color of awn, awn nature, lemma color.

Sumathi and Balamurugan (2014) evaluated 11 oat varieties and found that plant characters viz., stem hairiness on uppermost node, growth habit, flag leaf attitude, presence of awns and orientation of branches in panicle and seed morphological characters viz., seed color, color of coleoptile region were important morphological characters responsible for identification. Other plants characters viz., lower leaf hairiness of sheath and seedlings characters viz., sheath of first leaf, first leaf, anthocyanin pigmentation on coleoptiles were of secondary importance for variety identification.

Kaziu *et al.*, (2016) studied 32 oat genotypes for characterization based on morphological and quality characters and concluded that genotypes that have erect panicle, erect growth habit and presence of wax should be chosen for tolerance of abiotic stress.

2.2 Genetic variability parameters (*Avena sativa* L.)

Rezai and Frey (1988) studied 457 wild oats for variability in 6 seed characters in various geographical region. Concluded that occurrence of protein percentage, oil percentage and the number of spikelet per panicle was affected by region specific adaptation.

Matiello *et al.*, (1998) evaluated oat for assessment of variability for plant height and flowering date by introduction of different wild forms and came with positive result for variability.

Shankar *et al.*, (2002) evaluated 32 oat genotypes for different characters to assess genetic variability of a genotype and high genotypic coefficient was observed for trait leaf: stem ratio, green fodder yield and dry matter yield.

Prasad *et al.*, (2003) worked in 247 exotic forage oat and determined the genetic variability for various yield contributing components. All the characters studied showed moderate to high variability.

Bakhsh *et al.*, (2007) evaluated 10 oats varieties. All the traits studied showed significant differences among different varieties. The exotic oats varieties “Scott” and “Cuscade” produced significantly taller plants, more tillers per plant, higher leaf area and more leaves per tiller.

Neem *et al.*, (2007) evaluated seventeen varieties of oat and observed a significant differences for characters like plant height, number of tillers per plant, and green fodder yield where no. of leaves per tiller was found non- significant.

Hussain *et al.*, (2010) worked in nine exotic oat cultivars. Cultivar NZ-0034 produced high green fodder yield and dry matter yields. In comparison to other varieties NZ-0034 produced more stiffness of plants which was attributed by high fodder yields. So, NZ-0034 could be grow for high fodder yields.

Ilias and Costas (2010) evaluated 158 accessions of wild oats. All the quantitative characters studied viz., plant height, no. of leaves per plant, no. of tillers per plant, lemma hairiness, awn and floret length showed high CV was a clear indication of variability present within genotypes.

Iannucci *et al.*, (2011) characterized 109 accession for 13 bio agronomic traits. Accessions were studied specially for seed yield. Heading time and productivity characteristics were the major source of diversity among oat population studied.

Bibi *et al.*, (2012) studied 180 accession of oat for green fodder yield in augmented design and observed that number of tillers per meter row exhibited highest genotypic variance and genotypic coefficient variance whereas lowest GCV was recorded for number of leaves per plant.

Sangwan *et al.*, (2012) observed moderate GCV and PCV values for trait dry matter yield, green fodder yield, number of tillers and plant height. Lowest GCV and PCV was recorded for days to 50% flowering.

Krishna *et al.*, (2013). Highest GCV was recorded in grain weight. All the characters studied showed high to moderate variability for GCV. All the traits except, number of leaves, leaf breadth and leaf: stem ratio showed comparatively higher level of genotypic coefficient variance.

Zaheri *et al.*, (2013) investigated 21 oat genotypes in rainfed and irrigated conditions. Determined direct and indirect effect of different traits on grain yield. They observed that most of the traits measured had highly significant genotypic differences among them. High significant environmental differences were found in grain yield, straw yield, 1000 grain weight and biomass.

Chakraborty *et al.*, (2014) evaluated 24 oat accession and observed high GCV and PCV for green fodder yield, dry fodder yield, seed yield per plant, spikelet per panicle, flag leaf width, peduncle length and reducing sugar.

Dubey *et al.*, (2014) studied 34 oat genotypes for assessment of genetic variability. High PCV and GCV was reported in trait crude protein yield which was followed by leaf area, total dry matter yield and total green fodder yield. This indicated the high variability for these traits.

Surje and De (2014) found that traits like number of grain per panicle, grain yield per plant, crude protein content and weight of flag leaf showed significantly high GCV and PCV.

Kaziu *et al.*, (2016) determined the genetic variation for lodging resistance, hairiness of leaf sheath, lemma color, hairiness of lemma in 32 genotypes of oat. All the characters exhibit variation.

Poonia *et al.*, (2017) found highest variability for dry matter yield. Genotypes Algerian, OL-125 and JHO-99-1 had high value for dry matter yield.

Premkumar *et al.*, (2017) evaluated 48 oat genotypes for 14 different yield and yield attributing characters. Groats weight per panicle, kernel weight per panicle, harvest index, single plant groat yield and single plant kernel yield reported high genotypic and phenotypic coefficient of variation.

Rawat *et al.*, (2019) evaluated 21 released varieties of oats and results revealed that maximum GCV found for grain yield per plant, harvest index, leaf: stem ratio, dry matter yield, green fodder yield and straw yield per plant.

Singh *et al.*, (2019) Found variation for almost all the traits studied. Seedlings dry weight, green leaves weight per plant and green fresh weight of total tillers

showed moderately high variability for genotypic coefficient of variation. Green fresh weight showed highest GCV.

Sahu and Tiwari (2020). The highest value of GCV and PCV reported for dry matter yield. Leaf: stem ratio had moderate GCV and PCV value. Low GCV and PCV were recorded for most of the characters viz., days to 50% flowering, protein (%) and plant height. Phenotypic coefficient of variation were slightly higher than the genotypic coefficient of variation which indicates the environmental influence on genotypes.

2.3 Heritability and genetic advance

Singh (1999) evaluated 31 genotypes for 7 characters to derive heritability and genetic advance. High heritability combined with high GCV and PCV were recorded for traits plant height, no. of tillers per plant, no. of leaves per plant, green forage yield, dry forage yield and leaf: stem ratio. This indicated that selection for these traits will be beneficial for breeding program. Number of tillers per plant and green forage yield recorded high heritability and genetic advance as a percent mean.

Shankar *et al.*, (2002) observed that high heritability coupled with high PCV found in green fodder yield. High heritability and high genetic advance were recorded in green fodder yield and dry matter yield.

Prasad *et al.*, (2003) worked in 247 exotic forage oat genotypes. Studied for yields and yield attributing traits and found high heritability among them.

Pundir *et al.*, (2003) estimated high heritability with high genetic advance for character green fodder yield and leaf length. Higher values of genetic advance and heritability observed for almost all the characters studied.

Mall *et al.*, (2005) observed that dry matter yield per plant, green fodder yield per plant, number of grains per panicle, numbers of tillers per plant and grain yield

per plant had high broad sense heritability combined with high genetic advance whereas, 1000 seed weight had low heritability and low genetic advance indicated that high influence of environment on this character.

Bibi *et al.*, (2012) studied 180 accessions of oat for green fodder yield and found high heritability for traits numbers of tillers per plant, days to 50% flowering, green fodder yield and plant height indicated that selection on these traits would be effective for further improvement program.

Sangwan *et al.*, (2012) revealed from their studies that high heritability and moderate genetic advance observed in trait green fodder yield and dry matter yield.

Krishna *et al.*, (2013) estimated that high heritability coupled with high to moderate GCV were recorded for all the characters studied. Highest heritability was found in panicle length (92.2%) and lowest in leaf breadth (20.6%). Highest genetic advance as percent mean was found in grain weight (103.64), followed by dry matter yield (63.78 g), green fodder yield (55.07 g), panicle length (30.33 cm) and 1000 seed weight (31.68 g).

Chakraborty *et al.*, (2014) studied twenty-four genotypes from 16 different *Avena* spp. for yield, quality characters and disease reaction. They observed high heritability along with high genetic advance for green fodder yield, dry fodder yield, seed yield per plant, spikelets per panicle, flag leaf width, peduncle length and reducing sugar.

Surje and De (2014) evaluated fifteen oat genotypes for green forage and grain yield and estimated that high heritability, genetic advance found for trait green fodder yield, dry fodder yield, seed yield per plant, spikelets per panicle, flag leaf width, peduncle length and reducing sugar.

Premkumar *et al.*, (2017) evaluated 48 oat genotype for 14 different yield and yield attributing characters. They recorded high heritability coupled with high genetic advance for almost all the characters.

Rawat *et al.*, (2019) recorded high heritability and moderate to high genetic advance for plant height, leaf length, leaf: stem ratio, number of spikelet, dry matter yield, green fodder yield, straw yield per plant, grain yield per plant and harvest index.

Singh *et al.*, 2019 estimated that heritability varied from 6.65 % to 98.33%. The highest heritability was recorded in days to maturity and lowest in leave per plant. Moderate GCV coupled with high heritability observed for character seedlings dry weight, green fresh weight of total tillers and green leaves weight per plant. Among all the traits studied green fresh weight of total tillers estimated as comparatively higher genotypic coefficient variance, heritability and genetic advance. Green fresh weight of total tillers was exhibited highest genetic advancement as percent mean and plant height had moderate.

Sahu and Tiwari (2020). Highest heritability was exhibited by trait dry matter yield and highest genetic advance was recorded for green forage yield whereas high genetic advance as percent mean was reported for dry matter yield.

2.4 Association analysis in various yield contributing traits

2.4.1 Correlation analysis

Shrivastava *et al.*, (1995) observed that green and dry fodder yield were hugely associated with days to 50% flowering, plant height, number of tillers, leaf length, leaf width and leaf: stem ratio and revealed that traits plant height, number of leaves per plant, leaf size and leaf:stem ratio had high direct positive effects on fodder yield.

Nehvi *et al.*, (2000) observed that plant height, number of leaves per plant, green leaf and stem weight per plant are positively correlated with green fodder yield. Path coefficient analysis indicated that green leaf weight and green stem weight were the major deciding factor for fodder yield.

Ziya *et al.*, (2001) examined 17 oat accessions for determining the inter relation between different characters grain yield (g), plant height (cm), grain number per panicle, grain weight per panicle (g), 1000 grain weight (g), days to maturity, panicle number by evaluating correlation coefficient analysis.

Shanker *et al.*, (2002) recorded data for fourteen characters of oats to find out the inter relationship among various desirable characters and concluded that positive significant correlation found for days to 50% flowering, plant height, number of tillers per plant, green fodder yield, dry matter yield, panicle length, 1000-grain weight and grain yield.

Bukhari *et al.*, (2009) exhibited the correlation between the traits like days to 50% flowering, plant height, number of tillers, green fodder yield, dry fodder yield, leaf stem ratio and concluded that these traits are important for improvement of yield potential traits.

Bibi *et al.*, (2012) recorded that trait inter nodal length, leaf area, number of tillers and dry matter yield were significantly positive correlated with green fodder yield. Whereas, non-significant negative correlation shown by days to 50% flowering, days to 50% maturity and plant height.

Sangwan *et al.*, (2012) found significant positive correlation between green fodder yield and dry matter yield for genotypic coefficient of correlation and both traits were also showed high significance correlation with other traits like plant height, number of tillers/m and days to 50% flowering.

Sofi *et al.*, (2012) revealed that green fodder yield was highly correlated with plant height while seed yield significant positive correlation with plant height.

Ahmad *et al.*, (2013) evaluated 75 germplasm lines and recorded high positive correlation between grain yield and leaf length, leaf stem ratio and plant height was mainly obtained through indirect effect *via* green fodder yield.

Nirmalakumari *et al.*, (2013) worked out in 21 oats genotypes and revealed that single plant yield significant positive correlated with number of basal tillers per plant, number of productive tillers per plant, number of grains per panicle and dry matter yield per plant and they concluded that major contributing factor for yield were number of productive tillers per plant and number of grains per panicle.

Krishna *et al.*, (2014) plant height and leaf length showed positive correlation with maximum number of character studied.

Surje and De (2014) found that plant height, tiller number per plant, length of panicle and number of spikelet per panicle exhibited significant positive correlation with grain yield per plant. Total grain yield per plant and number of grains per panicle produced highest in genotype Kent and JHO-99-2 whereas NDO-609 was observed to produce highest green forage yield.

Tanoli *et al.*, (2016) assessed correlation analysis for 124 oat genotypes which indicated that seed yield per plant was highly significantly correlated with all the traits studied except days to 50% germination which exhibited non-significant correlation with seed yield per plant.

Poonia *et al.*, (2017) observed that plant height, seed yield per meter row length, green fodder yield per meter row length, flag leaf length, inter-node length, axis length, leaf length and germination percentage showed positive significant correlation for dry matter yield per meter row.

Premkumar *et al.*, (2017) revealed that trait single plant kernel yield exhibited significant positive correlation with various traits viz., total number of tillers per plant, number of groats per panicle, number of productive tillers per plant, number of groats per panicle, kernel weight per panicle, groat weight per panicle, 1000 groat weight, thousand kernel weight, fodder yield per plant, harvest index and single plant goat yield.

Poonia *et al.*, (2018) evaluated 92 oat genotypes. They found that plant height, number of tiller per plant and dry matter yield showed positive significant correlation with green fodder yield.

Sahu and Tiwari (2020) worked for correlation analysis in oat germplasm and observed that green fodder yield showed positive correlation with most of the traits studied except trait days to 50% flowering and plant height. Days to 50% flowering showed highly significant negative correlation with green forage yield. Genotypic and phenotypic correlation was observed for days to flowering initiation which was highly significant positive correlated with days to 50% flowering.

2.4.2 Path analysis

Choubey *et al.*, (2001) observed that number of tillers and leaf width had positive direct effect for green fodder yield. Dry matter yield had negative effect on green fodder yield. They also concluded that appropriate plant height with more number of tiller and number of leaves per plant with longer flag leaf length would produce high green fodder yield in their progenies so, selection on these traits would be beneficial.

Kumar *et al.*, (2004) studied various yield attributing trait of oats for green fodder yield and the data recorded were showed that trait plant height, number of tillers per plant and flag leaf length contributed direct effect towards green fodder yield.

Bukhari *et al.*, (2009) observed in his studies of path coefficient that days to 50% flowering, plant height, number of tillers, green fodder yield, dry fodder yield, leaf area index, leaf: stem ratio and crude protein content directly affect the yield of fodder oat.

Sangwan *et al.*, (2012) examined oat accession and found that dry fodder yield, plant height and number of tillers per plant had positive direct effect on green fodder yield whereas, days to 50% flowering exhibited negative direct effect towards green fodder yield.

Ahmad *et al.*, (2013) evaluated 75 germplasm lines and came with a conclusion that green fodder yield had maximum positive direct effect for grain yield which was followed by number of leaves per plant and leaf width.

Zaheri *et al.*, (2013) investigated 21 oat genotypes in rainfed and irrigated conditions. Determined the direct and indirect effect of various traits on grain yield. They measured highly significant genotypic difference among the traits studied. Grain yield, straw yield, biomass and 1000 grain weight exhibited highly significant environmental differences. Path analysis revealed that number of panicle per square metre had largest positive direct effect on grain yield.

Krishna *et al.*, (2014) estimated path analysis for 50 genotypes of oats. Leaf: stem ratio and dry matter yield contributed maximum positive direct effect towards green fodder yield. So, direct selection of these traits would be beneficial for the improvement of green fodder yield.

Poonia *et al.*, (2017) revealed that direct and positive effect on dry matter yield was exhibited by traits like green fodder yield, number of tillers per plant, plant height and seed yield per meter row length whereas days to 50% flowering, peduncle length, axis length, number of spikelets per panicle, and number of leaves per plant showed negative direct effect on dry matter yield.

Sahu and Tiwari (2020) observed that low crude protein contributed towards direct effect on green fodder yield. However, indirect effect was exhibited by most of the traits studied.

2.5 Genetic diversity in oats (*Avena sativa* L.)

2.5.1 Multivariate analysis using Mahalanobis D²-statistic

Sindhu and Mahndiratta (1981) studied 30 varieties of oats and by using multivariate analysis they grouped it into 11 clusters and indicated the presence of ample of genetic divergence in the genotypes. Traits contributed most towards genetic divergence was number of tiller followed by plant height and leaf width.

Souza and Sorrell (1989) studied coefficient of percentage among 205 oats cultivar to the major relative change in genetic diversity. They observed 7 clusters out of that 6 corresponded to the original germplasm.

Krishan *et al.*, (1993) made cluster analysis of data on 12 quantitative traits in 48 advanced lines. They grouped all the entries in all 11 clusters. Considerable genetic divergence was observed for all the traits among the genotypes.

Singh and Mishra (1996) made D² analysis in 2576 oat germplasm. Traits like 100 grain weight and seed width showed high genetic divergence.

Babbar *et al.*, (1997) based on D² statistics found that 20 oat genotypes were clustered in 7 groups. Result revealed that intra cluster means will be helpful in selection of diverse genotypes.

Choubey *et al.*, (2001) evaluated 300 germplasm lines of oat and grouped into 14 clusters by using D² statistic and reported that genotypes had high diversity which was measured by inter cluster distance. Selection among these genotypes is effective for improvement of yield of forage oat.

Kumarmall and Vishwakarma (2006) used Mahalanobis D^2 analysis to study the genetic divergence among 48 elite lines of oat for 10 different traits. Genotypes were divided into 7 clusters. Largest contribution for genetic divergence was recorded by traits dry matter yield per plant, number of grains per panicle, grain yield per plant, biological yield per plant and green fodder yield per plant.

Vieira *et al.*, (2006) genetic divergence was estimated in fifteen oat cultivars by using Mahalanobis D^2 statistics. They divided oat cultivars into 3 cluster groups, (I), (II) and (III). Cultivar which belongs to the cluster (III) showed difficulty in adapting in cultivating condition of cluster (II).

Ahemad *et al.*, (2011) evaluated 75 germplasm lines for 10 different traits. Germplasms were grouped into 9 clusters and concluded that days to 50% flowering, grain yield, green fodder yield and leaf: stem ratio contributed most towards genetic divergence.

Singh and Singh (2011) grouped 70 oat genotypes into 7 clusters based on D^2 analysis Crop duration, green fodder yield and plant showed maximum contribution towards genetic divergence.

Yadav *et al.*, (2011) studied 36 genotypes for genetic diversity in oats by using Mahalanobis D^2 statistics. Oat genotypes were grouped into 11 clusters. Highest number of genotypes was contributed by cluster I. The values of intra-cluster distance were ranged from 0.00 to 136.0 for all the 11 clusters. Values for inter-cluster was found highest between cluster VI and VII. Cluster VII exhibited highest mean values of traits green fodder per plant and plant height and in cluster VI highest mean value was observed in 50% flowering and plant height.

Sangwan *et al.*, (2012) evaluated 39 indigenous and 5 exotic genotypes of oat (*Avena sativa* L.) for 16 fodder and seed yield traits. Genetic divergence was

evaluated by hierarchical cluster analysis which divide genotypes into 6 clusters. Genotypes present in cluster I, II, and IV had high genetic divergence.

Krishna *et al.*, (2014) based on distance range 50 germplasms were distributed in 10 clusters. Cluster I had highest number of genotypes whereas cluster II, III, V, VI, VII, VIII and cluster X had lowest number of genotypes. This indicated that high genetic divergence present between the genotypes studied. It was estimated that genotypes present in cluster II had highest genetic diversity

Jaipal and Shekhawat (2016) grouped 30 genotypes into 4 clusters. Highest number of genotypes were recorded in Cluster I followed by 5 genotypes in cluster II and 1 in III and IV cluster. Highest inter cluster distance was found between cluster II and IV and these both cluster showed high genetic diversity.

Tanoli *et al.*, (2016) evaluated 124 oat genotypes. 124 oat genotypes were distributed into 5 clusters. Cluster III had highest number of genotypes *i.e.*, 50 and lowest in cluster V which contained 3 genotypes. Highest genetic divergence present in cluster V.

Kaur *et al.*, (2018) studied 96 oat genotypes to assess the genetic diversity. All the 96 genotypes were grouped into 6 clusters. Highest inter cluster distance was observed between cluster IV and V followed by VI and III, I and VI for oat accession. High genetic diversity present between all the clusters.

2.5.2 Principal component analysis

Kumar *et al.*, (2006) evaluated 100 germplasm lines of oat using the principal component method of factor analysis. Maximum contribution made by first six principal components could explain 76.7 percent of the total variation in the 22 quantitative attributes and were mainly associated with green fodder yield and its components, seed component traits, 100-grain weight and days to maturity. The remaining principal component made little contribution towards total variation and

thus cannot be considered of much practical value to plant breeders. The first three factor played a pivotal role towards diversity in oat.

Leisova *et al.*, (2007) studied 2707 accessions of spring barley and 1998 accessions of oats. Based on dendogram and Principal component analysis studies it revealed that there is a necessity of conservation of barley and oat germplasm because of negative impact of breeding process were observed on genetic diversity.

Sangwan *et al.*, (2012) evaluated 39 indigenous and 5 exotic genotypes of oat (*Avena sativa* L.) with 16 fodder and seed traits. Five principal components were identified by principal factor analysis which showed 69 percent of total variability.

Tang *et al.*, (2014) compared 114 accessions from 25 *Avena* species. First five components contributed 89.3 per cent of total variation. Investigation revealed that for high grain yield and lodging resistance breeding accessions like CN 25766 and CN 25787, PI 545459, CN 2170, Ciav 8330 were found good parents.

Tanoli *et al.*, (2016) studied 124 oat accessions including three checks. The principal components whose eigen value is more than 1 contributed for 71.06 per cent of total variation. These results gave the information for successful conservation of genetic resources of oats.

Qi *et al.*, (2017) studied 62 oat varieties. Principal component analysis was used for analysing fatty acid profile combined with gas chromatography and cluster analysis. PCA scores scatterplot was used to distinguish between the varieties 46 naked oats were identified.

CHAPTER 3

MATERIALS AND METHOD

The experiment entitled “Agro-morphological characterization of Oat (*Avena sativa* L.) accessions for forage yield and its contributing traits” was conducted at Research cum instructional farm IGKV, Raipur Chhattisgarh, *Rabi* 2019-20. The techniques followed and the materials used during the courses of investigation are presented below:

3.1 Experimental site

The experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India. Chhattisgarh is located between 17°14’N and 24°45’N latitudes and 79°16’E and 84°15’ E longitudes. Raipur is the capital of the Chhattisgarh state and lies at 21°16’N latitude and 81°36’ E longitude with an altitude of 289.60 meters above mean sea level.

3.2 Climate

Subtropical type of climate is found in Raipur. It receives 1200-1400 mm rainfall annually out of which about 8 percent is received during *Rabi* season. The temperature ranged from 27.8 °C to 43.1 °C during the growth period of crop.

The rainfall pattern varies from year to year. The unevenly distribution of rainfall adversely affect the crop growth. Monsoon breaks by the end of June and continues up to month of September.

