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CONTENTS

Association of germination and seedling vigour attributes with green forage yield in oat (*Avena sativa* L.) genotypes through correlation and path coefficient analysis

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ABSTRACT: The present investigation was carried out during the *Rabi* season of 2022–23 to evaluate thirteen oat (*Avena sativa* L.) genotypes for germination, seedling vigour, and their association with green forage yield. While seed quality parameters are routinely assessed in cereals, their potential as indirect selection criteria for green forage yield improvement in oat remains poorly documented, particularly for newly developed genotypes under north Indian agro-climatic conditions. The field experiment was conducted at the Dairy Farm, Nagla, Govind Ballabh Pant University of Agriculture and Technology (GBPUAT), Pantnagar, Uttarakhand, and the laboratory studies on seed quality parameters were carried out at the Seed Testing Laboratory, Breeder Seed Production Centre, GBPUAT, Pantnagar. The experiment was laid out in a Randomized Block Design with three replications. Ten genotypes (UPO-22-1 to UPO-22-10) along with three checks (UPO-212, UPO-10-2, and UPO-06-1) were evaluated for first count (%), standard germination (%), seedling root length (cm), germination index (GI), mean germination time (MGT), mean daily germination, time to 50% germination (T50), seedling fresh weight (g), seedling dry weight (g), seedling vigour index-I, seedling vigour index-II, speed of germination (SOG), relative growth index (RGI), and green forage yield (kg/plot). Significant genotypic variation was recorded for all traits studied. Genotype UPO-22-6 recorded the highest first count (93.67%) and standard germination (94.003%), while UPO-22-5 showed the lowest time to 50% germination (3.49 days) and UPO-22-9 exhibited the lowest mean germination time (3.94 days) and highest germination index (19.43), collectively identifying these genotypes as the most vigorous among those evaluated. Correlation analysis revealed that seedling fresh weight (SFW) was the only trait under given conditions with a significant positive association with green forage yield at both genotypic ($r = 0.431^{*}$) and phenotypic ($r = 0.431^{*}$) levels, while mean germination time showed a consistent negative trend with yield. Path coefficient analysis confirmed that SFW exerted the highest positive direct effect on green forage yield at both genotypic (+0.758) and phenotypic (+0.691) levels, establishing it as the most reliable indirect selection criterion for forage yield improvement. These findings suggest that simultaneous selection for high seedling fresh weight, high standard germination, and low mean germination time particularly in genotypes UPO-22-5 and UPO-22-6 would be an effective strategy for developing high-yielding, vigorous oat varieties.

Key words: *Avena sativa*, Germination, Seedling vigour, Path coefficient, Correlation, Green forage yield, Genotypic variation

Oat (*Avena sativa* L.) is an important cool-season cereal widely cultivated for forage due to its high biomass production, palatability, and adaptability under diverse agro-climatic conditions. In forage crops, early crop establishment is a critical determinant of final biomass yield, as it directly influences plant population, canopy development, and resource use efficiency. Seed germination and early seedling growth represent key physiological stages that govern successful establishment. High germination percentage ensures rapid and uniform emergence, leading to optimum plant stand, which is essential for maximizing light interception and minimizing inter-plant competition (Finch-Savage and Bassel, 2016). Early seedling vigour, characterized by traits such as root length, shoot length, and seedling biomass, plays a crucial role in determining the ability of plants to acquire water and nutrients during initial growth stages. A well-developed root system enhances soil exploration and nutrient uptake, while vigorous shoot growth supports early leaf area expansion and photosynthetic activity (Ellis, 1992).

These early advantages contribute to faster canopy establishment, improved radiation interception, and greater accumulation of photosynthates, which ultimately influence total biomass production and forage yield (Ghassemi-Golezani, 2014). Previous studies in oats and other cereal crops have reported positive associations between germination, seedling vigour traits, and yield components, indicating that early growth parameters can serve as useful indicators of crop performance under field conditions (Ghogare *et al*., 2022). Bukhari *et al*. (2009) demonstrated the usefulness of correlation and path coefficient analysis in identifying reliable selection criteria in fodder oat, reporting that traits such as plant height and tiller number exerted significant direct effects on forage yield.

Despite these advances, a critical knowledge gap persists: seed quality and seedling vigour parameters are rarely evaluated simultaneously with forage yield traits in oat, and their direct versus indirect causal contributions to green forage yield remain unquantified for newly developed genotypes under north Indian sub-humid conditions. Most available studies either focus on agronomic traits alone or examine germination parameters in isolation without linking them causally to field yield performance. Moreover, for the newly released GBPUAT oat genotypes evaluated here, no information on the relationship between seed vigour parameters and green forage productivity is available in the published literature. Identifying which specific seed quality traits exert genuine direct effects on forage yield, as opposed to traits whose apparent associations are confounded by indirect pathways, is essential for designing efficient early-generation selection schemes in oat breeding.

