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## MORPHO-PHYSIOLOGICAL EVALUATION OF SOYBEAN (*GLYCINE MAX* L.) GENOTYPES FOR YIELD IMPROVEMENT UNDER ARID ENVIRONMENTAL CONDITIONS OF QUETTA, BALOCHISTAN

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### ABSTRACT

Soybean is a major oilseed crop belongs to leguminous family with wide genetic variability for agro-morphological traits. The present study was conducted to assess the morphological and physiological variability among 20 soybean genotypes cultivated under the water limited conditions of upland Balochistan. Among the studied traits, 1000-seed weight and biological yield revealed significant variations ( $p < 0.001$ ), while no significant differences were recorded in other traits like days to flowering, plant height, and chlorophyll content (SPAD). Among the tested genotypes, superior agronomic performance was displayed by "GP-1" for chlorophyll content (42.2 SPAD), yield per plant (116.3 g) and 1000-seed weight (15.3 g). The Principal Component Analysis (PCA) indicated that first three principal components together explained 64.8% of total phenotypic variance, among which PC 1 (34.03 %) was mainly affected by variables like biomass yield, biological yield, LAI, SPAD, and seed yield. Correlation analysis revealed that seed yield exhibited a strong negative response with days to flowering ( $r = -0.67$ ), whereas a positive correlation with SPAD ( $r = 0.46$ ), LAI ( $r = 0.31$ ) and plant height ( $r = 0.24$ ) pointed to important characteristics that had a positive influence on the productivity. Hierarchical clustering classified genotypes into three groups as GP-1 has a unique cluster because it has high yield potential and early flowering. The results of present study provide a valuable framework for selecting high-yielding soybean genotypes that are well adapted to the arid regions of Balochistan.

**Keywords:** Balochistan, Morphological Traits, Physiological Traits, Yield, Correlation, Soybean.

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### INTRODUCTION

Soybean (*Glycine max* L.) is well-known as a "miracle legume crop" due to essential source of protein and edible oil for both livestock and human consumption (Khojely et al., 2018; Lukanda et al., 2023; Ullah et al., 2024), and it is regarded as a 4<sup>th</sup> most broadly cultivated crop globally (Chander et al., 2021). It is a self-pollinating crop of leguminous family with a wide allelic variability in wild and cultivated species (Sivabharathi et al., 2023). Soybean cultivation was primarily domesticated in China around

5000 year ago, followed by Japan and other countries. In the 18<sup>th</sup> century, it was introduced in Europe and later in USA during 19<sup>th</sup> century (Li et al. 2008; Valliyodan et al. 2016). Nutritionally, it generally contains approximately proteins (35-40%), lipids (20%), dietary fibre (9%) and moisture (8.5%) contents (Dukariya et al., 2020). Soy seeds also have acceptable levels of nutrients that have marginal importance like calcium, iron and zinc, and substantially greater levels (5%) of minerals than cereal seeds (1%) (Kahraman, 2017). The nutrient composition of soybean differs with the place,

varietal potential and climate of growing conditions. It is proven that soybean based foods contain significant amount of protein, vitamins, fibers and minerals as well as limit the amount of saturated fatty acids (Dukariya et al., 2020). Multiple soy based products have been processed for boiled soybean, tamari, soy yogurt, miso, tofu, soymilk, roasted soybean, soy mayonnaise, soy cheese, textured soy protein and textured vegetable protein (Jayachandran, & Xu, 2019). Global soybean production is reported to be approximately 350 million tons with an average yield of 2.8 tons (Ullah et al., 2021). Brazil is the leading producer country of soybean worldwide, sharing around 163 million tons, followed by United States (118 million tons), Argentina (48 million tons) and China (20.7 million tons) (FAO, 2022; USDA FAS, 2025). In Pakistan, Sindh province contributes highest production of soybean (33%), while other provinces share negligible in total production (Asad et al., 2020).

The improvement of high yielding soybean genotypes requires accurate information regarding yield related characteristics and their heritability in next generations. Improvements in yield-related traits are often reflected in grain yield traits (Li et al., 2024). Yield characteristics of soybean genotypes are quantitatively inherited and highly influenced by genotype -environmental interactions, it is therefore very important to choose cultivars that are well adapted to suitable environmental conditions to enhance the yield (Li et al., 2020). The strong genetic diversity and high heritability of major traits such as pods per plant, and seeds per pod have made the current breeding lines to contribute toward maintenance of valuable germplasm at a high level of genetic variability (Verma et al., 2024). Soybean genotypes are characterized by extensive morphological and physiological variations, which forms the basis of development of high-yielding and improved nutritionally cultivars (Mishra et al., 2021; Ullah et al., 2024), which is possibly owing to existence of inherent genetic diversity among soybean genotypes (Irshad et al., 2016). The cluster and the principal component analysis has identified discrete groups of genotypes with significant divergence indicating that hybridization between genotypes belonging to separate cluster, especially desirable yielding genotypes having desirable characteristics, can further increase genetic gain. The cluster and the principal component analysis have given a group wise division of genotypes with significant divergence, indicating the hybridization of genotypes in different clusters, especially economically good high-

yielding genotypes with desirable traits could provide extra genetic gain and genetic variation (Ullah et al., 2024; Saha et al., 2024).

Multivariate principal component analysis (PCA) effectively provides summarization of observed multivariate variation on the multiple traits which has helped the researchers to determine the main characters that play a pivotal role in influencing genetic diversity within the soybean genotypes (Sinha et al., 2023). The number of pods, clusters, and yield of a single plant are some of the phenotypic traits that are critical to plant genetic variation and thus be good selection criteria in soybean breeding (Sivabharathi et al., 2023). PCA in combination with cluster analysis is very effective in grouping genotypes based on phenotypic similarities and thus helps in the deliberate adoption of genotypes to be used in breeding and hybridization programs (Mekonen, 2023). On the other hand, Correlation analysis helps in identifying the relation of phenotypic traits (number of pods plant<sup>-1</sup>, seed weight, seed vigour, plant height and number of seeds per plant) to the final yield (Ullah et al., 2021; Ullah et al., 2024).

The present research study aimed to identify and select the diverse and promising soybean genotypes with high productivity, and more adaptation under the water limited conditions for the arid regions of Quetta, Balochistan.

## MATERIALS AND METHODS

### Field experimental study layout

A field experimental layout was carried under a completely randomized block design in the research area of the Department of Plant Breeding and Genetics at Balochistan Agriculture College, Quetta (30.1830° N latitude, and 66.9987° E longitude). The seeds were sown with three replications for each genotype in each block. The twenty seeds of each genotype were sown in well-drained loam soil with pH 7.5 at depth of 1.5-2 inches. Row-to row (45 cm) and plant-to plant distance (10 cm) were maintained for proper emergence. For seedbed preparation agronomic practices and raised bed was formed as per standard. One furrow irrigation was provided one week before sowing and supplemental irrigations were given every 10-14 days' interval at four critical phases (germination, flowering, pod formation and grain filling). However, one irrigation was escape at vegetative stage. NPK Fertilizer at optimal dosage (N:20–25 kg N, P: 40–60 kg P<sub>2</sub>O<sub>5</sub> per acre, P: 20–30 kg K<sub>2</sub>O per acre) was applied in bands 6 cm deep and 6 cm apart from the seed.