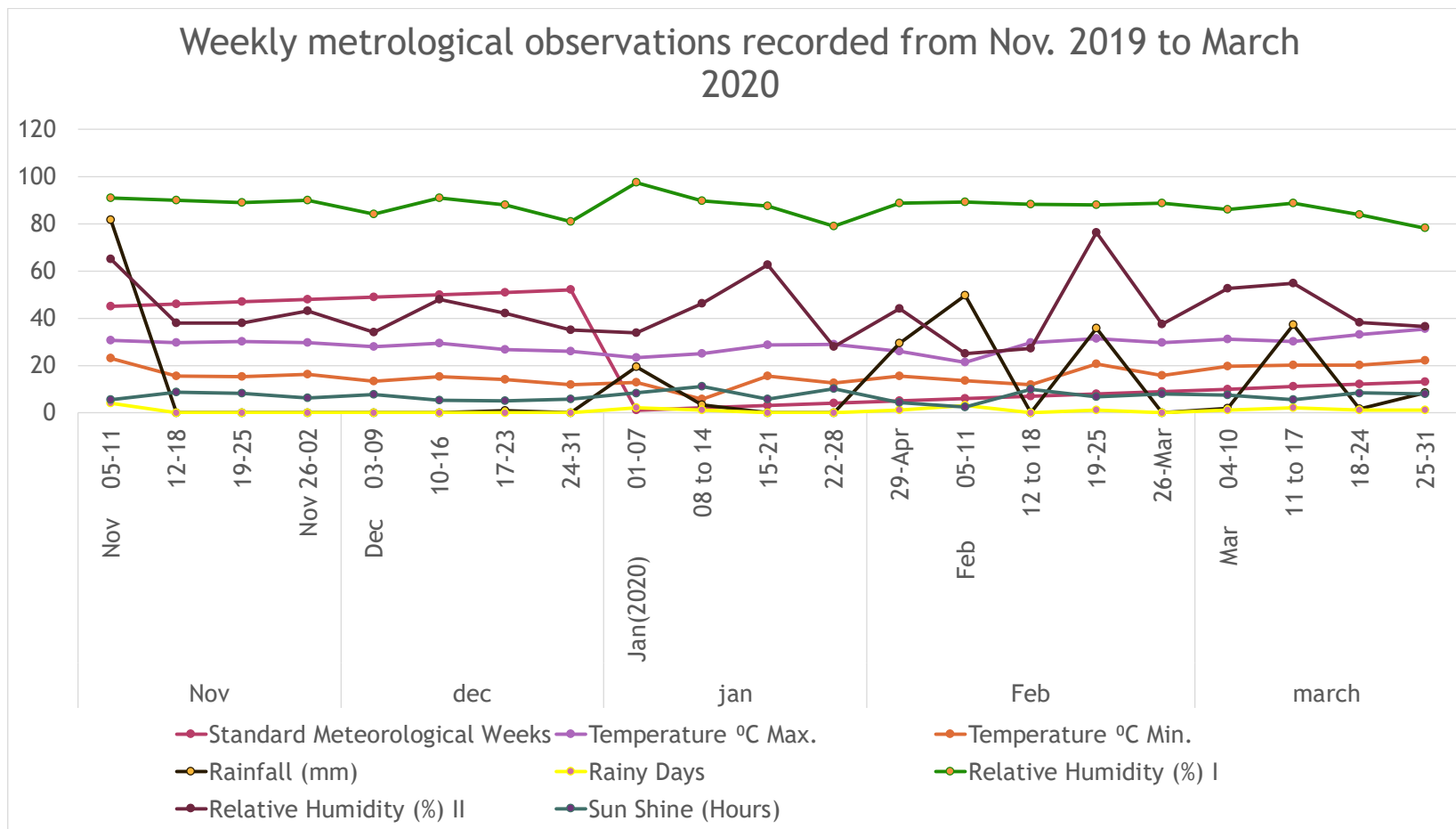


Fig. 3.1. Graph representing meteorological data observed during crop period of Oat (*Avena sativa* L.)

3.3 Experimental Material

The experimental materials comprised for Augmented design with 130 germplasm lines (including 5 checks- JHO-851, RO-19, JHO-822, UPO-212, JO-1) which contains both indigenous collection (IC) and exotic collection (EC) with 5 blocks, Department of Genetics and Plant Breeding, College of Agriculture Raipur, Indira Gandhi Krishi Vishwavidyalaya Raipur, Chhattisgarh, India.

Table 3.1 Experimental materials and their sources

S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype
1.	EC/209494	13.	EC/097538	25.	EC/097537	37.	EC/292328	49.	EC/014016	61.	EC/209211
2.	EC/0076710	14.	EC/097248	26.	EC/0102326	38.	EC/292363	50.	EC/035765	62.	EC/0107539
3.	EC/0101747	15.	EC/097528	27.	EC/060977	39.	EC/0292312	51.	EC/035768	63.	EC/0107524
4.	EC/009884	16.	EC/009890	28.	EC/060975	40.	EC/292362	52.	EC/0131307	64.	EC/0107528
5.	EC/009888	17.	EC/009883	29.	EC/0102324	41.	EC/292371	53.	EC/066172	65.	EC/029056
6.	EC/060978	18.	EC/009889	30.	EC/097533	42.	EC/292275	54.	EC/209196	66.	EC/035103
7.	EC/009885	19.	EC/097522	31.	EC/097532	43.	EC/0292369	55.	EC/0107017	67.	EC/035051
8.	EC/008539	20.	EC/030245	32.	EC/097530	44.	EC/0292340	56.	EC/039899	68.	EC/034585
9.	EC/097525	21.	EC/022079	33.	EC/097520	45.	EC/0292267	57.	EC/209215	69.	EC/034588
10.	EC/097536	22.	EC/022080	34.	EC/097539	46.	EC/036779	58.	EC/0108486	70.	EC/034587
11.	EC/097541	23.	EC/097519	35.	EC/097535	47.	EC/036821	59.	EC/096592	71.	EC/246147
12.	EC/097531	24.	EC/097241	36.	EC/097240	48.	EC/0035766	60.	EC/096541	72.	EC/246146

❖ Source: Procured from NBPGR (National Bureau of Plant Genetic Resources).

Contin....

S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype	S.N.	Genotype
73.	IC/282934	83.	GP-7	93.	GP-21	103.	GP-32	113.	GP-41	123.	RO-11
74.	IC/014555	84.	GP-8	94.	GP-12	104.	GP-30	114.	GP-37	124.	OL-1804
75.	IC/0625278	85.	GP-10	95.	GP-26	105.	GP-13	115.	GP-17	125.	OL-10
76.	EC/096591	86.	GP-33	96.	GP-28	106.	GP-39	116.	GP-11	126.	JHO-851
77.	GP-1	87.	GP-34	97.	GP-40	107.	GP-31	117.	GP-19	127.	RO-19
78.	GP-2	88.	GP-27	98.	GP-15	108.	GP-22	118.	GP-35	128.	JHO-822
79.	GP-3	89.	GP-25	99.	GP-16	109.	GP-43	119.	GP-36	129.	UPO-212
80.	GP-4	90.	GP-48	100.	GP-38	110.	GP-50	120.	UPO-12-1	130.	JO-1
81.	GP-5	91.	GP-44	101.	GP-18	111.	GP-42	121.	1760		
82.	GP-6	92.	GP-20	102.	GP-46	112.	GP-49	122.	405		

❖ Source: Procured from NBPGR (National Bureau of Plant Genetic Resources).

3.4 Observation and collection of data

Observations were recorded on five randomly selected plants in each entry in 5 blocks for screening of germplasm line of oats for the quantitative and qualitative characters. According to descriptor – Indian grassland and Fodder Research Institute, Jhansi, India. (Roy *et al.*, 2017).

3.4.1 Biometric character

Days to 50% flowering

The data recorded when 50% plant showed spike emergence from the date of sowing.

Plant height (cm)

The data noted on main tiller from ground level to tip of the main shoot at 50% flowering stage.

Number of leaves per plant

The data recorded at 50% flowering stage and no. of leaves per plant were counted.

Flag leaf length (cm)

Flag leaf length were noted from ligule to leaf tip at 50% flowering stage.

Flag leaf width (cm)

Flag leaf width were recorded at widest point of flag leaf at 50% flowering stage.

Leaf length (cm)

Leaf length were measured on 4th leaf from top at 50% flowering stage.

Leaf width (cm)

The data were measured at widest point on 4th leaf from the during at 50% flowering stage .

Culm diameter (cm)

Diameter of the main tiller were noted by means of vernier caliper.

Number of nodes on the main culm

Total number of nodes on the main tiller were noted during 50% flowering stage.

Number of tillers per plant

Number of tillers per plant was counted from 5 random plant at 50% flowering stage.

Peduncle length (cm)

The data was recorded from last node of main culm to the base of panicle.

Green fodder yield (kg or g)

The germplasms were harvested at 15 cm from ground at 50% flowering stage and weighted in gram by electronic balance.

Dry matter yield per plant (kg or g)

The plants were dried till its constant weight at 60-80°C in oven and dry weights were measured in grams.

Leaf dry weight per plant (g)

Green harvested leaf dried till its constant weight at 60-80°C in oven and dry weights were measured in grams.

Stem dry weight per plant (g)

Green harvested stem dried till its constant weight at 60-80°C in oven and dry weights were measured in grams.

Leaf: stem ratio

Calculated on the basis of dry leaf and stem weight.

Days to maturity

The days to maturity were recorded by counting the days from date of sowing to the date on which more than 70% plants become physiologically mature.

Seed yield per plant (g)

Seed yield per plant was recorded after harvesting and by threshing them. Electronic balance was used to measure the weight of seed.

1000 seed weight (g)

1000 seed of each genotype was measured by mixing the seed of randomly selected five plants. Seed was weighted by electronic balance.

3.4.2 Non-biometric character

$$\text{Frequency percent} = \frac{\text{No. of the genotype falling under certain category}}{\text{Total no. of genotypes}} \times 100$$

Table 3.2 Non-biometric agro-morphological characters

S.N.	Character Name	Class	Observational stage
1.	Early plant vigour	Poor Good Very good	After 20-25 days of sowing
2.	Growth habit	Erect Semi prostrate Prostrate Others	At start of spike emergence
3.	Leaf color	Green Dark green Others	At 50% flowering
4.	Leaf sheath pubescence	Absent Present	At 50% flowering
5.	Flag leaf attitude	Erect Drooping Semi-drooping	At spike emergence
6.	Stem solidness	Hollow Semi solid Solid	At 50% flowering

7.	Panicle attitude	compact Semi-compact Lateral Equilateral Others	At near maturity
8.	Awn per spikelet	Absent One Two	At maturity
9.	Primary floret pubescence	Absent Present	At full blossom stage
10.	Spikelet shattering	Shattering Non-shattering	At maturity
11.	Hullness	Absent Present	After harvesting
12.	Seed color	White Yellow Grey Black Others	After harvesting and seed drying
13.	Biotic stress susceptibility	Very low Low Intermediate High Very high	At 50% flowering

3.5 Experimental Design

All the experimental materials were sown in 7th November, 2019 in Augmented design. Total 130 germplasm (including checks) were allocated in experimental field. It included 5 checks and whole experimental field was divided into 5 blocks with 30 germplasm line in each block. Each check is replicated at every block and other 125 germplasm grown in a single row.

3.5.1 Statistical Analysis

Statistical analysis was done for 130 oats germplasm accessions on the basis of data recorded for different quantitative characters.

3.5.1.1 Analysis of Variance

Analysis of Variance is calculated for quantitative traits. ANOVA for Augmented Design, suggested by Federer (1961).

The skeleton of analysis of variance for Augmented Design:

S.V.	df	SS	MS	F _{value}
Total	(bc-1)	SST	MST	
Blocks	(b-1)	SSB	MSB	
Checks	(c-1)	SSC	MSC	
Error	(b-1) (c-1)	SSE	MSC	

Adjustment factor, r_j , for each block. This is computed as:

$$r_j = (1/c) (B_j - M)$$

Where,

r_j = Block effect

c = Number of check varieties

B_j = Block total

M = Sum of checks mean

$$\sum r_j = 0$$

Note: as a check on the computation,

$$j$$

3.6 Assessment of variability

Range, mean, standard deviation and coefficient of variation are the variability parameters.

3.6.1 Range

Range is calculated by computing difference between highest and lowest value of the character, which can be expressed as follows:

$$\text{Range} = \text{highest value} - \text{lowest value}$$

3.6.2 Mean

The average of recorded observations was calculated as follows:

$$\bar{X} = \sum \frac{X_i}{n}$$

Where,

Σx_i = Summation of all the observations

n = Total number of observations

3.6.3 Standard Deviation

It is defined as the positive square-root of the arithmetic mean of the Square of the deviations of the given observation from their arithmetic mean and calculated as:

$$S. D. = \sqrt{\frac{\sum (x_i - \bar{x})^2}{n - 1}}$$

Where,

S.D. (σ) = Standard deviation of Sample

X_i = An observation/variante value

$\bar{X}$ = Mean of sample

n = number of given observation

3.6.4 Standard Error

The standard deviation of the sampling distribution of a statistics (estimate) is known as the standard error of that statistics and calculated as:

$$S. E. = \frac{\sigma}{\sqrt{n}}$$

Where,

S.E. = Standard Error

σ = Standard deviation of Sample

n = Number of given observation

3.6.5 Coefficient of variation

The coefficient of variation is obtained by dividing the standard deviation by the mean and expressed in percentage and calculated as:

$$CV = \frac{\sigma}{\bar{X}} \times 100 \%$$

Where,

CV= coefficient of variation

σ = Standard deviation of Sample

$\bar{X}$ = Mean of sample

3.6.6 Phenotypic and Genotypic coefficient of variation

Estimation of genotypic and phenotypic coefficient of variation was calculated as suggested by Burton (1952). The phenotypic and genotypic components of variance were computed according to formulae given by Lush (1940).

However, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in percentage were calculated according to following formula;

$$\sigma^2 = \frac{Mt - Me}{r}$$

Where,

σ^2g = Genotypic variance,

Mt = Treatment mean sum of square,

Me = Error mean sum of square (σ^2e)

(a) Phenotypic coefficient of variation (PCV)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

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

Where,

$\sigma^2 p$ & σ^p = Phenotypic variance and its standard deviation,

$\sigma^2 g$ & σ^g = Genotypic variance and its standard deviation,

$\sigma^2 e$ = Environmental variance,

$\bar{X}$ = General mean.

(b) Genotypic coefficient of variation (GCV)

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

The estimates of PCV and GCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973). The magnitude of coefficient of variation was categorized as high (>20%), moderate (20%-10%) and low (<10%).

3.7 Heritability and genetic advance

Heritability estimates (Broad sense) was calculated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956).

$$\text{Heritability } h^2 (\text{bs}) (\%) = \sigma^2 g / \sigma^2 p \times 100$$

Where,

$h^2 (\text{bs})$ = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The broad sense heritability estimates were classified as low, moderate and high according to Robinson (1966) as follows:

0 - 50 % = Low

51 - 70% = Moderate, and

> 70% = High

3.7.1 Genetic advance

The expected genetic advance from one cycle of selection of best 5 percent individuals was calculated by adopting the formula given by Johnson *et al.*, (1955) as described below.

The genetic advance as percentage of mean was estimated as mentioned below:

$$GA = k \cdot h^2 \cdot \sigma_p$$

Where,

GA = Genetic advance,

k = Selection differential (at 5%, k= 2.06),

h^2 = Heritability estimate,

p = Phenotypic standard deviation

3.7.2 Genetic advance as percent of mean

GA was reported as percentage of mean and it was calculated as follows:

$$\text{Genetic advance as percentage of mean} = (GA / \bar{x}) \times 100$$

$\bar{x}$ The GA was categorized as,

>50% = High,

30-50% = Moderate,

< 30% =Low.

3.8 Association analysis

The genotypic and phenotypic correlation coefficients were estimated between the component characters for the entire environment under studied (Singh and Chaudhary, 1979).

3.8.1 Genotypic correlation

$$r_{xy}(g) = \sqrt{\frac{COV_{xy}(g)}{V_x(g) \times V_y(g)}}$$

Where,

COV_{xy}(p) = Phenotypic covariance between x and y

V_x(p) = Phenotypic variance of character x

V_y(p) = Phenotypic variance of character y

Significance of correlation was tested by following formula

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

Where,

t = Table value of t for n - 2 degree of freedom.

r = Correlation coefficient

n = Number of observations

3.8.2 Path coefficient analysis

Calculations for path coefficient analysis were carried out according to the method developed by Wright (1921) and as used by Dewey and Lu (1939).

The degree of influence of one variable on the other can be expressed in quantitative terms and path coefficient analysis is very efficient in this respect. It is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects. It measures the direct and indirect contribution of independent variables on dependent variable.

Path coefficients were obtained by the following simultaneous equations which express basic relationship between correlation and path coefficients.

$$1. r_{1n} = P_{1n} + r_{12} P_{2n} + \dots + r_{1(n-1)} P_{(n-1)n}$$

$$2. r_{2n} = P_{2n} + r_{21} P_{1n} + \dots + r_{2(n-1)} P_{(n-1)n}$$

.

.

.

$$(n-1) r_{(n-1)n} = P_{(n-1)n} + r_{(n-1)1} P_{1n} + \dots + r_{(n-1)(n-2)} P_{(n-2)n}$$

The residual effect is estimated as it permits precise explanation about the pattern of interaction of other possible components of yield. The unexpected variation of residual factor was obtained from the equation.

$1 = P_2 n P_{21n} + P_2 2n + \dots P_2 (n-1)n + P_1 n r_{12} P_2 n + 2p_{in} r_{13} P_1 n + \dots$
 $+ P (n-1) n r (n-2) n P_1 n$. Where, 1, 2, 3----- (n-1) are component characters and n is the character upon which direct and indirect effects are studied.

3.9 Methodology for Mahalanobis diversity analysis

The D^2 statistic was originally developed by P.C. Mahalanobis in 1936 and Rao (1952) suggested the application of this technique for the assessment of genetic divergence between the populations. The generalized distance between any two populations is given by formula,

$$\Delta = \sum \sum \lambda_{ij} \sigma_i \sigma_j$$

Where,

D^2 = Square of generalized distance

λ_{ij} = Reciprocal of the common dispersal matrix

$\sigma_{ai} = (\mu_i 1 - \mu_i 2)$

$\sigma_{aj} = (\mu_j 1 - \mu_j 2)$ μ = General mean

Since the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (Xs) to standardize uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

3.9.1 Clustering of D^2 values

All the $n(n-1)/2$ D^2 values were clustered using Tocher's method as described by Rao (1952).

3.9.2 Intra cluster distance

The intra cluster distance were calculated by the formula:

Square of intra cluster distance = D_i^2/n

Where,

$\sum D_i^2$ is the sum of distance between all possible combinations of the entries included in a cluster.

n = Number of all possible combinations.

3.9.3 Inter cluster distance

The inter cluster distance were calculated by the formula:

$$\text{Square of inter cluster distance} = \sum D_i^2 / n_{ij}$$

Where,

$\sum D_i^2$ is the sum of distance between all possible combinations (n_{ij}) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.10 Principal component analysis

Principal Component Analysis (PCA) was discovered by Karl Pearson in 1901. Principal component analysis is a multivariate statistical method that attempts to describe the total variation in a multivariate sample with fewer variables than in the original data set.

A principal component is concerned with explaining the variance. covariance structure through a few linear combinations of the original variables. Its general objectives are (1) Data reduction and (2) Interpretation

Algebraically, principal components are particular linear combinations of the p random variables $X_1, X_2, X_3, \dots, X_p$ geometrically, these linear combinations represent the selection of a new coordinate system obtained by rotating the original system with $X_1, X_2, X_3, \dots, X_p$ as the coordinate axes. The new axes represent the directions with maximum variability and provide a simpler and more parsimonious description of the covariance structure.

The principal component depends solely on the covariance matrix Σ (or the correlation matrix ρ) of $X_1, X_2, X_3, \dots, X_p$. The eigenvalue and eigenvector pairs created from data matrix is utilized to identify the principal components.

Let the random vector $X = [X_1, X_2, X_3, \dots, X_p]$ have the covariance matrix Σ with eigenvalues $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_p \geq 0$.

Consider the linear combinations

$$Y_1 = \ell_1 X = \ell_{11}X_1 + \ell_{21}X_2 + \ell_{31}X_3 + \dots + \ell_{p1}X_p$$

$$Y_2 = \ell_2 X = \ell_{12}X_1 + \ell_{22}X_2 + \ell_{32}X_3 + \dots + \ell_{p2}X_p \quad (3.1)$$

$$Y_p = \ell_p X = \ell_{1p}X_1 + \ell_{2p}X_2 + \ell_{3p}X_3 + \dots + \ell_{pp}X_p$$

$$\text{Then, } \text{var}(Y_i) = \ell_i \sum \ell_i \quad i=1,2,\dots,p \quad (3.2)$$

$$\text{Cov}(Y_i, Y_k) = \ell_i \sum \ell_k \quad i=1,2,\dots,p \quad (3.3)$$

The principal components are those uncorrelated linear combinations $Y_1, Y_2, \dots, Y_p$ whose variances in (3.2) are larger as possible.

The first principal component is the linear combination with the maximum variance i.e., it maximizes $\text{Var}(Y_1) = \ell_1 \sum \ell_1$. It is clear that $\text{Var}(Y_1) = \ell_1 \sum \ell_1$ can be increased by multiplying any ℓ_1 by some constant. To eliminate this indeterminacy, it is convenient to restrict attention to the coefficient vector of unit length.

The present study entitled as “Agro-morphological characterization of Oat (*Avena sativa* L.) accessions for forage yield and its contributing traits” was conducted in *Rabi* 2019-20. The main objective is to study the morphological characterization and genetic parameters for forage yield and its contributing traits of Oats as well as to estimate the genetic diversity and association analysis. Correlation and path coefficient analysis was used to estimate the contribution traits for green forage production. Genetic variability and genetic diversity was estimated to find out the variation present among the genotypes and difference among the traits studied for these genotypes.

The experiment was conducted at Research cum Instructional Farm, IGKV, Raipur. Investigation was presented in 130 Oat germplasm accessions including 5 checks in augmented design in five blocks. Total 32 traits were studied of biometric and non-biometric traits. The data were recorded according to the descriptor- Indian grassland and Fodder Research Institute, Jhansi, India. (Roy *et al.*, 2017) under the following subheads:

- 4.1 Characterization of oat germplasm accessions for forage yield and its contributing traits.
- 4.2 Estimation of genetic parameter for forage yield and its contributing traits.
- 4.3 Estimation of association analysis.
- 4.4 Genetic diversity for forage yield and its contributing traits.

4.1 Characterization of oat germplasm accessions for forage yield and its contributing traits

The data were recorded for non-biometric character is presented in Table 4.1. Total 130 germplasm accessions of Oat (*Avena sativa* L.) were observed for 13 qualitative traits. The result is presented below:

4.1.1 Early plant vigour, growth habit and leaf colour

Early plant vigour was classified into three classes *i.e.*, poor, good and very good. Out of 130 genotypes 66 were fell under poor, 48 under good and 16 under very good.

Growth habit had divided into four classes *i.e.*, erect, semi prostrate, prostrate and others. Ninety one genotypes were fell under erect, 36 under semi prostrate, 3 under prostrate and none of the genotypes were fell under other than these classes.

Leaf colour was classified into three categories *i.e.*, green, dark green and others. Fifteen genotypes were fell under green and 115 were under dark green. No any genotypes were fell in other categories.

