Received: 26 Aug 2023 | Revised: 22 Feb 2024 | Accepted: 27 Feb 2024

Electronic Journal of Plant Breeding

Research Article

Integrating principal component and regression analyses for genetic diversity and trait evaluation in oat genotypes

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Abstract
Oat holds significant importance in global agriculture and nutrition due to their adaptability and versatility. In the present study, Principal Component Analysis (PCA) and Regression analysis were carried out to identify the cause and effect relationship among various traits. PCA on 13 yield attributes revealed five main components contributing to 80.75% cumulative variance. PC1, associated with green fodder yield, dry matter yield, tillers per plant and seed yield was a prominent contributor. PC2 was influenced largely by days to 50% flowering and days to maturity. Biplot analysis identified two distinct trait groups. Multiple regression analysis revealed tillers per plant, test weight and number of spikelets as significant predictors of seed yield. The findings offer insights into genetic association among traits in oat by uncovering the quantitative relationships among them and to identify patterns of genetic variation among different oat genotypes. The analysis of individual trait regression graphs enhances understanding of trait contributions to seed yield. This study advances oat improvement strategies for enhanced crop productivity and resilience.

Keywords: Oat, Principal component, Regression analysis, Yield

INTRODUCTION

Oat (*Avena sativa* L.) is an essential cereal crop with a significant contribution to global agriculture and human nutrition (Chawla *et al.,* 2023; Ibrahim *et al*., 2020). With their exceptional adaptability to diverse environmental conditions, oat plays a crucial role in providing food, feed and fiber (Pankaj and Dhankar, 2023). In addition to being a staple diet for humans in the form of oat meal and other products (Poutanen *et al*., 2022), oats are also an important component of animal feed (Choudhary *et al*., 2023; Chawla *et al.,* 2022), supporting sustainable agricultural systems. Despite the extensive economic and nutritional significance of oats, there remains untapped potential for crop improvement to enhance yield, nutritional content and overall resilience. Traditional breeding methods have contributed to varietal improvements over the years; however, advancements in statistical techniques have paved the way for more precise and efficient approaches to oat enhancement. Two such techniques, Principal Component Analysis and Regression Analysis offer valuable insights into oat genetics, phenotype relationships and potential avenues for improvement (Bichewar *et al.,* 2023; Kumari and Kaushal, 2022).

Principal Component Analysis (PCA) provides a powerful tool to analyze complex data sets and identify underlying patterns in multivariate data (Saranprabhakaran *et al.,* 2021). By reducing the dimensionality of data while preserving critical variation, PCA enables the visualization of relationships between variables and samples (Ivosev *et al*., 2008). The resulting insights facilitate the identification of key traits driving variability, genotype clustering and the identification of potentially valuable genotypes in oat. Additionally, regression analysis, on the other hand, establishes quantitative relationships between variables, enabling predictive modeling and hypothesis testing. In oat improvement, regression analysis can help uncover the associations between genotype and phenotype, guiding breeding decisions to select desirable traits (Hisir *et al*., 2012). By leveraging these analytical tools, latent patterns within oat data sets can be uncovered to identify key variables influencing oat yield and predictive models can be developed to guide targeted breeding efforts. Ultimately, the integration of advanced statistical techniques with oat improvement strategies holds immense promise for enhancing crop yield, nutritional quality and resilience, ensuring the continued prosperity of this vital cereal crop.

MATERIALS AND METHODS

The research encompassed a total of 62 oat genotypes, which also included reference checks (OS 6, JHO 851 and UPO 212). These genotypes were collected from diverse geographical regions across the country and were evaluated in augmented design with three row plot of 3 m row length **(Table 1)**. The study was conducted during the *Rabi* season of the year 2019-20 at the Research Farm Area, Forage Section of the Department of Genetics and Plant Breeding at CCS Haryana Agricultural University, Hisar, Haryana.