Table 1: List of 20 soybean genotypes selected from previous study based on performance.

| S. No. | Gene Bank ID / Genotype Code | Donor variety | Origin    | Source of Acquisition | Biological Status |
|--------|------------------------------|---------------|-----------|-----------------------|-------------------|
| G1     | PI 24615                     | HM-8468       | China     | PGRP                  | Accession         |
| G2     | PI 24623                     | CH-Ssu-20     | China     | PGRP                  | Accession         |
| G3     | PI 24625                     | CH-Ssu-10     | China     | PGRP                  | Accession         |
| G4     | PI 24659                     | Youngyang     | S. Korea  | PGRP                  | Accession         |
| G5     | PI 24674                     | SOY-12        | S. Korea  | PGRP                  | Accession         |
| G6     | PI 24676                     | Nampung       | S. Korea  | PGRP                  | Accession         |
| G7     | PI 24678                     | Ransom        | USA       | PGRP                  | Accession         |
| G8     | NIBGE-102                    | Calland       | USA       | NIBGE                 | Accession         |
| G9     | NIBGE-183                    | AGS-93        | USA       | NIBGE                 | Accession         |
| G10    | NIBGE-218                    | Hawkeye       | USA       | NIBGE                 | Accession         |
| G11    | NARC-XI                      | Lincoln       | USA       | ORP (NARC)            | Advanced line     |
| G12    | NARC-XVI                     | Forrest       | USA       | ORP (NARC)            | Advanced line     |
| G13    | GP-29                        | Calquit       | USA       | ORP (NARC)            | Accession         |
| G14    | GP-30                        | Hongkong      | USA       | ORP (NARC)            | Accession         |
| G15    | GP-61                        | A3127         | USA       | ORP (NARC)            | Accession         |
| G16    | GP-66                        | Hutcheson     | USA       | ORP (NARC)            | Accession         |
| G17    | GP-85                        | Bragg         | Brazil    | ORP (NARC)            | Accession         |
| G18    | GP-91                        | Hampton       | Brazil    | ORP (NARC)            | Accession         |
| G19    | GP-108                       | Soja savanna  | Brazil    | ORP (NARC)            | Accession         |
| G20    | E-1531                       | Hayman        | Australia | AAUR                  | Breeding line     |

PGRP: Plant Genetics Resource Program, NIBGE: National Institute for Biotechnology and Genetic Engineering, ORP (NARC): Oilseed Research Program, National Agricultural Research Centre Islamabad, AAUR: Arid Agriculture University Rawalpindi

### Determination of morphological and physiological attributes

The following attributes of 20 soybean genotypes as shown in table 1 were determined for this experimental study.

#### Plant height (cm) and Number of branches per plant

Ten soybean plants per plot were arbitrarily selected at maturity stage. The height of each selected plants was measured from the soil surface to top of main stem using a meter scale and the height was recorded in centimeters and computed the mean. Moreover, Number of primary branches of ten randomly selected plants per plant were counted and the average value was calculated.

#### Days to flowering and Days to maturity

Plants were observed regularly after one month of sowing and date was recorded when 50% flowers appeared. The sowing date was subtracted to determine the days to flowering. However, each plant was monitored from three months after sowing and date was recorded when physiological maturity occurred. The sowing date was subtracted to record the days to maturity.

#### 1000-Seed weight (g) and Seed yield per plant (g)

Well-dried seeds were randomly selected after harvest and

weighed using a precise balance. The weight of 1000-seed was expressed in grams (g). Moreover, the seeds were harvested from ten randomly chosen plants, and then the seeds were dried and weighed from each plants. The mean yield per plant expressed in grams (g) was computed.

#### Germination percentage (%)

Total number of appeared seedlings 7-10 days after sowing were counted and following formula was used for recording the germination (%).

$$\text{Germination (\%)} = \frac{\text{Number of emerged plant}}{\text{Number of seed sown}} \times 100$$

#### Number of Pods Plant<sup>-1</sup> and Biomass yield per plant (kg)

Ten matured plants were selected arbitrarily. The number of pods per plant were counted and the mean values were calculated. However, at least ten plants were uprooted from each plot at maturity and air-dried them to constant weight in drying oven. The dried plants were weighed and the biomass yield per was averaged in kilogram (Kg).

#### Biological yield (ton/ha)

The net plot area was harvested and all the plant material including seeds and straw were dried. The total biomass was converted to tons per hectare using following formula;

$$\text{Biological yield (ton/ha)} = \frac{\text{Total biomass (Kg)}}{\text{Area of plot (m}^2\text{)}} \times 10$$

### Leaf area index (LAI)

The leaf area index (LAI) was measured using digital LAI meter

### SPAD (Chlorophyll Content)

SPAD (chlorophyll content) of top fully expanded trifoliate leaf of 5 plants/plot was measured using SPAD-502 meter. Three readings (tip, middle and based were taken and averaged them and then SPAD units were recorded.

### Statistical analysis

Data in terms of morphological and physiological attributes of 20 genotypes were evaluated through analysis of variance (ANOVA), and mean values comparison were analyzed using Tukey's Honest significant difference (HSD) test at probability value ( $P \leq 0.05$ ). Principal component analysis (PCA) and correlation analysis were performed in Rstudio version 2025. Heatmap clustering with hierarchical analysis and dendrogram were constructed in OriginPro 2024.

## RESULTS AND DISCUSSION

### Morpho-physiological characteristics

Soybean genotypes (GP-1 to GP-20) were thoroughly investigated in morphological and physiological study with aim at determining their agronomic performance under standard growing conditions. The data indicated the large variation of genotypes in more than a few traits but all parameters were not statistically significant ( $p \leq 0.05$ ) as depicted in Table 2.

#### Days to flowering

The genotypes represented average variation of days to flowering between 36 days (GP-1) and 46 days (GP-2 and GP-15) (Table 2). The difference was found significant ( $P = 0.04$ ) and that showed genetic variation in the date of flowering among the genotypes.

#### Days to Maturity

Days to maturity differs between 98.0 days (GP-1) and 114.3 days (GP-3) (Table 2). The results indicated a numerical difference although it was not significant in terms of statistics ( $P = 0.23$ ).

#### Plant Height

The GP-1 genotype (78.0 cm) was tallest and the GP-8 genotype (67.3 cm) was shortest (Table 2). In spite of this variation, the analysis of variance showed that the sample had no significant difference ( $P = 0.31$ ), meaning that height is not a critical discrimination between these genotypes.

#### Number of Branches per Plant

The range of 4 to 7 branches per plant was found more or less consistently in all genotypes and the variation was not

found to be significant ( $P = 0.72$ ), which shows that the trait of the plant was relatively uniform.

### 1000-Seed Weight

The weight of 1000 seeds was found to significantly differ ( $P = 0.0004$ ) with the greatest (15.3 g) and the least (6.0 g) weight in GP-1 and GP-20 respectively. The trait plays an important role in the quality and marketing of grain and GP-1, GP-10 and GP-14 have better seed yield.

### Seed Yield per Plant

The mean seed yield varied between 62.3g (GP-15) and 116.3 g (GP-1). Nonetheless, this difference was not recorded to be significant ( $P = 0.5$ ) although, GP-1 kept on performing better than other genotypes in the aspect of seed productivity.

### Germination Percentage

Overall, germination was high achieving a range of 44.7 to 95.3 percent (GP-20 to GP-1) and it was not statistically significant ( $P = 0.2$ ), which means that the seed viability among genotypes is good.

### Biomass Yield per Plant

Totals accumulation of biomass ranged 0.17kg (GP-15) to 0.45kg (GP-1). The variation though evident was not correlated as significant ( $P = 0.32$ ).

### Biological Yield (Ton/ha)

Significant differences were reported on the biological yield ( $P < 0.001$ ) values at 2.0 ton/ha (GP-19) to the highest 4.4 ton/ha (GP-1). This supports the hypothetical potential of high yielding genotype (GP-1).

### Physiological Attributes

#### Leaf area index

Significant difference ( $P = 0.000$ ) in leaf area index (LAI) was recorded, ranging from 2.0 (GP-19) to 4.4 (GP-1). The LAI was highest in GP-1 (4.4), GP-2 (4.2), and GP-11 (3.7), which are associated with the high productivity and seed yield. The lowest LAI was in GP-13 (2.2), GP-14 (2.1), GP-19 (2.0) and GP-12(2.7), which may restrict photosynthetic efficiency and biomass production.

#### SPAD value

The SPAD values of soybean ranged between 19.7 (GP-13) and 42.2 (GP-1) showing a physiological variability of noticeable significance among the different genotypes. The variation in SPAD values were not also of any statistical significance ( $P = 0.23$ ), but the numerical difference is likely to indicate the different chlorophyll content, which possibly has an effect on the photosynthetic efficiency. Highest SPAD index values were observed in GP-1 (42.2) and GP-2 (38.4) indicating better chlorophyll content as well as photosynthetic potential for vigorous growth and development.