So, out of 130 genotypes studied more number of genotypes were found poor in early plant vigour, erect in nature and dark green leaf. Frequency percentage was found highest for these classes.

4.1.2 Leaf sheath pubescence and flag leaf attitude

Leaf sheath pubescence was classified into two classes as presence and absence of pubescence on the basis of presence of hairs on the leaf sheath. Except one genotype all the genotypes studied had leaf sheath pubescence present.

Flag leaf attitude was grouped into three classes – erect, drooping and semi drooping. Three genotypes were found erect, 104 were drooping and 23 were semi drooping in nature.

So, most of the genotypes studied had leaf sheath pubescence present and flag leaf was drooping in nature. Frequency percentage was high for these classes.

4.1.3 Panicle attitude, awn per spikelet and seed colour

The trait panicle attitude is classified into five classes – compact, semi-compact, lateral, equilateral and others. All the genotypes studied were fell under only two categories *i.e.*, lateral and equilateral. Twelve genotypes had lateral panicle and 118 had equilateral panicle. Arora (2013) also found that most of genotypes he studied had equilateral panicle.

Awn per spikelet was grouped into three classes – absent, one and two. Two genotypes had awn absent, 126 genotypes had one awn and 2 genotypes had 2 awns.

Seed colour was classified into five classes – white, yellow, grey, black and others. One twenty nine genotypes had yellow seed colour and 1 genotype had black seed colour.

In all the genotypes studied most of the genotypes had equilateral panicle, one awn and yellow in seed colour. So, the frequency percentage was highest for these classes.

Traits namely, stem solidness, primary floret pubescence, spikelet shattering, hullness and biotic stress susceptibility were fell under single class *i.e.*, stem solidness was found as hollow, all accessions had primary floret pubescence presence, non-shattering type of spikelet, hullness present and all were exhibited as very low biotic stress susceptibility.

Table 4.1 Non-biometric agro-morphological characters for different germplasm accessions.

S.N.	CHARACTERISTICS	CLASS	SYMBOLS	NO. OF GENOTYPES RECORDED IN CLASS	FREQUENCY PERCENTAGE (%)
1.	Early plant vigour	Poor Good Very Good	1 2 3	66 48 16	50.76 36.92 12.3
2.	Growth habit	Erect Semi Prostrate Prostrate Others (specify)	1 2 3 9	91 36 3 0	70 27.69 2.3 0
3.	Leaf colour	Green Dark Green Others (specify)	1 2 9	15 115 0	11.54 88.46 0
4.	Leaf sheath pubescence	Absent Present	0 1	1 129	0.76 99.23
5.	Flag leaf attitude	Erect Drooping Semi-drooping	1 2 9	3 104 23	2.3 80 17.69
6.	Stem solidness	Hollow Semi solid Solid	1 2 3	130 0 0	100 0 0

7.	Panicle attitude	Compact	1	0	0
		Semi-compact	2	0	0
		Lateral	3	12	9.23
		Equilateral	4	118	90.77
		Others (specify)	9	0	0
8.	Awn per spikelet	Absent	0	2	1.54
		One	1	126	96.92
		Two	2	2	1.54
9.	Primary floret pubescence	Absent	0	0	0
		Present	1	130	100
10.	Spikelet shattering	Shattering	1	0	0
		Non-shattering	2	130	100
11.	Hullness	Absent	0	0	0
		Present	1	130	100
12.	Seed colour	White	1	0	0
		Yellow	2	129	99.23
		Grey	3	0	0
		Black	4	1	0.76
		Others (specify)	9	0	0
13.	Biotic stress susceptibility	Very low	1	130	100
		Low	3	0	0
		Intermediate	5	0	0
		High	7	0	0
		Very High	9	0	0

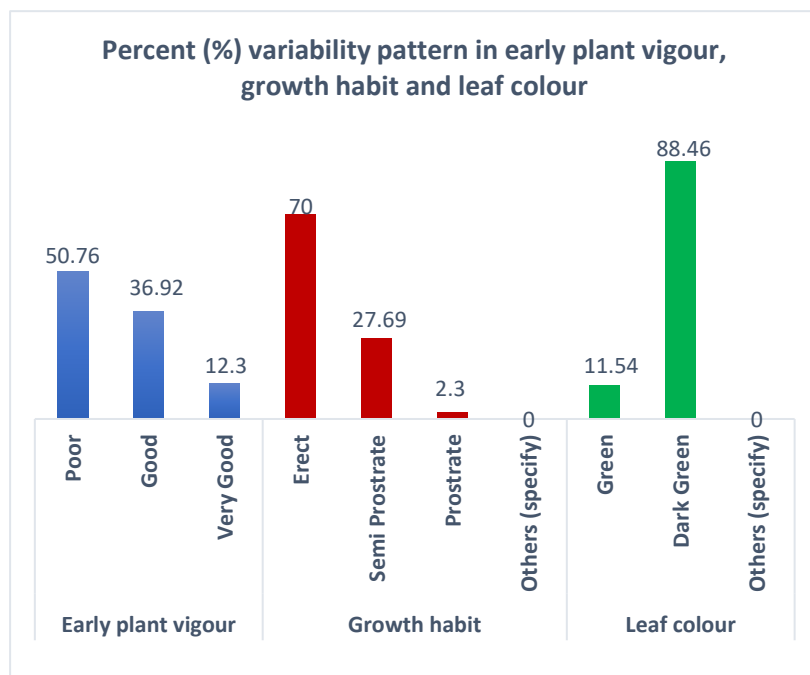


Fig 4.1.1

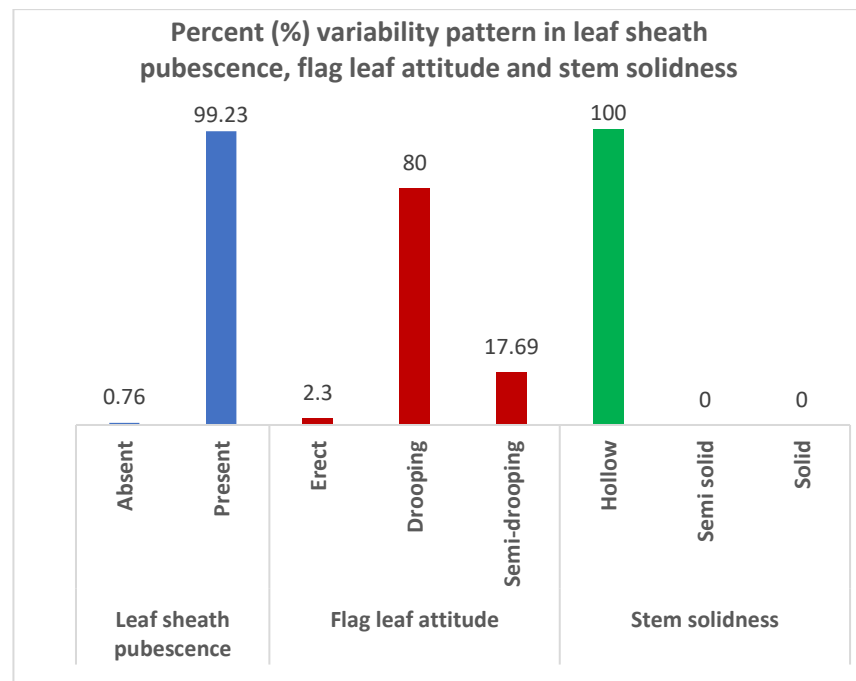


Fig 4.1.2

Fig. 4.1 Percent (%) variability pattern in non-biometric traits for different genotypes

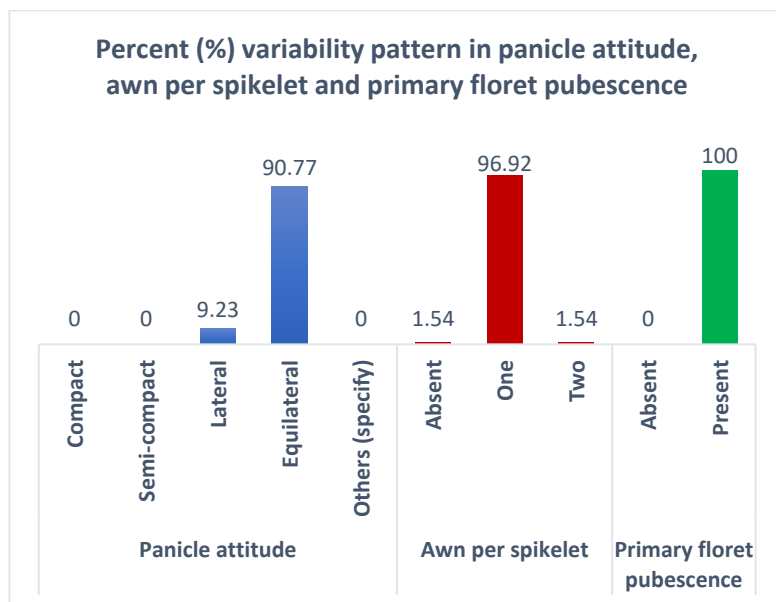


Fig 4.1.3

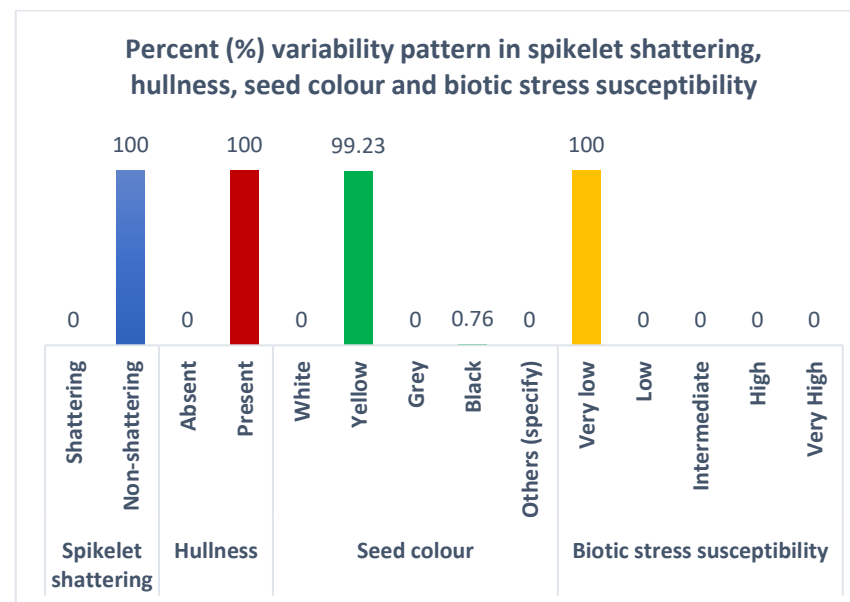


Fig 4.1.4

Fig. 4.1. Percent (%) variability pattern in non-biometric traits for different genotypes



Erect



Semi-prostrate



Prostrate

PLATE-(I)



Erect



Semi- drooping



Drooping

PLATE- (II)



Lateral



Equilateral

PLATE- (III)



Yellow seed



Black seed

PLATE- (IV)

PLATE (I) : Variation in growth habit

PLATE (II) : Variation in flag leaf attitude

PLATE (III) : Variation in panicle attitude

PLATE (IV) : Variation in seed colour

Fig 4.2. Variation present in different germplasm accessions for non-biometric traits

4.2 Estimation of genetic parameter for forage yield and its contributing traits

Genetic variability, heritability, and genetic advance provides the genetic information of any genotype. The result obtained from the present investigation are presented under the following heads:

4.2.1 Analysis of variance

4.2.2 Assessment of variability

4.2.1 Analysis of variance

Analysis of variance was carried out for 19 characters. There is considerable amount of variability present among the genotype studied are presented in the Table 4.2. Analysis of variance revealed that most of trait studied were found significant at 0.1%, 1% and 5% level of significance. Trait 1000 seed weight was significant at 0.1% level of significance, days to 50% flowering and leaf: stem ratio were found highly significant at 1% level of significance and trait like plant height, number of leaves per plant, flag leaf width, leaf length, number of tillers per plant, green fodder yield, stem dry weight per plant and seed yield per plant were significant at 5% level of significance. The above investigation presented indicated a better opportunity for a breeder to select a genotype for these traits.

Range and mean performance of Oat germplasm

Range, mean performance, standard deviation, standard error and coefficient of variation of 130 genotype were observed for different characters are presented in Table 4.3. Performance of individual character is described as:

1. Days to 50% flowering

Genotypes had a range of 67.24 days to 93.20 days with mean of 73.50 days. S. D. was observed as 4.20 and S.E. recorded for trait was 0.37 having 5.71 % of CV.

2. Plant height (cm)

Plant height ranged from 85.35 cm to 134.81 cm with mean of 107.73 cm. S.D. of this character recorded 9.33, S.E. was 0.82 and CV was observed 8.67 %.

3. Number of leaves per plant

No. of leaves lies between the range of 12.29 to 47.25. Mean of this trait was found as 27.82. S.D. was observed as 7.11 and S.E. was 0.62. CV recorded for this character was 25.58%.

4. Flag leaf length (cm)

Flag leaf length lies between the range of 18.94 cm to 36.66 cm. Mean of this trait was 30.22 cm. S.D. measured for this trait was 2.99 and S.E. was observed to be 0.26. Flag leaf length had 9.90 % of CV.

5. Flag leaf width (cm)

Range of flag leaf width was 1.52 cm to 2.42 cm having 1.95 cm mean. For flag leaf length S.D. was 0.19, S.E. was recorded 0.02 and 9.61% CV.

6. Leaf length (cm)

Range for leaf length was 31.29 cm to 64.91 cm with a mean of 46.89 cm. Leaf length exhibited 5.36 S.D. and 0.47 standard error. Per cent contribution for CV was 11.42 %.

7. Leaf width (cm)

Range was observed for the leaf width is 1.48 cm to 2.26 cm. Mean of leaf width was recorded as 1.82 cm. S.D. of leaf width was 0.15 and S.E. for this trait was 0.01 having 8.29 % of CV.

8. Culm diameter (cm)

It ranges from 5.14 cm to 7.38 cm with 6.13 cm mean. Value of S.D. was 0.46 for culm diameter and S.E. was recorded as 0.04. CV for culm diameter was recorded as 7.49 %.

9. Number of nodes on the main culm

Genotype have range of 2.92 to 6.52 for no. of nodes and had a mean of 4.91. This trait had 0.54 S.D. and 0.05 S.E., CV for this trait was recorded as 11.01%.

10. Number of tillers per plant

Number of tillers exhibited range of 2.43 to 11.35 with a mean of 5.95. S.D. observed for no. of tillers was 1.55 and S.E. was 0.14. CV was recorded to be 26.07 %.

11. Peduncle length (cm)

Range for peduncle length varies from 26.92 to 40.86 cm with a mean of 33.64 cm. S.D. recorded for this trait was 2.57 and S.E. was 0.23. CV was observed 7.64 %.

12. Green fodder yield (g)

Green fodder yield exhibited between the range of 27.10 g to 145.90 g with mean 96.31 g. S.D. observed for this trait was 22.47. It had 1.97 standard error and 23.33% of CV.

13. Dry matter yield per plant (g)

Range was observed to be 13.6 g to 40.20 g and have 26.41 g of mean. S.D. recorded for dry matter yield was 5.47 and S.E. was 0.48. CV was observed 20.73 %.

14. Leaf dry weight per plant (g)

Leaf dry weight ranged from 3.45 g to 13.85 g having a mean of 8.17 g. Value of S.D. was 1.80 and S.E. was 0.16. Leaf dry weight recorded 22.06 % of CV.

15. Stem dry weight per plant (g)

Stem dry weight recorded range from 8.69 g to 30.49 g with mean of 18.21 g. It had 4.46 S.D. and S.E. was 0.39. CV recorded for stem dry weight was 24.50 %.

16. Leaf: Stem ratio

Leaf: stem ratio ranged from 0.21 to 1.06 having mean of 0.46. S.D. was observed as 0.13 and S.E. was 0.01 for trait leaf: stem ratio. 28.35 % of CV was recorded.

17. Days to maturity

Ranges varies from 97.88 days to 120.08 days for maturity of genotypes. Mean of days to maturity recorded was 109.05 days. S.D. was observed 2.70 and S.E. was 0.24. CV of days to maturity was 2.47 %.

18. Seed yield per plant (g)

Seed yield ranged from 7.00 to 34.78 g and mean was 19.08 g. S.D. recorded for this trait was 5.53 and S.E. was 0.49. CV for seed yield was 28.99 %.

19. 1000 seed weight (g)

1000 seed weight ranged from 14.52 g to 54.72 g with a mean of 36.77 g. S.D. of this trait was recorded as 7.05 and S.E. was 0.62. CV was observed 19.17 %.

The result observed for mean performance showed that efficient amount of variability present among different genotypes. High CV was observed for seed yield per plant (g) (28.99 %), followed by leaf: stem ratio (28.35 %), number of tillers per plant (26.07 %), number of leaves per plant (25.56 %), stem dry weight per plant (g) (24.45 %), green fodder yield (g) (23.33 %), leaf dry weight per plant (g) (22.06 %) and dry matter yield per plant (g) (20.73 %). These findings are in harmony with

Ilias and Costas (2010) who also found high CV in plant height and number of leaves per plant, number of tillers per plant.

4.2.2 Assessment of variability

Phenotypic and genotypic coefficient of variation, heritability, genetic advance, skewness and kurtosis are commonly used parameters for assessment of variability. Assessment of all these parameters are represented in Table 4.4.

4.2.2.1 Genotypic and phenotypic coefficient of variation (GCV & PCV)

Value of genotypic coefficient of variation and phenotypic coefficient of variation indicate the influence of environment on the character studied. When phenotypic coefficient of variation is higher than genotypic coefficient of variation indicates the presence of environmental influence on character studied for study material. Krishna *et al.*, 2014 categorized genotypic and phenotypic coefficient of variation as low (<10%), moderate (10 to 20%) and high (>20%).

Highest GCV (21.96 %) was observed for leaf: stem ratio and seed yield per plant (20.78 %). Highest PCV (32.54 %) was recorded for trait green fodder yield followed by seed yield per plant (28.6 %), number of leaves per plant (27.17 %), leaf: stem ratio (26.82%), number of tillers per plant (25.77 %), leaf dry weight per plant (25.65 %), stem dry weight per plant (24.43 %) and dry matter yield per plant (22.66%).

Moderate GCV was recorded for 1000 seed weight (16.37 %), followed by green fodder yield (16.05 %) and (11.33 %) for leaf dry weight per plant. Moderate PCV was recorded for 1000 seed weight (17.37 %), leaf length (11.78 %) and number of nodes on the main culm (11.64 %)

The lowest value of GCV was recorded for culm diameter (-4.21 %) which was followed by dry matter yield (1.35 %), flag leaf width (1.49 %) and days to maturity (1.64 %). Lowest value for PCV was observed for days to maturity (2.44 %), followed by days to 50% flowering (4.90 %), culm diameter (7.72 %) and for peduncle length was (7.82 %).

Data presented in Table 4.4 revealed that phenotypic coefficient of variance were relatively higher than the genotypic coefficient of variation for all the character studied which indicate that variation present in the observation are influenced by environment also.

Leaf: stem ratio and seed yield per plant had high GCV and PCV values indicates the sufficient amount of variation. So, by selecting these traits would provide a good scope for crop improvement. Chakraborty *et al.*, 2014 and Surje and De, 2014 also found high GCV and PCV for seed yield per plant.

4.2.2.2 Heritability

Heritability is the degree of phenotypic variation present in a population due to genotypic variation among the genotype in that population. It indicates the percentage of transfer of character from one generation to another. Broad sense heritability exhibit the predominance of additive gene effect for the expression of any character.

According to Johnson *et al.*, 1955 broad sense heritability can be categorized as high (>60%), moderate (40-60%) and low (<40%). The investigation for heritability presented in the Table 4.4.

High heritability found in the character 1000 seed weight as (88.81%) and leaf: stem ratio (67.04%). This gives the indication of less influence of environment on the expression of this trait. Moderate heritability was recorded for trait leaf length (54.13%), seed yield per plant (52.78%), plant height (46.38%), days to maturity (45.42%) and days to 50% flowering (42.57%). Lowest heritability was found in culm diameter (-29.78%) followed by dry matter yield per plant (0.35%) and no. of leaves per plant (1.97%).

4.2.2.3 Genetic advance

Genetic advance is classified in 3 categories *i.e.* high (>20%), moderate (10-20%) and low (<10%) suggested by Johnson *et al.*, 1955.

High genetic advance was observed for leaf: stem ratio (37.04%), followed by 1000 seed weight (31.77%) and seed yield (31.1%). Moderate genetic advance found

in green fodder yield (16.30%), followed by leaf length (13.13%) and leaf dry weight (10.30%). Low genetic advance found in culm diameter (-4.73%), which was followed by dry matter yield (0.17%) and flag leaf width (0.52%).

The above result is closely related with the findings of Mall *et al.*, (2005), Krishna *et al.*, (2013), Chakraborty *et al.*, (2014), Surje and De (2014) and Rawat *et al.*, (2019).

High heritability combined with high genetic advance is the indication of additive gene action and selection based on this would be more effective. High heritability and high genetic advance was found in 1000 seed weight and leaf: stem ratio. This finding is relevant with the results of Krishna *et al.*, (2013) and Rawat *et al.*, (2019).

4.2.2.4 Skewness and Kurtosis

Skewness and kurtosis indicates relative mean performance and nature of distribution of traits. Skewness represent the asymmetry of a data distributed in normal distribution curve. It is a distortion of symmetry. If value ranges from -0.5 to 0.5 then the data is normally distributed *i.e.*, symmetrical. Kurtosis indicates the peakness or flatness of a tail of a curve. If the value is near 0 then the data is normally distributed. Kurtosis < 0 indicates the flatness of the curve *i.e.*, platykurtic and if it is > 0 then it indicates the peakness of a curve *i.e.*, leptokurtic (Kanavi *et al.*, 2020).

Skewness and kurtosis indicates the nature of gene action and number of genes controlling any trait. Positive skewness shows dominant and complementary gene action where negative skewness is associated with dominant and duplicate gene action (Pooni *et al.*, 1977). Leptokurtic (positive kurtosis) indicates that traits are governed by fewer number of genes and platykurtic (negative kurtosis) shows that traits are governed by large number of genes (Kapur *et al.*, 1981).

Most of the traits studied had skewness value ranged from (-0.5 to 0.5) are normally distributed except traits days to 50% flowering (1.5565), leaf : stem ratio (1.1931), leaf dry weight per plant (0.7823) and number of tillers per plant (0.5405) showed positive skewness means they shows dominant and complementary gene

action and flag leaf length (-0.5091) showed negative skewness *i.e.*, it exhibited dominant and duplicate gene action.

Plant height (cm) (-0.0981), flag leaf width (cm) (-0.0705), culm diameter (cm) (-0.1227), dry matter yield per plant (g) (-0.3133), stem dry weight per plant (g) (-0.2070) and seed yield per plant (g) (-0.3149) exhibited negative kurtosis (platykurtic) indicates traits are controlled by large number of genes and rest of the traits showed positive kurtosis (leptokurtic) are governed by small number of genes.

