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Morphological Diversity in Castor (*Ricinus communis* L.): A Metroglyph Analysis Approach to Reveal Hidden Patterns

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Abstract: An experiment was conducted to study the pattern of morphological variation for six characters in 22 elite castor inbred lines by Metroglyph and Index score method. Each genotype was represented by a closed circle, with the X-coordinate being seed yield per plant and the Y-coordinate being plant height. The remaining four characters were represented by rays of different positions on the glyph, with the length of the rays indicating the range. The line had a low value with no ray, medium value with a short ray, and a high value with a long ray. Scatter diagram revealed that maximum numbers of 7 genotypes were found in group IV. Metroglyph and Index score analysis revealed maximum variability for different characters in first and fourth group which comprised seven and four genotypes, respectively. The results unveiled seven distinct groups with unique morphological variations. The highest index score observed was 16 for genotypes RG-3041 while lowest score was 6 for JI-424. This study may be helpful for breeders, offering promising trait combinations available within the gene pool, paving the way for advances for castor improvement.

Key words: Metroglyph, castor, arid zone, clustering, index Score, variability.

Castor (*Ricinus communis* L.) plays a crucial role in agricultural contexts, especially in arid and semi-arid regions, where the challenges of water scarcity and harsh environmental conditions are prominent. Its remarkable adaptability to arid zones positions castor as a key player in addressing the impacts of climate change and maintaining agricultural productivity in regions facing water stress (Dangi *et al*., 2019). Its distinctive capacity to thrive in arid environments while yielding valuable oil-rich seeds underscores castor's promise as a resilient crop, capable of making substantial contributions to global energy security in the context of pressing environmental issues.

Castor is a highly diverse plant species with a wide range of morphological, biochemical, and genetic variation (Delvadiya *et al.*, 2024). The plant is known to exhibit a high degree of phenotypic plasticity, making it well-suited to adaptation to different environmental conditions (Debnath *et al.*, 2020). The diversity of castor is also reflected in its wide distribution, which spans from the tropics to temperate regions, as well as its wide range of uses, including as a source of biodiesel, industrial lubricants, and medicines (Eswaran *et al.*, 2019). Castor bean seeds were used by people dating from about 4000 BC and were thought to have originated in Eastern Africa, particularly Ethiopia (Qiu *et al.*, 2010). The application of castor in India, Saudi Arabia, Greece, and Rome has been documented as having anti-inflammatory, antiasthmatic, and cathartic effects (Ribeiro *et al.*, 2016). The genetic diversity of castor has been extensively studied using various molecular markers, such as SSRs, SNPs, and AFLPs, with many studies reporting high levels of genetic diversity and population differentiation (Zhang *et al.*, 2015 and Zhang *et al.*, 2016). Overall, the diversity of castor makes it a valuable genetic resource for breeding and genetic improvement programs, as well as a potential source of new bioactive compounds for various applications.

The importance of Metroglyph analysis in the realm of castor research cannot be emphasized enough. Castor presents a unique set of challenges and opportunities in plant breeding due to its extensive phenological marker diversity and the inheritance of many traits through mono and oligogenic characters. This inherent complexity sets castor apart from other crops. In the realm of plant breeding, precision and accuracy are of paramount importance. Metroglyph analysis, rooted in the principles of first-order statistics, offers a remarkably precise and error-free approach. Its enduring relevance and effectiveness make it a perfect fit for castor research, where the need for a robust analytical tool to decipher the genetic intricacies of this crop is crucial. An essential aspect of Metroglyph analysis is its semigraphical approach, which facilitates the comprehension and analysis of data through graphical representation. This approach simplifies the interpretation of results, making it easier for researchers to extract valuable insights. Furthermore, the suitability of Metroglyph analysis for castor research is enhanced by its ability to operate without replication, simplifying field experiments and data handling. This practicality streamlines the research process, making it more accessible and efficient. It has enabled researchers to delve into the complex genomic landscape of castor, resulting in the development of a more refined selection criterion. This underscores the pivotal role of Metroglyph analysis in contemporary plant breeding, especially when dealing with crops as distinctive and intricate as castor.

Materials and Methods

In a quest to unlock the morphological potential of castor, the investigation was conducted at the Main Oilseed Research station of Junagadh Agricultural University in Gujarat. A total of 22 genotypes were carefully selected and planted in a randomized block design with three replications (Table 1).

Each row extended 6 m, with a spacing of 120 cm between rows and 60 cm between individual plants. Ten plants were randomly selected from each genotype to examine, six key characters *viz.* days to flowering, plant height, length of primary raceme, number of capsules on primary raceme, shelling out turn, and seed yield per plant.