Table 2: Morphological and physiological attributes of soybean genotypes grown in uplands of Balochistan.

| Genotypes          | Days to flowering    | Days to maturity        | Plant height (cm)      | Number of branches per plant | 1000-seed weight (g)    | Seed yield per plant (g) | Plant Germination (%)   | No. of pod plant <sup>-1</sup> | Biomass yield per plant (kg) | Biological yield (ton/ha) | LA1                        | SPAD (Chlorophyll Content) |
|--------------------|----------------------|-------------------------|------------------------|------------------------------|-------------------------|--------------------------|-------------------------|--------------------------------|------------------------------|---------------------------|----------------------------|----------------------------|
| GP-1               | 36 <sup>a</sup> ±2.0 | 98.0 <sup>a</sup> ±1.7  | 78.0 <sup>a</sup> ±1.5 | 7 <sup>a</sup> ±0.7          | 15.3 <sup>a</sup> ±0.7  | 116.3 <sup>a</sup> ±7.2  | 95.3 <sup>a</sup> ±2.6  | 7 <sup>a</sup> ±0.7            | 36 <sup>a</sup> ±2.0         | 0.45 <sup>a</sup> ±0.02   | 4.4 <sup>a</sup> ±0.10     | 42.2 <sup>a</sup> ±1.2     |
| GP-2               | 46 <sup>a</sup> ±0.3 | 102.7 <sup>a</sup> ±4.2 | 69.3 <sup>a</sup> ±2.6 | 5 <sup>a</sup> ±1.2          | 14.0 <sup>a</sup> ±0.6  | 80.7 <sup>a</sup> ±8.4   | 47.3 <sup>a</sup> ±5.8  | 4 <sup>a</sup> ±1.2            | 46 <sup>a</sup> ±0.3         | 0.44 <sup>a</sup> ±0.02   | 4.2 <sup>ab</sup> ±0.12    | 38.4 <sup>a</sup> ±3.1     |
| GP-3               | 39 <sup>a</sup> ±1.9 | 114.3 <sup>a</sup> ±3.0 | 73.0 <sup>a</sup> ±3.5 | 5 <sup>a</sup> ±1.3          | 12.3 <sup>ab</sup> ±0.3 | 71.0 <sup>a</sup> ±13.1  | 54.3 <sup>a</sup> ±13   | 3 <sup>a</sup> ±0.6            | 39 <sup>a</sup> ±1.9         | 0.23 <sup>a</sup> ±0.08   | 3.4 <sup>abc</sup> ±0.42   | 34.7 <sup>a</sup> ±5.4     |
| GP-4               | 42 <sup>a</sup> ±3.5 | 112.7 <sup>a</sup> ±1.5 | 73.7 <sup>a</sup> ±4.3 | 6 <sup>a</sup> ±0.6          | 12.7 <sup>a</sup> ±1.9  | 95.3 <sup>a</sup> ±26.2  | 75.7 <sup>a</sup> ±15.3 | 7 <sup>a</sup> ±1.3            | 42 <sup>a</sup> ±3.5         | 0.33 <sup>a</sup> ±0.12   | 3 <sup>bcd</sup> ±0.50     | 31.4 <sup>a</sup> ±4.7     |
| GP-5               | 38 <sup>a</sup> ±1.8 | 105.0 <sup>a</sup> ±3.5 | 77.0 <sup>a</sup> ±1.7 | 4 <sup>a</sup> ±0.3          | 12.0 <sup>ab</sup> ±1.5 | 104.7 <sup>a</sup> ±7.7  | 65.0 <sup>a</sup> ±17.4 | 4 <sup>a</sup> ±1.2            | 38 <sup>a</sup> ±1.8         | 0.30 <sup>a</sup> ±0.1    | 3.2 <sup>abcde</sup> ±0.15 | 36 <sup>a</sup> ±2.7       |
| GP-6               | 40 <sup>a</sup> ±2.0 | 108.7 <sup>a</sup> ±5.4 | 69.7 <sup>a</sup> ±3.3 | 5 <sup>a</sup> ±0.6          | 14.0 <sup>a</sup> ±1.2  | 92.0 <sup>a</sup> ±18.3  | 50.0 <sup>a</sup> ±8.0  | 5 <sup>a</sup> ±1.5            | 40 <sup>a</sup> ±2.0         | 0.36 <sup>a</sup> ±0.04   | 3.3 <sup>abcde</sup> ±0.72 | 30.1 <sup>a</sup> ±4.3     |
| GP-7               | 45 <sup>a</sup> ±1.5 | 107.0 <sup>a</sup> ±5.3 | 72.0 <sup>a</sup> ±3.8 | 6 <sup>a</sup> ±1.2          | 13.3 <sup>a</sup> ±0.9  | 71.0 <sup>a</sup> ±1.5   | 72.7 <sup>a</sup> ±13.4 | 6 <sup>a</sup> ±1.9            | 45 <sup>a</sup> ±1.5         | 0.26 <sup>a</sup> ±0.05   | 2.9 <sup>cdef</sup> ±0.21  | 29.9 <sup>a</sup> ±7       |
| GP-8               | 41 <sup>a</sup> ±1.9 | 110.0 <sup>a</sup> ±2.6 | 67.3 <sup>a</sup> ±1.2 | 5 <sup>a</sup> ±1.3          | 14.0 <sup>a</sup> ±0.6  | 81.3 <sup>a</sup> ±19.2  | 87.7 <sup>a</sup> ±9.9  | 5 <sup>a</sup> ±1.2            | 41 <sup>a</sup> ±1.9         | 0.23 <sup>a</sup> ±0.1    | 3.1 <sup>cdef</sup> ±0.56  | 34.3 <sup>a</sup> ±7.1     |
| GP-9               | 38 <sup>a</sup> ±0.7 | 105.3 <sup>a</sup> ±2.9 | 71.3 <sup>a</sup> ±3.5 | 6 <sup>a</sup> ±0.9          | 14.0 <sup>a</sup> ±1.2  | 107.3 <sup>a</sup> ±8.0  | 74.0 <sup>a</sup> ±16.1 | 5 <sup>a</sup> ±1.7            | 38 <sup>a</sup> ±0.7         | 0.26 <sup>a</sup> ±0.07   | 2.3 <sup>def</sup> ±0.44   | 27.2 <sup>a</sup> ±6.1     |
| GP-10              | 38 <sup>a</sup> ±1.8 | 109.0 <sup>a</sup> ±1.0 | 70.7 <sup>a</sup> ±3.2 | 5 <sup>a</sup> ±1.5          | 14.7 <sup>a</sup> ±1.3  | 105.3 <sup>a</sup> ±17.7 | 58.7 <sup>a</sup> ±5.8  | 6 <sup>a</sup> ±1.3            | 38 <sup>a</sup> ±1.8         | 0.25 <sup>a</sup> ±0.1    | 2.3 <sup>def</sup> ±0.35   | 33.5 <sup>a</sup> ±4.5     |
| GP-11              | 42 <sup>a</sup> ±3.7 | 104.3 <sup>a</sup> ±1.5 | 67.7 <sup>a</sup> ±1.8 | 7 <sup>a</sup> ±1.3          | 12.3 <sup>ab</sup> ±1.5 | 74.0 <sup>a</sup> ±8.3   | 52.3 <sup>a</sup> ±9    | 5 <sup>a</sup> ±1.5            | 42 <sup>a</sup> ±3.7         | 0.3 <sup>a</sup> ±0.1     | 3.7 <sup>cdef</sup> ±0.17  | 27.6 <sup>a</sup> ±4.2     |
| GP-12              | 42 <sup>a</sup> ±1.0 | 107.7 <sup>a</sup> ±2.3 | 75.7 <sup>a</sup> ±2.8 | 5 <sup>a</sup> ±1.2          | 13.0 <sup>a</sup> ±1.7  | 75.7 <sup>a</sup> ±18.9  | 55.3 <sup>a</sup> ±10   | 6 <sup>a</sup> ±1.7            | 42 <sup>a</sup> ±1.0         | 0.3 <sup>a</sup> ±0.11    | 2.7 <sup>ef</sup> ±0.30    | 31 <sup>a</sup> ±9.6       |
| GP-13              | 44 <sup>a</sup> ±1.3 | 101.3 <sup>a</sup> ±2.0 | 72.0 <sup>a</sup> ±3.1 | 5 <sup>a</sup> ±0.7          | 11.0 <sup>ab</sup> ±2.0 | 64.3 <sup>a</sup> ±7.9   | 69.7 <sup>a</sup> ±11.3 | 7 <sup>a</sup> ±1              | 44 <sup>a</sup> ±1.3         | 0.3 <sup>a</sup> ±0.1     | 2.2 <sup>def</sup> ±0.15   | 19.7 <sup>a</sup> ±6.2     |
| GP-14              | 37 <sup>a</sup> ±0.3 | 108.0 <sup>a</sup> ±5.1 | 69.3 <sup>a</sup> ±3.4 | 5 <sup>a</sup> ±1.5          | 14.7 <sup>a</sup> ±0.9  | 79.0 <sup>a</sup> ±12.5  | 65 <sup>a</sup> ±18.6   | 4 <sup>a</sup> ±2              | 37 <sup>a</sup> ±0.3         | 0.21 <sup>a</sup> ±0.1    | 2.1 <sup>cdef</sup> ±0.56  | 30.3 <sup>a</sup> ±3.5     |
| GP-15              | 45 <sup>a</sup> ±1.5 | 104.7 <sup>a</sup> ±1.9 | 72.3 <sup>a</sup> ±3.4 | 6 <sup>a</sup> ±1.2          | 14.7 <sup>a</sup> ±0.7  | 62.3 <sup>a</sup> ±5.0   | 64.3 <sup>a</sup> ±15.6 | 6 <sup>a</sup> ±1              | 45 <sup>a</sup> ±1.5         | 0.17 <sup>a</sup> ±0.07   | 2.4 <sup>cdef</sup> ±0.40  | 28.2 <sup>a</sup> ±9.4     |
| GP-16              | 40 <sup>a</sup> ±3.9 | 109.0 <sup>a</sup> ±4.4 | 76.3 <sup>a</sup> ±1.7 | 6 <sup>a</sup> ±0.6          | 13.7 <sup>a</sup> ±0.7  | 66.7 <sup>a</sup> ±23.7  | 61.0 <sup>a</sup> ±14.6 | 2 <sup>a</sup> ±0.3            | 40 <sup>a</sup> ±4           | 0.26 <sup>a</sup> ±0.06   | 2.5 <sup>def</sup> ±0.26   | 34.5 <sup>a</sup> ±7.4     |
| GP-17              | 44 <sup>a</sup> ±1.0 | 110.3 <sup>a</sup> ±3.2 | 71.7 <sup>a</sup> ±1.2 | 5 <sup>a</sup> ±1.2          | 13.3 <sup>a</sup> ±0.7  | 79.7 <sup>a</sup> ±7.3   | 71.7 <sup>a</sup> ±13.7 | 5 <sup>a</sup> ±0.6            | 44 <sup>a</sup> ±1           | 0.34 <sup>a</sup> ±0.11   | 2.6 <sup>cdef</sup> ±0.25  | 35 <sup>a</sup> ±3.2       |
| GP-18              | 41 <sup>a</sup> ±2.6 | 106.3 <sup>a</sup> ±4.2 | 74.7 <sup>a</sup> ±1.2 | 4 <sup>a</sup> ±1.0          | 9.7 <sup>ab</sup> ±1.5  | 82.7 <sup>a</sup> ±12.7  | 84.7 <sup>a</sup> ±4.2  | 6 <sup>a</sup> ±1.2            | 41 <sup>a</sup> ±2.6         | 0.3 <sup>a</sup> ±0.1     | 2.4 <sup>def</sup> ±0.71   | 28 <sup>a</sup> ±3.4       |
| GP-19              | 42 <sup>a</sup> ±1.8 | 107.7 <sup>a</sup> ±6.1 | 73.0 <sup>a</sup> ±2.9 | 7 <sup>a</sup> ±0.7          | 9.0 <sup>ab</sup> ±1.7  | 87.3 <sup>a</sup> ±22.5  | 59.0 <sup>a</sup> ±3.2  | 5 <sup>a</sup> ±0.9            | 42 <sup>a</sup> ±2           | 0.3 <sup>a</sup> ±0.03    | 2 <sup>f</sup> ±0.3        | 20.7 <sup>a</sup> ±8.6     |
| GP-20              | 40 <sup>a</sup> ±1.5 | 113.0 <sup>a</sup> ±4.2 | 72.7 <sup>a</sup> ±0.9 | 5 <sup>a</sup> ±0.7          | 6.0 <sup>b</sup> ±1.0   | 93.3 <sup>a</sup> ±21.3  | 44.7 <sup>a</sup> ±8.7  | 5 <sup>a</sup> ±1.7            | 40 <sup>a</sup> ±1.5         | 0.2 <sup>a</sup> ±0.04    | 2.5 <sup>cdef</sup> ±0.41  | 27.9 <sup>a</sup> ±6.7     |
| SEM                | 2.06                 | 3.5                     | 2.71                   | 1.01                         | 1.204                   | 15.4                     | 11.7                    | 1.11                           | 0.06                         | 0.06                      | 0.23                       | 42.2 <sup>a</sup> ±1.2     |
| P <sub>value</sub> | 0.04                 | 0.23                    | 0.31                   | 0.72                         | 0.0004                  | 0.5                      | 0.2                     | 0.3                            | 0.32                         | 0.32                      | 0.000                      | 38.4 <sup>a</sup> ±3.1     |

