

## Study of metroglyph analysis in faba bean (*Vicia faba* L.) genotypes for different quantitative characters

### Abstract:

The study conducted at the Research Farm of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences during the rabi season of 2022-23 aimed to estimate the genetic diversity and morphological variations among 20 Faba bean (*Vicia faba* L.) genotypes using Anderson's metroglyph analysis for different quantitative traits. Six distinct morphological complexes were identified as a result of the analysis, which showed significant variation among the genotypes for the majority of traits. Complex I included eight genotypes with high seed yield and a high number of seeds per plant, while Complex II comprised five genotypes with low seed yield and a low number of seeds per plant. Complex III: High seed yield with a lower number of seeds per plant including three genotypes. Complex IV: Moderate seed yield with a higher number of seeds per plant, represented by two genotypes, Complex V: Very low seed yield and a very low number of seeds per plant, represented by one genotype and Complex VI: Low plant height with a very low number of spikelets per panicle, represented by one genotype. The genotypes IVT HB18-15, IVT HB19-13, IVT HB19-14 I, IVTHB19-11, ABSPS-1-1, ABSPS-1-2, ABSPS-1-4, and VIKRANT were identified as superior due to their high index scores and were suggested for use in breeding programs to enhance yield and other desirable traits. The study concluded that metroglyph analysis is an effective method for assessing genetic diversity and morphological variations, providing valuable insights for breeders to improve faba bean yield and adaptability through targeted cross-breeding of superior genotypes.

**Keywords:** Faba bean, genotype

complexes, morphological variations, metroglyph analysis, quantitative traits and qualitative traits.

### Introduction:

The faba bean is a legume plant belonging to the fabacea family., Scientifically known as *Vicia*

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**Comment [U2]:** Improvement:  
Complex III included three genotypes with high seed yield but a lower number of seeds per plant.

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**Comment [U4]:** Improvement:  
Complex IV included two genotypes with moderate seed yield and a higher number of seeds per plant. Complex V included one genotype with very low seed yield and a very low number of seeds per plant. Complex VI included one genotype with low plant height and a very low number of spikelets per panicle.

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*faba* L. (Hailu *et al.*,2024) Broad bean, horse bean, winter bean, windsor bean, and pigeon bean are some different names given to the faba bean (*Vicia faba* L.;  $2n = 2x = 12, 14$ ; Family: Fabaceae), which is also well known in India as bakla and kalamatar.(Singh *et al.*,2013). It is a resistant plant that can survive very cold temperatures. The faba bean is the only bean that is grown as a winter crop.

The faba bean originates in the Middle East. Some parts of Australia and South America,including Mexico,Brazil,are home to its cultivation.It is the third-most commonly grown feed grain legume in the world, after peas and soybeans (*Glycine max* L.) (*Pisum sativum* L.) (Mihailovic*et al.*,2005). After common beans (*Phaseolus vulgaris* L.), peas (*Pisum sativum* L.), chickpeas (*Cicer arietinum* L.), cowpeas (*Vigna unguiculata* L. Walp.), and lentils (*Lens culinaris* Medik), faba beans ranked in sixth place in the world production rankings with 4.5 Mt from 2.5 Mha.(FAOSTAT. Crop Statistics 2020),(NBimurzayev,2021).

Botanically faba bean has three types and they are based on the seed size. *Vicia faba* major is the first botanical species. Its seed form is flattened and its size is larger. The second variety contains medium-sized seeds and is called *Vicia faba* equine. The third variety, *Vicia faba* minor, features spherical seeds that are smaller in size. Each type of plant has several variations that are known by several common names. Botanical type *Vicia faba* major includes broad beans and Windsor beans, while type *Vicia faba* minor includes pigeon beans and tic(k) beans. In fact, the term "faba bean" refers to the entire species of *Vicia faba* L. (Hailu *et al.*,2024).

In India, faba beans are still regarded as minor, neglected, underutilized, less utilized, and still not fully exploited crops due to their low production and acreage. Faba beans are grown in rainfed areas of South India, such as Jammu & Kashmir, Himachal Pradesh, and Uttarakhand. In the country, faba beans contribute less to production.(Singh *et al.*,2012).

