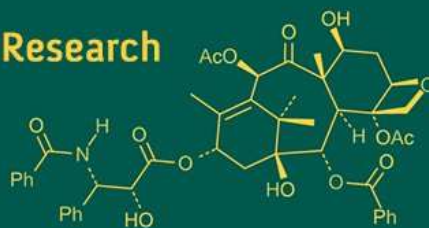
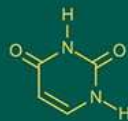
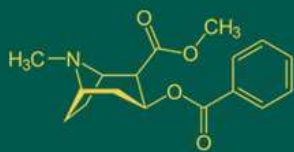


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Anchal Mishra
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya,
Raipur, Chhattisgarh, India

J H Kahodariya
Deputy Project Director,
ATMA, Department of
Agriculture, Cooperation and
Farmers Welfare, Botad,
Gujarat, India

Manoj Kumar
Assistant Professor-cum-
Junior Scientist, Department
of Genetics and Plant
Breeding, Bihar Agricultural
University, Sabour, Bihar,
India

Biju Sidharthan
Scientist, Department of Plant
Breeding and Genetics, College
of Agriculture, Vellanikkara,
Kerala Agricultural
University, Thrissur, Kerala,
India

Parshuram Sial
Associate Director of Research,
Regional Research and
Technology Transfer Station,
Odisha University of
Agriculture and Technology,
Semiliguda, Koraput, Odisha,
India

Corresponding Author:
Anchal Mishra
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya,
Raipur, Chhattisgarh, India

Genotypic and Phenotypic Correlation Architecture of Green Forage Yield and Its Component Traits in Grass Pea (*Lathyrus sativus* L.): Implications for Multi-Trait Selection in a Forty-Four-Accession Germplasm Panel

Anchal Mishra, JH Kahodariya, Manoj Kumar, Biju Sidharthan and Parshuram Sial

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Abstract

Grass pea (*Lathyrus sativus* L., $2n = 14$) is a hardy, protein-rich legume of marginal and moisture-stressed tracts, valued simultaneously as a pulse and a dual-purpose forage crop. Because green forage yield is a polygenic trait that represents the multiplicative end-product of numerous component characters, a precise understanding of the strength, direction and genetic basis of inter-trait association is a prerequisite for designing an efficient multiple-trait selection scheme. The present investigation was carried out on a genetically diverse panel of forty-four grass pea genotypes, comprising local landraces and improved breeding lines, evaluated in a randomized block design with three replications at the Research-cum-Instructional Farm of Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, during the Rabi season of 2024. Genotypic and phenotypic correlation coefficients were estimated for fifteen quantitative descriptors using the variance-covariance component approach of Al-Jibouri *et al.* (1958) and tested for significance against tabulated *r*-values at 42 degrees of freedom. Green matter yield per plant showed a highly significant positive genotypic correlation with dry matter yield per plant ($r_g = 0.605$), length of primary branch ($r_g = 0.376$), plant height ($r_g = 0.261$), leaflet width ($r_g = 0.259$) and number of primary branches ($r_g = 0.165$), together with a highly significant negative genotypic correlation with days to maturity ($r_g = -0.540$) and a significant negative correlation with seeds per pod ($r_g = -0.214$). In almost every trait pair the genotypic correlation coefficient exceeded its phenotypic counterpart in absolute magnitude, indicating a strong inherent genetic association between yield and its components that is partly masked at the phenotypic level by non-heritable environmental variance. Heat-map visualization of the complete 15×15 genotypic and phenotypic correlation matrices, together with a trait-association network constructed for $|r_g| \geq 0.30$, resolved three coherent trait clusters: a vegetative-growth cluster (plant height, primary branch length, leaflet width), a phenological cluster (days to first flowering and days to 50 per cent flowering, $r_g = 0.743$) and an antagonistic maturity-dry-matter cluster (days to maturity versus dry matter yield, $r_g = -0.658$). These findings provide empirical justification for indirect selection of high-forage-yielding grass pea genotypes through dry matter accumulation, branch elongation and plant stature, while cautioning against the use of late maturity or a high seed-per-pod count as selection criteria for improved green forage productivity.

Keywords: *Lathyrus sativus*; germplasm characterization; genotypic correlation; phenotypic correlation; green forage yield; correlation heat map; trait association network

Introduction

Grain and forage legumes occupy a pivotal position in resource-poor, rainfed agricultural systems because they combine biological nitrogen fixation with nutritional density, and among these, grass pea (*Lathyrus sativus* L.) stands out as one of the most climatically resilient. Grass pea is a diploid ($2n = 14$) member of the family Leguminosae, subfamily Papilionoideae, and is cultivated widely across the Indian subcontinent, sub-Saharan Africa, and parts of the Mediterranean basin, most often on residual soil moisture after the harvest of the preceding rice or other kharif crop (Mishra *et al.* 2025) [7]. In tracts where soil quality is poor and terminal drought, transient waterlogging or salinity routinely erode the productivity