There was also a good performance of these genotypes in seed and biomass yield signifying possible positive relationship with productivity. The lowest values of SPAD were found in genotypes like GP-13 (19.7) and GP-19 (20.7), and these genotypes have low Chlorophyll content reflecting that photosynthetic efficiency of plants and yield potential is low.

#### Principal component analysis

The present study was conducted to investigate the eleven physio-morphological attributes of soybean

genotypes based on principal component analysis, out of 11 PCs, in which 4 PCs exhibited > 1.00 Eigen value and contributed 75.4% of total variability (Table 3). While, other 7 PCs have Eigen values (> 1.00) and attributed 24.61 of total variance. Among the physio-morphological traits, PCI contributed the 34.03% total variability, however, other remaining (PC2-PC11) represented 16.98, 13.77, 10.61, 8.23, 4.98, 2.73, 1.44, 0.94 and 0% of total variance, respectively. Among eleven PCs, the first four PCs exhibited significant

contribution (75.40%) of total variability. Variance and Eigen value linked with each PC reduced slightly and cumulative variance raised slightly as shown in screen plot (Figure 2). Significantly, PC1 includes most of the total variation, is highly linked to traits that relate to plant productivity. Biomass yield per plot (0.44), biological yield (0.44) and seed yield per plant (0.31) had high positive loadings, showing that they make up a significant part of the first principal component.

Besides, LAI (0.38) and SPAD (0.31) also had moderate positive loadings, implying that both photosynthetic efficiency and canopy structure are important for greater biomass and yield. This factor could mean that more biomass generally gives plants more chance to produce seeds. PC2 has a positive factor load of 0.63 for days to flowering which implies that the genotypes that flower later are more associated with this axis. Alternatively, delayed flowering was found to be linked inversely to seed yield per plant (-0.46) and SPAD (-0.30). Taken together, this suggests that those that develop flowers early should attain more seeds than late-flowering plants which may choose to develop vegetatively before reproducing. PC3 suggests that lower coefficient values for germination percentage (-0.51) and number of pods per plant (-0.46) represent a group of genotypes where those with a higher germination percentage also have fewer pods. On the other hand, SPAD (0.38) has a positive factor loading which means that chlorophyll content could be separate from these traits. PC4 mainly reflects the relationship between the number of branches and SPAD in plants, clearly suggesting that genotypes with more branches are more likely to contain greater amounts of chlorophyll. This can result from the branches increasing photosynthesis by capturing more light. Plant height (0.74) appears to have the most influence on PC5, while LAI's influence is in the opposing direction, implying that more vertical growth often means less dense foliage. PC6 reveals that there is a positive relationship between germination rate (0.53) and the number of days to maturity (0.36) which suggests early-germinating varieties tend to take more time

to mature. PC7 reveals that late-maturing plants tend to produce greater numbers of pods, most likely because they remain in the reproductive stage for a longer period.