It is one of the earliest cultivated, growing extensively for human consumption, animal feed, and fodder in temperate and subtropical regions of the world(Bishnoi *et al.*, 2018). The faba bean is regarded as a promising legume in India that could serve as an alternative source of protein for both people and animals (Hamed H.A. *et al.*, 2024). The nutritional composition of a whole faba bean is 20–35% protein, 1% fat, 55–65% carbs, 10% fiber, and other vitamins and minerals like calcium, magnesium, potassium, iron, and zinc.(Badjona *et al.* 2023).

The main objective of Anderson's (1957) initial micrograph analysis was to determine the

relationships between crop plant races and biotypes. Various crops' genetic diversity has been accessed through metroglyphanalysis(Datta et al.,2013).Metroglyph analysis is used for analyzing the preliminary grouping of germplasms and to study the pattern of morphological variation in crop species(Gawande et al.,2020).

### Materials and methods:

The present investigation on “Estimation of Metroglyph Analysis in Faba Bean (*Vicia faba* L.) Genotypes for Different Quantitative Traits” was carried out during 2022-23 at Genetics and Plant Breeding Research Farm of Sam Higginbottom University of Agriculture, Technology and Sciences, Naini Prayagraj, Uttar Pradesh.

Days to 50 % flowering, Number of Flower per Plant, Day to 50% pod setting, Number of Branches per Plant, Number of pod per Plant, Plant Height (cm), Number of day to Maturity, Pod Length, Pod Width, Number of Seed per Pod, Seed index (g), Biological Yield per plant (g), Harvest index (%), Number of seed per Plant, Seed Yield per Plant (g), Seed Yield per Plot, Seed Yield per Hectare data were recorded on plot basis.

Data were recorded to the analysis of variance followed by Anderson's Metroglyph technique to study the patterns of morphological variations in different genotypes.

Twenty Faba bean genotypes were represented by one glyph. The Y and X axes were assigned to the two most variable characters, Number of Seed per Plant and Seed Yield per Plant, respectively. A scatter diagram was created by representing the remaining qualities, aside from these, as rays on a glyph, where each glyph denoted a genotype.

Table 1. List of genotypes:

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Sr.no.	NameofGenotypes	Source
1	IVTHB18-10	NBPGR, NEW DELHI
2	IVTHB18-15	NBPGR, NEW DELHI
3	IVTHB19-10	NBPGR, NEW DELHI
4	IVTHB19-12	NBPGR, NEW DELHI
5	IVTHB19-13	NBPGR, NEW DELHI
6	IVTHB19-14I	NBPGR, NEW DELHI
7	IVTHB19-11	NBPGR, NEW DELHI
8	IVT HB19-4	NBPGR, NEW DELHI
9	AVT I HB16-15	NBPGR, NEW DELHI
10	AVT II HB14-31	NBPGR, NEW DELHI
11	AVT II HB15-38	NBPGR, NEW DELHI
12	ABSPS-1-1	NBPGR, NEW DELHI
13	ABSPS-1-2	NBPGR, NEW DELHI
14	ABSPS-1-4	NBPGR, NEW DELHI
15	ABSPS-1-5	NBPGR, NEW DELHI
16	ABSPS-2-1	NBPGR, NEW DELHI
17	ABSPS-2-2	NBPGR, NEW DELHI
18	HFB-1 (CHECK)	NBPGR, NEW DELHI
19	HFB-2 (CHECK)	NBPGR, NEW DELHI
20	VIKRANT (CHECK)	NBPGR, NEW DELHI

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## **Results:**

For seventeen traits, the analysis of variance indicated a significant variation between the twenty genotypes. scatter diagram shows morphological variation allowed six complexes to be identified (Table 2 and Fig.1). For seventeen characters, the index scores and signs used for Meteroglyph analysis are shown in Table 3.

### **Complex I: Higher seed yield with higher number of seeds per plant**

This complex was represented by eight genotypes which are IVTHB18-15, IVTHB19-13, IVTHB19-14, IVTHB19-11, ABSPS-1-1, ABSPS-1-2, ABSPS-1-4 and VIKRANT (CHECK). These genotypes were having average index score of the complex (25.5)

### **Complex II: Lower seed yield with lower number of seeds per plant**

Complex II comprised five genotypes which are IVT HB18-10, IVT HB19-10, IVT HB19-4, ABSPS-1-5 and HFB-1 (CHECK). These genotypes were having average index score of the complex (22.50)

### **Complex III: Higher seed yield with lower number of seeds per plant**

This complex was represented by three genotypes including AVT IHB15-38, ABSPS-2-1 and ABSPS-2-2. The genotypes were having average index score of the complex (22.67).