A total of 13 phenotypic traits were evaluated including PH- Plant height (cm), TPL- Number of tillers/plant, NOL- Number of leaves/plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield/plant (g), DMY- Dry matter yield/plant (g), DFF- Days to 50% flowering, DM- Days to maturity, SY- seed yield/plant (g), TW- Test weight (1000 seed weight in g). The data on phenotypic traits were collected from five randomly chosen vigorous plants for each genotype except for DFF and DM which was recorded on a plot basis. The analysis was performed using R STUDIO software (2023.03.1+446). The figures and plots were made using the same software.

RESULTS AND DISCUSSION

PCA was applied to a dataset comprising 62 oat genotypes, encompassing 13 traits related to yield. Components with an eigenvalue exceeding one were preserved and the primary components contributing most significantly to the overall variation were identified through a scree plot (**Fig. 1**). These five main components contributed a cumulative variance of 80.75%, out of which PC 1 contributed (29.1%), followed by PC 2 (18.63%). A contribution of 14.62%, 10.29% and 9.11% was made from PC 3, PC 4 and PC 5, respectively. PC 1 was accounted largely by GFY, DMY, TPL and SY, while PC 2 was favorably impacted by DFF, DM, NOS and LL. It was further detected that PC 3 was loaded on PL and PH, PC 4 on LL and NOS and PC 5 on NOL, PL and DM (**Table 2**). The highest positive and negative values within a principal component are responsible for maximum differentiation in clustering (Bhatti *et al.,* 2022). Among these principal components, PC 1 can be regarded as a yield factor. Similar results were recorded by Poonia *et al.,* 2021; Zhang *et al.,* 2010. The prominence of yield traits on PC1 suggests that variations in GFY, DMY, TPL and SY play a pivotal role in shaping the overall variability observed among individuals within the population. This result aligns with the established understanding that yield traits are often critical determinants of a crop's economic and agronomic value (Poonia *et al.,* 2021). The observed relationship between PC1 and yield traits suggests that genetic factors associated with these traits are closely linked to the observed variation. It is plausible that specific genes related to yield traits are driving the variation captured by PC1. This finding could have significant implications for targeted breeding efforts.

Biplot visualization allows for diverse interpretations. The alignment of a variable vector with a principal component axis indicates its significant contribution specifically to that PC. The first group identified by biplot analysis (**Fig. 2**) comprised DM, DFF, SY, NOS and LL. Among these traits, the SY vector was found in close proximity to PCA 1 axis as it largely contributes to it. While all the remaining eight traits were contained in the second group. Among these traits, GFY, DMY, NOL, TP and PH vectors were closer to PCA 1 axis. GFY, DMY, DFF and DM vector had highest length as the length of the arrow indicates the proportion of total variance in the data explained by that variable along that principal component. Furthermore, the angle between two arrows (for e.g. between GFY and DMY; DFF and DM; SY and TPL indicates the correlation between the corresponding variables (Chawla *et al.,* 2021). Scores of genotypes that are close together share similar characteristics, while those farther apart are more dissimilar. The validation of clustering and association patterns was confirmed through the utilization of a heat map, serving as a conceptual model (**Fig. 3**). Upon careful examination of both the biplot and heat map, few outliers were identified, notably the genotypes RO 11-2-2, OS 403, and HFO 1108. The possible explanation for this is that RO 11-2-2 was earliest maturing genotype, while OS 403 displayed the highest seed yield. The genotype HFO 1108 displayed the highest green fodder and dry matter yield.

The multiple regression analysis results hold significant implications for our study, offering valuable insights into the relationships between yield attributes and their impact on seed yield (Sadras *et al.,* 2017). Through a comprehensive