of more sensitive pulses, grass pea continues to set pods and accumulate biomass, a trait that has earned it the reputation of an insurance crop of the poor (Palmer *et al.*, 1989)^[10]. Compared with other pulses, *Lathyrus* combines a favourable yield potential with an exceptionally high protein content, an efficient nitrogen-fixing symbiosis, and outstanding tolerance to drought, flooding and soil salinity. When grown in rotation, grass pea additionally improves soil physical structure, breaks pest and weed cycles, and reduces the operational cost of the succeeding cereal crop (Vaz Patto *et al.*, 2006)^[13]. Regionally known by names such as khesari, teora and lakhadi, it is a hardy, nutritionally dense crop reported to supply approximately 362 kcal of energy per 100 g along with 25.6–31.4 per cent protein, 48.0–52.3 per cent starch and appreciable mineral content, although the presence of the neuro-excitatory non-protein amino acid β -ODAP in the seed continues to necessitate breeding for safer, low-toxin cultivars (Rotter *et al.*, 1991)^[12]. Realizing the full agronomic potential of grass pea, whether as a pulse or as a green/dry fodder crop, depends on the systematic collection, characterization and conservation of its genetic diversity, particularly the vast reservoir of landraces still maintained by farmers in traditional cropping tracts. Morphological and agronomic characterization remains the first and most accessible entry point for describing this diversity because such descriptors are of direct and immediate interest to breeders and end-users alike. Translating this diversity into usable breeding material, however, requires more than a simple catalogue of trait means: it requires quantitative estimates of genetic and phenotypic variability, heritability, and — critically — the pattern of association that links individual component traits to the complex, multiplicative character of final yield. Green forage or green matter yield per plant is precisely such a complex character. It is not determined by any single gene or physiological process but emerges as the resultant of plant height, branching intensity, leaf area, stem thickness, the duration of the vegetative phase, and the partitioning of dry matter between leaf and stem tissue, each of which is itself under separate and only partially overlapping genetic control. Selection applied directly to green forage yield is consequently inefficient, both because the trait has comparatively low heritability relative to its components and because it is measured destructively, late in the crop cycle, when the breeding season is already largely spent. An indirect selection strategy — one built upon component traits that are easy to record non-destructively, early in ontogeny, and that show a strong and consistent statistical association with the target trait — is therefore of considerably greater practical value to the breeder. Correlation analysis provides the essential statistical bridge between individual component traits and a complex target trait such as green forage yield. A genotypic correlation coefficient isolates the portion of the observed phenotypic association between two traits that is attributable to shared or linked genetic factors — either pleiotropy, in which a single gene or gene cluster influences both traits, or gametic-phase linkage disequilibrium — after removing the confounding contribution of environmental covariance. A phenotypic correlation coefficient, in contrast, reflects the association actually visible in the field, incorporating both the genetic and the non-heritable environmental components together. Comparing the magnitude and, where relevant, the sign of these two coefficients across a comprehensive trait set offers a breeder immediate, actionable guidance: traits whose genotypic correlation with yield exceeds their phenotypic correlation are candidates for indirect selection

with a genuine expectation of correlated genetic gain, whereas traits in which the phenotypic correlation dominates are more likely to reflect transient developmental or environmental covariation of limited long-term selection value.

Despite the considerable breeding interest that grass pea has attracted in recent years as climate variability intensifies pressure on marginal cropping systems, quantitative studies that simultaneously document the genotypic and phenotypic correlation network among a wide battery of vegetative, phenological, reproductive and yield-related traits — and that visualize this network as an integrated whole rather than as an isolated list of pairwise coefficients — remain comparatively scarce. Against this background, the present study was undertaken with the specific objectives of (i) estimating genotypic and phenotypic correlation coefficients among fifteen quantitative traits in a diverse panel of forty-four grass pea genotypes evaluated under the agro-climatic conditions of Chhattisgarh, (ii) resolving the resulting 15×15 correlation architecture through heat-map and network visualization, and (iii) translating the observed association pattern into concrete recommendations for component-trait-based indirect selection for improved green forage yield in grass pea improvement programmes.

2. Materials and Methods

The present investigation was carried out at the Research-cum-Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, India, during the Rabi (post-monsoon, dry) season of 2024. The experimental protocol, plant material, trait descriptors and statistical procedures employed are described below.

2.1 Experimental Site

Chhattisgarh lies between approximately 17°14' N and 24°45' N latitude and 79°16' E and 84°15' E longitude in the eastern part of peninsular India. The experimental site at Raipur, the state capital, is situated at 21°16' N latitude and 81°36' E longitude at an elevation of 289.6 m above mean sea level, in the fertile alluvial plains of the Chhattisgarh basin.

2.2 Agro-Climatic Conditions

The region experiences a subtropical climate characterized by a hot, dry summer, a humid monsoon and a mild, dry winter. Mean annual rainfall ranges from 1200 to 1400 mm, of which only about 8 per cent is received during the Rabi season, so that the crop is grown predominantly on stored soil moisture and residual monsoon rain. During the crop growth period the maximum air temperature reached 35.5 °C and the minimum fell to 5.7 °C. Inter-annual variability in the onset, intensity and withdrawal of the south-west monsoon, which conventionally breaks toward the end of June and recedes by September, exerts a marked influence on soil-moisture carry-over and, consequently, on the expression of yield-related traits during the subsequent Rabi crop.

2.3 Experimental Material

The experimental material comprised forty-four grass pea genotypes, encompassing a mixture of locally adapted landraces and improved breeding lines, obtained through the All India Coordinated Research Project (AICRP) on MULLaRP (Mungbean, Urdbean, Lentil, *Lathyrus*, Rajmash and Pea), College of Agriculture, IGKV, Raipur. The complete list of genotypes evaluated is presented in Table 1.

Table 1: List of forty-four grass pea (*Lathyrus sativus* L.) genotypes evaluated in the study (Source: AICRP on MULLaRP, College of Agriculture, IGKV, Raipur).

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1	RLK-2	12	RLK-1397	23	RLK-1363	34	PUSA-24
2	RLK-74	13	RLK-1385	24	RLK-1379	35	KL-5
3	RLK-937	14	RLK-1317	25	RLK-1956	36	MAHATEORA
4	RLK-11	15	RLK-1412	26	RLK-1312	37	PRATEEK
5	RLK-127	16	RLK-202	27	RLK-895	38	JCL-19-3
6	RLK-870	17	RLK-1392	28	RLK-345	39	IVT-5
7	RLK-481	18	RLK-1391	29	RLK-875	40	JCL-19-2
8	RLK-277	19	RLK-779	30	RLK-1472	41	JCL-19-4
9	RLK-1073	20	RLK-1158	31	RLK-917	42	JCL-19-1
10	RLK-407	21	RLK-1158	32	RLK-114	43	RATAN
11	RLK-472	22	RLK-860	33	RLK-1950	44	BIOL-5

2.4 Experimental Design and Data Recording

The genotypes were laid out in a Randomized Block Design (RBD) with three replications. Each entry was raised in accordance with recommended agronomic package of practices for grass pea under rainfed Rabi conditions, and standard plant-protection measures were adopted uniformly across the trial to minimize confounding biotic stress. Observations were recorded on five randomly selected, competitive plants in each entry in every replication, for

fifteen quantitative and forty-three qualitative descriptors, following the descriptor list of the International Plant Genetic Resources Institute, Rome (IPGRI, 2000). Only the fifteen quantitative traits relevant to green forage yield and its components are analysed in the present communication; the corresponding qualitative descriptors are being reported separately.

The fifteen quantitative traits recorded, together with the stage and method of measurement, were as follows.

Table 2: Quantitative descriptors recorded and their stage/method of measurement.