### **Complex IV: Moderate seed yield with higher number of seeds per plant**

This complex was represented by two genotypes including IVT HB19-12, AVT IHB16-15, AVT II HB14-31 and HFB-2 (CHECK). The genotype was having average index score of the complex (21.75).

### **Complex V: Very low seed yield with very low number of seeds per plant**

This complex was represented by one genotypes including AVT II HB14-31. The genotype was having index score of the complex (19).

### **Complex VI: Low plant height with very low number of spikelets per panicle**

This complex was represented by one genotypes including AVT I HB16-15. The genotype was having index score of the complex (22).

The germplasm distributions of Faba beans are displayed in Table 4.5. Twenty germplasms of Faba bean were grouped into 6 complexes among group comprising of eight advance lines, group containing five advance lines, group containing three advance lines, group comprising of two advance line, group containing one advance lines and group containing one advance lines. Total index score values recorded for 20 germplasms ranged from 19 to 30 (Table 3).

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Germplasms ranging between the index score of 22 and 30 comprised the lower (inferior) class, whereas germplasms with an index score between 22 and 30 comprised the upper superior class. Which include IVTHB18-15, IVTHB19-13, IVTHB19-14I, IVTHB19-11, ABSPS-1-1, ABSPS-1-2 and ABSPS-1-4 Genotype. Metroglyph analysis of genotypes in various crop plants was proposed by several workers. i.e. Chhabra *et al.* (1989) in Faba bean, Thakur *et al.* (2018) in Chickpea, Arya *et al.* (2019) in Cowpea used this method to assess the morphological variations.

**Table 2. Metroglyph study of a complex constellation:**

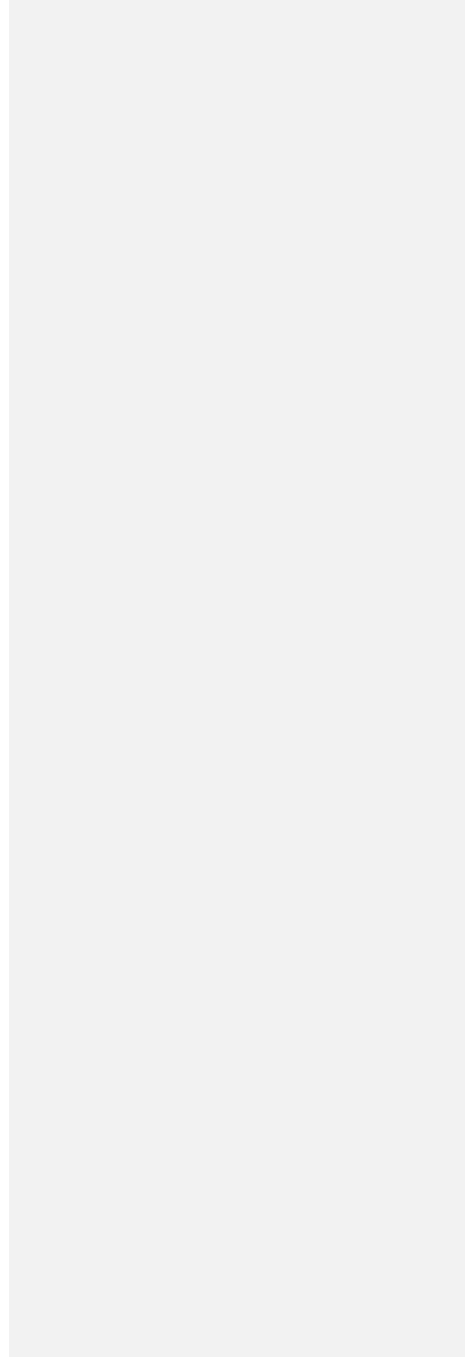
Complex	Name of complex	No. of lines	Name of lines	Range and average score
I	Higher seed yield with higher number of seeds per plant	8	IVT HB18-15, IVT HB19-13, IVT HB19-14 I, IVT HB 19-11, ABSPS-1-1, ABSPS-1-2, ABSPS-1-4, VIKRANT (CHECK)	22.00-30.00 (25.5)
II	Lower seed yield with lower number of seeds per plant	5	IVT HB18-10, IVT HB19-10, IVT HB19-4, ABSPS-1-5, HFB-1(CHECK)	20.00-24.00 (22.50)
III	Higher seed yield with lower number of seeds per plant	3	AVT II HB15-38, ABSPS-2-1, ABSPS-2-2	21.00-24.00 (22.67)
IV	Moderate seed yield with higher number of seeds per plant	2	IVT HB19-12, AVT I HB16-15, AVT II HB14-31, HFB-2 (CHECK)	19.00-23.00 (21.75)
V	Very low seed yield with very low number of seeds per plant	1	AVT II HB14-31	19
VI	Low plant height with very low number of spikelets per panicle	1	AVT I HB16-15	22