Table 1. Sixty-two oat genotypes along with their source

S. No.	Genotypes	Pedigree	Source	S. No.	Genotypes	Pedigree	Source
1	GP 65	HJ 8 X HFO 267	CCS HAU, Hisar	32	HFO 1109	OS 346 X Kent	CCS HAU, Hisar
2	GP 68	Selection from HFO 114	CCS HAU, Hisar	33	HFO 1111	Kent X SKO 148	CCS HAU, Hisar
3	GP 158	OS 6 X UPO 212	CCS HAU, Hisar	34	HFO 1112	HFO 114 X Kent	CCS HAU, Hisar
4	GP 192	Selection from HJ 8	CCS HAU, Hisar	35	HFO 1113	UPO 212 X SKO 148	CCS HAU, Hisar
5	GP 298	Kent X OS 6	CCS HAU, Hisar	36	HFO 1114	HFO 878 X OS 6	CCS HAU, Hisar
6	GP 492	HJ 8 X Kent	CCS HAU, Hisar	37	HFO 1115	HJ 8 X HFO 58	CCS HAU, Hisar
7	GP 580	Selection from OS 7	CCS HAU, Hisar	38	HFO 1116	OS 403 X OS 377	CCS HAU, Hisar
8	GP 781	OS 6 X JHO 851	CCS HAU, Hisar	39	HFO 1117	HJ 8 X OS 346	CCS HAU, Hisar
9	GP 875	Dulo, Introduction from Bulgaria	Bulgaria	40	HFO 1118	HJ 8 X JHO 822	CCS HAU, Hisar
10	HFO 424	HJ 8 X Kent	CCS HAU, Hisar	41	HFO 1121	FOS 1/29 X HJ 8	CCS HAU, Hisar
11	HFO 529	OS 6 X Kent	CCS HAU, Hisar	42	HFO 1122	OS 377 X HJ 8	CCS HAU, Hisar
12	HFO 607	HJ 8 X UPO-04-1	CCS HAU, Hisar	43	HFO 1123	OS 346 X OS 403	CCS HAU, Hisar
13	HFO 611	HJ 8 X UPO 212	CCS HAU, Hisar	44	HJ 8	OS 7 X S3021	CCS HAU, Hisar
14	HFO 707	JHO 822 X NGB 7021	CCS HAU, Hisar	45	OS403	HJ 8 X Algerian	CCS HAU, Hisar
15	HFO 806	OL 125 X UPO 212	CCS HAU, Hisar	46	OL 125	Appler X IPC-63	PAU, Ludhiana
16	HFO 818	JO 1 X HFO 267	CCS HAU, Hisar	47	OL 1861	HJ 8 x OL 1610	PAU, Ludhiana
17	HFO 901	UPO 212 X Kent	CCS HAU, Hisar	48	OL 1869-1	OL 9 X OL 125	PAU, Ludhiana
18	HFO 902	JHO 822 X NGB 6370	CCS HAU, Hisar	49	OL 1766-2	Advance breeding line	PAU, Ludhiana
19	HFO 903	OL 125 X OS 346	CCS HAU, Hisar	50	OL 1874-2	Advance breeding line	PAU, Ludhiana
20	HFO 915	UPO 212 X OS 346	CCS HAU, Hisar	51	Kent	Introduction	USA
21	HFO 917	NGB 6370 X NGB 4871	CCS HAU, Hisar	52	RO 11-2-2	Advance breeding line	MPKV, Rahuri
22	HFO 1003	HFO 878 X OS 6	CCS HAU, Hisar	53	RO 11-2-6	Advance breeding line	MPKV, Rahuri
23	HFO 1005	JHO 822 X NGB 7021	CCS HAU, Hisar	54	JHO 822	IGO 4268 X Indio-6-5-1	IGFRI, Jhansi
24	HFO 1013	UPO 212 X OS 6	CCS HAU, Hisar	55	JHO 99-1	OS 7 X IGO-320-1139-19	IGFRI, Jhansi
25	HFO 1016	UPO 212 X SKO 96	CCS HAU, Hisar	56	JHO 2006-1	Advance breeding line	IGFRI, Jhansi
26	HFO 1101	JHO 2006-1 X HJ 8	CCS HAU, Hisar	57	JO 1	Kent X UPO 50	JNKVV, Jabalpur
27	HFO 1104	HFO 878 X UPO 212	CCS HAU, Hisar	58	NDO 1	Local collection	NDUA&T, Faizabad
28	HFO 1105	UPO 212 X OS 6	CCS HAU, Hisar	59	PLP 1	Selection from Algerian material	CSKHPKV, Palampur
29	HFO 1106	Algerian X OS 6	CCS HAU, Hisar	60	OS 6 (C$_1$) *	HFO 10 X HFO 55	CCSHAU, Hisar
30	HFO 1107	HJ 8 X OS 6	CCS HAU, Hisar	61	JHO 851 (C$_2$)	Selection from Huga Kairyokuro	Introduction from Japan
31	HFO 1108	HFO 878 X OS 6	CCS HAU, Hisar	62	UPO 212 (C$_3$)	VS 1492 X Kent	GBPUAT, Pantnagar