The present study was, therefore, undertaken with the hypothesis that specific seed quality and seedling vigour traits exhibit significant genotypic variation and are causally associated with green forage yield, and can thus serve as reliable indirect selection criteria in oat improvement programmes. The specific objectives were: (i) to assess genotypic variation for germination and seedling vigour parameters among thirteen oat genotypes; (ii) to determine the nature and magnitude of association between seed quality traits and green forage yield through genotypic and phenotypic correlation analysis; and (iii) to partition these associations into direct and indirect causal components using path coefficient analysis, thereby identifying the most effective traits for indirect selection for forage yield improvement.

MATERIALS AND METHODS

The present investigation was carried out during the *Rabi* season of 2022–23. The field experiment for seed production was conducted at the Dairy Farm, Nagla, Govind Ballabh Pant University of Agriculture and Technology (GBPUAT), Pantnagar, Uttarakhand, while the laboratory studies on seed quality parameters were conducted at the Seed Testing Laboratory, Breeder Seed Production Centre, GBPUAT, Pantnagar. The experimental material consisted of ten oat genotypes (UPO-22-1 to UPO-22-10) along with three checks (UPO-212, UPO-10-2, and UPO-06-1). The experiment was laid out in a Randomized Block Design with three replications in plots of size 5×5 m^2 (25 m^2 per plot). Seeds were sown in rows with a row-to-row spacing of 25 cm and a plant-to-plant spacing of 10 cm, following the standard agronomic practices recommended for forage oat cultivation at GBPUAT, Pantnagar. Green forage yield was recorded at harvest by sampling plants from a 25 m^2 area within each plot. All plants within the sampled area were harvested and weighed immediately to obtain fresh biomass. The recorded weight was expressed on a per plot basis, and average values were calculated across replications. Germination test was conducted in three replications, each containing 100 seeds taken randomly from each genotype. Seeds were kept in between paper (B.P.) media. Then the samples were placed at 20^0C (±1°C) in a temperature-controlled germinator (Hercules-type; capacity 200 petri plates). Seedling fresh weight and dry weight were recorded using a digital electronic balance (accuracy 0.001 g). Seedling root and shoot lengths were measured with a standard metric ruler to the nearest millimetre. Only normal seedlings, as defined by ISTA (2022) rules, were counted on the 5th day and 10th day of test. Observations were recorded for days to first count (%), standard germination (%), seedling root length (cm), seedling shoot length (cm), seedling fresh weight (g) and seedling dry weight (g). After that other seed quality parameters were calculated –

Seedling vigour index

The seedling vigour index was calculated by two different methods (Abdul Baki and Anderson, 1973).

(a)- *Seedling vigour index-I*= Standard germination (%) x Seedling length (cm)

(b)- *Seedling vigour index- II*= Standard germination (%) x Seedling dry weight (g)

Speed of germination

After the seed start to germinate, they were examined daily at approximately the same time each day. Normal seedlings were removed from the test when they reached a predetermined size. This procedure was continued until all seed that could produce a normal seedling had germinated. An index was computed for each treatment by dividing the number of normal seedlings removed each day by the corresponding day of counting.

Relative growth index (RGI) (Brown and Mayer, 1988)

$$\text{RGI}=\frac{\text{No. of seed germinated at I count}}{\text{No. of seed germinated at final count}} \times 100$$

Germination index (GI)

Germination index (GI) was computed as described in the association of official seed Analysts (1983)[7] using the following formula:

$$\text{GI}=\frac{\text{No. of germinated seeds}}{\text{Days of first count}}+....+\frac{\text{No. of germinated seeds}}{\text{Days of final count}}$$

Mean Germination Time (MGT)(Days) (Ellis and Roberts, 1981)

$$\text{MGT}=\frac{\Sigma Dn}{\Sigma n}$$

Where, n is the number of seeds which were germinated on day D, and D is the number of days counted from the start of germination.

Mean Daily Germination (MDG)

$$\text{MDG}=\frac{\text{Final Germination Percentage}}{\text{Total number of days}}$$

Time to 50% Germination (T_{50}) (Coolbear et al., 1984; Farooq et al., 2005)

$$T_{50}=T_i+\frac{(\frac{N}{2}-n_i)(t_i-t_i)}{n_i-n_i}$$

where N = final number of seeds germinated, n_i and n = cumulative germination numbers at time t_i and t respectively when $n_i < N/2 < n_i$

Analysis of Variance (ANOVA)

To assess the presence of significant differences among genotypes for the studied traits, analysis of variance was performed as per the procedure given by Panse and Sukhatme (1985). The significance of the mean square values was tested using the *F-test* at 5% and 1% probability levels.

Correlation Analysis

The correlation coefficients were estimated using the following expressions: (Johnson *et al*., 1955)

Genotypic correlation coefficient

$$r_{g(xy)}=\frac{g\ Cov(x,y)}{\sqrt{g\ V_x \times g\ V_y)}}$$

Phenotypic correlation coefficient

$$r_{p(xy)}=\frac{p\ Cov(x,y)}{\sqrt{p\ V_x \times p\ V_y)}}$$

Significance of correlation coefficients was tested using *t*-values at 5% and 1% levels of probability.