Using the RBD design, the analysis of variance was carried out for all genotypes - to get a better understanding of the morphological characters in different crop species, the Metroglyph and index score method - as advocated by Anderson (1957) was used. Each genotype was represented by a closed circle (glyph), with seed yield per plant placed on X-coordinate and plant height placing on Y-coordinate on a scatter diagram. The remaining four characters were represented by rays of different positions on the glyph, with the length of the rays indicating the range. The line had a low value with no ray, medium value with a short ray, and a high value with a long ray (Table 2).

The index values were classified into three distinct classes: 1 - no ray, 2 - short ray and 3 - long ray. To determine the total index values, the index scores of all six characters studied were added up.

Result and Discussion

Upon examining the scatter diagram (Fig.1), the results revealed existence of seven distinct

Table 1. List of genotypes used in present study along with their pedigree and salient features

Name of genotypes	Pedigree	Origin	Salient features
JP 96	JP 66 × 454	JAU, Junagadh	G_3SP
JP 106	JP-89 × DCS-9	JAU, Junagadh	M_2SP
SKP 84	SKP 1 × VP 1	SDAU, S.K. Nagar	M_3SP
VP-1	(TSP-10-R × JI-15) F2 × (JP-5 × 26006) F2	Vijapur	G_3SP
JI 244	Selection from JI-112	JAU, Junagadh	G_3SP
JI 390	JP-83 × JI-227	JAU, Junagadh	M_3SP
JI 398	JP-82 × JI-258	JAU, Junagadh	M_3SP
JI 424	JP-88 × JI-303	JAU, Junagadh	G_2SP
JI 426	JP-96 × JI-398	JAU, Junagadh	G_3SP
JI 436	JP-90 × JI-340	JAU, Junagadh	G_3SP
JI-437	JP 89 × SKI- 291	JAU, Junagadh	M_2SP
SKI-215	SKI-8A × SA-2	SDAU, S.K. Nagar	M_2NSP
SKI-327	JP-83 × SKI-217	SDAU, S.K. Nagar	M_3SP
SKI-343	JI-244 × SH-72	SDAU, S.K. Nagar	G_3SP
SKI-392	SKP-84 × SKI-147	SDAU, S.K. Nagar	M_3SP
SKI-397	VP-1 × GEETA	SDAU, S.K. Nagar	M_3NSP
SKI-405	SKP-42 × PCS-124	SDAU, S.K. Nagar	M_2SP
RG-3041	Selection	IIOR, Hyderabad	G_3SP
RG-3073	Selection	IIOR, Hyderabad	M_3SP
JC-24	Selection	JNKVV, Chhindwara	M_2SP
PCS-124	PPL-4 × 48-1	ARS, Palem	G_2SP
500-2	Selection	IIOR, Hyderabad	M_2NSP

Stem color: M = Mahogany, G = Green; Bloom: 2 = Double, 3 = Triple; Capsule: SP = Spiny, NSP = Non-spiny

groups based on morphological variations. Table 2 showcased the Index scores and signs, which were instrumental in conducting the Metroglyph analysis on six different characters.

The first group, Group I, stood out with four genotypes (VP-1, JI-424, JI-436, and SKI-327), displaying low seed yield per plant and shorter plant height. Moving on to Group II, formed of a single genotype (RG-3073) displayed moderate seed yield per plant and a shorter stature. Again, Group III distinguished with single genotype (SKP-84), which exhibited high seed yield per plant but shared the characteristic of shorter plant height.

Table 2. Index scores and symbols for six characters in metroglyph analysis of castor germplasms

Categories	Range and genotype	Yield	Capsules	Length of Raceme	DF	PH	SH	Ray length
		X1	X2	X3	X4	X5	X6	
Low	Range	125.87-185.09	42.13-61.82	42-57.64	52-58.33	30.47-58.80	55-61.56	
	Genotype	2, 4, 5, 6, 8, 10, 11, 13, 14, 18, 20, 22	8, 12, 19	8, 11, 13, 16, 17, 19, 20, 22	4, 5, 8, 10, 16	3, 4, 8, 10, 13, 19	2, 4, 8, 10, 13, 14, 15, 16	
Medium	Range	185.09-244.31	61.82-81.51	57.64-73.29	58.33-64.67	58.80-87.14	61.53-68.11	
	Genotype	1, 7, 9, 16, 17, 19, 21	1, 7, 10, 13, 15, 20, 21, 22	3, 4, 5, 6, 9, 10, 12, 15, 21	1, 6, 7, 9, 11, 14, 19	1, 2, 5, 6, 7, 9, 11, 14, 16, 17, 20, 21, 22	1, 3, 7, 19	—
High	Range	244.31-303.53	81.51-101.20	73.29-88.93	64.67-71	87.14-115.47	68.11-74.67	
	Genotype	3, 12, 15	2, 3, 4, 5, 6, 9, 11, 14, 16, 17, 18	1, 2, 7, 14, 18	2, 3, 12, 13, 15, 17, 18, 20, 21, 22	12, 15, 18	5, 6, 9, 11, 12, 17, 18, 20, 21, 22	———
Ray posotion		For X axis	⇧	⇨	⇩	For Y axis	⇦	