examination of multiple traits, patterns that shed light on the factors influencing seed yield was discerned. Based on these results (**Table 3**), the predicting model equation for the seed grain yield (SY) was formulated as: SY = -23.782280 + 0.045708 * PH + 1.858241 * TPL - 0.101173 * NOL + 0.040303 * LL + 0.503800 * LW - 0.100978 * PL + 0.205511 * NOS - 0.009421 * GFY - 0.036908 * DMY - 0.053072 * DFF + 0.010333 * DM + 0.369131 * TW. These coefficients indicate the anticipated alteration in the dependent variable (seed yield) resulting from a unitary adjustment in the respective independent variable, with all other variables maintained at constant level. These traits emerged as statistically significant contributors to the model (Kumari and Kaushal, 2022). Notably, TPL exhibited a highly positive coefficient of 1.858 indicating that an increase in TPL is associated with a substantial increase in seed yield. TW is another trait that emerged as a predictor within the regression model which significantly influences the determination of seed yield. Lastly, NOS demonstrated a positive coefficient of 0.205, implying that an elevated NOS corresponds to a notable improvement in the seed yield. Conversely, GFY displayed coefficients near zero, suggesting a more limited influence on the outcome. Furthermore, it is worth highlighting that certain

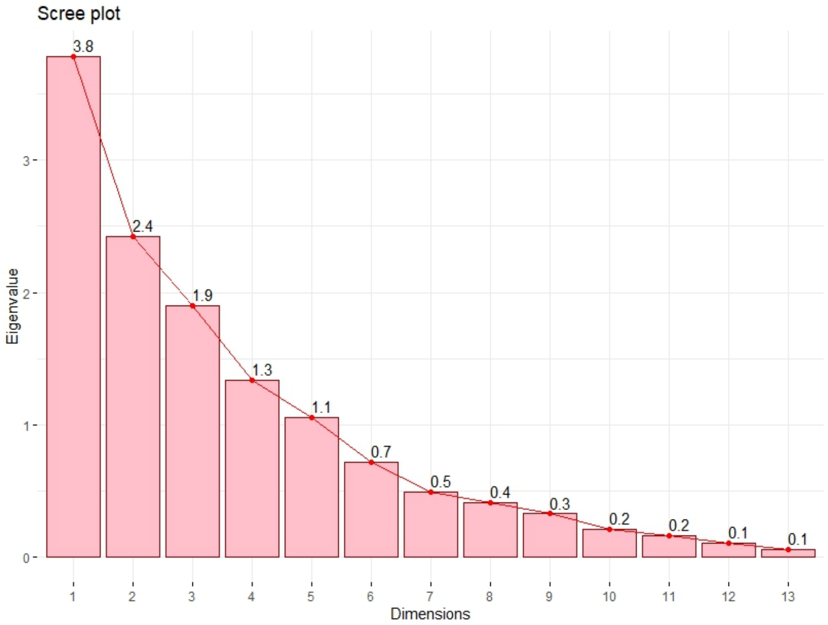

Fig. 1 Scree plot depicted eigen values for respective principal components

Table 2. Variance attributable to principal components along with loadings of various traits