Path Coefficient Analysis

The path analysis method, pioneered by Wright (1921), provides standardized partial regression coefficients. These coefficients allow for dissecting the correlation coefficient into direct and indirect influences, as further developed by Dewey and Lu (1959). Path coefficient analysis partitions correlation coefficients into direct and indirect effects, enabling identification of traits that directly influence yield as well as those that act indirectly through other traits.

RESULTS AND DISCUSSION

Mean Performance of Genotypes for Germination and Seedling Vigour Traits

The mean performance of thirteen oat (*Avena sativa* L.) genotypes evaluated for germination and seedling

Table 1: **Mean performances by different genotypes for various parameters**

Genotypes	First count (%)	Standard germination (%)	Seedling root length (cm)	Germination index (GI)	Mean germination time (MGT)	Mean daily germination	Time to 50% germination (T50)
UPO-22-1	76.34	87.337	17.633	17.297	4.817	9.057	4.063
UPO-22-2	82.003	90.337	18.997	19.253	4.437	9.687	3.693
UPO-22-3	76.673	88.34	15.533	17.17	4.147	8.953	3.55
UPO-22-4	74.003	86.003	18.247	17.187	4.65	9.133	4.373
UPO-22-5	85.003	94	18.707	18.807	4.283	9.94	3.493
UPO-22-6	93.67	94.003	17.38	18.877	4.033	9.547	3.543
UPO-22-7	87.673	93.007	16.927	19.037	4.347	9.757	3.677
UPO-22-8	76.003	89.007	16.443	16.467	4.637	8.477	3.913
UPO-22-9	90.67	86.34	14.513	19.427	3.943	9.523	3.513
UPO-22-10	65.007	88.34	16.663	17.743	5.057	9.15	4.177
UPO-212	28.603	80.673	17.633	15.647	4.367	8.107	3.997
UPO-10-2	77.67	89.337	17.12	18.293	4.573	10.163	3.903
UPO-06-1	60.673	71.337	15.057	14.16	4.917	7.267	4.177
Mean	74.92	87.54	16.99	17.64	4.48	9.14	3.85
CV	2.05	2.19	2.27	2.57	2.5	2.46	2.63
Sem	0.89	1.11	0.22	0.26	0.06	0.13	0.06
CD at 5%	2.59	3.23	0.65	0.76	0.19	0.38	0.17
CD at 1%	3.5	4.38	0.88	1.04	0.26	0.51	0.23
Minimum	28.6	71.34	14.51	14.16	3.94	7.27	3.49
Maximum	93.67	94	19	19.43	5.06	10.16	4.37
Replication	NS	NS	NS	NS	NS	NS	NS
Treatment	S	S	S	S	S	S	S

Table 1a: **Analysis of Variance (ANOVA) for germination and seedling vigour parameters in oat genotypes**

Sl. No.	Character	Replication MSS (d.f.=2)	Treatment MSS (d.f.=12)	Error MSS (d.f.=24)
1	First count (%)	4.901	843.815**	2.356
2	Standard germination (%)	0.275	110.353**	3.672
3	Seedling root length (cm)	0.006	5.488**	0.149
4	Seedling fresh weight (g)	0.004	0.420**	0.003
5	Seedling dry weight (g)	0.003	0.019**	0.002
6	Seedling vigour index-I	2147.478	434727.052**	4463.843
7	Seedling vigour index-II	0.179	167.844**	0.178
8	Speed of germination	0.259	25.282**	0.344
9	Relative growth index (RGI)	4.975	146.696**	4.733
10	Germination index (GI)	0.151	7.270**	0.206
11	Mean germination time (MGT)	0.001	0.342**	0.012
12	Mean daily germination	0.0002	1.934**	0.050
13	Time to 50% germination (T… €)	0.004	0.260**	0.010
14	Green forage yield (kg/plot)	2.013	407.306**	94.054

MSS = Mean Sum of Squares; ** Significant at 1% level of significance; NS = Non-Significant; d.f. = degrees of freedom. Source: Thesis Table 4.1.1 (Manish Mehra, 2024, GBPUAT Pantnagar).

vigour parameters is presented in Table 1. The analysis of variance (ANOVA) presented in Table 1a revealed highly significant differences ($p \leq 0.01$) among genotypes for all germination and seedling vigour traits studied. The treatment mean sum of squares (MSS) was remarkably high for first count (843.815) and standard germination (110.353), reflecting strong genotypic differentiation for these key germination parameters. Similarly, seedling vigour index-I recorded an exceptionally large treatment MSS (434727.052) owing to the multiplicative nature of its computation. Among individual parameters, germination index (7.270), mean germination time (0.342), speed of germination (25.282), and relative growth index (146.696) also showed highly significant treatment MSS, confirming that genotypic differences were consistent across all aspects of germination

Table 2: **Combined Genotypic (upper right) and Phenotypic (lower left) Correlation Matrix**