Savitha and Kumari (2015) observed platykurtic and left skewed distribution for days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, hundred grain weight and single plant yield in rice. Kanavi *et al.*, (2020) reported all the quantitative traits studied in germplasm accessions exhibited skewness values between -0.5 and 0.5 except for the traits leaf water potential (0.69) and seed yield per plant (0.66) indicating normal distribution for these traits in the population in green gram. Neelima *et al.*, (2020) found days to silking, tassel length, the number of tassel branches, leaf length, leaf breadth, cob length, the number of kernels per row, cob weight, 100 kernel weight and single plant yield had positive skewness and platykurtic nature in maize.

Table 4.2 Analysis of variance for green fodder yield and its attributing traits in Oat (*Avena sativa* L.)

Mean sum of square (MSS)											
Source of variation	Degree of freedom	Days to 50% flowering	Plant height	No. of leaves/ plant	Flag leaf length	Flag leaf width	Leaf length	Leaf width	Culm diameter	No. of nodes/ plant	No. of tillers/ plant
Block	4	30.657	1644.311	521.406	48.747	0.082	174.731	0.198	0.612	2.342	18.257
Treatment	129	28.022**	80.519*	48.155*	9.164	0.031*	28.709*	0.024	0.207	0.298	2.232*
Checks	4	354.740	118.758	153.829	26.073	0.097	33.289	0.060	0.185	0.884	7.534
Error	16	7.415	63.794	55.797	7.595	0.029	13.973	0.022	0.291	0.238	2.121
Mean sum of square (MSS)											
Source of variation	Degree of freedom	Peduncle length	Green fodder yield/ plant	Dry matter yield/ plant	Leaf dry weight/ plant	Stem dry weight/ plant	Leaf: stem ratio	Days to maturity	Seed yield/ plant	1000 seed weight	
Block	4	53.706	24165.020	346.118	51.097	141.464	0.043	53.727	201.953	309.327	
Treatment	129	6.077	479.290*	31.453	3.438	18.774*	0.015**	7.708	34.739*	51.047***	
Checks	4	6.104	1599.926	155.780	14.590	72.430	0.010	43.660	289.602	372.060	
Error	16	5.369	741.201	35.689	3.529	19.034	0.005	3.861	14.075	4.610	

*** Significant at 0.1% probability level, ** Significant at 1% probability level, * Significant at 5% probability level

Table 4.3 Genetic variability parameters for forage yield and its contributing traits in Oat (*Avena sativa* L.)

S.N.	Character	Maximum	Minimum	Grand mean	S.D.	S.E.	CV (%)
1	DT50%F	93.20	67.24	73.50	4.20	0.37	5.71
2	PH	134.81	85.35	107.73	9.33	0.82	8.67
3	NOL	47.25	12.29	27.82	7.11	0.62	25.58
4	FLL	36.66	18.94	30.22	2.99	0.26	9.90
5	FLW	2.42	1.52	1.95	0.19	0.02	9.61
6	LL	64.91	31.29	46.89	5.36	0.47	11.42
7	LW	2.26	1.48	1.82	0.15	0.01	8.29
8	CD	7.38	5.14	6.13	0.46	0.04	7.49
9	NON	6.52	2.92	4.91	0.54	0.05	11.01
10	NOT	11.35	2.43	5.95	1.55	0.14	26.07
11	PL	40.86	26.92	33.64	2.57	0.23	7.64
12	GFY	145.90	27.10	96.31	22.47	1.97	23.33
13	DMY	40.20	13.60	26.41	5.47	0.48	20.73
14	LDW	13.85	3.45	8.17	1.80	0.16	22.06
15	SDW	30.49	8.69	18.21	4.46	0.39	24.50
16	L: S	1.06	0.21	0.46	0.13	0.01	28.35
17	DTM	120.08	97.88	109.05	2.70	0.24	2.47
18	SY	34.78	7.00	19.08	5.53	0.49	28.99
19	1000 SW	54.72	14.52	36.77	7.05	0.62	19.17

DT50%F = Days to 50% flowering

FLW (cm) = Flag leaf width

NON = No. of nodes on the main culm

DMY (g) = Dry matter yield per plant

DTM = Days to maturity

PH (cm) = Plant height

LL (cm) = Leaf length

NOT = No. of tillers per plant

LDW (g) = Leaf dry weight per plant

SY (g) = Seed yield per plant

NOL = No. of leaves per plant

LW (cm) = Leaf width

PL (cm) = Peduncle length

SDW (g) = Stem dry weight per plant

1000 SW (g) = 1000 seed weight

FLL (cm) = Flag leaf length

CD (cm) = Culm diameter

GFY (g) = Green fodder yield

L:S = leaf: stem ratio

Table 4.4 Variability parameters for Oat (*Avena sativa* L.)

S.N.	Character	PCV (%)	GCV (%)	H ² (bs) %	GA	GA (as % of mean)	Kurtosis	Skewness
1	DT50%F	4.90	3.20	42.57	3.15	4.30	4.9270 ***	1.5565 ***
2	PH	10.13	6.90	46.38	10.42	9.68	-0.0981	0.3195
3	NOL	27.17	3.82	1.97	0.31	1.11	0.2220	0.1182
4	FLL	10.21	4.61	20.42	1.30	4.30	0.8760 *	-0.5091 *
5	FLW	8.87	1.49	2.83	0.01	0.52	-0.0705	0.2601
6	LL	11.78	8.66	54.13	6.15	13.13	0.7641	-0.0067
7	LW	8.95	3.87	18.68	0.06	3.45	0.1256	0.3338
8	CD	7.72	-4.21	-29.78	-0.29	-4.73	-0.1227	0.1846
9	NON	11.64	6.05	27.01	0.32	6.48	0.9199 *	-0.2796
10	NOT	25.77	7.98	9.59	0.30	5.09	1.2819 **	0.5405 *
11	PL	7.82	3.72	22.64	1.23	3.65	0.5177	0.0913
12	GFY	32.54	16.05	24.32	15.68	16.30	0.4788	-0.4585 *
13	DMY	22.66	1.35	0.35	0.04	0.17	-0.3133	0.0022
14	LDW	25.65	11.33	19.51	0.84	10.31	1.2165 **	0.7823 ***
15	SDW	24.43	4.76	3.80	0.35	1.91	-0.2070	0.0055
16	L: S	26.82	21.96	67.04	0.17	37.04	3.3157 ***	1.1931 ***
17	DTM	2.44	1.64	45.42	2.49	2.28	3.8678 ***	0.3631
18	SY	28.60	20.78	52.78	5.94	31.10	-0.3149	0.1239
19	1000 SW	17.37	16.37	88.81	11.74	31.77	0.7646	-0.1270

DT50%F = Days to 50% flowering

FLW (cm) = Flag leaf width

NON = No. of nodes on the main culm

DMY (g) = Dry matter yield per plant

DTM = Days to maturity

PH (cm) = Plant height

LL (cm) = Leaf length

NOT = No. of tillers per plant

LDW (g) = Leaf dry weight per plant

SY (g) = Seed yield per plant

NOL = No. of leaves per plant

LW (cm) = Leaf width

PL (cm) = Peduncle length

SDW (g) = Stem dry weight per plant

1000 SW (g) = 1000 seed weight

FLL (cm) = Flag leaf length

CD (cm) = Culm diameter

GFY (g) = Green fodder yield

L:S = leaf: stem ratio

4.3 Estimation of association analysis

4.3.1 Estimation of coefficient of correlation

Relationship between different variables is represented by coefficient of correlation. It is used to indicate the character on which selection can be based for further breeding programme.

Coefficient of correlation were worked out in various combination of characters in Table 4.5 for green fodder yield.

Days to 50% flowering had significant positive correlation with trait days to maturity (0.279), leaf width (0.230), leaf: stem ratio (0.215), leaf length (0.185) and culm diameter (0.165) whereas negative significant correlation coefficient exhibited by seed yield per plant (-0.396).

Plant height exhibited significant positive correlation with flag leaf length (0.350) which was followed by leaf length (0.330), number of nodes on the main culm (0.286), seed yield per plant (0.250), flag leaf width (0.179) and peduncle length (0.161).

Positive significant correlation of number of leaves per plant was exhibited by number of tillers per plant (0.787) and negative significant correlation with leaf length (-0.224) followed by leaf dry weight per plant (-0.209) and culm diameter (-0.187).

Flag leaf length had significant positive correlation with trait plant height (0.350) followed by culm diameter (0.296), flag leaf width (0.293), 1000 seed weight (0.224), leaf length (0.205) and number of nodes on the main culm (0.166).

Positive significant correlation of flag leaf width is exhibited by culm diameter (0.296), flag leaf length (0.293), leaf width (0.201), leaf length (0.185) and plant height (0.179).

Leaf length had positive significant correlation with leaf width (0.359), plant height (0.330), flag leaf length (0.205), culm diameter (0.186), flag leaf width and days to 50% flowering (0.185) and no. of nodes on the main culm (0.170). Negative

correlation is associated with traits, number of leaves per plant (-0.224) and no. of tillers per plant (-0.167).

Leaf width exhibited positive significant correlation with leaf length (0.359), days to 50% flowering (0.230), days to maturity (0.219) and flag leaf width (0.201) whereas negative significant correlation exhibited by seed yield per plant (-0.173).

Culm diameter had positive correlation with flag leaf length and flag leaf width (0.296), leaf length (0.186) and days to 50% flowering (0.165) whereas significant negative correlation is associated with number of leaves per plant and number of tillers per plant as (-0.187) and (-0.186) respectively.

Number of nodes on the main culm exhibited positive significant correlation with plant height (0.286), leaf length (0.170) and flag leaf length (0.166).

Number of tillers per plant had significant positive correlation with number of leaves per plant (0.787) and seed yield per plant (0.195) whereas negative significant correlation is associated with leaf dry weight per plant (-0.288), dry matter yield (-0.249), culm diameter (-0.186), stem dry weight per plant (-0.180) and leaf length (-0.167).

Peduncle length exhibited positive significant correlation with seed yield per plant (0.199) and plant height (0.161) whereas days to maturity (-0.254) and leaf: stem ratio (-0.187) showed negative significant correlation.

Dry matter yield per plant laid positive significant correlation with stem dry weight per plant (0.897) and leaf dry weight per plant (0.732) whereas negative significant correlation with number of tillers per plant (-0.249) and leaf: stem ratio (-0.165).

Leaf dry weight per plant had positive significant correlation with dry matter yield (0.732), stem dry weight per plant (0.513) and leaf: stem ratio (0.465) whereas negative significant correlation is exhibited by number of tillers per plant (-0.288), 1000 seed weight (-0.211), number of leaves per plant (-0.209) and seed yield per plant (-0.188).

Stem dry weight per plant exhibited significant positive correlation with dry matter yield (0.897) and leaf dry weight per plant (0.513). Negative significant correlation shown by leaf stem: ratio (-0.487) and number of tillers per plant (-0.180).

Leaf: stem ratio had positive significant correlation with leaf dry weight per plant (0.465) and days to maturity (0.215) while negative significant correlation exhibited by stem dry weight per plant (-0.487), peduncle length and seed yield (-0.187) and dry matter yield (-0.165).

Significant positive correlation for days to maturity exhibited by trait days to 50% flowering (0.279) and leaf width (0.219) whereas negative significant correlation exhibited by peduncle length (-0.254), 1000 seed weight (-0.218) and seed yield (-0.212).

Seed yield displayed significant positive correlation with plant height (0.250), 1000 seed weight (0.214), peduncle length (0.199) and number of tillers per plant (0.195). Negative correlation showed days to 50% flowering (-0.396), days to maturity (-0.212), leaf dry weight per plant (-0.188), leaf: stem ratio (-0.187) and leaf width (-0.173).

1000 seed weight showed significant positive correlation by flag leaf length (0.224) and seed yield (0.214) whereas negative significant correlation shown by days to 50% flowering (-0.288), days to maturity (-0.218) and leaf dry weight (-0.211).

As green fodder yield taken as dependent characters the study of relation of green fodder yield with other characters is very important. Green fodder yield found positive significant correlation with leaf dry weight per plant (0.506) which was followed by dry matter yield per plant (0.479), stem dry weight per plant (0.392), leaf width (0.262), culm diameter (0.227**) and days to maturity (0.224*) indicating that selection of these traits will lead to rapid progress of production of green fodder yield. Negative significant correlation with number of tillers per plant (-0.376) followed by number of leaves per plant (-0.320) and plant height (-0.229).

In investigation presented green fodder yield showed positive but non-significant correlation with leaf: stem ratio (0.100) followed by days to 50% flowering (0.065) and leaf length (0.058) whereas negative non-significant correlation with number of nodes on the main culm (-0.162) and flag leaf length (-0.061).

From the above result it was concluded that selection for traits like leaf dry weight per plant, dry matter yield per plant, stem dry weight per plant and leaf width will be helpful in new variety development for high green fodder yield as they are significantly positive correlated with green fodder.

These above results obtained are in harmony with the research findings of Nehvi *et al.*, (2000) and Bibi *et al.*, (2012) who found positive correlation of green fodder yield with stem dry weight per plant and dry matter yield respectively.

Table 4.5 Correlation analysis for green forage yield and its attributing traits in oat (*Avena sativa* L.)

	PH	NOL	FLL	FLW	LL	LW	CD	NON	NOT	PL	DMY	LDW	SDW	L:S	DTM	SY	1000SW	GFY
DT50 %F	-0.112	0.047	0.019	0.102	0.185*	0.230*	0.165*	0.079	0.015	-0.153	-0.074	0.086	-0.148	0.215**	0.279***	-0.396***	-0.288	0.065
PH	1	-0.090	0.350***	0.179*	0.330***	0.073	0.152	0.286***	-0.034	0.161*	0.028	-0.046	0.092	-0.149	-0.084	0.250**	0.145	-0.229**
NOL		1	-0.072	-0.029	-0.224**	-0.055	-0.187*	-0.158	0.787***	0.022	-0.147	-0.209*	-0.105	-0.114	0.017	0.107	0.087	-0.320**
FLL			1	0.293***	0.205*	0.006	0.296***	0.166*	0.0145	0.062	-0.148	-0.143	-0.087	-0.050	0.014	0.091	0.224*	-0.061
FLW				1	0.185*	0.201*	0.296***	0.054	0.017	-0.022	-0.055	-0.003	-0.032	0.005	0.133	0.026	-0.032	0.189*
LL					1	0.359***	0.186*	0.170*	-0.167*	0.079	-0.094	-0.029	-0.069	0.006	0.063	-0.046	0.060	0.058
LW						1	0.157	-0.100	-0.036	-0.105	0.013	0.097	-0.012	0.128	0.219**	-0.173*	-0.004	0.262*
CD							1	0.071	-0.186*	0.049	0.094	0.101	0.084	-0.008	0.111	-0.098	0.069	0.227**
NON								1	-0.077	0.062	0.048	0.042	0.032	0.017	-0.120	0.050	0.027	-0.162
NOT									1	-0.008	-0.249**	-0.288***	-0.180*	-0.106	-0.047	0.195*	0.103	-0.376**
PL										1	0.055	-0.086	0.103	-0.187*	-0.254**	0.199*	0.050	-0.209*
DMY											1	0.732***	0.897*	-0.165*	0.069	-0.023	-0.079	0.479**
LDW												1	0.513***	0.465***	0.138	-0.188*	-0.211**	0.506**
SDW													1	-0.487***	0.010	0.044	-0.012	0.392**
L:S														1	0.157	-0.187*	-0.1550	0.100
DTM															1	-0.212**	-0.218**	0.224*
SY																1	0.214**	-0.239**
1000SW																	1	-0.188*

DT50%F = Days to 50% flowering

FLW (cm) = Flag leaf width

NON = No. of nodes on the main culm

DMY (g) = Dry matter yield per plant

DTM = Days to maturity

PH (cm) = Plant height

LL (cm) = Leaf length

NOT = No. of tillers per plant

LDW (g) = Leaf dry weight per plant

SY (g) = Seed yield per plant

NOL = No. of leaves per plant

LW (cm) = Leaf width

PL (cm) = Peduncle length

SDW (g) = Stem dry weight per plant

1000 SW (g) = 1000 seed weight

FLL (cm) = Flag leaf length

CD (cm) = Culm diameter

GFY (g) = Green fodder yield

L:S = leaf: stem ratio

4.3.2 Estimation of path coefficient analysis

Path coefficient analysis estimates the direct and indirect effect of independent variable on dependent variable. This provides an idea about the direct selection of a trait which directly affect the dependent trait for their yield production.

In the investigation presented in Table 4.6 green fodder yield was taken as dependent character in which maximum positive direct effect shown by dry matter yield (0.273) was followed by leaf dry weight per plant (0.193), flag leaf width (0.170), leaf width (0.158), culm diameter (0.111), leaf length (0.065), flag leaf length (0.059), stem dry weight per plant (0.028) and days to maturity (0.024). So, selecting directly these traits will be effective for green fodder production. Green fodder yield was negative but directly associated with plant height (-0.275), number of leaves per plant (-0.166), peduncle length (-0.153), number of nodes on the main culm (-0.134), 1000 seed weight (-0.120), days to 50% flowering (-0.093), number of tillers per plant (-0.087), leaf: stem ratio (-0.054) and seed yield per plant (-0.043) indicating that increase in the yield of these traits will decrease the yield of green fodder. So, special attention should be given during selecting these traits.

Direct and indirect effect shown by yield attributing traits of green fodder yield:

Days to 50% flowering

Days to 50% flowering showed positive and indirect effect with plant height (0.010), peduncle length (0.014), dry matter yield per plant (0.007), stem dry weight per plant (0.014), seed yield per plant (0.037) and 1000 seed weight (0.027) while negative indirect effect with number of leaves per plant (-0.004), flag leaf length (-0.002), flag leaf width (-0.010), leaf length (-0.017), leaf width (-0.021), culm diameter (-0.015), number of nodes on the main culm (-0.007), number of tillers per plant (-0.001), leaf dry weight per plant (-0.008), leaf: stem ratio (-0.020) and days to maturity (-0.026). Positive correlation was showed for days to 50% flowering with green fodder yield (0.065).

Plant height (cm)

Plant height had positive indirect effect with the trait days to 50% flowering (0.031), number of leaves per plant (0.025), number of tillers per plant (0.009), leaf

dry weight per plant (0.013), leaf: stem ratio (0.041) and days to maturity (0.023) whereas negative indirect effect showed by flag leaf length (-0.096), flag leaf width (-0.049), leaf length (-0.091), leaf width (-0.020), culm diameter (-0.042), number of nodes on the main culm (-0.079), peduncle length (-0.044), dry matter yield per plant (-0.008), stem dry weight per plant (-0.025), seed yield per plant (-0.069) and 1000 seed weight (-0.040). Plant height had significant negative correlation with green fodder yield (-0.229) this is due to the negative indirect effect of plant height with other traits.

Number of leaves per plant

Number of leaves per plant showed positive indirect effect with plant height (0.015), flag leaf length (0.012), flag leaf width (0.005), leaf length and leaf width (0.037), culm diameter (0.031), number of nodes on the main culm (0.026), dry matter yield per plant (0.024), leaf dry weight per plant (0.035), stem dry weight per plant (0.017), leaf: stem ratio (0.019) and 1000 seed weight (0.015). Negative indirect effect with days to 50% flowering (-0.008), number of tillers per plant (-0.131), peduncle length (-0.004), days to maturity (-0.003) and seed yield per plant (-0.018). It showed negative significant correlation with green fodder yield (-320).

Flag leaf length (cm)

It showed positive indirect effect with days to 50% flowering (0.001), plant height (0.021), flag leaf width (0.017), leaf length and leaf width (0.012), culm diameter (0.018), number of nodes on the main culm (0.010), number of tillers per plant (0.001), peduncle length (0.004), days to maturity (0.001), seed yield per plant (0.005) and 1000 seed weight (0.013) whereas negative indirect effect exhibited by other traits. Flag leaf length showed negative correlation with green fodder yield (-0.061).

Flag leaf width (cm)

Flag leaf width had positive indirect effect with trait days to 50% flowering (0.017), plant height (0.031), flag leaf length (0.050), leaf length (0.032), leaf width (0.034), culm diameter (0.042), number of nodes on the main culm (0.009), number of tillers per plant (0.003), leaf: stem ratio (0.001), days to maturity (0.023) and seed yield per plant (0.004) while other characters showed negative indirect effect with

flag leaf width. It showed positive significant correlation with green fodder yield (0.189).

Leaf length (cm)

Leaf length showed positive indirect effect with days to 50% flowering (0.012), plant height (0.021), flag leaf length (0.013), flag leaf width (0.012), leaf width (0.023), culm diameter (0.012), number of nodes on the main culm (0.011), peduncle length (0.005), days to maturity and 1000 seed weight (0.004) while other traits showed negative indirect effect. It showed positive correlation with green fodder yield (0.057).

Leaf width (cm)

Leaf width showed positive indirect effect with days to 50% flowering (0.036), plant height (0.012), flag leaf length (0.001), flag leaf width (0.032), leaf length (0.057), culm diameter (0.025), dry matter yield per plant (0.002), leaf dry weight per plant (0.015), leaf: stem ratio 0.020) and days to maturity (0.035). Rest of the characters showed negative indirect effect with the leaf width. It had positive significant correlation with green fodder yield (0.262).

Culm diameter (cm)

It had negative indirect effect with number of leaves per plant and number of tillers per plant (-0.021), leaf: stem ratio (-0.001) and seed yield per plant (-0.011) while other characters showed positive direct effect. Culm diameter showed positive significant correlation with green fodder yield (0.277).

Number of nodes on the main culm

It showed positive indirect effect with number of leaves (0.021), leaf width (0.014), number of tillers per plant (0.010) and days to maturity (0.016) whereas other characters showed negative indirect with number of nodes on the main culm. It exhibited negative correlation with green fodder yield (-0.162).

Number of tillers per plant

Number of tillers per plant had negative indirect effect with days to 50% flowering and flag leaf length (-0.001), number of leaves per plant (-0.068), flag leaf

width (-0.002), seed yield per plant (-0.017) and 1000 seed weight (-0.009) while other characters showed negative indirect effect with number of tillers per plant. It showed negative significant correlation with green fodder field (-0.376).

Peduncle length (cm)

Peduncle length exhibited positive indirect effect with character days to 50% flowering (0.023), leaf width (0.016), number of tillers per plant (0.001), leaf dry weight per plant (0.013), leaf: stem ratio (0.029) and days to maturity (0.039) whereas rest of the other characters showed negative indirect effect. It showed negative significant correlation with (-0.209).

Dry matter yield per plant (g)

It exhibited positive indirect effect with leaf width (0.004), culm diameter (0.026), number of nodes on the main culm (0.013), peduncle length (0.015), leaf dry weight per plant (0.200), stem dry weight per plant (0.245) and days to maturity (0.019) whereas other character showed negative indirect effect. Dry matter yield per plant showed positive significant correlation with green fodder yield (0.479).

Leaf dry weight per plant (g)

Leaf dry weight per plant showed positive indirect effect with days to 50% flowering (0.017), leaf width and culm diameter (0.019), number of nodes on the main culm (0.008), dry matter yield per plant (0.141), stem dry weight per plant (0.099), leaf: stem ratio (0.090) and days to maturity (0.027) whereas rest of the characters showed negative indirect effect. It had positive significant correlation with green fodder yield (0.506).