Opposite effects were seen for germination percentage (0.47) and LAI (-0.58) in PC8, which implies that abundant germination is not always linked to better canopy formation. PC9 exhibited that days to flowering (0.59) and yield of seeds per plant (0.47) have positive correlation, meaning that not all late-flowering plants have low seed yields. PC10 revealed the contrast effects between SPAD (-0.59) and seed yield per plant (0.44), which suggests that high chlorophyll content has no correlation with optimal yield. PC11 particularly divides biomass yield per plot (0.71) and biological yield (-0.71) because of their scale differences (per plot vs. per hectare). These traits are positively correlated among each other, PCA biplot (Figure 1) revealed that days to flowering, seed yield per plant (g), biological yield (ton/ha) and biomass yield per plot (kg) have potential contributions to both components (PC1 and PC2). These traits are positively correlated among each other, which implies that genotypes producing more yield often result in better biomass and biological yields as well. No. of branches per plants, plant germination (%) and plant height reveal moderate contributions and less influence on both PCs, clustering collectively adjacent origin point. Days to maturity and days to flowering have negative correlation with yield-related traits, falling in directions opposite to yield components. Genotypes that develop later may have lower productivity in terms of important yield components.

Table 3: Principal component analysis of 20 soybean genotypes (GP-1 and GP-20) for physio-morphological traits.

| Parameters                         | PC1   | PC2   | PC3   | PC4   | PC5   | PC6   | PC7   | PC8   | PC9   | PC10  | PC11  |
|------------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Plant height (cm)                  | 0.15  | -0.19 | -0.36 | -0.17 | 0.74  | 0.37  | 0.13  | -0.26 | -0.02 | 0.11  | 0.00  |
| Germination (%)                    | 0.23  | -0.02 | -0.51 | 0.13  | -0.32 | 0.53  | -0.22 | 0.47  | 0.13  | -0.02 | 0.00  |
| Days to flowering                  | -0.11 | 0.63  | 0.18  | -0.04 | 0.08  | 0.26  | 0.31  | 0.04  | 0.59  | 0.18  | 0.00  |
| Day to maturity                    | -0.31 | -0.32 | 0.24  | 0.11  | -0.09 | 0.36  | 0.63  | 0.29  | -0.32 | 0.13  | 0.00  |
| Number of branches per plant       | 0.18  | 0.20  | 0.06  | 0.75  | 0.32  | -0.16 | -0.10 | 0.20  | -0.19 | 0.39  | 0.00  |
| Seed yield plant <sup>-1</sup> (g) | 0.31  | -0.46 | -0.13 | -0.06 | -0.13 | -0.39 | 0.29  | 0.09  | 0.47  | 0.44  | 0.00  |
| No. of pods per plant              | 0.23  | 0.29  | -0.46 | 0.21  | -0.19 | -0.21 | 0.57  | -0.25 | -0.19 | -0.33 | 0.00  |
| Biomass yield (kg)                 | 0.44  | 0.15  | 0.21  | -0.31 | 0.09  | -0.04 | 0.08  | 0.29  | -0.20 | -0.05 | 0.71  |
| Biological yield (ton/ha)          | 0.44  | 0.15  | 0.21  | -0.31 | 0.09  | -0.04 | 0.08  | 0.29  | -0.20 | -0.05 | -0.71 |
| LAI                                | 0.38  | 0.01  | 0.25  | 0.05  | -0.38 | 0.37  | -0.07 | -0.58 | -0.16 | 0.37  | 0.00  |
| SPAD                               | 0.31  | -0.30 | 0.38  | 0.38  | 0.12  | 0.16  | 0.04  | -0.07 | 0.36  | -0.59 | 0.00  |
| Eigenvalue                         | 3.74  | 1.87  | 1.51  | 1.17  | 0.90  | 0.69  | 0.55  | 0.30  | 0.16  | 0.10  | 0.00  |
| Variance (%)                       | 34.03 | 16.98 | 13.77 | 10.61 | 8.23  | 6.29  | 4.98  | 2.73  | 1.44  | 0.94  | 0.00  |
| Cumulative (%)                     | 34.03 | 51.02 | 64.78 | 75.40 | 83.62 | 89.91 | 94.89 | 97.62 | 99.06 | 100.0 | 100.0 |

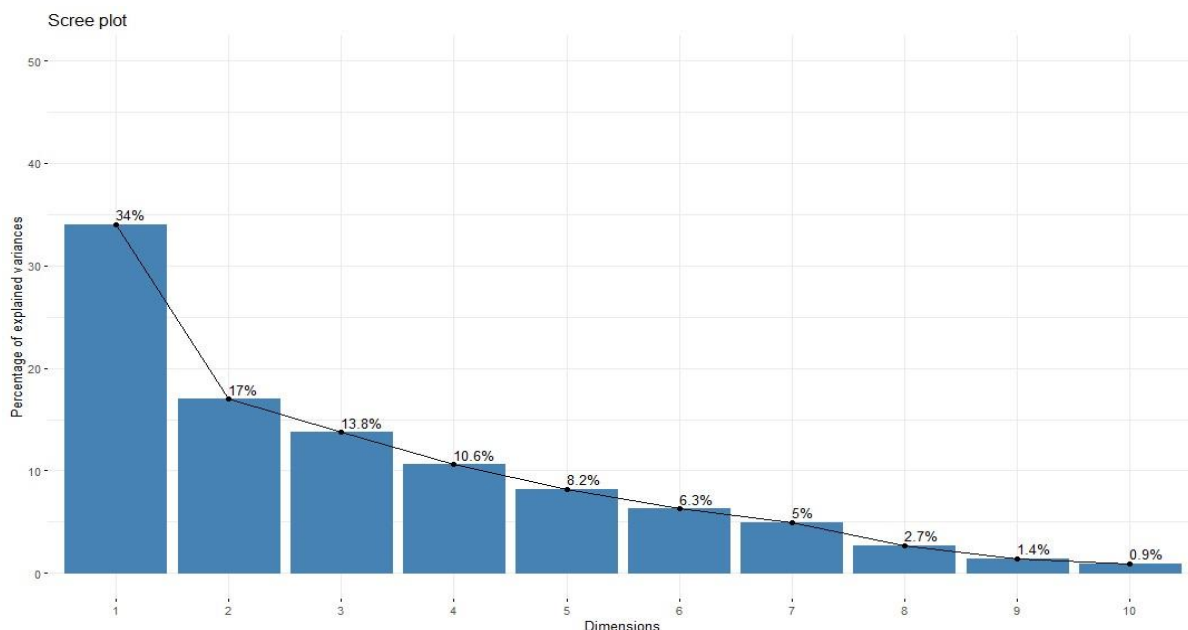


Figure 1: Screen plot indicating the cumulative variance of measured morpho-physiological traits.

The biplot depicted the distribution of twenty genotypes with the first two PCs, explaining 34.03% and 16.99% of total variability (51%). Genotypes (GP-3, GP-4, GP-5, GP-6, GP-7, GP-20, and GP-19) are positively correlated with morphological traits like days to flowering and day to maturity, which means these genotype have longer vegetative periods and mature lately. Genotypes (GP-1 and GP-2) locate on the left side of PC1, likely linked with traits such as plant height (cm), seed yield per plant and biomass yield. Genotypes (GP-10, GP-12, GP-13, GP-14, GP-16 and GP-17) have no particular contribution to both components, exhibiting average performance around most important traits. Genotypes (GP-8 and GP-9) located particularly in lower part of PC2 (vertical axis), exhibited lower performance in physio-morphological traits such as no. of pod/ plant, plant germination (%) and SPAD value. Genotypes (GP-1, GP-2 and GP-9) located far away from the center point, exhibit high variability and these genotypes are useful for selecting in breeding strategies depending upon target characters.