Variances	**Principal Components**				
	PC1	**PC2**	**PC3**	**PC4**	**PC5**
Standard deviation	1.95	1.56	1.38	1.16	1.03
Eigen values	3.8	2.4	1.9	1.3	1.1
Proportion of Variance (%)	29.10	18.63	14.62	10.29	8.11
Cumulative Proportion (%)	29.1	47.73	62.35	72.64	80.75
Factor Loadings					
Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
PH	-0.23	-0.13	**-0.44**	-0.27	-0.22
TPL	**-0.39**	-0.07	0.41	-0.13	-0.15
NOL	-0.37	-0.11	0.33	-0.12	**-0.32**
LL	-0.04	**-0.38**	-0.14	**0.47**	-0.16
LW	-0.17	0.24	-0.18	0.40	-0.23
PL	-0.05	-0.14	**-0.59**	-0.13	**-0.29**
NOS	-0.19	**0.38**	-0.10	**0.41**	-0.23
GFY	**-0.43**	-0.22	-0.10	-0.12	0.06
DMY	**-0.41**	-0.17	-0.05	-0.18	0.21
DFF	-0.18	**0.48**	-0.22	-0.20	0.17
DM	-0.22	**0.45**	-0.08	-0.10	**0.29**
SY	**-0.38**	0.06	0.13	0.39	0.10
TW	-0.12	-0.31	-0.18	0.28	0.66

[PH- Plant height (cm), TPL- Number of tillers/plant, NOL- Number of leaves/plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield/plant (g), DMY- Dry matter yield/plant (g), DFF- Days to 50% flowering, DM- Days to maturity, SY- seed yield/plant (g), TW- Test weight]

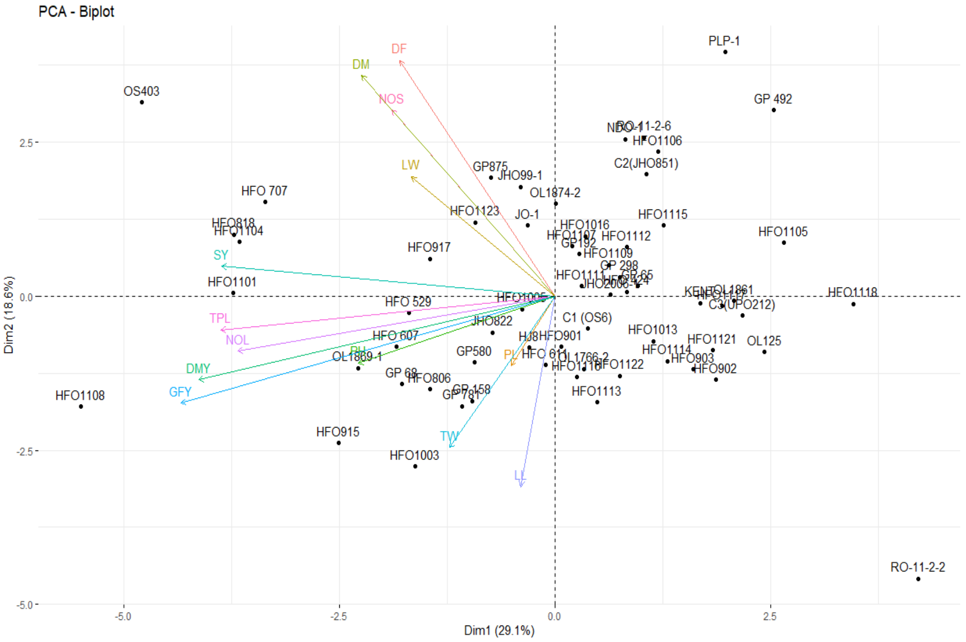

Fig. 2 Biplot showing relationships between variables and observations in a multivariate dataset