	SG (%)	SRL (cm)	SSL (cm)	SFW (g)	SDW (g)	SVI-I	SVI-II	SOG	RGI	MGT	GFY (kg/plot)
SG (%)	1	0.418*	0.469*	0.417*	0.117	0.803**	0.308	0.777**	0.377*	-0.409*	0.150
SRL (cm)	0.418*	1	0.060	0.644**	0.578**	0.529**	0.630**	0.208	-0.019	0.082	0.006
SSL (cm)	0.470*	0.060	1	0.064	0.133	0.580**	0.197	0.631**	0.737**	-0.747**	0.007
SFW (g)	0.417*	0.644**	0.064	1	0.733**	0.369*	0.776**	0.225	0.184	-0.212	0.431*
SDW (g)	0.117	0.578**	0.133	0.733**	1	0.250	0.972**	0.115	0.129	-0.200	0.134
SVI-I	0.804**	0.529**	0.580**	0.370*	0.250	1	0.427*	0.864**	0.466*	-0.484*	0.085
SVI-II	0.308	0.630**	0.197	0.776**	0.972**	0.427*	1	0.303	0.208	-0.267	0.166
SoG	0.778**	0.208	0.631**	0.225	0.115	0.865**	0.303	1	0.619**	-0.715**	0.122
RGI	0.377*	-0.019	0.738**	0.184	0.130	0.469*	0.210	0.620**	1	-0.827**	0.295
MGT	-0.409*	0.082	-0.748**	-0.212	-0.200	-0.485*	-0.268	-0.715**	-0.828**	1	-0.290
GFY (kg/plot)	0.150	0.007	0.007	0.431*	0.134	0.085	0.166	0.123	0.296	-0.290	1

(Values presented are Pearson's genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients. Note- SG Standard germination (%), SRL Seedling root length (cm.), SSL Seedling shoot length (cm.), SFW Seedling fresh weight (g), SDW Seedling dry weight (g), SVI-I Seedling vigour index-I, SVI-II Seedling vigour index- II, SOG Speed of germination, RGI Relative growth index (RGI), MGT Mean germination time (MGT), GFY Green forage yield (kg/plot), $^{*}P \leq 0.05$, $^{**}P \leq 0.01$)

Table 3: **Genotypic path coefficients for traits**

	SG	SRL	SSL	SFW	SDW	SVI-I	SVI-II	SOG	RGI	MGT	GFY
SG	+0.0236	-0.1271	-0.1931	+0.3161	+0.0366	+0.1066	-0.1950	-0.0098	+0.1360	+0.0561	0.150
SRL	+0.0099	-0.3040	-0.0247	+0.4882	+0.1808	+0.0702	-0.3988	+0.0026	-0.0069	-0.0112	0.006
SSL	+0.0111	-0.0182	-0.4117	+0.0485	+0.0416	+0.0770	-0.1247	+0.0080	+0.2731	+0.1024	0.007
SFW	+0.0098	-0.1958	-0.0263	+0.7580	+0.2293	+0.0490	-0.4912	+0.0028	+0.0664	+0.0291	0.431*
SDW	+0.0028	-0.1757	-0.0548	+0.5556	+0.3128	+0.0332	-0.6153	+0.0014	+0.0465	+0.0274	0.134
SVI-I	+0.0190	-0.1608	-0.2388	+0.2797	+0.0782	+0.1327	-0.2703	+0.0109	+0.1681	+0.0663	0.085
SVI-II	+0.0073	-0.1915	-0.0811	+0.5882	+0.3041	+0.0566	-0.6330	+0.0038	+0.0751	+0.0366	0.166
SOG	-0.0183	-0.0632	-0.2598	+0.1706	+0.0360	+0.1146	-0.1918	+0.0126	+0.2234	+0.0980	0.122
RGI	+0.0089	+0.0058	-0.3117	+0.1395	+0.0404	+0.0618	-0.1317	+0.0078	+0.3608	+0.1134	0.295
MGT	-0.0097	-0.0249	+0.3075	-0.1607	-0.0626	-0.0642	+0.1690	-0.0090	-0.2984	-0.1371	-0.290

(Note- SG Standard germination (%), SRL Seedling root length (cm.), SSL Seedling shoot length (cm.), SFW Seedling fresh weight (g), SDW Seedling dry weight (g), SVI-I Seedling vigour index-I, SVI-II Seedling vigour index- II, SOG Speed of germination, RGI Relative growth index (RGI), MGT Mean germination time (MGT), GFY Green forage yield (kg/plot), $^{*}P \leq 0.05$, $^{**}P \leq 0.01$)

performance. Seedling fresh weight (0.420) and seedling dry weight (0.019), though smaller in absolute magnitude, were likewise highly significant, attesting to genuine genotypic variation in early seedling biomass accumulation. The replication mean sum of squares was non-significant for all traits, indicating field uniformity and confirming the reliability of the experimental layout. The coefficient of variation (CV) ranged from 2.05% (first count) to 2.63% (T50), reflecting a high degree of experimental precision.