#### Biplot

The biplot (Figure 2) depicted the distribution of twenty genotypes with the first two PCs, explaining 34.03% and 16.99% of total variability (51%). Genotypes (GP-3, GP-4, GP-5, GP-6, GP-7, GP-20, and GP-19) are positively correlated with morphological traits such as days to flowering and days to maturity, indicating that these genotypes have longer vegetative periods and mature later. Genotypes (GP-1 and GP-2) locate on the left side of PC1,

likely linked with traits such as plant height (cm), seed yield per plant and biomass yield. Genotypes (GP-10, GP-12, GP-13, GP-14, GP-16 and GP-17) have no particular contribution to both components, exhibiting average performance around most important traits. Genotypes (GP-8 and GP-9) located particularly in lower part of PC2 (vertical axis), exhibited lower performance in physio-morphological traits such as no. of pod/ plant, plant germination (%) and SPAD value. Genotypes (GP-1, GP-2 and GP-9) located far away from the center point, exhibit high variability and these genotypes are useful for selecting in breeding strategies depending upon target characters.

#### Pearson correlation analysis

The Pearson correlation analysis (Figure 3) represents the between the morphological and physiological attributes of eleven soybean genotypes population. Biomass yield per plot and biological yield revealed a potential positive correlation ( $r = 1$ ), which intends that increment in biomass yield are directly related to rise in biological yield. Physiological trait such as Leaf Area Index (LAI) positively correlated with biological yield ( $r = 0.61$ ) and biomass yield ( $r = 0.61$ ), implying that larger leaf area supports strong photosynthetic activity and leads to more biomass yield. SPAD value has a moderate correlation with Leaf area index ( $r = 0.44$ ), biological yield ( $r = 0.41$ ) and biomass yield ( $r = 0.41$ ), implying the effect of chlorophyll content on biomass yield and biological yield. Seed yield per plant has strong negative correlation with days to blooming ( $r = -0.67$ ), intending that soybean

genotypes with earlier blooming produce maximum seed yields. Biomass and Biological yield inversely correlate with day to maturity ( $r = -0.52$ ), which means that there is a no role of prolonged vegetative stages of soybean

genotypes. SPAD value revealed a negative correlation with days to flowering ( $r = -0.33$ ), implying that earlier flowering in soybean genotypes can happen because of a greater amount of chlorophyll.

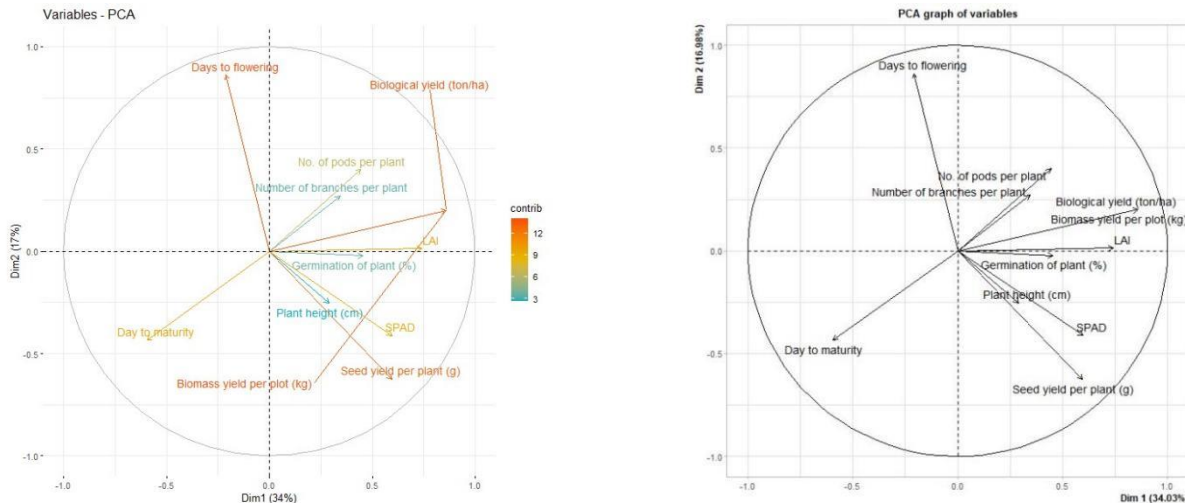


Figure 2: Biplot representation for 11 morph-physiological variables of 20 soybean genotypes based on PCA analysis.

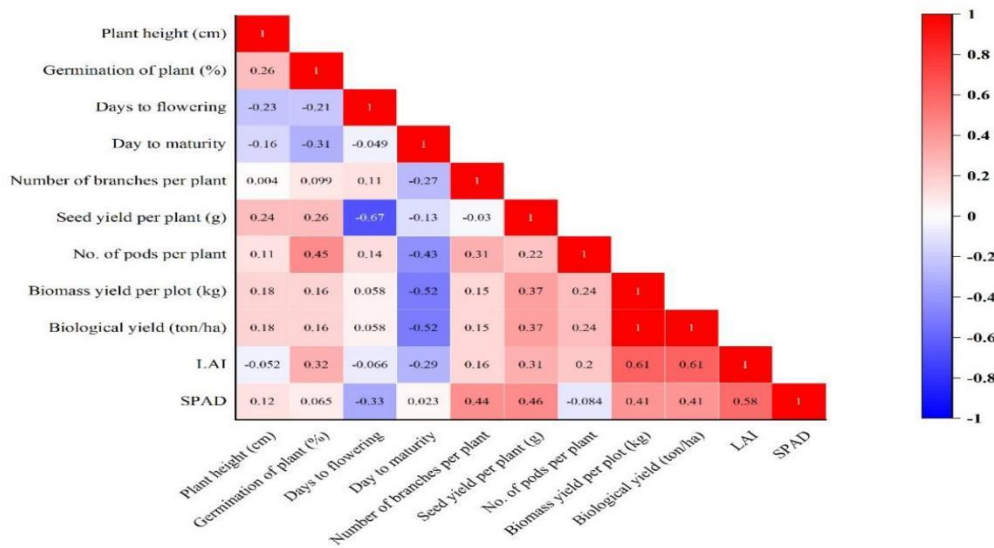


Figure 3: Pearson correlation analysis for morphological and physiological attributes of eleven soybean genotypes.

### Dendrogram with hierarchical cluster analysis of soybean genotypes

The dendrogram (Figure 4) exhibit the hierarchical cluster analysis of twenty soybean genotypes (GP-1 to GP-20) based on their physio-morphological traits and divides into three clusters (A, B and) at similarity threshold of nearly 42. The cluster A (red color) comprises of soybean genotypes (GP-1, GP-5, GP-9 and GP-10) shows similar physio-morphological performance from the rest of

soybean genotypes. Genotype (GP-1) is noticeably a most divergent member, exhibiting higher level of divergence from other members within this cluster A and is placed into a separate sub-cluster, which means this genotype has one or more distinctive phenotypic traits than other genotypes population. Cluster B includes genotypes (GP-2, GP-6, GP-20, GP-3, GP-16, GP-11, GP-12 and GP-19), is most heterogeneous and the largest group. This cluster B is further divided into several subgroups. Genotypes (GP-2

and GP-6) group adjacently and share similar agronomic performance. Additionally, genotypes (GP-3 and GP-16) construct a strong sub-cluster. Cluster C includes genotypes (GP-14, GP-17, GP-8, GP-18, GP-7, GP-13,

GP-15), exhibit tight grouping between genotypes (GP-13 and GP-15), which implies that these two genotypes have homology in agronomic performance and genotypic makeup.