Stem dry weight per plant (g)

Stem dry weight per plant exhibited positive indirect effect with plant height (0.003), culm diameter (0.002), number of nodes on the main culm (0.001), peduncle length (0.003), dry matter yield per plant (0.025), leaf dry weight per plant (0.014) and seed yield per plant (0.001) whereas other characters exhibited negative indirect effect with stem dry weight per plant. It showed positive significant correlation with green fodder yield (0.392).

Leaf: stem ratio

Leaf: stem ratio had negative indirect effect with days 50% flowering (-0.012), leaf width (-0.007), number of nodes on the main culm (-0.001), leaf dry weight per plant (-0.025) and days to maturity (-0.009) whereas other traits showed positive indirect with leaf: stem ratio. It had positive correlation with green fodder yield (0.100).

Days to maturity

Days to maturity showed negative indirect effect with plant height (-0.002), number of nodes on the main culm (-0.003), number of tillers per plant (-0.001), peduncle length (-0.006), seed yield and 1000 seed weight (-0.005) while other characters showed positive indirect effect. Days to maturity was positively significant correlated with green fodder yield (0.224).

Seed yield per plant (g)

Seed yield had positive indirect effect with days to 50% flowering (0.017), leaf length (0.002), leaf width (0.007), culm diameter (0.004), dry matter yield (0.001), leaf dry weight per plant and leaf: stem ratio (0.008), and days to maturity (0.009). Rest of the characters showed negative indirect effect. Seed yield per plant had negative significant correlation with green fodder yield (-0.239).

1000 seed weight (g)

Trait 1000 seed weight showed negative indirect effect with plant height (-0.017), flag leaf length (-0.027), leaf length (-0.007), culm diameter (-0.008), number of nodes on the main culm (-0.003), number of tillers per plant (-0.012), peduncle length (-0.006) and seed yield (-0.026) while other characters showed positive indirect with 1000 seed weight. 1000 seed weight had negative significant correlation with green fodder yield (-0.188).

Optimum number of tillers and leaves requires for high green fodder yield. So, here in our studies we observed significant negative correlation as well as negative direct effect of traits number of tillers per plant, number of leaves per plant, seed yield per plant, plant height, peduncle length and 1000 seed weight towards green fodder yield. Therefore, if the selection planned then optimum number of tillers and

number of leaves per plant and plant height should be considered. Low to medium 1000 seed weight may contribute for higher green fodder yield because source and sink distribution proportionate for high green forage and about all energy used for forage production purpose.

Leaf dry weight per plant followed by dry matter yield per plant, stem dry weight per plant, culm diameter and leaf width showed significant positive correlation as well as positive direct effect on dependent character green fodder yield indicating a true relationship among traits. Therefore, plant with high leaf dry weight, high dry matter yield, high stem dry weight and leaf width with increased culm thickness should be considered as selection criterion for enhancing the yield of green fodder in Oat.

This result was confirmed by Sangwan *et al.*, (2012) and Krishna *et al.*, (2014) who also found that dry matter yield showed positive direct effect and significant positive correlation with green fodder yield. Choubey *et al.*, (2001) and Ahmad *et al.*, (2013) found true relationship of leaf width with green fodder yield as it showed positive direct effect and significant positive correlation with green fodder yield.

Table 4.6 Path matrix for green forage yield in Oats (*Avena sativa* L.)

	DT50%F	PH	NOL	FLL	FLW	LL	LW	CD	NON	NOT	PL	DMY	LDW	SDW	L:S	DTM	SY	1000SW	R ² with GFY
DT50%F	-0.093	0.010	-0.004	-0.002	-0.010	-0.017	-0.021	-0.015	-0.007	-0.001	0.014	0.007	-0.008	0.014	-0.020	-0.026	0.037	0.027	0.065
PH	0.031	-0.275	0.025	-0.096	-0.049	-0.091	-0.020	-0.042	-0.079	0.009	-0.044	-0.008	0.013	-0.025	0.041	0.023	-0.069	-0.040	-0.229**
NOL	-0.008	0.015	-0.166	0.012	0.005	0.037	0.037	0.031	0.026	-0.131	-0.004	0.024	0.035	0.017	0.019	-0.003	-0.018	0.015	-0.320**
FLL	0.001	0.021	-0.004	0.059	0.017	0.012	0.012	0.018	0.010	0.001	0.004	-0.009	-0.009	-0.005	-0.003	0.001	0.005	0.013	-0.061
FLW	0.017	0.031	-0.005	0.050	0.170	0.032	0.034	0.042	0.009	0.003	-0.004	-0.009	-0.007	-0.006	0.001	0.023	0.004	-0.005	0.189*
LL	0.012	0.021	-0.015	0.013	0.012	0.065	0.023	0.012	0.011	-0.011	0.005	-0.006	-0.002	-0.005	0.000	0.004	-0.003	0.004	0.057
LW	0.036	0.012	-0.009	0.001	0.032	0.057	0.158	0.025	-0.016	-0.006	-0.017	0.002	0.015	-0.002	0.020	0.035	-0.027	-0.001	0.262**
CD	0.018	0.017	-0.021	0.033	0.027	0.021	0.017	0.111	0.008	-0.021	0.005	0.010	0.011	0.009	-0.001	0.012	-0.011	0.008	0.277**
NON	-0.011	-0.038	0.021	-0.022	-0.007	-0.023	0.014	-0.010	-0.134	0.010	-0.008	-0.007	-0.006	-0.004	-0.002	0.016	-0.007	-0.004	-0.162
NOT	-0.001	0.003	-0.068	-0.001	-0.002	0.014	0.003	0.016	0.007	-0.087	0.001	0.022	0.025	0.016	0.009	0.004	-0.017	-0.009	-0.376**
PL	0.023	-0.025	-0.003	-0.009	-0.003	-0.012	0.016	-0.007	-0.10	0.001	-0.153	-0.008	0.013	-0.016	0.029	0.039	-0.030	-0.008	-0.209*
DMY	-0.020	-0.002	-0.040	-0.040	-0.015	-0.026	0.004	0.026	0.013	-0.068	0.015	0.273	0.200	0.245	-0.045	0.019	-0.006	-0.022	0.479**
LDW	0.017	-0.009	-0.040	-0.028	-0.001	-0.006	0.019	0.019	0.008	-0.055	-0.017	0.141	0.193	0.099	0.090	0.027	-0.036	-0.041	0.506**
SDW	-0.004	0.003	-0.003	-0.002	-0.001	-0.002	0.000	0.002	0.001	-0.005	0.003	0.025	0.014	0.028	-0.014	0.000	0.001	0.000	0.392**
L:S	-0.012	0.008	0.006	0.003	0.000	0.000	-0.007	0.000	-0.001	0.006	0.010	0.009	-0.025	0.026	-0.054	-0.009	0.010	0.008	0.100
DTM	0.007	-0.002	0.000	0.000	0.003	0.002	0.005	0.003	-0.003	-0.001	-0.006	0.002	0.003	0.000	0.004	0.024	-0.005	-0.005	0.224*
SY	0.017	-0.011	-0.005	-0.004	-0.001	0.002	0.007	0.004	-0.002	-0.008	-0.009	0.001	0.008	-0.002	0.008	0.009	-0.043	-0.009	-0.239**
1000SW	0.034	-0.017	0.010	-0.027	0.004	-0.007	0.001	-0.008	-0.003	-0.012	-0.006	0.010	0.025	0.001	0.019	0.026	-0.026	-0.120	-0.188*

DT50%F = Days to 50% flowering

FLW (cm) = Flag leaf width

NON = No. of nodes on the main culm

DMY (g) = Dry matter yield per plant

DTM = Days to maturity

PH (cm) = Plant height

LL (cm) = Leaf length

NOT = No. of tillers per plant

LDW (g) = Leaf dry weight per plant

SY (g) = Seed yield per plant

NOL = No. of leaves per plant

LW (cm) = Leaf width

PL (cm) = Peduncle length

SDW (g) = Stem dry weight per plant

1000 SW (g) = 1000 seed weight

FLL (cm) = Flag leaf length

CD (cm) = Culm diameter

GFY (g) = Green fodder yield

L:S = leaf: stem ratio

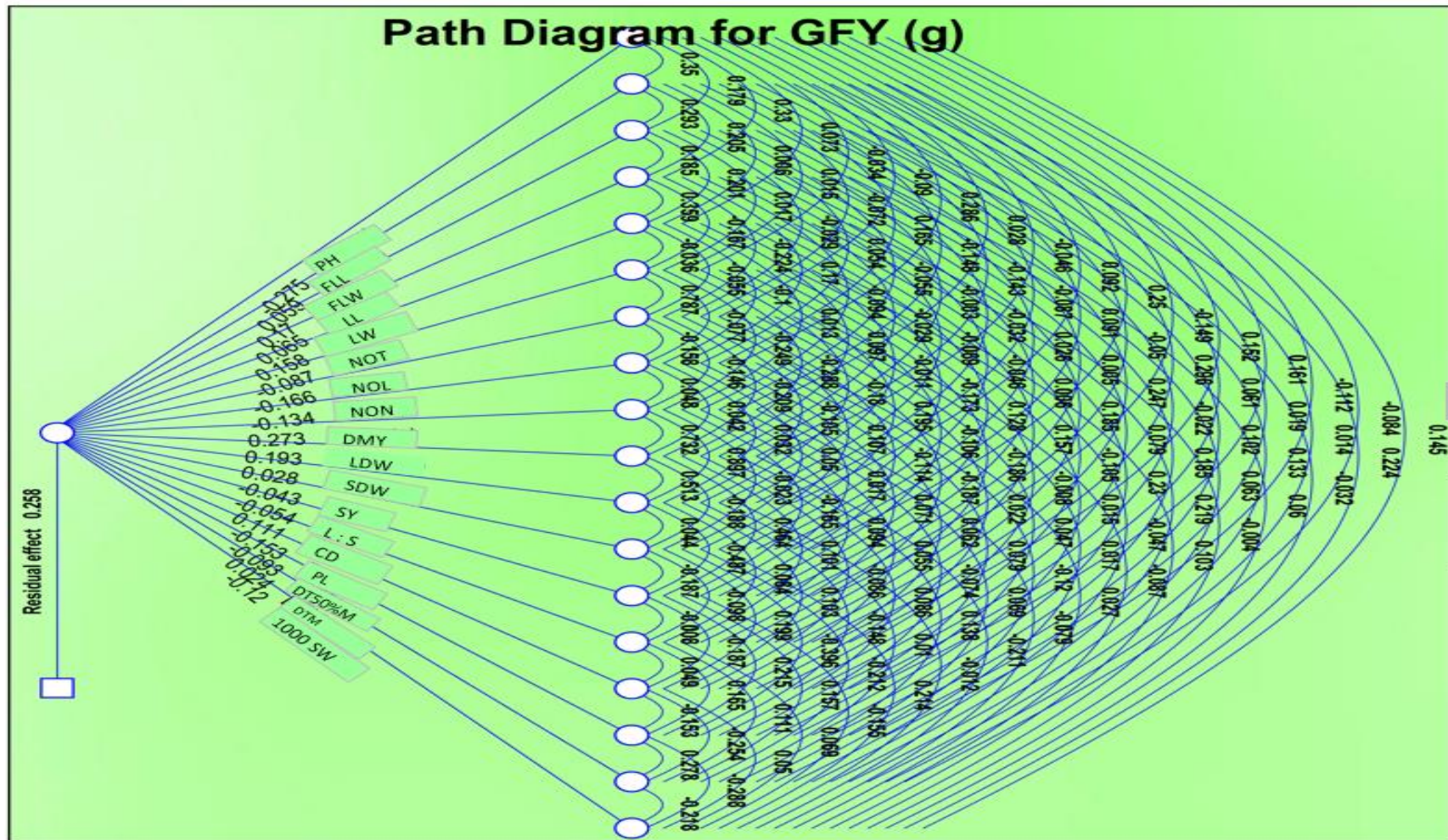


Fig.4.3. Path diagram showing direct and indirect effect of independent traits on green fodder yield

4.4 Genetic diversity for forage yield and its contributing traits

Genetic divergence can be described as the degree of differentiation between or within the species. Intra and inter specific differences are the base for any crop improvement programme. Genetically divergent parents are important to get wide array of recombination for any hybridization programme. The knowledge of genetic diversity among the accession is necessary for crop improvement.

4.4.1 D² statistics

Result of cluster analysis has been presented in tables. One thirty genotypes were used to obtain D² value for 19 traits *i.e.*, days to 50% flowering, plant height(cm), number of leaves per plant, flag leaf length (cm), flag leaf width (cm), leaf length (cm), leaf width (cm), culm diameter (cm), number of nodes on the main culm, number of tillers per plant, peduncle length (cm), green fodder yield (g), dry matter yield per plant (g), leaf dry weight per plant (g), stem dry weight per plant (g), leaf: stem ratio, days to maturity, seed yield per plant (g) and 1000 seed weight (g) and they are grouped into 12 clusters (Table 4.7) by Tocher method. Cluster I comprised by 66 genotypes followed by cluster III (33), cluster V (14), cluster X (9), and cluster VI (4). Seven cluster II, IV, VII, VIII, IX, XI, XII had 1 genotype. (Yadav *et al.*, 2011; Krishna *et al.*, 2014; Jaipal and Shekhawat, 2016) also reported highest number of genotype in cluster I. Clustering pattern of genotypes revealed that there is ample amount of genetic divergence present among themselves. Genotypes belongs to the same sources were clustered into different groups indicating changes in the different characters under selection. Genetic drift, selection pressure and environment could be the cause of this changes which leads to high genetic diversity instead of genetic distance (Marsan *et al.*, 1998; Senior *et al.*, 1998; Wende *et al.*, 2013).

Cluster mean

Cluster means for different characters are given in (Table 4.8). The highest cluster mean for trait days to 50% flowering was obtained in cluster XII (92) and lowest in cluster VI (12.25). Plant height exhibit highest cluster mean in cluster VI (132.33) and lowest in cluster IX (92.16). Highest cluster mean was recorded in cluster IX (39.4) for number of leaves per plant and lowest in cluster XI (17.4).

Cluster VI had the highest cluster mean (32.45) for flag leaf length and lowest in cluster XII (24.82). For flag leaf width cluster VI (2.04) had highest cluster mean and cluster IV (1.62) had lowest. Highest cluster mean was recorded for trait leaf length in cluster II (49.80) and lowest was recorded in cluster IV (39.72). Cluster II (2.04) had highest cluster mean value for leaf width and cluster I (1.78) had lowest.

Culm diameter on the main culm had highest cluster mean in cluster XII (6.46) and lowest in cluster VII (5.70). The highest cluster mean for number of nodes were contributed by cluster VI (5.75) and lowest by cluster XI (4.40). Number of tillers per plant had highest cluster mean in cluster IX (10.20) and lowest in XI (3.8). For peduncle length highest cluster mean was contributed by cluster VI (36.66) and lowest was by cluster IX (29.90).

The highest value of cluster mean was recorded by cluster XI (201.60) and lowest in cluster X (55.22) for green fodder yield. The cluster mean was highest in cluster XI (41.80) for dry matter yield and the lowest value exhibited by cluster IX (17.80). For leaf dry weight highest cluster mean was obtained by cluster XI (14.20) and lowest by cluster X (6.91). Stem dry yield had highest cluster mean value in cluster XI (28.6) and cluster IX (10.80) had lowest cluster mean value.

Leaf: stem ratio contains highest cluster mean value in cluster II and IX (0.64) and lowest in cluster IV (0.39). For days to maturity highest cluster mean value exhibited by cluster XII (116.00) and lowest by cluster VII (105.00). Seed yield comprised for highest cluster mean value in cluster VII (23.40) and lowest in cluster XII (10.8). 1000 seed weight had highest cluster mean in cluster VII (49.00) and lowest in cluster XII (15.00).

From above result it was observed that Cluster VII had highest cluster mean for seed yield per plant and lowest for days to maturity indicated genotypes with early maturity were high grain yielder. Similarly, cluster XII had highest cluster mean for days to 50% flowering and days to maturity whereas lowest cluster mean for seed yield per plant indicating late flowering and late maturity genotypes had decreased the yield of seed. Highest cluster mean for plant height, peduncle length and lowest cluster mean for days to 50% flowering were recorded in cluster VI. As peduncle length is associated with high seed yield it can also be affected by

flowering time. Cluster IX reported highest cluster for leaf: stem ratio whereas lowest for dry matter yield per plant and stem dry weight per plant indicated leaf: stem ratio can be increased by decreasing the stem dry weight. It also represented that dry matter yield will decrease if stem dry weight will decrease which convey that the yield of both these traits were associated.

Wide range of values for cluster means obtained among the character studied showed that variation present among the genotypes studied. Yadav *et al.*, (2011) recorded highest cluster mean for plant height in cluster VI.

Inter and Intra cluster distance

Cluster distance obtained by D^2 was grouped into 12 clusters and the intra cluster distance ranges from 0 to 1506.42 (Table 4.9). This wide range of values indicates the ample of diversity present. Highest intra cluster distance obtained by cluster VI (1506) contains 4 genotypes represent the high genetic diversity among the genotypes. It is followed by cluster X (1331.27) having 9 genotypes, cluster III (972.27) having 30 genotypes, cluster V (925.05) having 14 genotypes and cluster I (834.01) having 66 genotypes.

The inter cluster distance varied from 429.41 to 23009.13. The result of this analysis indicated the presence of commendable amount of genetic divergence in the study material. The highest inter cluster distance found between Cluster X and XI had relatively higher mean for the trait plant height, leaf width, number of nodes on the main culm, peduncle length, green fodder yield, dry matter yield, leaf dry weight per plant and stem dry weight per plant. Genotypes which fell under cluster X and XI *i.e.*, (GP-30, GP-17, GP-12, GP-21, EC/246146, JHO-851, IC/014555, EC/209215, EC/0107524 and EC/097519) will also show high genetic diversity. Lowest inter cluster distance was observed between cluster II and IX therefore genotypes (EC/097520, EC/097532) which belongs to these clusters were less diverse. So, selection for these traits and genotypes will be effective for further breeding programme.

From the study it was observed that values of inter cluster distance is higher than the intra cluster distance which indicates that high genetic divergence found between the genotypes.

Percent Contribution by different traits for genetic divergence

The percent contribution for genetic divergence of each character is shown in (Table 4.10). 1000 seed weight contributes largest (16.62%) towards genetic divergence followed by green fodder yield (14%), seed yield per plant (12%), number of nodes on the main culm and leaf: stem ratio (8%), peduncle length (7%), number of leaves per plant (6.34%), culm diameter (6%), number of tillers per plant (5%), flag leaf width (4.50) and (4%) by leaf width. This is because the 1000 seed weight and seed yield directly affect green fodder yield. Flag leaf length, leaf length, no. of tillers, no. of nodes, leaf: stem ratio and culm diameter contributed lowest towards divergence in percent as well as ranking position.

The above result was in harmony with Sindhu and Mahndiratta (1981), Kumarmall and Vishwakarma (2006), Ahemad *et al.*, (2011) and Singh and Singh (2011) who also observed high genetic diversity contributed by trait plant height, leaf width, number of tillers per plant, green fodder yield, dry matter yield per plant, leaf: stem ratio and seed yield.

Elite genotypes were identified for agro-morphological characters (Table 4.11). Genotype RO-19 and EC/097519 were identified for high green fodder yield, GP-48, UPO-12-1, 1760, 405 and RO-11 were for high plant height, JHO-822 for more number of tillers per plant, EC/009888 for early maturity, EC/0131307 and EC/096541 for early days to 50% flowering, EC/0101747, EC/097537, EC/060977, GP-1, GP-21 and GP-50 for high leaf: stem ratio and genotypes EC/097522, EC/097537, EC/014016, 405, GP-21 were identified for high leaf width.