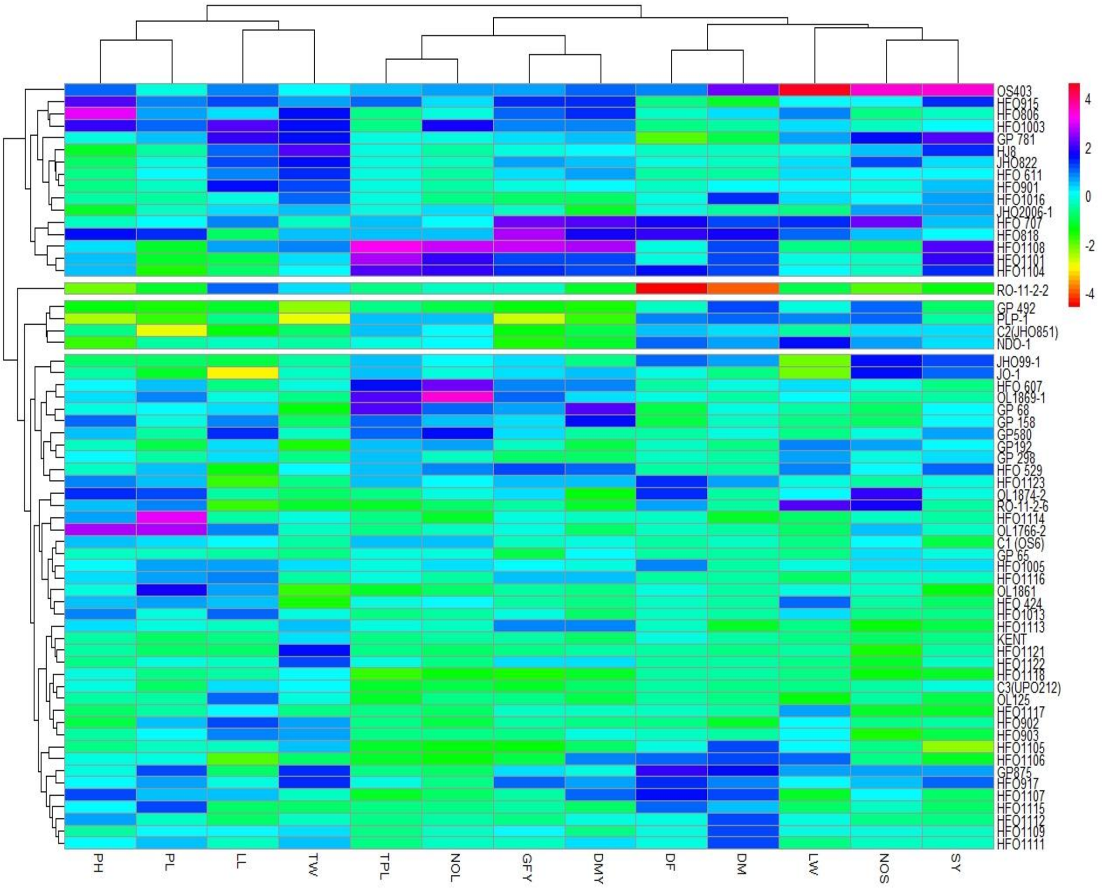

Fig. 3 Heat Map using R studio

Table 3. Multiple regression analysis of different morphological traits

	Regression coefficients	Estimate Std. Error	t value	Pr(>|t|)	
(Intercept)	-23.782	10.660	-2.231	0.030	*
PH	0.046	0.023	1.937	0.059	.
TPL	1.858	0.388	4.784	$1.62e^{-05}$	***
NOL	-0.101	0.056	-1.794	0.079	.
LL	0.040	0.065	0.613	0.543	
LW	0.503	0.823	0.612	0.543	
PL	-0.101	0.066	-1.521	0.135	
NOS	0.205	0.029	7.155	$3.81e^{-09}$	***
GFY	-0.0094	0.027	-0.343	0.733	
DMY	-0.037	0.094	-0.394	0.695	
DFF	-0.053	0.115	-0.461	0.647	
DM	0.010	0.083	0.125	0.901	
TW	0.369	0.073	5.056	$6.38e^{-06}$	***