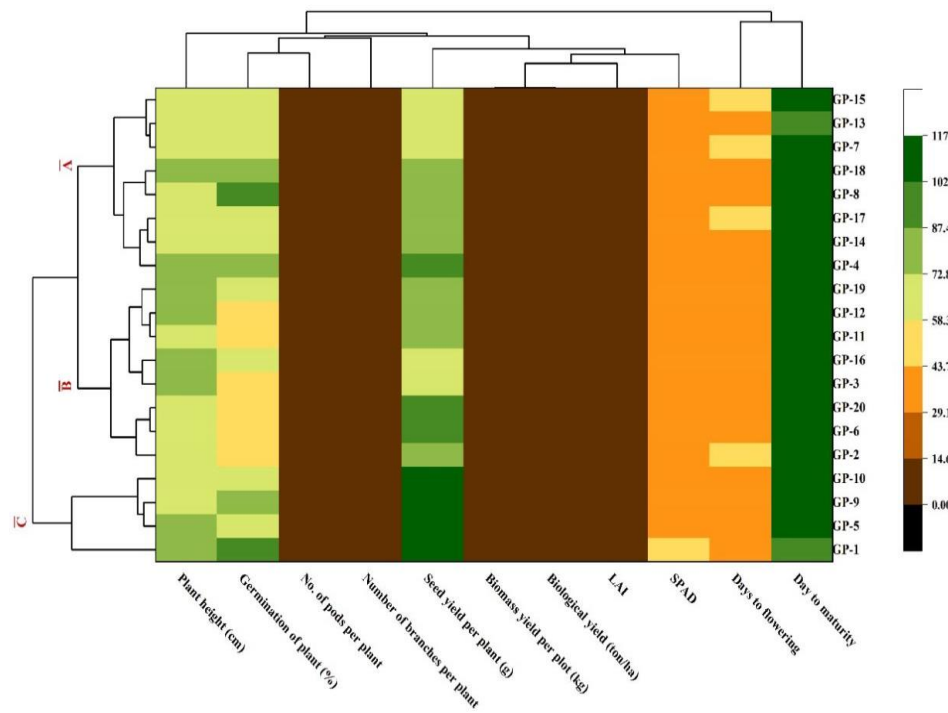


Figure 4: Dendrogram with hierarchical cluster analysis of 20 soybean genotypes and physio-morphological traits.

**Descriptive analysis of growth attributes of soybean genotypes**

The descriptive analysis of morph-physiological attributes of soybean genotypes exhibited significant difference among traits (Table 4). Days to maturity with low coefficients of variation value (3.74%) and plant height (CV= 4.08%) are suggested to be highly stable under environmental factors. Similarly, days to flowering with low variability value (CV = 7.01%) exhibited uniform flowering across each soybean genotype. High coefficient variability of 25.22%, 25.22%), 23.91%), and 23.46% were recorded in traits such as biomass yield, biological yield, number of pods per plant and leaf area index (LAI), respectively,

which means these genotypes having these traits are more useful for selection in breeding strategies to improve the yield. Germination percentage, seed yield per plant and branches per plant with moderate coefficient variability (20.89%), (18.2%) and (16.05%) respectively, may perform well in breeding program to improve the plant architecture. Physiological trait such SPAD with variability (CV = 8.48%), indicated chlorophyll content remain uniform across each soybean genotypes. Overall, traits such as biomass yield, biological yield, and pods per plant with high coefficient variability are more useful for selection in breeding programs to improve the productivity and architecture of soybean genotypes.

Table 4: Descriptive analysis of morph-physiological attributes of 20 soybean genotypes.

| Variables         | Mean   | Standard Deviation | Sum     | Minimum | Median | Maximum | CV%   |
|-------------------|--------|--------------------|---------|---------|--------|---------|-------|
| Plant height (cm) | 72.37  | 2.95               | 1447.33 | 67.33   | 72.17  | 78.00   | 4.08  |
| Germination (%)   | 65.42  | 13.66              | 1308.33 | 44.67   | 64.67  | 95.33   | 20.89 |
| Days to flowering | 40.97  | 2.87               | 819.33  | 36.00   | 40.83  | 45.67   | 7.01  |
| Day to maturity   | 107.25 | 4.01               | 2145.00 | 98.00   | 107.67 | 114.33  | 3.74  |

|                              |       |       |         |       |       |        |       |
|------------------------------|-------|-------|---------|-------|-------|--------|-------|
| Number of branches per plant | 5.53  | 0.89  | 110.67  | 3.67  | 5.33  | 7.33   | 16.05 |
| Seed yield per plant (g)     | 84.50 | 15.37 | 1690.00 | 62.33 | 81.00 | 116.33 | 18.18 |
| No. of pods per plant        | 5.17  | 1.24  | 103.33  | 2.33  | 5.00  | 7.33   | 23.91 |
| Biomass yield per plot (kg)  | 4.35  | 1.10  | 87.00   | 2.60  | 4.20  | 6.80   | 25.22 |
| Biological yield (ton/ha)    | 0.29  | 0.07  | 5.76    | 0.17  | 0.28  | 0.45   | 25.22 |
| LAI                          | 2.94  | 0.69  | 58.70   | 2.00  | 2.90  | 4.50   | 23.46 |
| SPAD                         | 37.33 | 3.17  | 746.67  | 31.33 | 37.17 | 45.00  | 8.48  |

**Dendrogram with hierarchical cluster analysis of soybean genotypes**

The dendrogram (Figure 5) exhibit the hierarchical cluster analysis of twenty soybean genotypes (GP-1 to GP-20) based on their physio-morphological traits and divides into three clusters (A, B and) at similarity threshold of nearly 42. The cluster A (red color) comprises of soybean genotypes (GP-1, GP-5, GP-9 and GP-10) shows similar physio-morphological performance from the rest of soybean genotypes. Genotype (GP-1) is noticeably a most divergent member, exhibiting higher level of divergence from other members within this cluster A and is placed into a separate sub-cluster, which means this genotype has

one or more distinctive phenotypic traits than other genotypes population. Cluster B includes genotypes (GP-2, GP-6, GP-20, GP-3, GP-16, GP-11, GP-12 and GP-19), is most heterogeneous and the largest group. This cluster B is further divided into several subgroups. Genotypes (GP-2 and GP-6) group adjacently and share similar agronomic performance. Additionally, genotypes (GP-3 and GP-16) construct a strong sub-cluster. Cluster C includes genotypes (GP-14, GP-17, GP-8, GP-18, GP-7, GP-13, GP-15), exhibit tight grouping between genotypes (GP-13 and GP-15), which implies that these two genotypes have homology in agronomic performance and genotypic makeup.

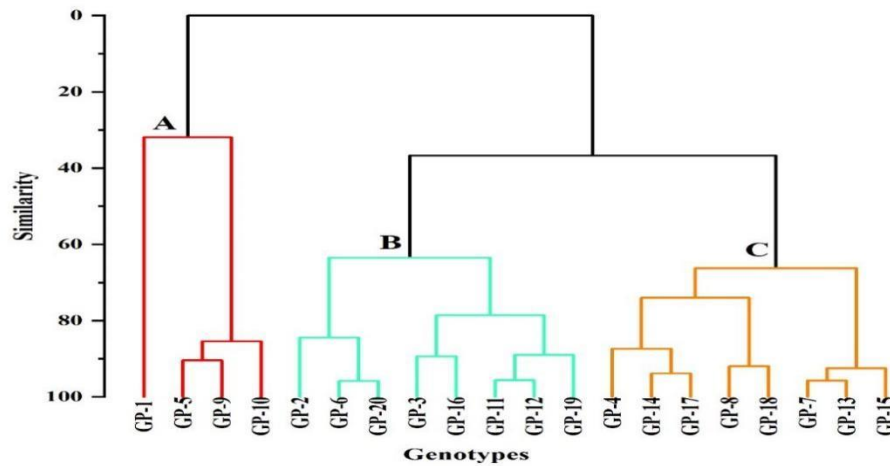


Figure 5: Dendrogram with hierarchical cluster analysis of soybean genotypes based on their physio-morphological variables.

**Dendrogram with hierarchical cluster analysis of variables**

The dendrogram (Figure 6) shows the grouping of agronomic variables resulting from hierarchical cluster analysis using the similarity threshold around 40 of their expression among soybean genotypes. The dendrogram is divided into three main clusters (A, B and C). Cluster A comprises of growth and development characters such plant height (cm), germination of plant (%), number of pods per plant, number of branches per plant and seed yield per plant

(g). The traits such "number of branches" and "number of pods" have a strong effect on "seed yield", it seems that these traits are essential for producing high yields. High plant height and plant germination (%) observed from this study implies that early development and vegetative growth lead to higher yields. Cluster B includes yield and physiological attributes such as Biomass yield per plot (kg), Biological yield (ton/ha), Leaf Area Index (LAI) and SPAD. It is clear from the grouping that biomass and leaf area formation are highly correlated. The correlation between

SPAD and biomass is moderate, so chlorophyll appears to be involved in the formation of biomass yield. The Cluster C includes phenological attributes such as days to flowering and days to maturity. These phenological characters forms

independent group and are explicitly isolated from the other traits, implying that traits are mainly independent of physio-morphological traits such as growth, and yield as well as other physiological traits.