First Count (%)

The first count percentage, which reflects the initial speed and uniformity of germination, ranged widely from 28.60% (UPO-212) to 93.67% (UPO-22-6), with a grand mean of 74.92% (Table 1). Genotype UPO-22-6 recorded the highest first count (93.67%), followed by UPO-22-9 (90.67%) and UPO-22-7 (87.67%), all of which were significantly superior to the general mean. In contrast, UPO-212 (28.60%) and UPO-06-1 (60.67%) performed consistently below the mean, indicating poor early germination capacity. The wide range observed for this trait underscores the differential potential of these genotypes for rapid and uniform seedling establishment, a characteristic of practical importance under field conditions. Similar variability in first count among genotypes has been documented in cereal crops (Mut and Akay, 2010).

Table 4: **Phenotypic path coefficients for traits**

	SG	SRL	SSL	SFW	SDW	SVI-I	SVI-II	SOG	RGI	MGT	GFY
SG	-0.0798	-0.1172	-0.1647	+0.2881	-0.1479	+0.2829	+0.3057	-0.5131	+0.0839	+0.2122	0.150
SRL	-0.0334	-0.2805	-0.0210	+0.4449	-0.7305	+0.1861	+0.6253	-0.1372	-0.0042	-0.0425	0.007
SSL	-0.0375	-0.0168	-0.3505	+0.0442	-0.1681	+0.2041	+0.1955	-0.4161	+0.1642	-0.0042	0.007
SFW	-0.0333	-0.1806	-0.0224	+0.6908	-0.9264	+0.1302	+0.7703	-0.1484	+0.0409	+0.1642	0.431*
SDW	-0.0093	-0.1621	-0.0466	+0.5063	-1.2639	+0.0880	+0.9648	-0.0758	+0.0289	+0.0409	0.134
SVI-I	-0.0642	-0.1484	-0.2033	+0.2556	-0.3160	+0.3519	+0.4238	-0.5704	+0.1043	+0.0289	0.085
SVI-II	-0.0246	-0.1767	-0.0691	+0.5361	-1.2285	+0.1503	+0.9926	-0.1998	+0.0467	+0.1043	0.166
SOG	-0.0621	-0.0583	-0.2212	+0.1554	-0.1453	+0.3044	+0.3008	-0.6595	+0.1379	+0.0467	0.123
RGI	-0.0301	+0.0053	-0.2587	+0.1271	-0.1643	+0.1650	+0.2084	-0.4089	+0.2225	+0.1379	0.296
MGT	+0.0326	-0.0230	+0.2622	-0.1464	+0.2528	-0.1707	-0.2660	+0.4715	-0.1842	-0.5188	-0.290

(Note- SG Standard germination (%), SRL Seedling root length (cm.), SSL Seedling shoot length (cm.), SFW Seedling fresh weight (g), SDW Seedling dry weight (g), SVI-I Seedling vigour index-I, SVI-II Seedling vigour index- II, SOG Speed of germination, RGI Relative growth index (RGI), MGT Mean germination time (MGT), GFY Green forage yield (kg/plot), $^{*}P \leq 0.05$, $^{**}P \leq 0.01$)

Standard Germination (%)

Standard germination percentage, a key indicator of seed quality and lot viability, ranged from 71.34% (UPO-06-1) to 94.003% (UPO-22-6), with a mean of 87.54%. Genotypes UPO-22-6 (94.003%) and UPO-22-5 (94.00%) recorded the maximum standard germination and were statistically at par with each other, followed by UPO-22-7 (93.007%). These three genotypes consistently exceeded the 90% threshold, which is generally considered acceptable for certified seed lots (AOSA 1983). UPO-06-1 recorded the lowest standard germination (71.34%), well below the population mean. The close agreement between first count and standard germination rankings for the top performers (UPO-22-6, UPO-22-5) suggests that these genotypes possess inherently superior seed quality characteristics. These results are consistent with earlier studies reporting significant differences among oat genotypes for germination percentage (Willenborg *et al*., 2005).

Seedling Root Length (cm)

Seedling root length, an important indicator of seedling establishment potential and early root development, varied from 14.51 cm (UPO-22-9) to 19.00 cm (UPO-22-2), with a mean of 16.99 cm. Genotype UPO-22-2 exhibited the longest root length (18.997 cm), followed by UPO-22-5 (18.707 cm) and UPO-22-4 (18.247 cm). Interestingly, UPO-22-9, which was a top performer for germination percentage and speed, recorded the shortest root length (14.51 cm), indicating that germination speed and root elongation may be independently regulated processes. UPO-06-1 also showed a below-average root length (15.06 cm). Seedling root length is known to be an important contributor to seedling vigour and early nutrient acquisition (Barik *et al*., 2022).

Germination Index (GI)

The germination index (GI), which integrates germination speed and percentage, ranged from 14.16 (UPO-06-1) to 19.43 (UPO-22-9), with a mean of 17.64. UPO-22-9 recorded the highest GI (19.427), followed by UPO-22-2 (19.253) and UPO-22-7 (19.037), while UPO-06-1 showed the lowest GI (14.16) and UPO-212 (15.65) also performed poorly. A higher GI indicates more vigorous and rapid seed germination (Reed *et al*., 2022). The superior performance of UPO-22-9 and UPO-22-2 for GI, despite their contrasting root length values, reflects the multi-dimensional nature of seedling vigour, where different component traits may be governed by distinct genetic mechanisms.