Trait	Stage / method of recording
Plant height (cm)	Measured from ground level to the tip of the main branch at 50 per cent flowering, averaged over five representative plants per entry.
Number of primary branches	Counted on the main stem at 50 per cent flowering, averaged over five representative plants.
Length of primary branch (cm)	The longest primary branch on each of five representative plants was measured and averaged.
Leaflet length (cm)	Measured on the mid-leaflet of the fifth fully expanded leaf from the base at 50 per cent flowering.
Leaflet width (cm)	Measured at the widest point of the central leaflet of the fifth fully expanded leaf at 50 per cent flowering.
Peduncle length (cm)	Mean length of randomly selected peduncles recorded at physiological maturity.
Pods per plant	Mean number of pods counted on randomly selected plants at physiological maturity.
Seeds per pod	Mean number of seeds counted on randomly selected pods at physiological maturity.
100-seed weight (g)	Weight of 100 randomly selected, physiologically mature seeds at 8–10 per cent (air-dry) moisture content.
Days to first flowering	Number of days from sowing to opening of the first flower.
Days to 50 per cent flowering	Number of days from sowing to the stage at which 50 per cent of plants in the plot had flowered.
Days to maturity	Number of days from sowing to the stage at which 80 per cent of plants bore mature pods.
Dry matter yield per plant (g)	Total plant dry weight after sun-drying, averaged over five representative plants.
Leaf : stem ratio	Ratio of leaf dry weight to stem dry weight, averaged over five representative plants.
Green matter yield per plant (g)	Total fresh weight of foliage, including stem, recorded at 50 per cent flowering, averaged over five representative plants.

2.5 Statistical Analysis

Data recorded on individual plants were pooled over replications and subjected to standard analysis of variance for a randomized block design to partition total variance into replication, genotypic and error components. Genotypic and phenotypic variances and covariances between all possible pairs of the fifteen quantitative traits were computed from the corresponding mean sum of squares and mean sum of products following the standard method described by Al-Jibouri *et al.* (1958) and later elaborated by Miller *et al.* (1958) and Falconer and Mackay (1996).

For any two traits x and y , the genotypic (rg) and phenotypic (rp) correlation coefficients were computed as:

$$rg(x,y) = \text{Cov } g(x,y) / \sqrt{[Vg(x) \times Vg(y)]} \text{ and } rp(x,y) = \text{Cov } p(x,y) / \sqrt{[Vp(x) \times Vp(y)]}$$

where $\text{Cov } g(x,y)$ and $\text{Cov } p(x,y)$ denote the genotypic and phenotypic covariance between traits x and y , and Vg and Vp denote the corresponding genotypic and phenotypic variances of the individual traits. Phenotypic variance was partitioned as $Vp = Vg + Ve$, where Ve is the environmental (error) variance obtained from the residual mean sum of squares of the analysis of variance.

The significance of each estimated correlation coefficient was tested by comparing its absolute value against tabulated critical values of the product-moment correlation coefficient at $(g - 2)$ degrees of freedom, where g is the number of genotypes ($g = 44$, giving 42 degrees of freedom), at the 5 per cent and 1 per cent probability levels. Coefficients exceeding the 5 per cent and 1 per cent critical values are indicated in the tables and figures by single (*) and double (**) asterisks, respectively.

The complete genotypic and phenotypic correlation matrices were visualized as lower-triangular heat maps using the Python data-visualization libraries pandas, NumPy, Matplotlib and seaborn, with a diverging red–blue colour scale centred on zero to allow simultaneous appreciation of the sign and magnitude of every pairwise coefficient. A trait-association network graph was additionally constructed, using the NetworkX package, by retaining only those genotypic correlation edges with $|rg| \geq 0.30$, to permit rapid visual identification of tightly co-inherited trait clusters and of the traits most centrally connected to green matter yield. All statistical computation and graphical rendering were performed in Python 3 (pandas 2.x, NumPy, Matplotlib, seaborn and NetworkX); the underlying analysis-of-variance and variance-component estimation followed standard procedures outlined by Panse and Sukhatme (1985).

3. Results

The genotypic (rg) and phenotypic (rp) correlation coefficients estimated for all 105 possible pairwise combinations among the fifteen quantitative traits are presented in Table 2, and the corresponding heat maps are

presented in Figures 1 and 2. Of the 105 trait pairs, 45 genotypic correlations (34 significant at 1 per cent and 11 at 5 per cent) and 23 phenotypic correlations (16 significant at 1 per cent and 7 at 5 per cent) differed significantly from zero, confirming that the genotypic correlation matrix was, on the whole, both denser and of higher magnitude than its phenotypic counterpart — a pattern consistent with the expectation that non-heritable environmental variation attenuates, and in some trait pairs partially masks, the underlying genetic association.

In the majority of trait combinations the genotypic correlation coefficient exceeded the corresponding phenotypic correlation coefficient in absolute value, and the two coefficients were almost always concordant in sign. Exceptions to this concordance were informative in their own right: days to maturity, for instance, showed a highly significant negative genotypic correlation with green matter yield ($rg = -0.540$) but a highly significant positive phenotypic correlation with the same trait ($rp = 0.247$), a sign reversal that points to an environmentally driven covariance between late maturity and standing biomass at the time of measurement that runs contrary to the underlying genetic relationship, and which is discussed further below.

Table 3: Genotypic (G) and phenotypic (P) correlation coefficients among fifteen quantitative traits of grass pea. Shaded cells denote statistical significance (light orange = $p \leq 0.01$; light yellow = $p \leq 0.05$).