Table 4.7 Clustering pattern of different Oat (*Avena sativa* L.) genotypes

Cluster No.	No. of genotypes	% of total genotype	Name of genotype
I	66	50.77	EC/0107017, GP-10, GP-18, EC/034588, EC/292328, EC/096541, EC/035103, GP-50, GP-28, GP-36, GP-41, GP-40, UPO-212, GP-5, GP-6, EC/209196, EC/0292267, GP-34, GP-35, GP-42, GP-44, EC/066172, GP-26, GP-7, EC/034587, GP-16, EC/0035766, GP-1, GP-37, EC/036821, EC/039899, EC/014016, EC/0292312, GP-46, GP-11, JHO-822, GP-48, GP-49, EC/096591, EC/0292340, EC/246147, JO-1, EC/0292369, OL-10, GP-33, GP-13, GP-39, EC/097528, EC/034585, GP-31, EC/029056, GP-32, GP-38, GP-20, GP-19, RO-19, GP-22, RO-11, GP-27, GP-15, EC/209211, EC/097541, EC/097533, EC/009888, EC/0131307, EC/097539
II	1	0.77	EC/097520
III	30	23.08	EC/0108486, EC/035051, EC/0107528, GP-8, EC/06097, EC/035765, GP-25, EC/0102324, EC/009884, EC/022079, EC/035768, EC/292275, EC/036779, EC/292362, EC/292363, EC/097248, EC/097536, EC/209494, GP-3, EC/097240, EC/009890, GP-2, EC/060975, EC/097538, IC/282934, EC/292371, EC/097530, EC/060978, EC/0102326, EC/097535
IV	1	0.77	EC/0107539
V	14	10.77	EC/008539, EC/009889, EC/009883, EC/009885, EC/097522, EC/030245, EC/097525, EC/022080, EC/0101747, EC/097531, EC/097537, GP-4, EC/0076710, EC/097241
VI	4	3.08	1760, 405, UPO-12-1, OL-1804
VII	1	0.77	GP-43
VIII	1	0.77	EC/096592
IX	1	0.77	EC/097532
X	9	6.92	GP-30, GP-17, GP-12, GP-21, EC/246146, JHO-851, IC/014555, EC/209215, EC/0107524
XI	1	0.77	EC/097519
XII	1	0.77	IC/0625278

Table 4.8 Cluster means of different characters among Oat genotypes

	DT50% F	PH	NOL	FLL	FLW	LL	LW	CD	NON	NOT	PL	GFY	DMY	LDW	SDW	L: S	DTM	SY	1000S W
Cluster 1	72.26	112.24	28.68	30.67	1.92	46.89	1.78	6.14	4.89	6.20	33.76	78.66	25.11	7.47	17.71	0.43	108.23	20.94	39.14
Cluster 2	77.0	92.42	28.80	31.72	1.98	49.80	2.04	6.19	4.60	6.00	34.20	93.80	21.40	8.40	13.00	0.64	112.00	13.20	38.00
Cluster 3	74.03	101.05	26.24	30.28	1.98	47.16	1.83	6.17	4.81	5.55	33.69	114.74	27.27	8.61	18.53	0.47	109.13	17.09	35.20
Cluster 4	76.00	95.94	38.60	25.84	1.62	39.72	1.84	6.16	5.40	7.20	33.30	89.80	36.40	10.20	26.20	0.39	109.00	12.60	31.00
Cluster 5	73.93	104.00	23.07	29.39	2.03	48.72	1.92	6.22	4.89	4.93	31.41	158.10	31.27	9.96	21.01	0.50	111.00	16.64	34.93
Cluster 6	12.25	132.33	25.25	32.45	2.04	48.92	1.81	6.44	5.75	6.05	36.66	82.05	30.80	10.20	20.50	0.49	108.50	20.65	27.75
Cluster 7	70.00	98.24	24.20	28.30	1.92	41.36	1.84	5.70	5.40	5.60	35.44	56.00	25.00	8.80	14.35	0.61	105.00	23.40	49.00
Cluster 8	72.00	101.24	37.20	29.92	1.82	40.88	1.92	6.16	5.40	6.60	30.58	56.40	19.40	7.20	12.20	0.59	108.00	17.00	34.00
Cluster 9	81.00	92.16	39.40	28.62	1.86	42.84	1.80	5.83	5.60	10.20	29.90	81.00	17.80	7.00	10.80	0.64	109.00	16.20	36.00
Cluster 10	76.78	101.6	31.18	28.07	1.92	46.63	1.80	5.82	5.16	6.62	36.38	55.22	21.67	6.91	14.76	0.49	109.56	19.44	33.33
Cluster 11	70.00	108.54	17.40	28.66	1.96	40.96	2.02	6.45	4.40	3.80	33.48	201.60	41.80	14.20	28.60	0.49	111.00	18.00	35.00
cluster 12	92.00	104.34	31.40	24.82	1.96	40.20	1.88	6.46	4.60	5.80	30.90	105.00	33.60	11.80	21.80	0.54	116.00	10.80	15.00

DT50%F = Days to 50% flowering

FLW (cm) = Flag leaf width

NON = No. of nodes on the main culm

DMY (g) = Dry matter yield per plant

DTM = Days to maturity

PH (cm) = Plant height

LL (cm) = Leaf length

NOT = No. of tillers per plant

LDW (g) = Leaf dry weight per plant

SY (g) = Seed yield per plant

NOL = No. of leaves per plant

LW (cm) = Leaf width

PL (cm) = Peduncle length

SDW (g) = Stem dry weight per plant

1000 SW (g) = 1000 seed weight

FLL (cm) = Flag leaf length

CD (cm) = Culm diameter

GFY (g) = Green fodder yield

L:S = leaf: stem ratio

Table 4.9 Distance between different centriole (intra and inter cluster distance) of different genotypes of Oats (*Avena sativa* L.)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	834.01											
II	1177.38	0										
III	2355.20	1104.19	972.27									
IV	1332.28	725.57	1535.59	0								
V	7364.43	4942.37	2834.89	5596.67	925.05							
VI	1596.41	2660.01	3190.99	2421.89	7701.12	1506.42						
VII	1311.88	1907.41	4259.75	2136.30	11341.12	3033.02	0					
VIII	1251.84	1721.59	4155.23	1710.81	11285.17	2700.98	523.37	0				
IX	1196.91	429.41	2120.71	786.98	7196.66	2932.41	1372.74	802.77	0			
X	1764.03	2271.02	4707.68	2349.33	11871.73	3062.69	1024.76	743.29	1548.97	1331.27		
XI	16192.89	12878.85	8557.65	13265.84	2644.84	15852.71	22136.30	22382.06	16429.80	23009.13	0	
XII	2504.86	1438.70	1566.96	957.30	4205.59	2799.35	4583.61	3611.58	1865.39	4060.47	10651.32	0

Table 4.10 Relative contribution of individual traits to the genetic divergence

Source	Contribution (%)	Times ranked first	Cumulative frequency
Days to 50% flowering	0.84	70	0.84
Plant height	3.00	250	3.84
Number of leaves per plant	6.34	528	10.18
Flag leaf length	0.13	11	10.31
Flag leaf width	4.50	375	14.81
Leaf length	2.10	175	16.91
Leaf width	4.00	333	20.91
Culm diameter	6.00	500	26.91
Number of nodes on the main culm	8.00	667	34.91
Number of tillers per plant	5.00	417	39.91
Peduncle length	7.00	583	46.91
Green fodder yield	14.00	1167	60.91
Dry matter yield per plant	2.15	179	63.06
Leaf dry weight per plant	0.01	1	63.07
Stem dry weight per plant	0.19	16	63..26
Leaf: stem ratio	8.00	667	71.26
Days to maturity	0.12	10	71.38
Seed yield per plant	12.00	1000	83.38
1000 seed weight	16.62	1385	100

Table 4.11 Elite gene identified for different agro-morphological characters in Oat (*Avena sativa* L.)

S. No.	Characters	Elite genotype
1	Green fodder yield	RO-19, EC/097519
2	Plant height	GP-48, UPO-12-1, 1760, 405, RO-11
3	Number of tillers per plant	JHO-822
4	Early maturity	EC/009888
5	Early days to 50% flowering	EC/0131307, EC/096541
6	Leaf: stem ratio	EC/0101747, EC/097537, EC/060977, GP-1, GP-21, GP-50
7	Leaf width	EC/097522, EC/097537, EC/014016, 405, GP-21

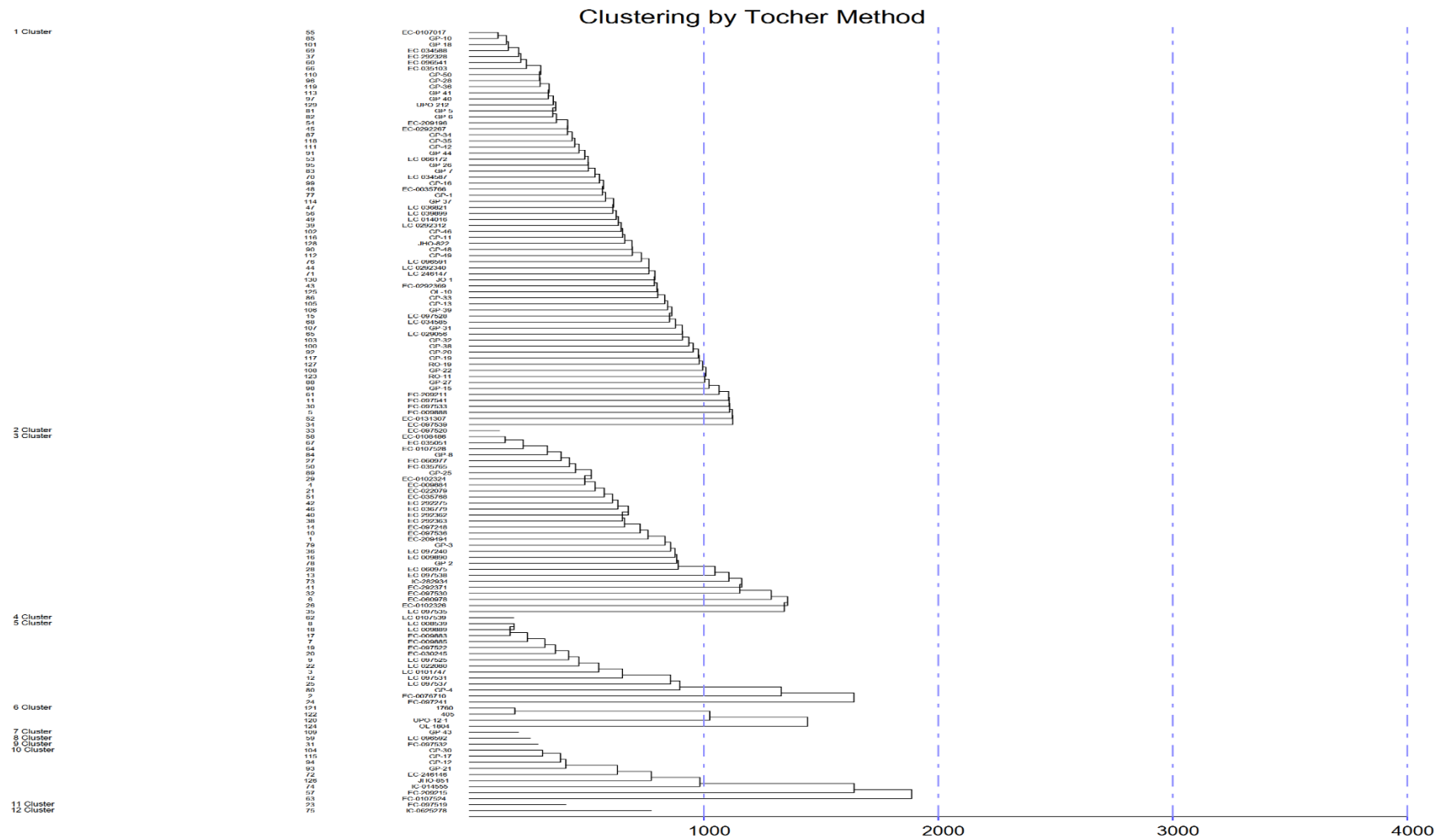


Fig 4.4. Dendrogram showing genotypes falling under different clusters

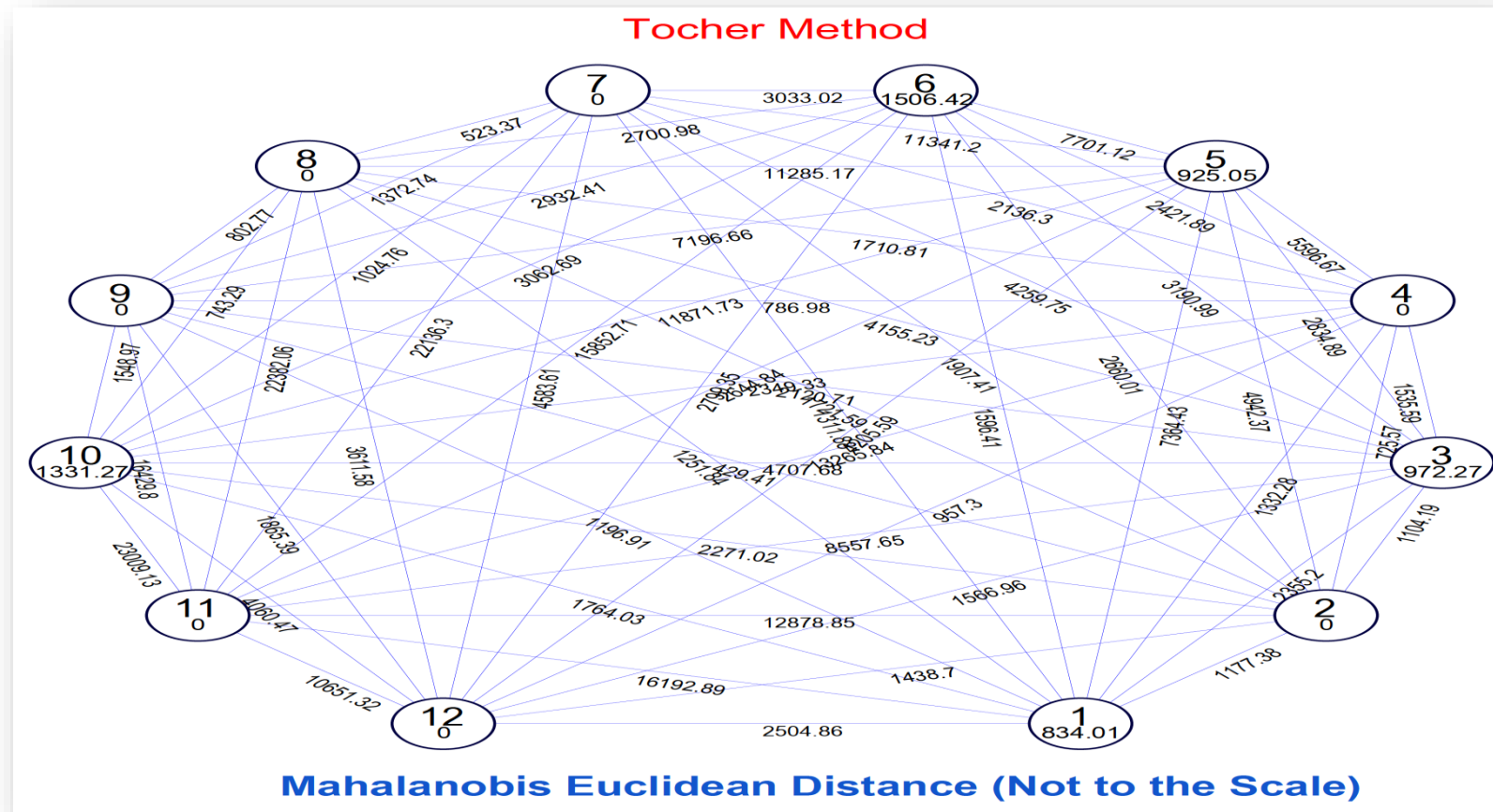


Fig 4.5. Cluster diagram showing Intra and Inter cluster distance

Fig 4.6. Traits showing per cent contribution towards genetic divergence

4.5 Principal Component Analysis

Principal component analysis can be used to know about the relationship between variables.

Principal component analysis divided total variability into 6 PCs presented in (Table 4.12). All the 6 PCs contributed 65.60 % of total variability present in germplasm accessions. First principal component (17.19%) contributed most towards total variability which is followed by subsequent principal components *i.e.* PC II (13.89%), PC III (12.39%), PC IV (8.68%), PC V (6.94%) and PC VI (6.51%).

In PC I trait green fodder yield contributed most heavily towards negative loading (-0.43571), followed by leaf dry weight per plant (-0.42560) and dry matter yield (-0.37168) whereas number of tillers per plant (0.33005) and number of leaves per plant (0.27582) showed high contribution towards positive loading.

The trait days to 50% flowering (-0.35897) contributed most towards negative loading in PC II followed by leaf: stem ratio (-0.30870), days to maturity (-0.25790) and leaf width (-0.23773) whereas stem dry weight per plant (0.44969) contributed heavily toward positive loading followed by dry matter yield (0.38182) and seed yield per plant (0.30526).

In PC III number of leaves per plant (-0.24262) contributed most heavily towards negative loading whereas leaf length (0.45111), plant height (0.39867), flag leaf length (0.39111) and culm diameter (0.35478) contributed towards positive loading.

In PC IV high negative loading showed towards leaf: stem ratio (-0.27682) and number of nodes on the main culm (-0.25152) whereas number of leaves per plant (0.44398), number of tillers per plant (0.42070) and days to maturity (0.30450) contributed most towards positive loading.

In PC V 1000 seed weight (-0.41675) and green fodder yield (-0.21224) contributed towards negative loading whereas days to 50% flowering (0.44146) contributed most heavily toward positive loading followed by number of nodes on the main culm (0.42813) and number of leaves (0.31798).

In PC VI peduncle length (-0.30422) and days to 50% flowering (-0.24354) heavily contributed towards negative loading whereas leaf: stem ratio (0.60734) and leaf dry weight per plant (0.38440) contributed towards positive loading.

From the above results trait days to 50% flowering, number of leaves per plant, flag leaf width, no. of tillers per plant, dry matter yield per plant, leaf dry weight per plant and leaf: stem ratio contributed most strongly toward genetic divergence. So, during selection more emphasis should be pay on these traits.

The 3-D biplot of PCA I score and PCA II score (Fig. 4.7) showed that the genotypes falling in the same cluster are closer to each other. The clusters only had single genotype showed distant between the genotypes present in these clusters and had a desirable mean value for traits *i.e.* GP-43 (high seed yield and low maturity duration), EC/097532 (low plant height and peduncle length), EC/097519 (high green fodder yield a most desirable character) and IC/0625278 (high days to 50% flowering, high days to maturity and lowest seed yield).

Table 4.12 Principal component analysis in Oat (*Avena sativa* L.)

	PC I	PC II	PC III	PC IV	PC V	PC VI
Eigene value (Root)	3.26621	2.63987	2.35432	1.64967	1.31809	1.23655
% Var. Exp.	17.19057	13.89403	12.39117	8.68250	6.93733	6.50815
Cum. Var. Exp.	17.19057	31.08460	43.47577	52.15827	59.09560	65.60375
Days to 50% flowering	-0.09434	-0.35897	0.08422	0.01815	0.44146	-0.24354
Plant height	0.08188	0.24775	0.39867	0.00838	0.18269	0.09493
No. of leaves per plant	0.27582	-0.05646	-0.24262	0.44398	0.31798	0.07490
Flag leaf length	0.10030	0.06762	0.39111	0.19900	-0.03231	0.22161
Flag leaf width	-0.03457	-0.09915	0.31128	0.30700	-0.07636	0.07340
Leaf length	-0.05820	-0.07989	0.45111	-0.06169	0.06259	-0.16405
Leaf width	-0.14556	-0.23773	0.21144	0.27907	-0.10930	-0.03411
Culm diameter	-0.10472	-0.01543	0.35478	0.14824	0.07901	-0.03437
No. of nodes on the main culm	0.01345	0.14767	0.24918	-0.25152	0.42813	0.17600
No. of tillers per plant	0.33005	-0.03415	-0.15705	0.42070	0.25239	0.19896
Peduncle length	0.15715	0.20913	0.07939	-0.16805	0.25079	-0.30422
Green fodder yield	-0.43571	-0.02886	-0.03170	0.17190	-0.21224	-0.00537
Dry matter yield per plant	-0.37168	0.38182	-0.11156	0.15500	0.16867	0.02277
Leaf dry weight per plant	-0.42560	0.12880	-0.09603	-0.03641	0.24162	0.38440
Stem dry weight per plant	-0.28204	0.44969	-0.07390	0.24809	0.09248	-0.18284
Leaf: stem ratio	-0.13691	-0.30870	-0.03263	-0.27682	0.11794	0.60734
Days to maturity	-0.19508	-0.25790	-0.00114	0.30450	0.05439	0.03260
Seed yield per plant	0.24794	0.30526	-0.00885	0.02764	-0.02795	0.24542
1000 seed weight	0.14411	0.20470	0.16982	0.09959	-0.41675	0.25943

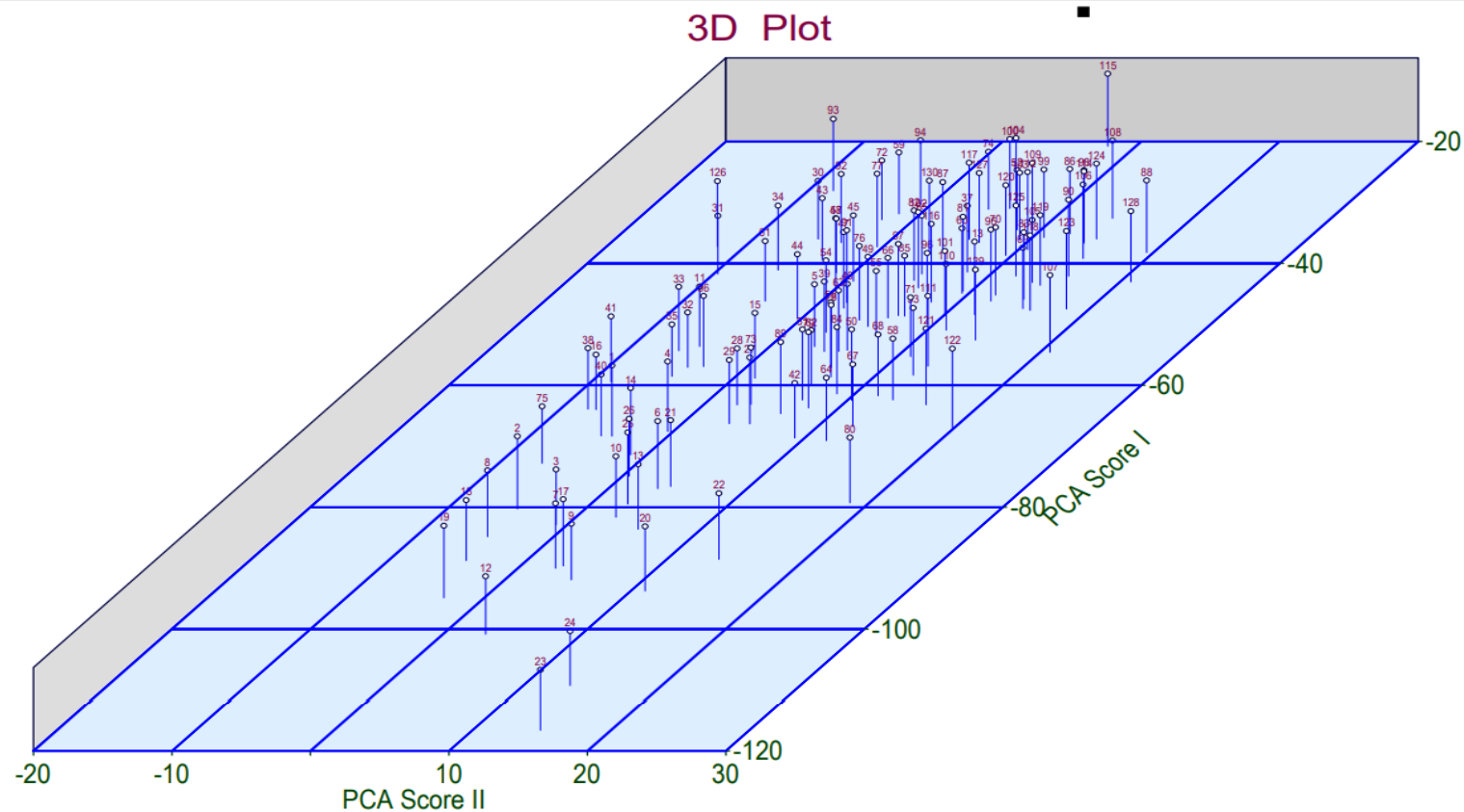


Fig. 4.7. 3D PCA plot

SUMMARY AND CONCLUSIONS

The present study entitled “Agro-morphological characterization of Oat (*Avena sativa* L.) accessions for forage yield and its contributing traits” was carried out at Department of Genetics and Plant Breeding, Research Cum Instructional Farm, IGKV, Raipur (C.G.). Total 130 accessions (including five checks) were grown in augmented design in five blocks. Five checks are replicated in each block and rest 125 accession were grown only once in their respective blocks. The crop was grown in *Rabi* season. All the genotypes were classified into different classes for their respective traits showing morphological variation. Randomly five plants were selected to study about genetic parameters, association analysis and genetic divergence for nineteen characters. Genotypes were subjected to study about their genetic variability, association analysis and genetic diversity. To estimate genetic variability range, mean, standard deviation, standard error, coefficient of variation, genotypic and phenotypic coefficient of variation, heritability, genetic advance, skewness and kurtosis was computed. To estimate association analysis correlation was insufficient to provide information about the relation between genotypes and for this path coefficient analysis was worked out. Genotypes were grouped into clusters by Tocher method and principal component analysis was evaluated to estimate genetic divergence.

➤ As per the result obtained following conclusion are made:

Morphological Characterization

According to DUS descriptor all the genotypes were classified into different classes for 13 qualitative characters.

- ❖ Based on early plant vigour 66 genotypes had poor, 48 had good and 16 had very good early plant vigour.
- ❖ For growth habit 91 genotypes were fell under erect, 36 under semi prostrate, 3 under prostrate and none of the genotypes were fell under other than these classes.