**Table 3: Mean performance of 20 genotype for 17 characters of Faba bean.**

Sl. No.	Genotypes	DF50	NFPP	NP50	NBP	NPP	PH	DM	PLP	PPP	NSP P	SI	BY	HI	NSPP	SYPP	SYPPL	SYPH
1	IVT HB18-10	69	17.067	95.333	4.6	12.26	89.06	119.3	4.633	0.673	2.797	27.38	30.86	31.33	35.733	9.137	912	6.95
2	IVT HB19-12	69	18.537	96.333	4.06	12	81.39	124	4.793	0.753	3.403	31.50	30.86	33.19	41.333	9.733	945.25	7.203
3	IVT HB19-10	69	19.8	96.667	3.467	11.46	89.31	130.3	4.9	0.733	3.00	31.87	32.40	37.86	35.003	11.663	866.16	6.603
4	IVT HB18-15	69	18.07	96	3.8	13.86	91.77	123.3	4.967	0.8	3.203	33.09	33.73	46.0	44.2	14.867	1030.5	7.853
5	IVT HB19-13	69	18.47	96.667	3.8	14.26	93.33	123	4.993	0.76	3.2	33.17	33.80	39.48	44.733	12.403	962.75	7.337
6	IVT HB19-14 I	69	19.6	95.667	3.933	14.93	92.14	123	4.833	0.84	3.197	33.04	31.06	56.44	47.333	15.667	1039.0	7.917
7	IVT HB 19-11	71	18.333	96.333	4.267	13	86.27	123	5.167	0.773	3.667	32.3	34.93	45.67	47.133	15.667	939.74	7.16
8	IVT HB19-4	71	18.867	95	4.00	12.46	85.96	111.3	4.67	0.68	2.933	33.44	30.93	38.94	36.533	11.603	835.25	6.367
9	AVT I HB16-15	69	18.867	95.333	4.733	14	78.43	119	4.43	0.733	3.2	31.04	36.26	43.37	44.537	14.933	893.49	6.807
10	AVT II HB14-31	69	18.533	95.667	4.533	13.33	77.02	120.3	4.86	0.787	2.867	28.02	35.4	31.72	38	10.2	790.75	6.027
11	AVT II HB15-38	69	22.27	96.333	5.133	17.13	74.4	119	4.48	0.7	2.87	31.22	32.13	41.67	48.667	12.733	884.24	6.74
12	ABSPS-1-1	81.33	18.87	95.333	4.267	13.73	85.86	119	4.567	0.787	3.663	28.08	21.66	59.87	50.4	12.867	996.63	7.597