PH	G	1.00	0.312**	0.495**	0.002	-0.007	0.104	0.083	0.061	0.133	-0.212*	0.092	-0.544**	0.168	0.084	0.261**
	P		0.240**	0.450**	0.018	-0.013	0.097	0.088	-0.015	0.122	-0.075	0.136	0.077	0.167	0.070	0.243**
NPB	G		1.00	0.036	-0.152	-0.217*	0.010	-0.160	-0.400**	-0.140	-0.348**	-0.291**	0.212*	-0.113	-0.156	0.165**
	P			0.025	-0.132	-0.190*	0.028	-0.150	-0.290**	-0.111	-0.154	-0.196*	0.014	-0.124	-0.136	0.170**
LPB	G			1.00	0.143	0.323**	0.199*	0.051	0.133	0.131	0.325**	0.253**	-0.299**	0.303**	0.126	0.376**
	P				0.121	0.312**	0.178*	0.041	0.077	0.122	0.135	0.208*	0.061	0.279**	0.123	0.348**
LL	G				1.00	-0.280**	0.016	0.044	-0.209*	0.220**	0.086	0.087	-0.212*	-0.062	-0.035	-0.028
	P					-0.280**	0.015	0.053	-0.145	0.197*	0.110	0.059	0.069	-0.043	-0.041	-0.031
LW	G					1.00	0.318**	0.142	-0.118	-0.099	0.302**	0.253**	0.176*	0.026	0.037	0.259**
	P						0.309**	0.139	-0.084	-0.092	0.115	0.177*	-0.110	0.033	0.034	0.243**
PL	G						1.00	0.091	0.014	0.091	0.313**	0.241**	-0.062	-0.178*	-0.155	0.118
	P							0.078	-0.038	0.107	0.128	0.171*	-0.098	-0.132	-0.149	0.101
P/P	G							1.00	0.082	0.400**	-0.146	0.258**	-0.114	-0.019	-0.030	0.090
	P								0.107	0.362**	-0.052	0.155	0.006	0.021	-0.020	0.068
S/P	G								1.00	0.082	-0.051	0.216*	0.490**	0.069	0.406**	-0.214*
	P									0.051	-0.035	0.056	-0.114	0.060	0.252**	-0.116
100SW	G									1.00	0.295**	0.091	-0.217*	0.101	0.024	0.052
	P										0.119	0.047	0.049	0.092	0.018	0.054
DFF	G										1.00	0.743**	-0.248**	0.043	0.272**	0.012
	P											0.251**	-0.048	0.011	0.139	0.025
D50%F	G											1.00	-0.027	-0.018	0.045	0.115
	P												-0.021	-0.025	0.039	0.082
DM	G												1.00	-0.658**	0.356**	-0.540**
	P													0.155	-0.108	0.247**
DMY	G													1.00	0.061	0.605**
	P														0.050	0.530**
L/S	G														1.00	0.045
	P															0.041
GMY	G															1.00
	P															

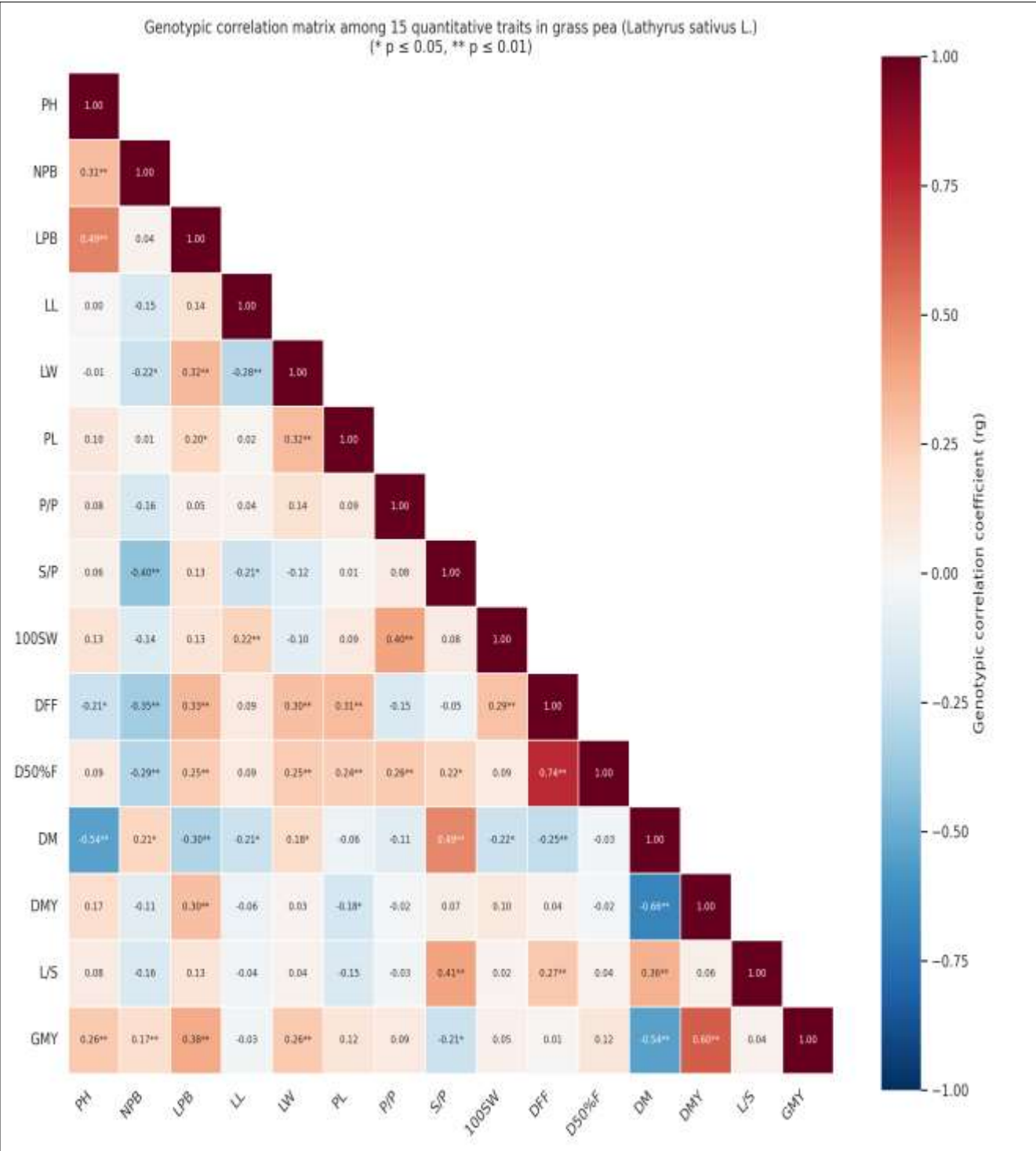


Fig 1: Heat map of the genotypic correlation matrix among fifteen quantitative traits of grass pea. Colour intensity and hue jointly encode the magnitude and sign of r_g (red = positive, blue = negative); * $p \leq 0.05$, ** $p \leq 0.01$.