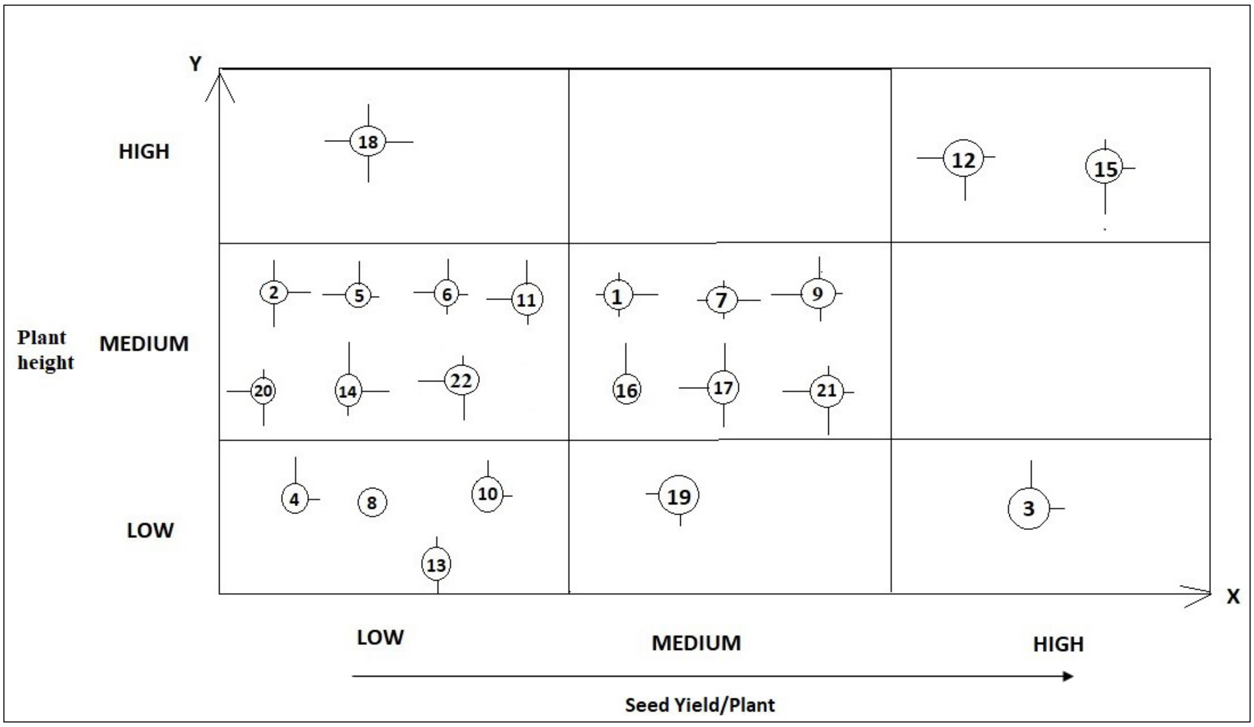
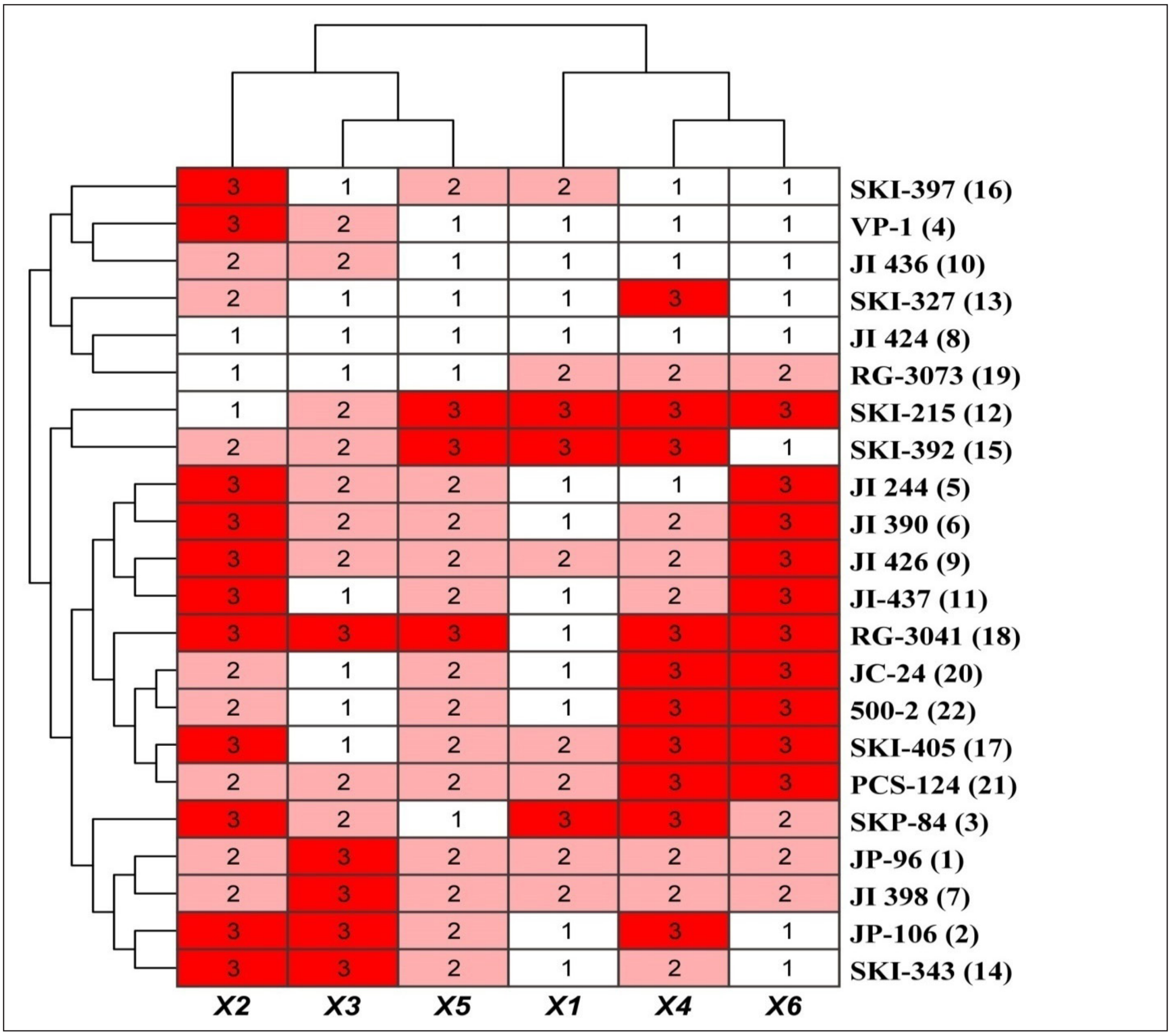