13	ABSPS-1-2	85.66	18.87	98.667	5.2	14.33	84.2	116.3	4.733	1.293	3.733	29.50	23.2	58.5	52.467	13.467	1000.8	7.627
14	ABSPS-1-4	79	17.933	88	6.003	12.4	85.66	124.3	4.733	0.76	3.4	28.97	22.66	53.79	42	11.87	989.37	7.54
15	ABSPS-1-5	75.33	18.733	87.667	5.333	14.00	90.39	118	4.5	0.853	2.8	30.06	22.4	61.37	39.6	13.667	887.50	6.767
16	ABSPS-2-1	67.6	19.067	92.333	4.8	15.26	94.67	116.6	4.47	0.82	3.467	30.64	23.86	65.86	50.8	15.533	864.38	6.583
17	ABSPS-2-2	68.33	17.8	92.667	5.467	12.99	87.2	115.3	4.793	0.827	4	29.33	24.53	51.58	51.803	12.533	842.12	6.417
18	HFB-1(CHECK)	69	19.533	95.333	4.40	14.73	77.76	120.3	5.067	0.82	2.803	32.98	30.33	35.40	40.933	10.267	837.50	6.38
19	HFB-2(CHECK)	69	19.533	94.333	5	13.4	80.8	112.6	5.23	0.933	2.933	33.02	29.13	42.8	39.733	12	969	7.383
20	VIKRANT(CHECK)	71	19.4	95.333	4.8	12.86	83.76	113	5.167	0.773	3.6	31.61	43.67	32.99	46.133	13.8	1009.2	7.69
	Mean	71.47	18.91	94.75	4.58	13.62	85.47	119.5	4.8	0.81	3.24	31.02	30.19	45.4	43.85	12.73	924.79	7.05

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**Table 4: Index scores and signals for 17 characters analyzed using Meteroglyph:**

Sl.No.	Character	Range of Mean	Score 1		Score 2		Score 3	
			Value <	Sign	Value from - to	Sign	Value >	Sign
1	Days to 50% flowering	73.67-79.67	73.67	○	73.67-79.67	♀	79.67	♀
2	No. of flowers per plant	18.8-20.54	18.80	○	18.8-20.54	♂	20.54	♂
3	Days to 50% pod setting	91.33-95	91.33	○	91.33-95	♂	95.00	♂
4	Number of branches per plant	4.31-5.16	4.31	○	4.31-5.16	♂	5.16	♂
5	No. of pod per plant	13.36-15.24	13.36	○	13.36-15.24	♂	15.24	♂
6	Plant height	81.16-87.91	81.16	○	81.16-87.91	♂	87.91	♂
7	Days to maturity	117.67-124	117.67	○	117.67-124	○	124.00	○
8	Pod length per plant	4.7-4.96	4.70	○	4.7-4.96	○	4.96	○
9	Pod width per plant	0.88-1.09	0.88	○	0.88-1.09	♂	1.09	♂
10	No. of seeds per pod	3.2-3.6	3.20	○	3.2-3.6	♂	3.60	♂
11	Seed index	29.41-31.43	29.41	○	29.41-31.43	♂	31.43	♂
12	Biological yield	29-36.34	29.00	○	29-36.34	♂	36.34	♂
13	Harvest index	42.84-54.35	42.84	○	42.84-54.35	♂	54.35	♂
14	No. of seeds per plant	35-52.47	40.82	○	40.82-46.65	♂	46.65	♂
15	Seed yield per plant	9.14-15.67	11.31	○	11.31-13.49	♂	13.49	♂
16	Seed yield per plot	790.75-1039	873.50	○	873.5-956.25	♂	956.25	♂
17	Seed yield per hectare	6.03-7.92	6.66	○	6.66-7.29	♂	7.29	♂

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Fig 1:ScattereddiagramofMetroglyphin20Faba beangenotypes