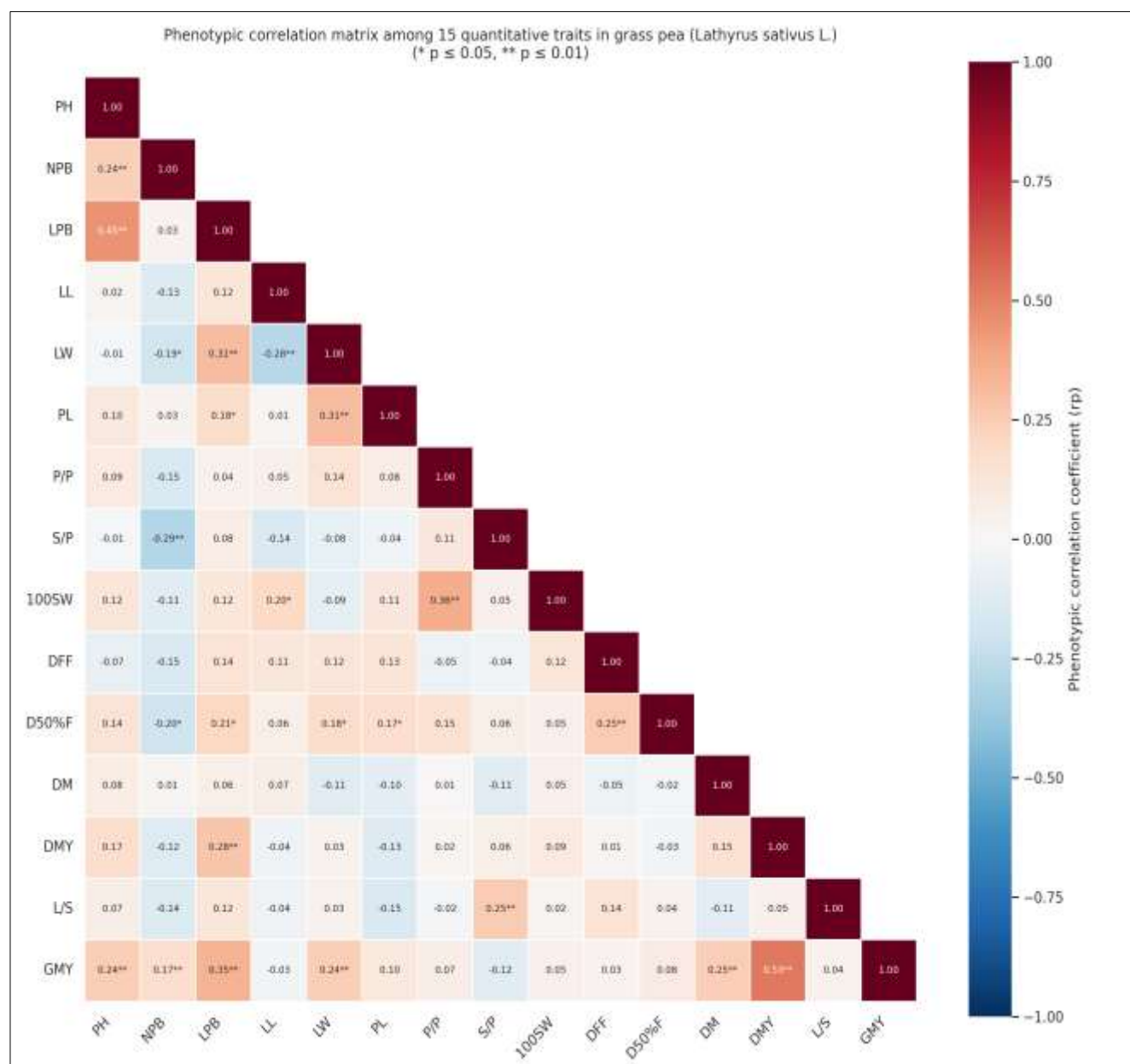


Fig 2: Heat map of the phenotypic correlation matrix among fifteen quantitative traits of grass pea. Colour intensity and hue jointly encode the magnitude and sign of r_p (red = positive, blue = negative); * $p \leq 0.05$, ** $p \leq 0.01$.

3.1 Association of Component Traits with Green Matter Yield

Green matter yield per plant (GMV) is the primary target trait of the present analysis, as it directly determines the productivity of grass pea as a fodder crop. At the genotypic level, GMV showed highly significant positive correlation with dry matter yield per plant ($r_g = 0.605$), length of primary branch ($r_g = 0.376$), plant height ($r_g = 0.261$), leaflet width ($r_g = 0.259$) and number of primary branches ($r_g = 0.165$); a highly significant negative correlation with days to maturity ($r_g = -0.540$); and a significant negative correlation with seeds per pod ($r_g = -0.214$). Peduncle length, pods per plant, 100-seed weight, days to first flowering, days to 50 per cent flowering, leaf:stem ratio and leaflet length showed positive but statistically non-

significant genotypic association with GMV, while leaflet length alone showed a negligible negative trend ($r_g = -0.028$). At the phenotypic level the pattern was broadly similar in direction, with dry matter yield ($r_p = 0.530$), plant height ($r_p = 0.243$), leaflet width ($r_p = 0.243$), length of primary branch ($r_p = 0.348$) and number of primary branches ($r_p = 0.170$) again emerging as the most consistent positive correlates, whereas the phenotypic correlation of seeds per pod and of days to maturity with GMV, as noted above, did not mirror their genotypic counterparts either in magnitude or, for days to maturity, in sign. Figure 3 ranks all fourteen component traits by the absolute magnitude of their genotypic correlation with GMV and juxtaposes the corresponding phenotypic estimate for direct visual comparison.