Mean Germination Time (MGT)

Mean germination time (MGT) is a negative indicator of germination performance, with lower values reflecting faster germination. MGT ranged from 3.94 days (UPO-22-9) to 5.06 days (UPO-22-10), with a mean of 4.48 days. UPO-22-9 exhibited the shortest MGT (3.943 days), followed by UPO-22-6 (4.033 days) and UPO-22-5 (4.283 days), confirming the superior germination speed of these genotypes. UPO-22-10 (5.057 days) and UPO-22-1 (4.817 days) showed the longest MGT, indicating delayed germination. The negative relationship of MGT with other germination traits is expected, as genotypes that germinate faster inherently have lower mean germination time. Similar variations in MGT among oat and cereal genotypes have been reported (Mut and Akay, 2010).

Mean Daily Germination and Time to 50% Germination (T50)

Mean daily germination ranged from 7.27 (UPO-06-1) to 10.163 (UPO-10-2), with a population mean of 9.14. UPO-10-2 recorded the highest mean daily germination (10.163), closely followed by UPO-22-5 (9.94) and UPO-22-7 (9.757), indicating a high rate of daily seed germination. UPO-06-1 (7.267) and UPO-212 (8.107) showed the poorest daily germination rates. Time to 50% germination (T50), another negative indicator, ranged from 3.49 days (UPO-22-5) to 4.37 days (UPO-22-4). UPO-22-5 reached 50% germination earliest (3.493 days), followed by UPO-22-3 (3.55 days) and UPO-22-6 (3.543 days), further confirming the vigour superiority of these genotypes.

Overall, considering all germination and seedling vigour parameters evaluated, genotypes UPO-22-6 and UPO-22-5 emerged as the most consistently superior performers, recording the highest values for first count, standard germination, mean daily germination, and the lowest T50 and MGT. UPO-22-9 was outstanding specifically for germination index and MGT, while UPO-22-2 excelled for seedling root length and GI. On the other hand, UPO-212 and UPO-06-1 consistently underperformed across most parameters. These genotypic differences reflect the inherent genetic diversity for seed quality and vigour among the studied oat accessions, which can be exploited in breeding programmes aimed at improving germination and early seedling establishment.

Correlation Analysis

Correlation analysis was performed to determine the nature and magnitude of association between germination and seedling vigour traits with green forage yield (GFY, kg/plot) as well as inter-trait associations. Both genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients were estimated and are presented in Table 2. In general, genotypic correlations were slightly higher in magnitude than the corresponding phenotypic correlations, suggesting that the associations between traits are largely under genetic control with minimal environmental interference (Fazlul Islam *et al*., 2021). This pattern is commonly observed in cereal crops and indicates that the observed trait associations are heritable and can be effectively exploited in selection programmes (Tesfaye *et al*., 2020).

Correlation of Traits with Green Forage Yield (GFY)

Among all germination and seedling vigour traits examined, seedling fresh weight (SFW) was the only trait to exhibit a significant positive correlation with GFY at both the genotypic ($r = 0.431^*$) and phenotypic ($r = 0.431^*$) levels. This consistent significant association at both levels further strengthens the reliability of SFW as a trait associated with forage yield potential. The positive direction of this relationship indicates that genotypes with higher seedling fresh weight tend to produce greater forage yield, possibly reflecting early biomass accumulation capacity as a determinant of productive potential (Barik *et al*., 2022).

Mean germination time (MGT) showed a negative correlation with GFY at both genotypic (r = -0.290) and phenotypic (r = -0.290) levels, though these did not attain statistical significance. The negative direction of this association is biologically meaningful, as genotypes that germinate more slowly (higher MGT) tended to produce lower forage yields, suggesting that germination speed has some bearing on overall plant productivity. Relative growth index (RGI) showed a positive but non-significant genotypic (r = 0.295) and phenotypic (r = 0.296) correlation with GFY. Seedling vigour index-II (SVI-II) also showed a positive association (genotypic r = 0.166; phenotypic r = 0.166), though non-significant. The remaining traits — SG, SRL, SSL, SDW, SVI-I, and SOG — showed very low and non-significant correlations with GFY at both levels, indicating their limited direct linear association with forage yield under the present experimental conditions.

Inter-trait Correlations

Examination of inter-trait associations revealed several noteworthy relationships. Seedling vigour index-I (SVI-I) showed highly significant positive genotypic correlations with standard germination (r = 0.803**), speed of germination (SOG) (r = 0.864**), and seedling shoot length (SSL) (r = 0.580**), indicating that SVI-I integrates information from multiple germination and growth components, as expected from its computational formula. Similarly, SDW and SVI-II were highly correlated with each other (r = 0.972**) at the genotypic level, reflecting the near-perfect biological relationship between these traits since SVI-II is derived from SDW (Dewey & Lu, 1959).