- ❖ For leaf colour 15 genotypes were fell under green and 115 genotypes were fell under dark green colour.
- ❖ Leaf sheath pubescence was classified into two classes as presence and absence of pubescence. Except one genotype all the genotypes had leaf sheath pubescence present.
- ❖ Based on flag leaf attitude 104 genotypes were drooping, 23 were semi drooping and 3 genotypes were erect in nature.
- ❖ Based on panicle attitude 12 genotypes had lateral panicle and 118 had equilateral panicle.
- ❖ Based on awn per spikelet 126 genotypes had one awn, 2 genotypes had two awn and 2 genotypes had no awn.
- ❖ In seed colour 129 genotypes were yellow and 1 was black in seed colour.
- ❖ Traits namely, stem solidness, primary floret pubescence, spikelet shattering, hullness and biotic stress susceptibility were fell under single class *i.e.*, hollow stem, primary floret pubescence present, non-shattering type of spikelet, hullness present and all were exhibited as very low biotic stress susceptibility.

Assessment of genetic variability parameter

- ❖ Analysis of variance showed high genetic variability among genotypes at 0.1%, 1% and 5% level of significance in oats.
- ❖ Highest GCV (21.96 %) was observed for leaf: stem ratio and seed yield per plant (20.78 %). Highest PCV (32.54 %) was recorded for trait green fodder yield followed by seed yield per plant (28.6 %), number of leaves per plant (27.17 %) and leaf: stem ratio (26.82%). The lowest value of GCV was recorded for culm diameter (-4.21 %). Lowest value for PCV was observed for days to maturity (2.44 %). Leaf: stem ratio and seed yield per plant coupled with high GCV and PCV. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicates that genotypes were influenced by environment also
- ❖ Highest heritability found in the character 1000 seed weight as (88.81%) and leaf: stem ratio (67.04%). Moderate heritability was recorded for trait leaf length (54.13%), seed yield per plant (52.78%), plant height (46.38%), days to maturity

(45.42%) and days to 50% flowering (42.57%). Lowest heritability was found in culm diameter (-29.78%) and followed by dry matter yield per plant (0.35%) and no. of leaves per plant (1.97%). High heritability indicates that traits are controlled at genetic level.

- ❖ High genetic advance was observed for leaf : stem ratio (37.04%), followed by 1000 seed weight (31.77%) and seed yield per plant (31.1%). Moderate genetic advance found in green fodder yield (16.30%) followed by leaf length (13.13%) and leaf dry weight per plant (10.3%). Low genetic advance found in culm diameter (-4.73%), which was followed by dry matter yield (0.16%) and flag leaf width (0.51%).
- ❖ High heritability and high genetic advance was recorded in trait 1000 seed weight and leaf: stem ratio and selection for these traits will be effective to understand the genetic level of any genotype for future breeding programme of oat.
- ❖ Most of the traits studied had skewness value ranged from (-0.5 to 0.5) are normally distributed except traits days to 50% flowering (1.5565), Leaf : stem ratio (1.1931), leaf dry weight per plant (0.7823) and number of tillers per plant (0.5405) showed positive skewness means they shows dominant and complementary gene action and flag leaf length (-0.5091) showed negative skewness *i.e.*, it exhibited dominant and duplicate gene action.
- ❖ Plant height (cm) (-0.0981), flag leaf width (cm) (-0.0705), culm diameter (cm) (-0.1227) dry matter yield per plant (g) (-0.3133), stem dry weight per plant (g) (-0.2070) and seed yield per plant (g) (-0.3149) exhibited negative kurtosis (platykurtic) indicates traits are controlled by large number of genes and rest of the traits showed positive kurtosis (leptokurtic) are governed by small number of genes.

Association analysis

- ❖ Association analysis provides information about the relation between traits and which are directly or indirectly affecting each other. It provides a good opportunity for a breeder to select a trait based on the relation with the other traits.
- ❖ Selection for the trait like leaf dry weight per plant (0.506**), dry matter yield per plant (0.479**), stem dry weight per plant (0.392**) and leaf width (0.262*)

will directly boost the yield of green forage as they are significantly positive correlated with green fodder yield. Significant positive correlation values of these traits with green fodder yield as (0.506**), (0.479**), (0.392**), (0.262*) respectively. But traits number of tillers per plant (-0.376**), number of leaves per plant (-0.320**) and plant height (-0.229**) showed highly significant negative correlation with green fodder yield. So, breeder should avoid to select these traits.

- ❖ Trait leaf: stem ratio (0.100), days to 50% flowering (0.065) and leaf length (0.058) showed non-significant but positive correlation with green fodder yield so these traits is also a good choice for selection whereas number of nodes on the main culm (-0.162) and flag leaf length (-0.061) had negative and non-significant correlation with green fodder yield so these traits should be directly avoid for selection.

Positive correlation between the traits enhance the productivity of both trait whereas negative correlation between the traits suppress the productivity of that both traits.

- ❖ Path coefficient analysis was used to identify the nature of relationship between the green fodder yield and its yield attributing traits. It was used to identify the direct and indirect effect of other traits on green fodder yield.
- ❖ Optimum number of tillers and leaves requires for high green fodder yield. So, here in our studies we observed significant negative correlation as well as negative direct effect of traits number of tillers per plant, number of leaves per plant, seed yield per plant, plant height, peduncle length and 1000 seed weight towards green fodder yield. Therefore, if the selection planned then optimum number of tillers and number of leaves per plant and plant height should be considered. Low to medium 1000 seed weight may contribute for higher green fodder yield because source and sink distribution proportionate for high green forage and about all energy used for forage production purpose.
- ❖ Leaf dry weight per plant followed by dry matter yield per plant, stem dry weight per plant, culm diameter and leaf width showed significant positive correlation as well as positive direct effect on dependent character green fodder yield indicating

a true relationship among traits. Therefore, plant with high leaf dry weight, high dry matter yield, high stem dry weight and leaf width with increased culm thickness should be considered as selection criterion for enhancing the yield of green fodder in Oat.

Genetic divergence

- ❖ Genetic divergence indicates the degree of distinction between genotypes of same species or different species. The high the genetic divergence more is the chance of crop improvement.
- ❖ Total 130 genotypes were studied for 19 characters. All the genotypes were divided into 12 clusters by Tocher method. Cluster I comprised by 66 genotype followed by cluster III (33), cluster V (14), cluster X (9), and cluster VI (4). Seven cluster II, IV, VII, VIII, IX, XI, XII had 1 genotype. Wide range of values for cluster means obtained among the character studied which showed that ample of variation present among the genotypes studied.
- ❖ Intra cluster distance ranges from 0 to 1506.42. This wide range of values indicates the ample of diversity present. Highest intra cluster distance obtained by cluster VI (1506) contains 4 genotypes represent the high genetic diversity among the genotypes. It is followed by cluster X (1331.27) having 9 genotypes, cluster III (972.27) having 30 genotypes, cluster V (925.05) having 14 genotypes and cluster I (834.01) having 66 genotypes.
- ❖ Inter cluster distance ranged from 429.41 to 23009.13. The highest inter cluster distance found between Cluster X and XI. Genotype GP-30, GP-17, GP-12, GP-21, EC/246146, JHO-851, IC/014555, EC/209215, EC/0107524 and EC/097519 which fell under these both cluster showed high genetic divergence. Cluster X and XI had relatively higher mean for trait plant height, leaf width, number of nodes on the main culm, peduncle length, green fodder yield, dry matter yield, leaf dry weight per plant and stem dry weight per plant. So, selection on the basis of these traits will be effective for further breeding programme.
- ❖ Trait 1000 seed weight contributes largest (16.62%) towards genetic divergence followed by green fodder yield (14%), seed yield per plant (12%), number of nodes on the main culm and leaf: stem ratio (8%) whereas leaf dry weight per

plant (0.01%), days to maturity (0.12%), flag leaf length (0.13%) and stem dry weight per plant (0.19%) contributed lowest towards genetic divergence.

❖ Total variability was divided into 6 PCs by principal component analysis.

All the 6 PCs contributed 65.60 % of total variability present in germplasm accessions. First principal component (17.19%) contributed most towards total variability which is followed by subsequent principal components *i.e.* PC II (13.89%), PC III (12.39%), PC IV (8.68%), PC V (6.94%) and PC VI (6.51%).

In PC I trait green fodder yield contributed most heavily towards negative loading (-0.43571), followed by leaf dry weight per plant (-0.42560) and dry matter yield (-0.37168) whereas number of tillers per plant (0.33005) and number of leaves per plant (0.27582) showed high contribution towards positive loading.

The trait days to 50% flowering (-0.35897) contributed most towards negative loading in PC II followed by leaf: stem ratio (-0.30870), days to maturity (-0.25790) and leaf width (-0.23773) whereas stem dry weight per plant (0.44969) contributed heavily toward positive loading followed by dry matter yield (0.38182) and seed yield per plant (0.30526).

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In PC V 1000 seed weight (-0.41675) and green fodder yield (-0.21224) contributed towards negative loading whereas days to 50% flowering (0.44146) contributed most heavily toward positive loading followed by number of nodes on the main culm (0.42813) and number of leaves (0.31798).

In PC VI peduncle length (-0.30422) and days to 50% flowering (-0.24354) heavily contributed towards negative loading whereas leaf: stem ratio (0.60734) and leaf dry weight per plant (0.38440) contributed towards positive loading.

CONCLUSION

- From the studies it was concluded that there is sufficient amount of morphological variation present as all the genotypes studied were showing variation for most of the traits.
- From the investigation presented we can conclude that there is ample of variation present between the genotypes which gives the greater opportunity for improvement of genotype.
- It is concluded that there is significant variation observed for most of the trait studied which is a requirement for any breeding programme instead of all these it also provides opportunity for improvement of genotypes.
- By looking at result obtained for GCV and PCV values conclusion is drawn that there is lot of variability present among the genotypes studied at both genotypic and phenotypic levels so selection can be effectively used for enhancement of genotypes.
- PCV values are relatively higher than the GCV values which provide a scope for selection on the phenotypic level.
- High genetic advance was recorded for traits leaf: stem ratio, 1000 seed weight and seed yield per plant. This indicated that these traits are governed by additive gene and due to this these traits should be selected for further improvement of genotype's performance.
- High heritability with high genetic advance as percent mean was observed for leaf: stem ratio and 1000 seed weight, indicating preponderance of additive gene action. Selection based on these traits may be effective for improvement of green fodder yield.
- Significant positive correlation of green fodder yield with dry leaf weight per plant, dry matter yield per plant, stem dry weight per plant and leaf width respectively. "Positive association of correlation between desirable traits is beneficial because it simultaneously helps in improvement of both the traits."

- As green fodder yield is considered as dependent traits in path analysis maximum positive direct effect was shown by dry matter yield per plant, leaf dry weight per plant, flag leaf width and leaf width. This indicated the true relationship between the characters for green fodder yield. The analysis revealed that direct selection of these traits will be rewarding for green fodder yield.
- Genetic divergence analysis revealed that there is ample of divergence present among the germplasm accessions. Intra cluster distance ranges from 0 to 1506.42. This result clearly revealed appreciable amount of genetic divergence present in study material. The inter cluster distance varied from 429.41 to 23009.13. It indicated wide range of diversity among genotypes. The highest inter cluster distance found between Cluster X and XI. So, superior recombinants can be obtain by hybridization between the genotypes fell under these both clusters.
- Total variance was partitioned into 6 PCs in principal component analysis. Trait days to 50% flowering, number of leaves per plant, flag leaf width, no. of tillers per plant, dry matter yield per plant, leaf dry weight per plant and leaf: stem ratio contributed most strongly toward genetic divergence indicating that more importance should pay for these traits during selection.

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Appendix-A

Weekly meteorological data during crop growth period of Oat (*Avena sativa* L.) Rabi 2019-20

Wk. No.	Date	Max. Temp. (°C)	Min. Temp. (°C)	Rainfall	Rainy days	Relative Humidity (%) I	Relative Humidity (%) II	Sun Shine (hours)
45	Nov 5-11	30.6	23	81.6	4	91	65	5.5
46	12-18	29.6	15.5	0	0	90	38	8.7
47	19-25	30.2	15.2	0	0	89	38	8.2
48	Nov 26-02	29.7	16.3	0	0	90	43	6.3
49	Dec 03-09	28	13.3	0	0	84	34	7.6
50	10-16	29.5	15.3	0	0	91	48	5.2
51	17-23	26.7	14.1	0.8	0	88	42	4.9
52	24-31	26.1	11.9	0	0	81	35	5.7
1	Jan (2020) 01-07	23.3	12.9	19.4	2	97.4	33.7	8.3
2	08-14	25.1	5.7	3.2	1	89.4	46.3	11.1
3	15-21	28.6	15.4	0	0	87.4	62.7	5.7
4	22-28	28.8	12.6	0	0	78.9	28	10.2
5	29-04	26.1	15.6	29.5	1	88.7	44.1	4.3
6	Feb 05-11	21.3	13.6	49.6	3	89.3	25	2.4
7	12-18	29.7	11.9	0	0	88.1	27.3	9.8
8	19-25	31.4	20.6	35.8	1	88	76.3	6.6
9	26-03	29.6	15.8	0	0	88.7	37.4	7.9
10	Mar 04-10	31.1	19.7	1.8	1	86.1	52.6	7.4
11	11-17	30.2	20.1	37.2	2	88.7	54.7	5.6
12	18-24	33.1	20.2	1.6	1	83.7	38.1	8.3
13	25-31	35.4	22	8.4	1	78.1	36.6	8

Appendix-B

Performance of germplasm accessions of 19 biometric traits in augmented design in 5 blocks

Name of genotype	Days to 50% flowering	Plant height	No. of leaves per plant	Flag leaf length	Flag leaf width	Leaf length	Leaf width	Culm diameter	No. of nodes on the main culm	No. of tillers per plant	Peduncle length	Green fodder yield	Dry matter yield per plant	Leaf dry weight per plant	Stem dry weight per plant	Leaf: stem ratio	Days to maturity	Seed yield per plant	1000 seed weight
JHO-851	91	106.26	17.8	25.4	2.06	57.6	1.86	5.54	4.4	3.8	32.88	116.8	17	6.8	12.4	0.54	119	5.6	19
RO-19	76	113.28	21.4	25.32	1.96	52.48	2.10	6.45	5.4	4.6	32.92	203.4	42.4	14	28.4	0.49	108	16	34
JHO-822	72	94.04	19.4	31.8	1.68	46.44	1.66	6.15	5.4	4.2	31.28	173.6	42	10.4	31.6	0.32	113	26	40
UPO-212	77	109.38	21	28.44	1.72	44.92	1.62	6.06	4.8	4.4	28.64	129.2	28.2	9.6	18.6	0.51	109	14.2	37
JO-1	73	114.6	27	28.64	2.2	54.22	2.00	5.46	4.6	5.6	33.66	175.6	33.6	8.4	25.2	0.33	108	23.4	35
EC/209494	83	109.96	18.6	26.98	2.26	57.32	1.90	5.65	4.4	4.2	29	108	25.4	8.4	17	0.49	112	15.4	27
EC/0076710	78	104.52	19.6	25.8	2.48	68.54	1.92	5.93	4.4	5.2	32.12	134	26	9.6	16.4	0.58	111	9.2	34
EC/0101747	70	95.78	25.8	26.64	2	35.74	1.92	5.86	3.8	5.6	31.24	156.4	24.6	10.2	14.4	0.71	107	15.4	36
EC/009884	77	101.94	24.4	31.16	1.86	58.12	2.02	6.43	4	4.6	39.5	119.8	24.6	8.8	15.8	0.55	110	16.2	36
EC/009888	70	96.24	27.6	27	1.78	48.12	1.86	6.22	4.8	6.2	31.4	97.2	23.6	7.8	15.8	0.49	100	17.6	39
EC/060978	76	108.92	24	24.12	1.66	53.74	1.88	5.72	4.4	4.8	34.94	139.6	26.8	8.8	18	0.48	107	15.4	41
EC/009885	73	101.34	19.8	27.22	2.08	54.3	1.86	6.37	5.2	4.4	32.62	151.2	33.8	8.6	21.2	0.4	114	14.8	32
EC/008539	78	100.02	22.4	31.3	1.96	52.76	1.96	6.35	5	4.8	32.5	156	25.2	5	16.2	0.3	109	12.4	32
EC/097525	70	94.76	27.4	25.02	1.78	45.28	2.10	6.73	4.4	6	28.64	155	35.8	10	25.8	0.38	113	14	35
EC/097536	70	96.64	24.6	26.9	1.94	50.12	1.78	6.39	4.8	4.8	33.28	129.4	34.2	15.4	18.8	0.82	111	9.2	35
EC/097541	72	91.06	28.2	26.94	1.84	47.04	1.72	5.72	4.8	5.4	31.68	87.2	22.6	8.2	14.4	0.56	113	13	34
EC/097531	70	93.66	21.4	28.22	1.98	45.52	1.68	6.24	4.8	4.8	31.42	177.8	32.8	9.8	23	0.42	113	15.8	34
EC/097538	76	103.16	20.8	26.84	2.04	51.38	1.96	5.62	4.4	4.8	35.1	136.4	34	10	24	0.41	109	9.6	38
EC/097248	71	97.14	12.6	31.38	1.94	51.04	1.92	6.11	4.6	3.2	32.7	113.4	25.4	8.6	16.8	0.511	110	11	31
EC/097528	70	99.8	17.8	27.3	2	47.1	1.82	5.61	4.8	3.8	31.1	94.4	22.6	9.6	16.6	0.57	112	16.2	39
EC/009890	77	96.58	34.4	17.56	1.7	45.42	1.74	6.52	5	5.6	32.6	113.6	22.2	6.8	15.4	0.44	108	14.8	22
EC/009883	76	106.7	22.4	30.56	1.9	50.48	1.86	6.89	4.6	4.6	29.98	164.4	27.4	8.8	20.6	0.42	111	20.2	37
EC/009889	77	99.66	26	26.57	2.02	47.32	1.80	6.66	5.4	4.4	32.16	163	25.2	9.4	15.8	0.59	109	16.8	26
EC/097522	79	110.18	20.2	35.28	2.22	58	2.18	6.08	5.4	4.4	25.78	163.4	29	10.6	18.4	0.57	112	8.6	33
EC/030245	75	107.6	24	34.04	1.9	45.48	1.96	6.25	5.4	5.4	33.36	162	37.6	9.8	27.8	0.35	111	16	37
EC/022079	78	109.66	19.6	30.12	2	45.48	1.84	5.66	5.2	4.6	32.88	128.8	29.8	9.2	20.6	0.44	110	16.8	31
EC/022080	70	116.58	21.8	29.92	2.02	43.12	2.00	6.13	4.4	5	33.66	157	35	11	23.4	0.47	108	17.6	38
EC/097519	70	108.54	17.4	28.66	1.96	40.96	2.02	6.45	4.4	3.8	33.48	201.6	41.8	14.2	28.6	0.49	111	18	35
EC/097241	70	98.86	17.4	27.84	1.94	34.92	1.76	5.57	4.4	4.4	30.7	185.4	41.6	12.8	29.2	0.43	112	20.4	35
EC/097537	79	113.24	27.4	31.28	2.04	56.74	2.22	6.12	5.4	5	31.16	146.4	27.8	14.2	13.6	1.04	115	26.4	40
JHO-851	98	103.4	30.2	30.8	1.94	42.46	1.80	5.73	4.4	7.2	28.8	55.2	9.4	3.4	6	0.56	116	4.4	14

RO-19	79	112.64	30.8	31.26	1.86	51.48	2.10	6.38	5.6	6.6	29.9	171.8	29.2	10.4	18.8	0.55	112	18.8	33
JHO-822	73	98.88	56.6	29.02	1.68	45.7	1.52	4.33	5.2	13	28.8	51	16.8	5.2	11.6	0.44	110	24.6	40
UPO-212	74	97.68	30.8	26.34	1.7	46.18	1.84	5.57	4.6	7.2	32.6	99.2	28.2	8.4	19.8	0.42	109	15.2	36
JO-1	77	89.86	27.8	31.92	2.08	49.92	1.82	6.18	4.2	6.6	32.1	99.8	25.6	7.4	18.2	0.42	108	21.4	34
EC/0102326	73	91.94	33	30.9	2.4	41.2	2.06	7.09	3.8	6.6	32.4	140.4	27	8.2	18.8	0.43	108	14.8	41
EC/060977	73	104.32	19.6	33.04	2.06	43.28	1.96	6.66	5	6.4	32.7	119.8	25.6	11.8	13.8	0.85	109	23.4	40
EC/060975	74	88.18	31.6	29.74	1.9	42.8	1.82	7.07	4.2	6	33.4	100.4	32	10.2	21.8	0.46	113	16.2	37
EC/0102324	76	98.3	34	34.68	2.12	49.42	1.98	6.15	4.8	7	37.6	124.6	27.6	8.4	19.2	0.43	107	19.6	36
EC/097533	72	94.48	34.8	29.46	1.96	38.24	1.82	5	3.4	7.6	31.4	69.2	16.6	5.8	10.8	0.53	111	17.4	37
EC/097532	81	92.16	39.4	28.62	1.86	42.84	1.80	5.83	5.6	10.2	29.9	81	17.8	7	10.8	0.64	109	16.2	36
EC/097530	72	85.1	22.6	27.66	1.76	33.84	1.72	6.23	4.4	6	32.8	102	20.2	7.6	12.6	0.6	106	13.6	39
EC/097520	77	92.42	28.8	31.72	1.98	49.8	2.04	6.19	4.6	6	34.2	93.8	21.4	8.4	13	0.64	112	13.2	38
EC/097539	73	99.76	21.4	31.64	2.06	37.56	1.74	5.89	5.4	5.4	34.7	67.8	16.4	6.6	9.8	0.67	113	9.6	37
EC/097535	74	82.88	39.2	29.9	1.98	39	1.82	5.61	3.4	10.4	25.3	119.8	21.4	6	15.4	0.38	112	26.8	41
EC/097240	76	101.12	22.4	32.54	1.78	57.2	2.02	5.76	5.6	5.6	35.6	97.4	21.4	6.8	14.6	0.46	107	11	34
EC/292328	69	109.02	35.4	30.64	1.92	48.56	1.90	5.65	5.6	8.6	33.4	79.2	24.4	7.2	17.2	0.41	108	24.4	38
EC/292363	75	93.3	26.6	32.48	2	43.26	1.60	6.71	4.6	6.8	29.8	114.6	20.4	8	12.4	0.64	110	10.8	33
EC/0292312	72	102.02	19.4	32.16	2.06	54.1	1.94	6.67	4.8	4.6	32.4	91.6	24.2	6.4	17.8	0.36	107	22	35
EC/292362	76	91.28	28.8	31.46	2.04	49.24	2.00	6.18	4.6	6.4	37.6	122.2	24	8	16	0.50	109	11	33
EC/292371	78	89.7	18.6	34.02	1.98	46.9	1.90	6.65	5.2	4.6	33.7	95.8	21.6	6.6	12.8	0.51	112	6.4	38
EC/292275	69	95.28	33.4	24.96	1.92	43.56	1.94	5.38	4.6	5.6	32.8	120.2	32.8	7.4	25.4	0.29	108	25.2	31
EC/0292369	70	100.54	32.6	28.32	1.88	42.42	1.66	6.14	4.8	6.2	32.6	76.4	16.2	5	11.2	0.44	113	22.4	31
EC/0292340	73	109.68	34.4	32	2.04	43.62	1.74	5.94	4.4	6.8	34.1	94.2	20.4	7.4	13	0.56	108	20.2	25
EC/0292267	76	110.04	39.8	32.84	1.86	44.82	1.94	6.27	4.6	10.2	31.6	88.4	20.6	6.6	14	0.47	112	20.6	41
EC/036779	76	112.42	36.2	30.52	2.12	48.34	1.84	5.85	4.6	8.2	31.6	103.2	26.2	7.2	19	0.37	114	28	36
EC/036821	74	119.3	18.6	30.68	1.98	54.3	1.90	6.2	4.6	4.4	31.6	80.8	19.8	5.8	13.2	0.43	112	21.8	32
EC/0035766	70	114.68	26.6	31.24	1.94	46.14	1.84	5.91	4.2	5.6	31.6	75.4	19.6	7	12.2	0.57	115	18.2	29
EC/014016	70	119.42	31.2	31.22	2.12	51.26	2.12	6.14	4.4	6.8	29.8	89.4	24	6.4	18.2	0.35	109	21.6	24
EC/035765	75	110.58	22.6	33.22	1.94	54.36	1.94	5.63	4.8	5	32.6	104	31	9.4	21.6	0.43	111	27	36
JHO-851	97	101.16	31	22.68	1.98	38.86	1.60	5.51	4.4	4.6	34.84	64.2	29.8	9	20.8	0.43	117	5.6	15
RO-19	75	103.52	34.6	25.98	2	46.04	1.64	5.97	5	6.4	32.5	91.4	35.6	11.4	24.2	0.47	108	22.6	37
JHO-822	71	104.68	37.4	36.5	1.94	43.9	1.44	6.39	4.6	6.6	35.92	109.8	30.4	9.8	20.6	0.47	107	36	38
UPO-212	76	118.02	27.2	31.94	1.78	47.26	1.72	5.78	5.2	6	35.1	85.4	31.4	9.4	22	0.42	109	20	37
JO-1	75	108.36	22.2	30.26	1.84	45.98	1.64	5.16	5.6	4.4	34.74	55.4	19.2	5.6	13.6	0.41	106	18.8	37
EC/035768	76	114.58	34.4	33.88	1.76	56.44	1.70	6.43	5.4	5.6	34.48	107.6	30.4	9	21.4	0.42	111	19.6	30
EC/0131307	68	100.1	35.4	31.96	2.06	40.5	1.44	4.98	4.2	6.8	33.76	66.8	23.6	7.8	15.8	0.49	110	36.4	31
EC/066172	72	114.02	20.4	29.32	1.9	45.34	1.64	5.39	4.6	3.6	34.84	87.8	32.6	10	22.6	0.44	105	18.4	30
EC/209196	79	110.4	21	34.72	1.94	48.34	1.72	6.85	4.6	4.6	33.42	81.8	24.8	7.8	17	0.45	107	14.4	36
EC/0107017	70	102.52	29.4	31.62	1.96	40.3	1.46	5.55	5.4	5.6	28.68	86	27.4	8	19.4	0.41	110	20.4	37