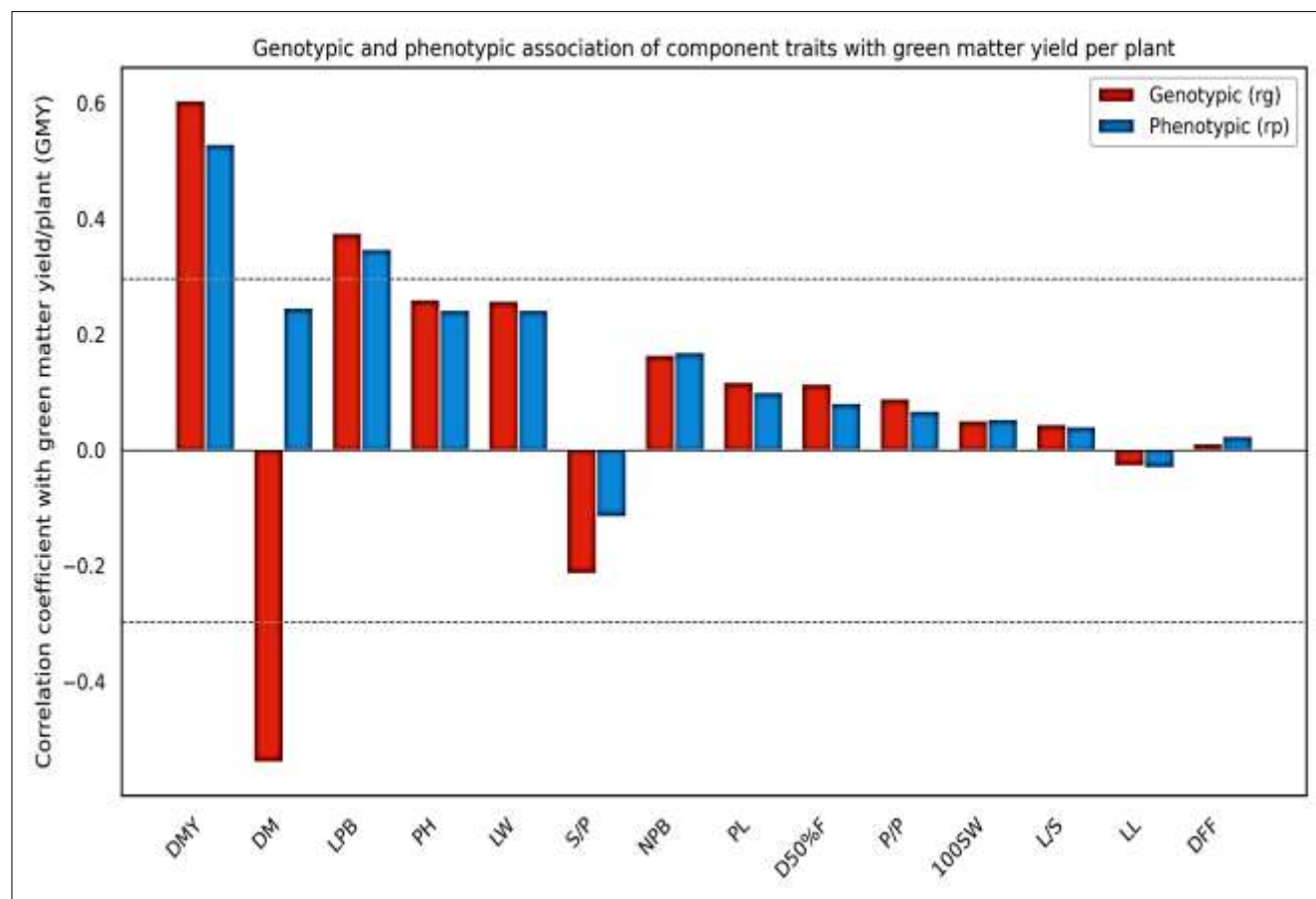


Fig 3: Genotypic (rg) and phenotypic (rp) correlation of fourteen component traits with green matter yield per plant (GMY), ranked by absolute genotypic correlation magnitude. Dashed lines mark the approximate 5% critical value of r .

3.2 Inter-Relationship Among Component Traits

Beyond their individual association with green matter yield, the component traits themselves formed several internally coherent clusters, most readily appreciated in the heat maps (Figures 1 and 2) and in the trait-association network restricted to $|rg| \geq 0.30$ (Figure 4). A vegetative-growth cluster was evident among plant height, length of primary branch and leaflet width, all of which were mutually and positively correlated at both the genotypic and phenotypic levels (plant height–length of primary branch, $rg = 0.495^{**}$; length of primary branch–leaflet width, $rg = 0.323^{**}$), consistent with a shared developmental basis rooted in vigorous vegetative growth.

A tightly linked phenological cluster was formed by days to first flowering and days to 50 per cent flowering, which showed the strongest genotypic association recorded in the entire matrix ($rg = 0.743^{**}$, $rp = 0.251^{**}$), as expected for two sequential measurements of the same developmental transition. Days to maturity, in turn, was negatively and significantly correlated with days to first flowering at the genotypic level ($rg = -0.248^{**}$) but showed a strong

negative genotypic association with dry matter yield ($rg = -0.658^{**}$) and with green matter yield ($rg = -0.540^{**}$), while its genotypic correlation with leaf:stem ratio was positive and significant ($rg = 0.356^{**}$). This antagonistic maturity–dry-matter cluster indicates that, within the present germplasm panel, genotypes that matured earlier tended to accumulate greater dry and green biomass, an agronomically important finding for a crop frequently grown as a short-duration, dual-purpose fodder–grain option.

Seed-related traits displayed a more complex association pattern: seeds per pod was negatively correlated with number of primary branches ($rg = -0.40^{**}$) and with green matter yield ($rg = -0.214^{*}$), but positively correlated with days to 50 per cent flowering ($rg = 0.216^{*}$), dry matter yield ($rg = 0.490^{**}$) and leaf:stem ratio ($rg = 0.406^{**}$), suggesting that allocation of assimilate toward seed number within the pod occurs partly at the expense of vegetative branching and fresh-forage accumulation, even while contributing positively to total dry matter and to the leafiness of the plant.