MGT showed significant negative genotypic correlations with SSL (r = -0.747**), RGI (r = -0.827**), and SOG (r = -0.715**), confirming that delayed germination is associated with reduced growth rate and lower germination speed a biologically consistent pattern. RGI and SSL also showed a high positive genotypic correlation (r = 0.737**), suggesting that seedling shoot growth and relative growth are closely linked processes. Standard germination (SG) was significantly positively correlated with SVI-I (r = 0.803**) and SOG (r = 0.777**) at the genotypic level, affirming that genotypes with higher germination percentage also tend to germinate more quickly and produce more vigorous seedlings. These inter-trait correlations are consistent with findings reported in earlier studies on oat and other cereal species (Barik *et al.*, 2022).

Path Coefficient Analysis

Path coefficient analysis was carried out to partition the correlation coefficients of each germination and seedling vigour trait with green forage yield (GFY) into direct and indirect effects, thereby identifying traits that exert genuine causal influence on yield versus those whose correlations are mediated indirectly through other traits. Genotypic and phenotypic path coefficients are presented in Tables 3 and 4, respectively. The analysis is based on the principle that the correlation of each trait with GFY equals the sum of its direct path coefficient and its indirect effects through all other traits included in the model (Dewey and Lu, 1959).

Genotypic Path Coefficients

At the genotypic level, seedling fresh weight (SFW) exhibited the highest positive direct effect on GFY (direct path coefficient = +0.7580), indicating that it exerts a strong and genuine positive causal influence on forage yield independent of other traits. This finding is further validated by its significant positive genotypic correlation with GFY (r = 0.431*), establishing SFW as the most important and reliable selection criterion for improving forage yield in oat. The correspondence between a high direct effect and significant correlation for SFW confirms that this trait's association with GFY is real and direct, not confounded by indirect pathways (Bukhari *et al.*, 2009).

Relative growth index (RGI) also showed a moderately high positive direct effect on GFY (direct path = +0.3608), and its positive but non-significant correlation (r = 0.295) with GFY may be partially attributable to negative indirect effects operating through other traits, particularly through SSL (-0.3117) and MGT (+0.1134), which partly offset its direct contribution. Seedling dry weight (SDW) showed a moderately positive direct genotypic effect (+0.3128), however its low correlation with GFY (r = 0.134) suggests that its direct contribution is suppressed by negative indirect effects, primarily *via* SVI-II (-0.6153) and SFW (+0.5556). Seedling vigour index-I (SVI-I) had a positive direct effect of +0.1327, while standard germination (SG) and speed of germination (SOG) had negligible direct effects (+0.0236 and +0.0126 respectively), suggesting minimal direct causal contribution to GFY.

Seedling vigour index-II (SVI-II) recorded the highest negative direct genotypic effect on GFY (-0.6330), followed by seedling shoot length (SSL) (-0.4117) and seedling root length (SRL) (-0.3040).

The high negative direct effect of SVI-II, despite its positive correlation with GFY (r = 0.166), reveals a classic case of suppression, where large positive indirect effects (particularly through SFW: +0.5882 and SDW: +0.3041) mask the negative direct relationship. This underscores the importance of path analysis in correctly identifying the true nature of trait relationships when correlation alone may be misleading [Dewey & Lu (1959)]. MGT showed a moderate negative direct genotypic effect (-0.1371) on GFY, consistent with the biological expectation that delayed germination may have some unfavorable influence on subsequent plant productivity.

Phenotypic Path Coefficients

At the phenotypic level, the direct effects showed broadly similar trends to the genotypic path analysis, though with some notable differences in magnitude, reflecting the additional influence of environmental effects at the phenotypic level. Seedling fresh weight (SFW) again recorded the highest positive direct phenotypic effect on GFY (+0.6908), reinforcing its central role as a primary driver of forage yield. Seedling vigour index-II (SVI-II) showed the highest positive direct phenotypic effect (+0.9926), a reversal from its negative genotypic direct effect, indicating that at the phenotypic level, environmental co-variation alters the nature of its influence. This divergence between genotypic and phenotypic path coefficients for SVI-II highlights the considerable environmental component in the expression of this trait and counsels caution in using it as a selection index at the phenotypic level.

Seedling vigour index-I (SVI-I) also showed a positive direct phenotypic effect (+0.3519), and RGI recorded a moderate positive direct effect (+0.2225). On the negative side, SDW exhibited the largest negative direct phenotypic effect (-1.2639), suggesting strong suppressor effects at the phenotypic level likely because its high phenotypic correlation with SVI-II (r = 0.972) creates a situation where most of its contribution to GFY is confounded. SOG (-0.6595), MGT (-0.5188), SSL (-0.3505), and SRL (-0.2805) also showed negative direct phenotypic effects of varying magnitudes. SG showed a negligible negative direct effect (-0.0798) at the phenotypic level.

Taken together, both genotypic and phenotypic path analyses consistently identify seedling fresh weight (SFW) as the single most important trait with a large, positive direct effect on green forage yield at both genotypic (+0.758) and phenotypic (+0.691) levels. This consistency across both analytical levels constitutes a clear finding of this study and validates SFW as the most reliable criterion for indirect selection for forage yield in oat.