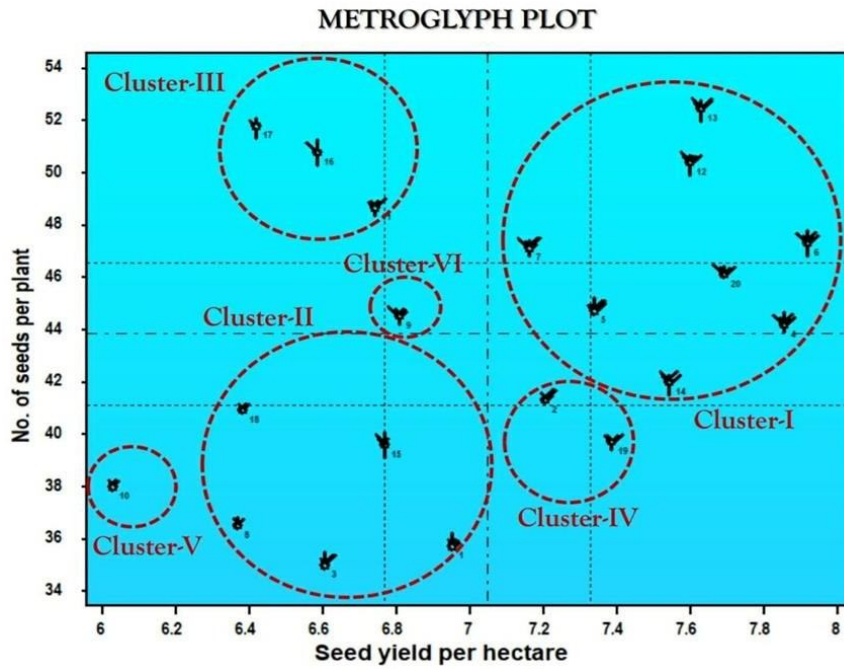
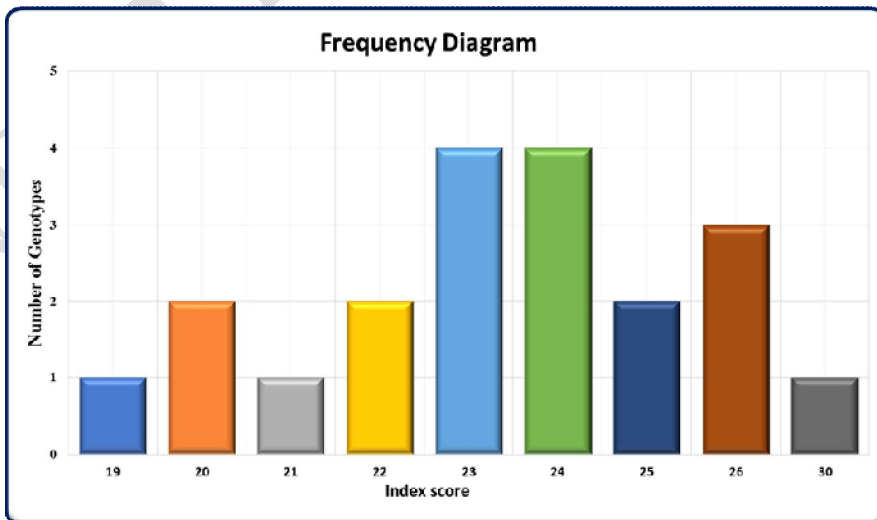
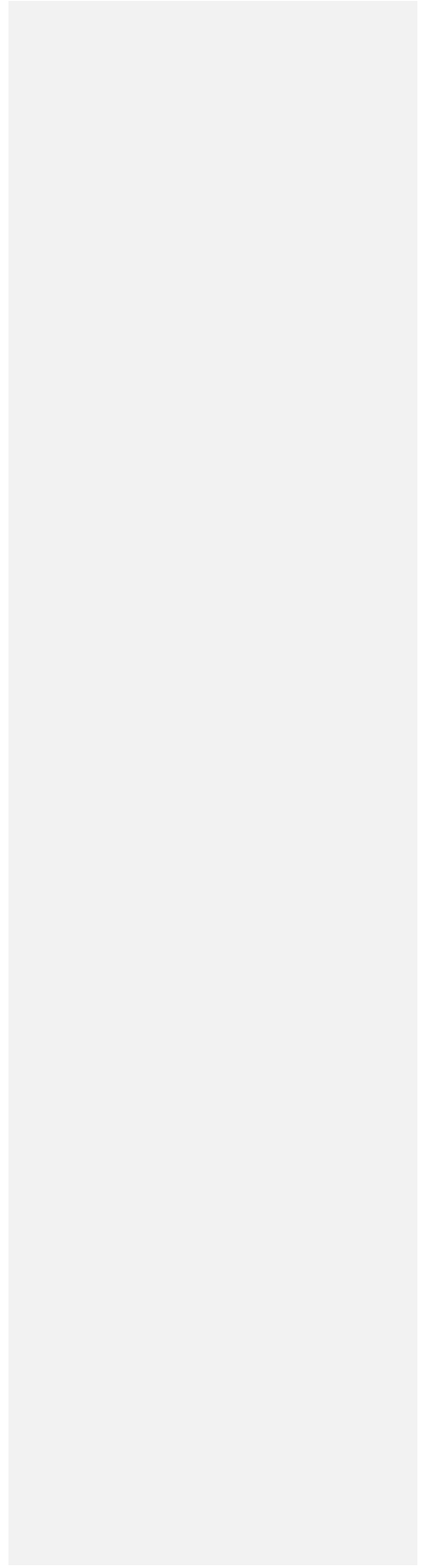