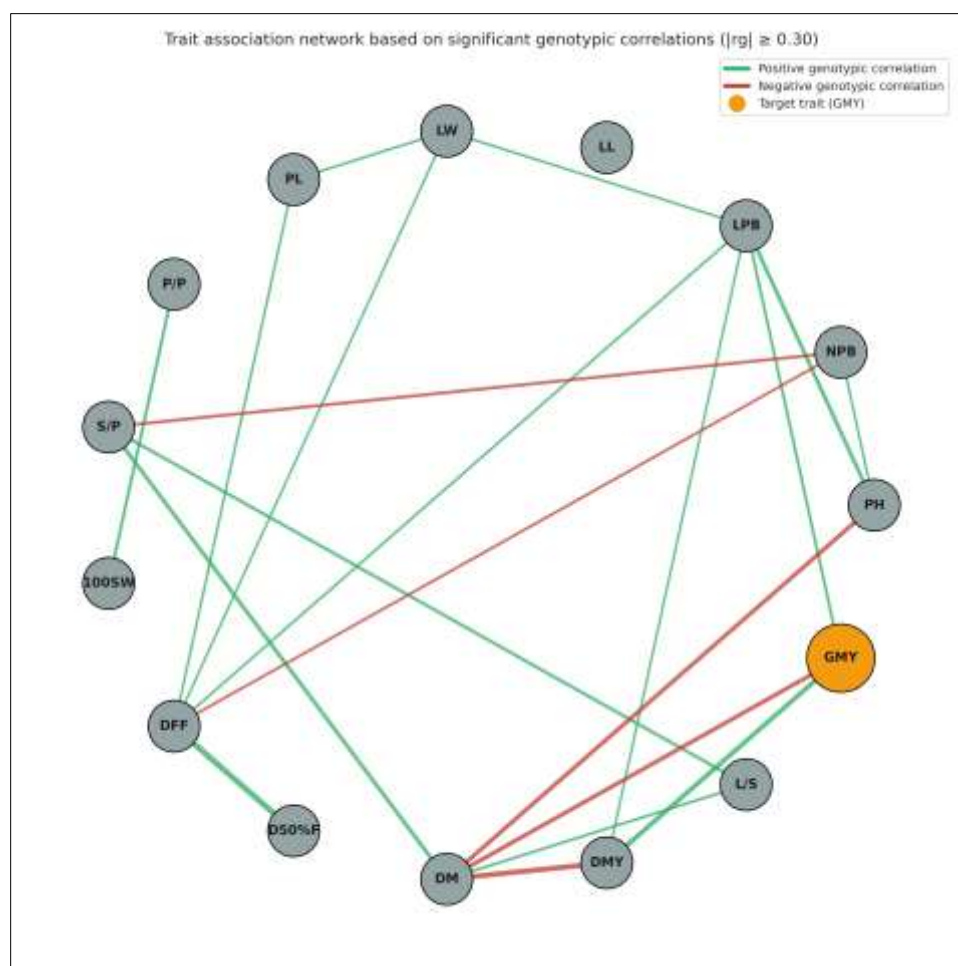


Fig 4: Trait-association network based on genotypic correlations of magnitude $|r_g| \geq 0.30$. Green edges denote positive and red edges negative genotypic correlation; edge thickness is proportional to $|r_g|$. Green matter yield (GMV) is highlighted in orange.

3.3 Genotypic Versus Phenotypic Correlation: Magnitude Comparison

Across the full trait set, the genotypic correlation coefficient exceeded the corresponding phenotypic correlation coefficient in absolute magnitude for the great majority of significant trait pairs, and in several instances substantially so — for example, plant height–days to maturity ($r_g = -0.544^{**}$ versus $r_p = 0.077$, ns), number of primary branches–seeds per pod ($r_g = -0.40^{**}$ versus $r_p = -0.29^{**}$), and days to maturity–green matter yield ($r_g = -0.540^{**}$ versus $r_p = 0.247^{**}$). This consistent pattern indicates that environmental variance, rather than reinforcing the genetic association between component traits, more often acted to dilute or, in a minority of trait pairs, to obscure and even reverse it, underscoring the importance of estimating genotypic correlation — rather than relying on phenotypic correlation alone — when selecting indirect selection criteria for a genetically complex trait such as green forage yield.

4. Discussion

The overall preponderance of genotypic over phenotypic correlation coefficients recorded in the present study is consistent with the broader body of correlation and character-association literature in *Lathyrus sativus* and allied grain legumes, which has repeatedly reported that the true genetic association between yield and its components is stronger, and more useful for selection purposes, than the association apparent from raw phenotypic observation

alone. Character-association studies conducted on grass pea landraces have similarly identified pod number, branching intensity and flowering-related traits as genotypically linked to seed and biomass yield, reinforcing the view that these traits constitute reliable, genetically anchored indirect selection criteria across diverse germplasm sets and growing environments (cf. character-association and path-analysis work reported in the Indian Journal of Plant Genetic Resources on grass pea landraces).

The strongest single correlate of green matter yield identified in the present panel was dry matter yield per plant, at both the genotypic ($r_g = 0.605^{**}$) and phenotypic ($r_p = 0.530^{**}$) levels. This close association is biologically expected, since green and dry matter yield are sequential measurements of the same standing biomass, differing principally in moisture content; nonetheless, the magnitude of the genotypic correlation confirms that genotypes selected for superior dry-fodder accumulation can be expected, with a high degree of confidence, to also rank highly for fresh green-forage productivity, allowing breeders to rely on the more storage-stable and logistically convenient dry-matter measurement as a proxy trait where field capacity for fresh-weight recording is limited.

The positive and significant genotypic association of green matter yield with plant height, length of primary branch, leaflet width and number of primary branches reflects the straightforward physiological logic that a taller, more profusely branched plant bearing broader leaflets presents greater photosynthetic surface area and structural biomass,

and consequently accumulates more green matter per plant. Comparable positive linkages between vegetative vigour traits and forage or biomass yield have been documented across a range of recent grass pea evaluation trials spanning South Asian rice-fallow systems and Central European multi-environment nurseries, where pod position, branch number and plant stature were similarly implicated as productivity-determining traits, even though the specific trait emphasis differed somewhat between pulse-type and dual-purpose leaf-type genetic material (Bubolz *et al.*, 2026; recent rice-fallow dual-purpose breeding evaluations of grass pea)^[2]. The convergence of this vegetative-growth signal across geographically and genetically distinct grass pea panels lends considerable external support to the pattern observed in the present Chhattisgarh-grown material and suggests that plant height, branch length and leaflet width can be recommended with reasonable generality as early, non-destructive selection criteria for forage-type grass pea improvement.

The negative genotypic correlation between days to maturity and both green matter yield ($rg = -0.540^{**}$) and dry matter yield ($rg = -0.658^{**}$) merits particular attention because it runs counter to a frequently assumed, though not universally observed, positive relationship between crop duration and biomass accumulation in indeterminate legumes. Within the present panel, later-maturing genotypes evidently redirected a larger share of assimilate toward extended reproductive development and pod-filling at the expense of standing vegetative biomass at the reference sampling stage, whereas early-maturing genotypes retained a higher proportion of green, leafy tissue. The corresponding phenotypic correlation between days to maturity and green matter yield was, by contrast, positive and significant ($rp = 0.247^{**}$) — a sign reversal between the genotypic and phenotypic estimates that is most plausibly explained by environmentally mediated covariance, in which favourable microplot conditions (superior soil moisture retention, more uniform stand establishment) simultaneously extended the vegetative duration of certain plots and increased standing biomass, thereby superimposing an environmental correlation of opposite sign onto the underlying genetic relationship. This divergence illustrates concretely why phenotypic correlation alone can mislead a breeder: selection on the phenotypic association here would favour late maturity as a route to higher forage yield, whereas the genotypic evidence indicates the opposite, and early duration is the genetically sound selection target for maximizing standing green biomass, an outcome that is also agronomically desirable given the premium on short-duration options for double-cropped or moisture-limited rice-fallow systems.