An unexpected finding of this study was the reversal in the direction of the direct path coefficient of seedling vigour index-II (SVI-II) between the genotypic (-0.6330) and phenotypic (+0.9926) levels. At the genotypic level, SVI-II exerted a strong negative direct effect on GFY despite its positive correlation (r = 0.166), indicating a classic suppressor relationship where its large positive indirect effects through SFW (+0.5882) and SDW (+0.3041) mask the underlying negative direct contribution. At the phenotypic level, however, SVI-II showed a high positive direct effect (+0.9926), which can be attributed to the strong environmental co-variation between SVI-II and GFY: since SVI-II is computed as the product of standard germination percentage and seedling dry weight, both of which respond to seasonal environmental conditions, the phenotypic path coefficient absorbs a substantial environmental covariance component that inflates its apparent direct contribution. This divergence between genotypic and phenotypic path coefficients for SVI-II is consistent with observations in other cereal crops where derived index traits show greater sensitivity to environmental fluctuations than their component traits (Tesfaye *et al*., 2020). This finding underscores the importance of estimating path coefficients at both levels and basing selection decisions on genotypic path coefficients when the objective is to exploit heritable genetic variation. These findings are in agreement with earlier reports emphasizing the utility of path analysis in identifying key selection criteria in forage crops (Bukhari *et al*., 2009).

It is important to clearly distinguish between the empirical findings of this study and the inferences drawn from them. The findings are: (i) SFW showed a significant positive genotypic and phenotypic correlation with GFY ($r = 0.431^{*}$); (ii) SFW exerted the highest positive direct path effect on GFY at both levels; (iii) treatment mean squares were highly significant for all fourteen traits evaluated; and (iv) replication effects were non-significant, confirming field homogeneity. The inferences drawn from these findings are: that SFW reflects early biomass accumulation capacity and is heritably linked to forage productivity; that simultaneous selection for high SFW, high standard germination percentage, and low MGT would be an effective indirect selection strategy; and that genotypes UPO-22-5 and UPO-22-6 are the most promising candidates for further advancement. These inferences are supported by the data but represent interpretations based on the biological mechanisms of seedling growth and forage yield formation.

Certain limitations of this study must be acknowledged. First, the experiment was conducted over a single season (Rabi 2022-23) at one location; hence, the stability of the observed associations across seasons and environments remains to be confirmed. Genotype-by-environment interaction may alter the relative ranking of genotypes and the magnitude of trait-yield correlations in different agro-climatic conditions. Second, the path coefficient analysis included only the seed quality and seedling vigour traits studied here; agronomic traits such as plant height, tillering capacity, and canopy architecture, which are also known to influence forage yield, were not included in the path model, which may have inflated or deflated some indirect effects. Third, although SFW showed a significant positive association with GFY, the overall coefficient of determination of the path model was not maximized, suggesting that additional traits beyond those studied may contribute to the unexplained variation in forage yield. Future studies should evaluate these genotypes across multiple environments, include a broader set of morpho-physiological traits in the path model, and validate the identified selection indices in advanced-generation populations.

Synthesizing the results from mean performance, correlation, and path coefficient analyses, genotypes UPO-22-5 and UPO-22-6 demonstrate the most consistent superiority for germination and seedling vigour parameters, while UPO-22-2 and UPO-22-9 are notable for specific traits. From a trait perspective, seedling fresh weight (SFW) emerges as the most critical trait, being the only parameter with a significant positive correlation with GFY and consistently the highest positive direct effect in both genotypic and phenotypic path analyses. Therefore, selection based on SFW, alongside high standard germination percentage and low MGT, would be the most effective strategy for improving green forage yield in oat breeding programmes. Genotypes UPO-212 and UPO-06-1 showed consistent inferiority across parameters and may be excluded from further selection cycles unless specific traits of interest are identified.

CONCLUSION

The present investigation on thirteen oat (*Avena sativa* L.) genotypes evaluated for germination, seedling vigour, and their association with green forage yield led to several important conclusions of breeding significance. Considerable and statistically significant genotypic variation was recorded for all traits studied, confirming the presence of exploitable genetic diversity within the experimental material. Among the genotypes evaluated, UPO-22-6 and UPO-22-5 emerged as the most consistently superior performers across germination and seedling vigour parameters, recording the highest standard germination, first count, and the most favourable germination speed indices, making them promising candidates for use as parents in hybridization programmes or for direct varietal advancement.

Correlation analysis revealed that seedling fresh weight (SFW) was the only trait to show a significant positive association with green forage yield at both genotypic and phenotypic levels under given conditions, while mean germination time (MGT) showed a consistent negative trend with yield, reinforcing the biological importance of early and rapid germination for subsequent crop productivity. Path coefficient analysis further validated these findings by demonstrating that SFW exerted the highest positive direct effect on green forage yield at both levels of analysis, establishing it as the most reliable and effective criterion for indirect selection for forage yield improvement.

In conclusion, simultaneous selection for high seedling fresh weight, high standard germination percentage, and low mean germination time, particularly in genotypes such as UPO-22-5 and UPO-22-6, would be the most productive strategy for improving green forage yield in oat. These results provide a valuable foundation for future breeding efforts aimed at developing high-yielding, vigorous oat varieties suited to varied agro-climatic conditions.

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