Significance codes: '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1

Multiple R-squared: 0.793, Adjusted R-squared: 0.743

[PH- Plant height (cm), TPL- Number of tillers/plant, NOL- Number of leaves/plant, LL- Leaf length (cm), LW- Leaf width (cm), PL- Peduncle length (cm), NOS- Number of spikelets/panicle, GFY- Green fodder yield/plant (g), DMY- Dry matter yield/plant (g), DFF- Days to 50% flowering, DM- Days to maturity, SY- seed yield/plant (g), TW- Test weight]

variables, including PH and NOL, exhibited coefficients with p-values marginally above conventional significance thresholds. While their direct impact on the outcome might be subject to further investigation, their proximity to significance underscores their potential relevance in certain contexts. While interpreting these results, it's essential to consider the overall model fit, as indicated by the Multiple R-squared value of 0.793. This indicates that a significant portion of the variance in the dependent variable can be explained collectively by the included independent variables. The adjusted R-squared value of 0.742 accounts for the model's complexity, providing a balanced assessment of goodness of fit. The overall F-statistic, along with its p-value of 7.197e-13, highlights the collective predictive power of the model. This reaffirms that, collectively, the selected traits significantly contribute towards explaining the variability in the dependent variable. It can be concluded that this analysis offers a nuanced understanding of the relationships between various yield attributes and their influence on seed yield (Krishna *et al.,* 2014). These findings provide a robust foundation for future research endeavors, enabling the optimization of plant breeding strategies and the raising of healthier, more productive crops.

A comprehensive regression analysis was conducted to elucidate the relationships between various yield attributes and their influence on the seed yield. Regression analysis graphs were generated to visually represent these relationships for each trait (**Fig. 4 & 5**). These graphs offer valuable insights into the associations between the traits and the estimated outcome, helping to unravel the intricate interplay of factors that affect seed yield.

While traditional breeding methods have made strides, advanced statistical techniques like Principal Component Analysis and Regression Analysis offer transformative avenues for oat improvement. PCA revealed that 80.75% of total variability was contributed by five major components. Traits i.e., green fodder yield, dry matter yield, tillers per plant and seed yield significantly shape the oat population's variability, underlining their economic importance. Regression analysis quantifies relationships between variables, showcasing how traits i.e., tillers per plant, test weight and number of spikelets intricately influence seed yield. Combining these insights paints a promising future for oat improvement. As the world's population grows, the need for productive and resilient crops intensifies. By harnessing advanced statistical analyses, we embark on a journey to develop hardy oat varieties with improved yield and nutrition. This synergy between science and agriculture not only cultivates crops but also cultivates a future where sustenance and sustainability harmonize.

ACKNOWLEDGMENT

The corresponding author sincerely appreciates the support of CCSHAU, Hisar in supplying the necessary research materials and laboratory facilities for the experiment.