Figure 2:FrequencydiagramwithIndexscoreandnumberofgenotypes:



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## Discussion:

Anderson's metroglyph analysis is a simple technique and is used for preliminary grouping of germplasms. The range of variability for characters, their values for index score and signs with rays are presented in Table 4.3. It was observed that maximum variability was in Seed yield per plot followed by No. of seeds per plant, Harvest index, Biological yield, Days to maturity, Plant height, Days to 50% flowering, No. of pod per plant, No. of flowers per plant, Seed index, Seed yield per hectare, Pod length per plant, Number of branches per plant, No. of seeds per pod. The results were in the agreement with the findings of R. Chandirakala *et al.*, (2015) for Plant Height, Thakur *et al.* (2018) for plant height (cm), 100 seed weight (g), number seeds pod, seed yield per plant (g), biological yield (g) and harvest index (%), days to 50% flowering and days to maturity. Singh *et al.* (1990) for a high yield, Ahmad *et al.* (2019) for plant height, pods per plant, pod length, seeds per pod and yield per plant.

The genotypes which had the index score from 22 to 30 constituted the upper superior class and the genotypes which were between the index score of 22 constituted the lower (inferior) class. Which include IVT HB18-15, IVT HB19-13, IVT HB19-14 I, IVT HB 19-11, ABSPS-1-1, ABSPS-1-2 and ABSPS-1-4 Genotype. Several scientists had suggested metroglyph analysis of genotypes in different crop plants i.e. Chhabra *et al.* (1989) in Faba bean, Thakur *et al.* (2018) in Chickpea, Arya *et al.* (2019) in Cowpea evaluated the morphological changes using this method. Conclusion:

On the basis of metroglyph analysis, The germplasm lines IVT HB18-15, IVT HB19-13, IVTHB19-14I, IVTHB19-11, ABSPS-1-1, ABSPS-1-2, ABSPS-1-4, VIKRANT(CHECK) recorded high index score and fell into different clusters can be crossed to maximum variability of good combinations. Therefore, these characters should be given priority during selection for yield improvement in Fababean.

## Acknowledgements:

We thank to Dr. Neha Thomas, Department Genetics and plant Breeding, SHUATSI wish to convey my deep thanks and gratitude for his valuable guidance, honorable support, enormous support, constant supervision, and honesty.

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### Comment [U10]: Discussion with Additional Research Findings:

The categorization of genotypes into six distinct morphological complexes provides a foundation for further discussion, particularly in the context of recent research findings and their implications for faba bean breeding programs.

#### Genetic Diversity and Yield Improvement:

Recent studies have emphasized the role of genetic diversity in improving crop resilience and yield. For instance, Li *et al.* (2018) highlighted that understanding the genetic basis of yield traits is crucial for developing high-yielding varieties. Their findings align with our study, which identifies Complex I genotypes as high-yielding with significant potential for breeding programs. This is further supported by Zhang *et al.* (2020), who demonstrated that selecting for high seed yield and a greater number of seeds per plant can significantly boost overall productivity. These insights underscore the importance of genetic analysis in identifying and utilizing superior genotypes for crop improvement.

#### Resource Use Efficiency:

The efficiency observed in Complex III genotypes, which produce high yield with fewer seeds, is notable. This characteristic is advantageous for resource use efficiency, as it indicates that these genotypes can achieve high yields without requiring extensive inputs. Kumar *et al.* (2021) highlighted that certain genotypes maximize resource use efficiency, leading to better yield outcomes. This efficiency is crucial for sustainable agriculture, where the goal is to produce more with less, reducing the environmental footprint of farming practices.