The very strong genotypic correlation between days to first flowering and days to 50 per cent flowering ($rg = 0.743^{**}$) is unsurprising, given that both traits index the same underlying floral-transition event at slightly different population thresholds, but its magnitude confirms that either descriptor can be recorded interchangeably as a proxy for the other without meaningful loss of information, a practical simplification of value in large-panel germplasm screening where recording time is constrained.

The negative genotypic correlation of seeds per pod with green matter yield ($rg = -0.214^{*}$) and with number of primary branches ($rg = -0.40^{**}$), set against its positive correlation with dry matter yield ($rg = 0.490^{**}$) and

leaf:stem ratio ($rg = 0.406^{**}$), is consistent with a resource-allocation trade-off in which genotypes investing more heavily in seed number per pod partition proportionally less assimilate toward vegetative branching and fresh-leaf accumulation, even as total dry biomass and stem-to-leaf partitioning shift in their favour. From a dual-purpose breeding perspective, this trade-off implies that simultaneous maximization of both green forage yield and seed-per-pod count may require an index-selection approach rather than tandem or single-trait selection, since strong genetic selection pressure on one trait would be expected to erode genetic gain in the other.

Taken together, the correlation architecture uncovered in the present study — a coherent vegetative-growth cluster positively linked to yield, a tightly co-inherited phenological cluster, and an antagonistic maturity–biomass relationship — is broadly consistent with the trait-association patterns reported across the recent grass pea literature, even though the precise magnitude of individual coefficients naturally varies with germplasm composition, environment and measurement stage (Frontiers in Sustainable Food Systems, 2025; Legume Science, 2026). Such convergence across independent germplasm panels strengthens confidence that plant height, branch length, leaflet width and dry matter accumulation are robust, generalizable indirect selection criteria for green forage yield improvement in *Lathyrus sativus*, whereas both excessive crop duration and a disproportionate seed-per-pod emphasis should be approached with caution when the primary breeding objective is fodder productivity rather than grain yield.

A limitation of the present communication, reflecting the scope of the primary dataset analysed, is that it is confined to correlation coefficients rather than extending to path-coefficient decomposition of direct and indirect effects, or to estimates of genetic advance and heritability, all of which would further refine the selection recommendations offered here. Complementary path analysis, partitioning each component trait's total genotypic correlation with green matter yield into direct and indirect effects transmitted through other traits, together with estimation of genotypic and phenotypic coefficients of variation, broad-sense heritability and expected genetic advance, is recommended as the logical next step for confirming and quantitatively ranking the indirect selection criteria identified in the present correlation analysis. Similar Results were found by Mishra *et al* 2025^[7].

5. Conclusion

The present study characterized, for the first time in this Chhattisgarh-grown germplasm panel, the complete genotypic and phenotypic correlation architecture linking fifteen quantitative traits to green forage yield in grass pea. Dry matter yield, plant height, length of primary branch, leaflet width and number of primary branches emerged as consistent, genetically anchored positive correlates of green matter yield, whereas days to maturity and seeds per pod emerged as negative genotypic correlates whose phenotypic expression, in the case of maturity duration, was actively misleading. The systematic excess of genotypic over phenotypic correlation magnitude observed across the trait set confirms that indirect selection decisions in this crop should be grounded in genotypic, rather than purely phenotypic, correlation estimates.

From an applied breeding standpoint, the results support a selection strategy that favours early-to-medium-maturing, tall, well-branched genotypes with broad leaflets and high dry-matter accumulation as the most efficient route to superior green forage yield in grass pea, while cautioning that selection for extended crop duration or for a high seed-per-pod count, if pursued without regard to correlated response, is likely to depress rather than enhance fodder productivity. These findings offer breeders a practical, statistically grounded framework for multi-trait selection in grass pea forage-improvement programmes and provide a quantitative baseline against which future path-coefficient and heritability studies on this germplasm panel can be benchmarked.

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References

1. Al-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agron J*. 1958;50(10):633–636.
2. Bubolz, *et al.* Characterisation of grass pea (*Lathyrus sativus* L.) genotype diversity identified key agronomic traits for Central European environments. *Legume Sci*. 2026.
3. Evaluation of grass pea (*Lathyrus sativus* L.) landraces for genetic variability and character association for growth, yield and quality attributes. *Indian J Plant Genet Resour*.
4. Falconer DS, Mackay TFC. Introduction to quantitative genetics. 4th ed. Harlow: Longman; 1996.
5. International Plant Genetic Resources Institute. Descriptors for *Lathyrus* species. Rome: International Plant Genetic Resources Institute; 2000.
6. Miller PA, Williams JC, Robinson HF, Comstock RE. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agron J*. 1958;50(3):126–131.
7. Mishra A, Gore P, Sahu M. Principal component analysis of 100 indigenous and exotic accessions of pigeonpea [*Cajanus cajan* (L.) Millsp.] of the Indian National Seed Bank. *J Adv Biol Biotechnol*. 2025;28(1):603–611. doi:10.9734/jabb/2025/v28i11913.
8. Mishra A, Sahu M, Pandey HK. Assessment of variability and association among green forage yield and contributing traits in indigenous genotypes of grass pea [*Lathyrus sativus* (L.)]. *J Adv Biol Biotechnol*. 2025;28(1):503–512. doi:10.9734/jabb/2025/v28i11904.
9. Optimizing grass pea (*Lathyrus sativus* L.) for rice-fallow systems: phenotypic and genetic insights for dual-purpose breeding. *Front Sustain Food Syst*. 2025.
10. Palmer R, Freeman J, Skarbek T. Grass pea as a food and forage crop of marginal environments. *Trop Agric*. 1989;66(4):305–310.
11. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 4th ed. New Delhi: Indian Council of Agricultural Research; 1985.
12. Rotter R, Marquardt RR, Campbell CG. Nutritive value of *Lathyrus sativus* seed as a partial replacement for a soybean-based protein source. *J Sci Food Agric*. 1991;55(4):615–629.
13. Vaz Patta MC, Skiba B, Pang ECK, Ochatt SJ, Lambein F, Rubiales D. *Lathyrus* improvement for resistance against biotic and abiotic stresses: from classical breeding to marker-assisted selection. *Euphytica*. 2006;147(1–2):133–147.