EC/039899	76	114.92	19.2	33.88	1.74	53.38	1.62	6.17	4.8	4.4	33.98	92.4	28.2	9.2	19	0.48	106	11.2	39
EC/209215	77	89.78	45.2	29.12	1.88	44.64	1.52	5.52	5.2	10.2	40.66	76.8	25.4	7.8	17.6	0.44	108	22.6	23
EC/0108486	70	105.02	38.8	31	2.02	45.56	1.60	5.87	5.2	7.4	33.98	113	35	10.4	22.6	0.46	106	22.4	40
EC/096592	72	101.24	37.2	29.92	1.82	40.88	1.92	6.16	5.4	6.6	30.58	56.4	19.4	7.2	12.2	0.59	108	17	34
EC/096541	68	109.1	36.8	31.76	1.62	46.66	1.54	5.78	4.6	7	30.32	76	28.8	8.8	20	0.44	107	16.4	40
EC/209211	76	96.9	33.2	33.12	1.74	40.04	1.74	6.4	4.4	6	32.46	72.6	22	7.8	17.8	0.43	110	9	29
EC/0107539	76	95.94	38.6	25.84	1.62	39.72	1.84	6.16	5.4	7.2	33.3	89.8	36.4	10.2	26.2	0.39	109	12.6	31
EC/0107524	77	84.14	25.2	31.3	1.72	48.44	1.86	5.65	5.8	4.2	34.04	81	31.8	9.8	22	0.44	107	20.2	43
EC/0107528	70	105.86	20.6	29.04	1.68	40.9	1.66	5.83	5.2	3.6	32.52	110.6	33.4	10.2	23.2	0.43	109	18.8	37
EC/029056	76	106.5	45	29.22	1.92	39.26	1.64	5.99	4.4	7.4	34.96	74.6	27.6	8.2	19.4	0.42	108	21.2	29
EC/035103	76	102.96	35.8	31.48	1.82	39.02	1.74	5.55	4.4	7	35.48	77.8	30.8	9.2	21.6	0.42	108	13.8	35
EC/035051	71	109.68	34.4	29.88	1.8	44.76	1.74	5.7	4.6	6.2	33.48	108.4	37	13.2	23.8	0.55	107	15.6	35
EC/034585	70	101.28	27.2	29.12	1.76	43.28	1.64	6.54	4.6	4.6	34.52	96.4	34.6	10.6	24	0.44	109	19.4	37
EC/034588	69	104.98	33.4	27.44	1.78	41.2	1.92	6	4.4	6.4	36.58	78.6	32.6	8.4	24.2	0.34	108	24.6	40
EC/034587	69	120.14	27.8	29.02	1.64	40.28	1.76	5.54	4.2	5.4	38.52	71.6	29	7.6	20	0.38	111	14	37
EC/246147	75	112.7	26.8	22.4	1.88	33.6	1.64	6.45	4.6	5	32.24	87	35.2	10.4	17.6	0.59	106	23.2	31
EC/246146	82	95.6	34.8	24.72	1.88	44.04	1.64	5.23	4.6	5.8	38.82	47.2	23.6	6.6	17	0.38	107	16.2	29
IC/282934	76	91.76	31.4	33	2.04	41.26	1.76	6.25	6.4	5.6	31.6	94.4	34.4	11	23.4	0.47	110	15.6	27
IC/014555	73	98.02	48.8	25.52	2.06	45.68	2.02	6.03	4.6	10.8	37.6	56	27	8.2	18.8	0.43	111	22	37
IC/0625278	92	104.34	31.4	24.82	1.96	40.2	1.88	6.46	4.6	5.8	30.9	105	33.6	11.8	21.8	0.54	116	10.8	15
JHO-851	96	105.22	27.6	29.16	1.98	40.02	1.74	6.02	4.6	4.8	33.38	73.8	18.2	7.2	11	0.65	111	6.4	20
RO-19	77	132.08	27.6	29.16	1.66	49.86	2.08	5.57	6.4	5.2	31.24	92.8	27	8	19	0.42	108	23.2	36
JHO-822	72	108.08	54.4	29.88	1.66	48.3	1.64	5.79	5.8	10.6	32.82	86.8	30.8	9.2	21.6	0.42	106	19.2	35
UPO-212	76	106.4	27.6	31.78	1.82	41.12	1.74	6.49	4.6	6.6	39.82	100.2	22	6.4	13.6	0.47	110	17.6	38
JO-1	76	112.46	20.2	34.64	2.3	50.06	1.66	6.67	5.4	4.4	35.72	122	22.2	6.2	16	0.38	107	25.2	35
EC/096591	74	111.44	17	29.66	1.98	53.36	1.78	6.15	4.8	4.8	32.48	93.8	18.4	6.6	11.8	0.55	107	28	42
GP-1	73	116.06	27	30.4	1.74	48.92	1.88	5.91	4.6	5.2	37.92	77	13.8	5.6	7.8	0.71	108	18	39
GP-2	71	96.06	16.4	28.72	1.92	42.5	1.68	5.58	5.6	3.4	38.46	102.4	23	5.4	17.6	0.30	106	28.8	31
GP-3	72	124.64	24.2	35.82	2.24	48.96	1.62	7.06	5.4	4.8	38.74	121.4	23.2	6.6	16.6	0.39	108	15.6	35
GP-4	70	113.12	27.4	31.76	2.08	43.94	1.60	5.95	5.8	5	34.44	141.4	36	9.6	28.4	0.33	109	25.4	40
GP-5	76	117.5	29	37.18	2.1	47.06	1.84	6.82	5	6.4	37.2	83	24.2	6	18.6	0.32	111	19.8	47
GP-6	73	115.58	36	35.3	2.06	43.82	1.66	6.69	4.4	6.2	33.06	84	20.6	7.2	15.4	0.46	110	16.6	45
GP-7	73	119.32	37.2	33.48	1.96	38.58	1.68	6.08	4.8	7.2	33.06	92.4	27	5	22	0.22	108	25.8	45
GP-8	70	106.24	20	33.52	2.36	39.4	1.54	6.24	5.6	4.6	32.98	109.2	25.8	5.8	20	0.29	106	15.2	44
GP-10	70	105.3	29.6	26.5	2.12	36.6	1.66	5.68	4.6	6.6	34.38	89.6	24.4	7	17.4	0.40	107	21	39
GP-33	69	108.94	32.4	28.74	1.88	40.14	1.94	5.59	4.2	6.4	32.44	64.6	25.2	6.2	19	0.32	106	23.4	49
GP-34	70	110.76	29.2	30.44	1.88	44.64	2.10	5.79	4.2	7.2	32.2	78.6	17.6	3.6	14	0.25	108	18	51
GP-27	69	124.9	37	33.14	1.88	48.8	1.84	5.77	3.2	7.2	35.14	62.6	32.8	7.4	25.4	0.29	109	20	45
GP-25	70	109.26	19.4	33.24	2.1	49.92	1.84	7.04	4.4	4.2	36.7	121.8	22.4	5	17.4	0.28	108	19	41
GP-48	70	133.04	32.6	31.82	1.9	51.1	1.76	5.46	5.6	7	32.12	77	26.8	7.6	20	0.38	109	22.2	42

GP-44	73	120.86	33.6	32.58	2.06	49.54	2.08	6.45	5.2	6.6	28.28	87.8	20.2	6	14.4	0.41	109	14.6	37
GP-20	76	112.4	48.6	34	2.18	50.18	2.00	6.77	5	5.6	33.64	77.8	17.2	4.6	12.6	0.36	111	14.8	36
GP-21	79	107.32	29.6	30.74	1.74	52.48	2.28	5.96	4.6	6.2	32.72	53.2	12	5	7	0.71	113	19	37
GP-12	76	105.66	32.2	25.74	2.04	42.64	1.82	6.39	5.4	7.2	34.34	43.6	21.8	8	13.8	0.57	117	14.8	41
GP-26	70	124.72	37	29.14	2.18	50.6	1.84	6.4	4.6	6.6	38.02	88	26.2	6.2	20	0.31	109	20.8	37
GP-28	72	108.62	24.4	30.38	1.78	52.4	1.88	6.21	5.2	4.6	33.52	83.6	28	8.6	17.4	0.49	109	22.6	45
GP-40	73	112.78	27.2	32.1	1.88	50.5	1.82	6.7	4.8	5.4	32.24	90.2	23	8.6	14.4	0.59	106	23	42
GP-15	70	106.84	20.6	30.52	1.92	47.48	1.50	6.41	5.4	5.8	33.42	60.6	25.6	6.6	19	0.34	107	27.2	52
GP-16	71	110	39.4	29.12	1.74	49.08	1.58	6.46	5.2	8.4	37.16	78.8	22.6	6.4	16.2	0.39	108	28.6	51
GP-38	75	109.86	44.4	35.48	2.36	52.24	1.82	6.09	5.2	9	35.76	65.8	22.6	7.2	15.4	0.46	106	24	41
JHO-851	84	101.68	21.6	23.82	1.68	48.44	1.68	5.83	4.8	5	38.14	55.8	14.6	4.2	10.4	0.40	109	13	18
RO-19	76	117.64	27.4	26.58	1.54	47.44	1.52	6.24	5.8	6.8	30.8	57.4	24.2	7.8	16.6	0.46	105	20.4	33
JHO-822	72	120.72	25.4	30.32	1.58	45.5	1.66	6.06	5.4	6.8	35.72	72	32.2	10.8	21.4	0.50	105	32.6	41
UPO-212	72	120.3	25.8	28.98	2.08	48.26	1.86	6.68	6.2	6	33.32	83	32	11	21	0.52	107	22.6	34
JO-1	76	108.6	30.4	31.88	1.94	55	1.82	6.09	4.6	6.4	35.18	64.8	23	7.2	15.8	0.45	105	21.8	32
GP-18	71	104.38	27	28.22	2.06	45.08	1.80	5.46	5.8	6	36.56	78.6	28.8	5.4	23.4	0.23	109	18.4	39
GP-46	72	120.46	18.6	30.02	2.06	51.28	1.82	6.1	5.2	5.8	33.46	78.6	12.2	9.2	18.8	0.48	104	18.2	37
GP-32	72	105.34	28.8	25.44	1.66	51.46	2.04	6.4	4.2	6.2	35.3	60.2	25.2	5.8	19.4	0.29	106	25.2	41
GP-30	74	116.3	19.8	30.9	2.04	48.82	1.76	6.07	5.8	4.4	34.94	41.8	22.8	6.2	16.6	0.37	108	18.2	33
GP-13	69	99.3	24.6	24.4	1.76	47.02	1.66	6.32	4.6	6.4	38.48	71.4	28.8	6.4	22.4	0.28	105	30.4	37
GP-39	74	113.26	21.6	35.16	1.88	50	1.78	6.37	5.6	10.6	33.46	63.6	29.4	7	22.4	0.31	106	23	49
GP-31	71	124.32	20.4	33.06	2.04	51.32	1.84	7.36	4.8	4.8	35.2	85.8	34.2	8.2	26	0.31	117	27.4	48
GP-22	74	119.66	25.8	33.64	1.94	52.88	1.74	6.56	5.6	6.4	35.8	61	23.8	7.4	16.4	0.45	106	28	51
GP-43	70	98.24	24.2	28.3	1.92	41.36	1.84	5.7	5.4	5.6	35.44	56	25	8.8	14.35	0.61	105	23.4	49
GP-50	70	110.02	23.2	28.36	1.76	42.86	1.66	5.64	5.8	5	32.42	83.2	33.4	10.4	13	0.80	107	22.2	43
GP-42	74	114	19.6	26.86	1.42	47.12	1.58	6.06	5.8	5.2	32.32	90	31	9.4	21.6	0.43	108	17.6	49
GP-49	76	121.82	27.8	34.72	2.04	50.04	1.68	6.72	5.4	7	33.38	70.6	23.2	6.8	16.4	0.41	106	18	54
GP-41	75	117.96	26.6	30.88	2.16	50.84	2.06	6.65	5	6	35.16	78	29.8	9.2	20.6	0.44	107	18.4	43
GP-37	71	124.14	38	31.98	1.96	47.96	1.96	6.19	5.6	8.2	37.48	71.2	26.4	7.2	19.2	0.37	109	24.8	40
GP-17	69	115.88	23.4	30.74	2.28	44.52	1.66	5.7	5.6	5.8	36.18	41.6	16	6.4	9.6	0.66	106	29	39
GP-11	75	120.8	21	28.18	2.22	55.58	2.02	6.66	5.8	5.2	32.34	76	24	6	18	0.33	108	13	50
GP-19	78	128.86	28	33.56	2.16	47.44	1.80	6.83	5.8	6.8	32.32	63.8	20.8	5.8	15	0.38	109	18.4	35
GP-35	72	121.86	24	30.4	2.16	51.08	1.90	6.39	5	5.4	32.62	84.6	27.6	6.6	21	0.31	107	26	47
GP-36	69	115.46	26.2	33.3	2.08	44.36	1.80	5.46	4.6	6.6	36.82	83	25.4	7.2	18.2	0.39	106	27	43
UPO-12-1	72	132.54	38.8	31.18	2.14	44.86	1.90	6.45	5.8	9.4	34.04	76.8	23.6	7.6	16	0.47	109	28	20
1760	70	133.46	22.2	32.38	1.92	49.64	1.64	6.32	5.4	5.4	37.34	97.8	34.4	11.6	22.4	0.51	110	10.8	33
405	78	140.24	17.6	31.8	2.24	49.64	2.18	6.82	6.2	4.4	37.68	97.4	38.8	13.6	25.2	0.53	108	15.4	31
RO-11	69	131.5	22.6	32.74	1.9	54.4	1.70	6.59	5	5.4	34.88	70.2	32.4	10	22.4	0.44	110	23	32
OL-1804	69	123.06	22.4	34.44	1.86	51.54	1.52	6.17	5.6	5	37.56	56.2	26.4	8	18.4	0.43	107	28.4	27
OL-10	69	115.72	19	28.78	1.72	48.4	1.86	6.28	5.4	4.6	35.94	68.6	25	8.4	16.6	0.5	105	29.6	28

Appendix-C

Principal component Vectors

	PCA I	PCA II	PCA III
Genotype	X Vector	Y Vector	Z Vector
EC-209494	-68.345	-4.049	84.558
EC-0076710	-80.272	-4.914	86.868
EC-0101747	-82.863	-0.828	66.103
EC-009884	-67.57	-0.419	83.58
EC-009888	-53.632	3.217	74.41
EC-060978	-76.958	3.56	80.835
EC-009885	-90.015	2.706	77.585
EC-008539	-84.835	-4.79	79.157
EC-097525	-91.901	4.794	66.955
EC-097536	-81.632	2.885	72.839
EC-097541	-53.625	-5.088	71.484
EC-097531	-100.834	3.071	69.291
EC-097538	-83.626	5.48	77.708
EC-097248	-71.405	-1.158	79.893
EC-097528	-58.831	1.515	78.025
EC-009890	-63.982	-7.384	65.763
EC-009883	-89.636	3.074	79.79
EC-009889	-88.749	-4.37	72.3
EC-097522	-94.866	-2.928	86.239

EC-030245	-93.762	11.055	77.267
EC-022079	-76.582	4.308	79.194
EC-022080	-88.548	13.775	78.938
EC-097519	-116.589	14.906	72.226
EC-097241	-109.253	13.384	65.238
EC-097537	-79.471	2.651	85.573
EC-0102326	-74.911	0.474	68.701
EC-060977	-66.322	4.896	79.31
EC-060975	-63.226	2.432	67.552
EC-0102324	-66.287	3.389	76.09
EC-097533	-36.013	-5.322	69.559
EC-097532	-41.728	-9.704	69.519
EC-097530	-57.064	-4.221	65.685
EC-097520	-54.321	-6.237	76.436
EC-097539	-41.096	-5.681	77.107
EC-097535	-58.518	-4.633	61.95
EC-097240	-56.932	-3.147	84.509
EC-292328	-41.436	8.163	79.18
EC-292363	-63.905	-7.999	72.831
EC-0292312	-54.464	4.345	83.557
EC-292362	-68.32	-4.839	73.561
EC-292371	-59.403	-8.587	78.131
EC-292275	-68.645	9.297	65.744
EC-0292369	-39.404	-3.329	73.591
EC-0292340	-49.008	-0.327	76.558
EC-0292267	-42.935	0.681	78.811

EC-036779	-54.239	5.896	79.104
EC-036821	-47.328	2.171	90.753
EC-0035766	-43.891	-0.122	82.422
EC-014016	-50.339	5.433	83.227
EC-035765	-62.481	10.326	84.923
EC-035768	-62.406	6.736	84.37
EC-0131307	-34.49	8.271	71.319
EC-066172	-58.333	12.699	80.435
EC-209196	-51.306	2.886	85.916
EC-0107017	-51.365	6.546	73.79
EC-039899	-58.622	6.89	89.188
EC-209215	-41.56	-1.239	64.874
EC-0108486	-62.379	13.258	73.21
EC-096592	-31.877	-1.565	73.373
EC-096541	-44.919	9.52	77.664
EC-209211	-46.187	-4.065	71.789
EC-0107539	-59.787	6.067	64.438
EC-0107524	-54.429	5.357	72.734
EC-0107528	-69.082	11.803	75.215
EC-029056	-41.744	5.028	69.794
EC-035103	-48.946	6.174	71.696
EC-035051	-66.732	12.541	74.093
EC-034585	-61.712	11.851	73.231
EC-034588	-47.413	15.156	72.679
EC-034587	-45.194	12.078	80.895
EC-246147	-55.286	10.982	70.738

EC-246146	-32.839	-2.308	70.843
IC-282934	-63.131	3.384	68.022
IC-014555	-31.116	4.53	68.6
IC-0625278	-72.784	-6.873	68.037
EC-096591	-49.317	4.305	88.614
GP-1	-37.296	-0.426	87.423
GP-2	-57.096	6.154	74.796
GP-3	-63.697	7.819	90.562
GP-4	-79.276	18.598	77.993
GP-5	-44.563	9.415	89.023
GP-6	-42.802	4.995	83.742
GP-7	-45.902	14.473	80.238
GP-8	-61.39	8.713	79.679
GP-10	-48.654	7.239	72.215
GP-33	-35.143	12.417	77.448
GP-34	-38.07	4.704	83.1
GP-27	-38.229	19.499	86.18
GP-25	-64.662	6.291	85.693
GP-48	-42.108	15.804	91.429
GP-44	-46.443	1.965	86.482
GP-20	-36.595	-3.373	81.98
GP-21	-28.08	-8.202	85.802
GP-12	-30.418	-0.728	77.319
GP-26	-46.185	12.236	85.508
GP-28	-49.944	9.515	84.772
GP-40	-48.564	6.742	85.574

GP-15	-36.363	14.059	84.765
GP-16	-35.753	10.854	81.338
GP-38	-31	6.014	82.963
GP-18	-48.562	10.1	77.155
GP-46	-44.015	5.906	90.542
GP-32	-36.14	9.291	80.228
GP-30	-31.54	6.725	88.207
GP-13	-43.135	13.699	74.66
GP-39	-39.186	15.397	88.423
GP-31	-54.567	20.7	92.066
GP-22	-32.613	14.229	92.986
GP-43	-34.084	9.177	76.708
GP-50	-50.957	11.396	79.322
GP-42	-56.861	13.033	84.025
GP-49	-37.742	10.669	92.83
GP-41	-48.403	12.17	87.263
GP-37	-36.682	14.203	85.821
GP-17	-20.78	7.972	86.673
GP-11	-46.343	8.01	93.4
GP-19	-36.069	5.605	91.729
GP-35	-47.712	15.833	89.756
GP-36	-43.594	14.501	83.946
UPO-12-1	-38.704	9.569	83.978
1760	-63.187	16.056	91.08
405	-66.984	19.853	94.865
RO-11	-47.472	18.329	93.189

OL-1804	-35.998	14.767	90.181
OL-10	-42.09	12	84.418
JHO-851	-37.238	-11.983	78.158
RO-19	-36.58	6.593	83.079
JHO-822	-43.043	20.775	84.563
UPO-212	-52.575	14.319	84.153
JO-1	-37.996	3.699	84.311

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Awards/ Recognitions (If any):

Publications (If any) :


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