https://doi.org/10.37992/2024.1501.012

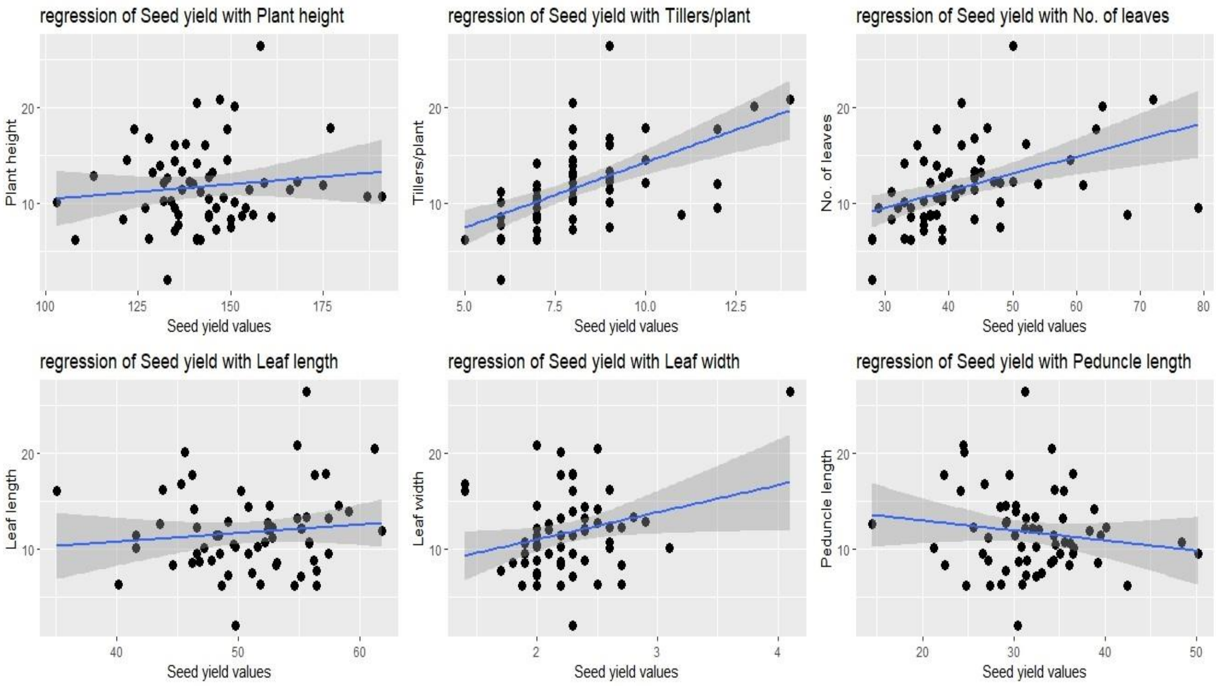

Fig. 4. **Regression graph of first six yield contributing traits. Each regression graph displays the trait of interest on the x-axis (seed yield) and the estimated outcome on the y-axis**

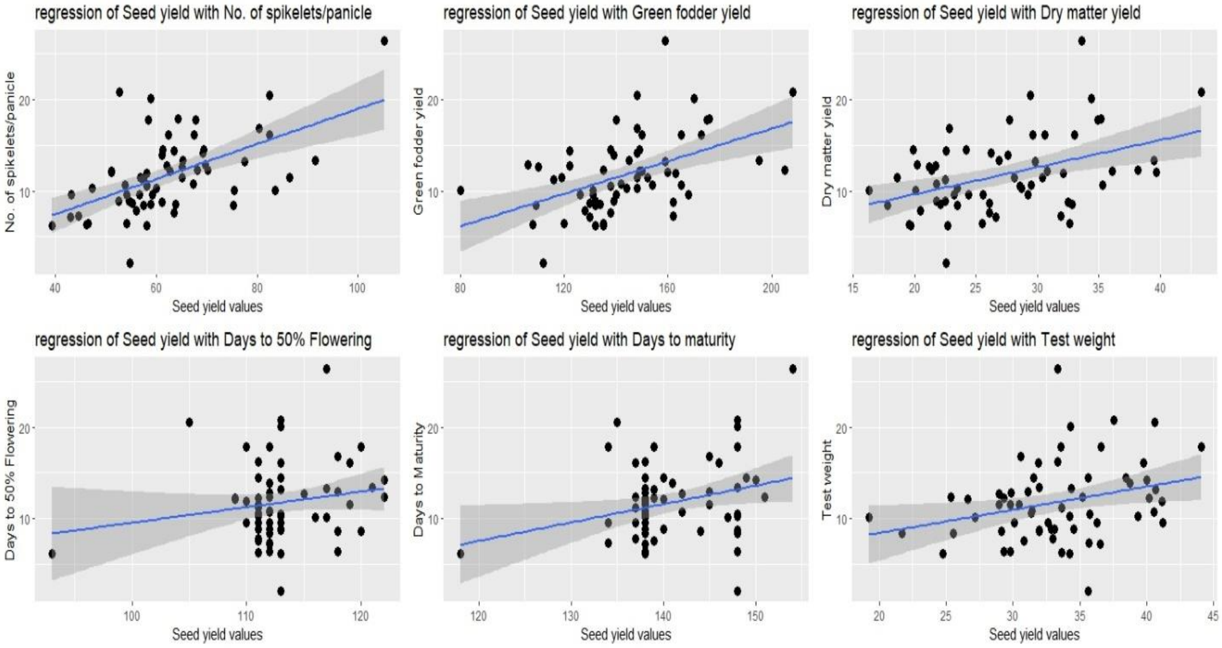

Fig. 5. Regression graph of next six yield attributes. Each regression graph displays the trait of interest on the x-axis (seed yield) and the estimated outcome on the y-axis

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