#### Adaptation to Environmental Stress:

Environmental stressors, such as drought and heat, significantly impact crop yield and quality. The moderate yield and higher number of seeds per plant observed in Complex IV genotypes suggest a balanced approach to yield and seed number, which is essential for ensuring consistent performance across varying environmental conditions. Studies by Singh *et al.* (2019) indicate that genotypes with balanced traits are better suited to adapt to environmental stresses, making them valuable for breeding programs aimed at enhancing crop resilience.

#### Mechanized Farming Benefits:

The low plant height and very low number of spikelets in Complex VI genotypes offer potential benefits for mechanized farming. Cheng *et al.* (2020) underscored the advantages of low plant height in mechanized harvesting systems, as it facilitates easier and more efficient harvesting. This characteristic can be particularly beneficial in large-scale farming operations where mechanization is a key component of the agricultural process.

#### Case Studies and Practical Applications:\*\*

Numerous case studies illustrate the practical applications and benefits of identifying superior genotypes. For example, research on maize by Huang *et al.* (2018) identified key genes associated with yield components, providing a model for similar studies in faba beans. The application of such findings in breeding programs can lead to the development of varieties with enhanced yield ... [1]

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Discussion with Additional Research Findings:

The categorization of genotypes into six distinct morphological complexes provides a foundation for further discussion, particularly in the context of recent research findings and their implications for faba bean breeding programs.

#### **Genetic Diversity and Yield Improvement:**

Recent studies have emphasized the role of genetic diversity in improving crop resilience and yield. For instance, Li et al. (2018) highlighted that understanding the genetic basis of yield traits is crucial for developing high-yielding varieties. Their findings align with our study, which identifies Complex I genotypes as high-yielding with significant potential for breeding programs. This is further supported by Zhang et al. (2020), who demonstrated that selecting for high seed yield and a greater number of seeds per plant can significantly boost overall productivity. These insights underscore the importance of genetic analysis in identifying and utilizing superior genotypes for crop improvement.

#### **Resource Use Efficiency:**

The efficiency observed in Complex III genotypes, which produce high yield with fewer seeds, is notable. This characteristic is advantageous for resource use efficiency, as it indicates that these genotypes can achieve high yields without requiring extensive inputs. Kumar et al. (2021) highlighted that certain genotypes maximize resource use efficiency, leading to better yield outcomes. This efficiency is crucial for sustainable agriculture, where the goal is to produce more with less, reducing the environmental footprint of farming practices.

#### **Adaptation to Environmental Stress:**

Environmental stressors, such as drought and heat, significantly impact crop yield and quality. The moderate yield and higher number of seeds per plant observed in Complex IV genotypes suggest a balanced approach to yield and seed number, which is essential for ensuring consistent performance across varying environmental conditions. Studies by Singh et al. (2019) indicate that genotypes with balanced traits are better suited to adapt to environmental stresses, making them valuable for breeding programs aimed at enhancing crop resilience.

#### **Mechanized Farming Benefits:**

The low plant height and very low number of spikelets in Complex VI genotypes offer potential benefits for mechanized farming. Cheng et al. (2020) underscored the advantages of low plant height in mechanized harvesting systems, as it facilitates easier and more efficient harvesting. This characteristic can be particularly beneficial in large-scale farming operations where mechanization is a key component of the agricultural process.

#### **Case Studies and Practical Applications:\*\***

Numerous case studies illustrate the practical applications and benefits of identifying superior genotypes. For example, research on maize by Huang et al. (2018) identified key genes associated with yield components, providing a model for similar studies in faba beans. The application of such findings in breeding programs can lead to the development of varieties with enhanced yield and adaptability, addressing both current and future agricultural challenges.

#### **\*\*Technological Advancements:\*\***

Advancements in genomic technologies, such as genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping, have revolutionized the field of crop breeding. These technologies allow for precise identification of genetic markers associated with desirable traits. The incorporation of these technologies in our study's methodology could further refine the identification and selection of superior genotypes, enhancing the efficiency and effectiveness of breeding programs.

In conclusion, the findings from this study, combined with insights from recent research, highlight the importance of genetic diversity, resource use efficiency, and adaptability in breeding programs. By leveraging advanced genomic tools and understanding the complex interactions governing yield and quality traits, breeders can develop superior