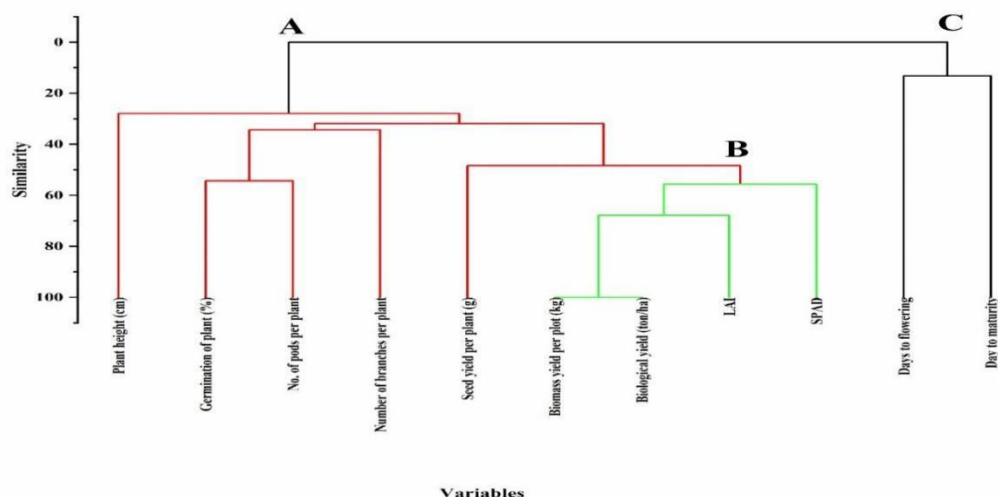


Figure 6: Dendrogram with hierarchical cluster analysis for eleven quantitative variables.

## DISCUSSION

Measurement of a wide range of soybean genotypes in Balochistan indicated notable difference in various morphological as well as physiological characteristics. Most of the phenotypic traits did not have any significant genotype effect, however, significant variation in 1000-seed weight ( $P = 0.0004$ ) and leaf area index (LAI,  $P = 0.000$ ) was noted. 1000-seed weight and LAI were noted to be two sensitive measures of genotype effects. Mean days to flowering among the measured parameters varied ranging from 38.1-45.9 with development consistency in various heterogeneous environments whereas mean days to maturity was between 97.9-114.2 days. Current study is aligned with findings of Grant et al. (2025) who studied the same parameters and highlight the fact that, in soybean, flowering time and maturity are regulated by major genes, namely the E1-E4, whose alleles are largely different between genotypes and environments. Moreover, these traits have been reported to be highly heritable and thus have a high probability of being selected using gene selection in breeding programs (Irshad et al., 2016). Similar to the results obtained in past studies that investigated soybean maturation, there was very little genotype by environment interaction in maturity date implying that there was a low scale of variability in maturation date among cultivars under different environmental conditions (Miranda et al., 2020).

In our study, plant height data tend to be concentrated in the mid-70s of cm, 4-7 branches per plant. In spite of the fact that all of these trends were not statistically significant in the present study, similar trends have also been reported to be past reviews carried out in Pakistan (Ahmad et al., 2023), where both traits may be exploited in genetic improvement programs, indicating a high level of phenotypic range and a moderate level of heritability. In the current finding, there was a significant difference ( $P < 0.001$ ) in 1000-seed weight, in a range of nearly 6 and 15 g. In earlier studies, the estimates of broad-sense heritability have been extremely high with all the values being above the highest mark of 0.97 (Irshad et al., 2016), affirming that weight of seeds is mainly governed by genes, which make it a potential breeding trait. The seeds per plant exhibited a significant difference, ranging from 62-116 g, but did not attain the significance at  $P < 0.05$  level. The field trials on soybean performed in Pakistan with similar findings by Irshad et al. (2016). There are no direct comparisons, but more recent studies have shown chlorophyll to be different in relation to physiological performance; improving SPAD is more commonly associated with increased photosynthesis rates (Fritschi et al., 2007; Hu et al., 2025). The increased SPAD genotypes like GP 1 could therefore be adapted to conditions of the semi-arid environment of Balochistan. Correlation analysis confirmed that a potential relationship

between biomass accumulation and biological yield occurs as biomass accounts for a large part of dry matter. Our findings were aligned with the previous study of Esegbe et al. (2024), who found a strong positive correlation between biological yield and grain yield. The positive correlation between LAI and yield ( $r \approx 0.61$ ) corresponds to finding to Malone et al (2002), explaining that at least 3.5–4.0 LAI during reproduction period provide the optimal yield of soybean. Leaf chlorophyll and nitrogen status are well reflected in SPAD values, making them predictors of both the plant's photosynthetic ability and projected yield. Research study on soybean has found that SPAD readings during the R5 and R6 stage are related to higher grain yields (Yokoyama et al., 2018). Our results exhibit moderate correlations between pod number and germination, and seed yield with plant height, implying that plants established early and evenly have better chances of producing greater yields. Wang et al., (2025) reported that a higher number of seeds and larger canopies are related to larger yields in soybean yield-components. The inverse correlations of biomass and biological yield with days to maturity ( $r = -0.52$ ), seed yield with days to flowering ( $r = -0.67$ ), SPAD value with days to flowering ( $r = -0.33$ ), indicate that both early flowering and timely maturity contribute to accumulation of more biomass and seeds in the plants. Previous studies described that soybean bloom and reproduce well under existence of optimal environmental conditions, resultantly tend to provide a maximum yield (Esegbe et al., 2024).

Principal Component Analysis (PCA) was carried out to estimate the variability and correlation of the association between 11 agro-morphological and physiological traits in twenty soybean genotypes (GP-1 and GP-20) grown in agro-ecological conditions of the Balochistan province. A preliminary principal component analysis (PCA) performed on soybean variety SB-1 and SB-20 which was under cultivation in the semi-arid environment of Balochistan suggested that yield-related traits were the major attributes defining genotypic diversification. Namely, PC1 that contributed to 34.03 % of the total variance had mostly the biomass yield per plot, biological yield, seed yield per plant, number of pods per plant, and plant height and they were all the factors that are often cited as productivity and vigor indicators of plants. This finding is in agreement with the findings by Ullah et al. (2024) as they recorded biological and seed yield to be the most important variables to influence the phenotypic variation of soybean with the top five principal components explaining over 81% of the whole variance. Likewise, previous researchers found the

explanatory variables that were selected as having the major loading importance on the first principal component (PC1) in a sequence of soybean genotypes grown under semi-arid conditions in a field in Tandojam, Pakistan, were the significantly relevant variables in determining the crop production in a water-limited environment (Manzoor et al. 2024). The predominant component 3 (PC3) explained 13.77 per cent of the total variance meaning that it had significant impact in the phenotypic variation. The results of the analyses of the loading values of PC3 showed that the highest positive correlation of PC3 was with the germination percentage and pod number, thereby demonstrating the significance of early plant vitality and reproductive effectiveness during soybean evolution. The current study supports the results of Perez-de-Cataldo et al. (2023), who reported that the germination characteristics and pod features make up the variables that have been most decisively distinct in the principal component analysis of a distinguished South American soybean genotype. Their findings highlighted that notable variables that affected the variation in crop yield were pod number and the duration in flowering to maturity. Likewise, the relevance of phenological characteristics and seed features was emphasized by Adie and Krisnawati (2017) in terms of PCA-based genotype characterization of soybeans in the tropical environment.

## CONCLUSION

The present findings suggested that genotype clusters (GP-1 and GP -20) are not localized in a specific geographic location, but are representative of strong genetic designs that can be employed in legume improvement across global soybean breeding programs. The current observations confirm the hypothesis that PCA analysis is a very sound multivariate method of genotype characterization and selection. The future research ought to focus on multi-environmental testing and compatibility of genomic tools so as to confirm trait association in various agro-ecological zones. These efforts will improve accuracy and efficiency of the breeding initiatives to develop more resilient, high-yielding and diversified soybean varieties with capacity to overcome the harsh climate conditions.

## AUTHOR'S CONTRIBUTIONS

All authors contributed equally in the manuscript.

## COMPETING OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this paper.

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