Fig. 1. Scattered diagram of metroglyph analysis of castor germplasm.

Group IV presented a diverse mix of seven genotypes, primarily showcasing moderate grain yield per plant, a moderate number of primary branches per plant, early flowering (days to 50% flowering), medium 100-seed weight, and an average number of pods per plant. Comprising six genotypes (JP-96, JI-398, JI-426, SKI-397, SKI-215, and PCS-124), Group V displayed its unique characteristics in the study. Both Group VI and Group VIII were found to be devoid of any genotypes that fit the observed criteria. Group VII, on the other hand contained a single genotype (RG-3041) with high seed yield per plant and shorter plant height, setting it apart in the analysis. The final group, Group IX, comprised of two genotypes (SKI-215 and SKI-392), which show cased high seed yield per plant and a greater plant height.

In the present study, we observed that each type of plant had a wide range of traits, creating a diverse and intricate pattern of differences. The majority of them, through, had both moderate seed yield and a moderate plant height. However, it's worth noting that each genotype still exhibited distinct values across the studied traits, contributing to the overall diversity of the findings. Group IX consisted of two genotypes (SKI-215 and SKI-392) from a showed high seed yield plant^{-1} and tall plant height. Findings similar to ours have been reported by various researchers. Laiju *et al.* (2002) conducted a study that revealed a wide range of index scores within Hordeum species, spanning from 12 to 23. The most prominent index score was 20, found in six genotypes. Two genotypes, Pusa 256 and PG042, stood out with the highest index score of 23. Some genotypes clustered around index scores of 17 and 21, showcasing their unique characteristics. A few individual genotypes had index scores of 14, 15, and 18. Additionally, rare gems with index scores of 13, 16, 18, 21, and 22 were discovered within the Hordeum species. These findings highlighted the rich tapestry of diversity among the 30 genotypes under investigation.

Furthermore, Bhargava *et al.* (2009) reported similar findings in their study of Chenopodium species. Group IV contained three genotypes characterized by high grain yield and a medium to high number of primary branches per plant, along with medium plant height. In contrast, Group VIII had a single genotype (PG 053) with exceptionally high grain yield per plant and a moderate number of primary branches per plant. This group also demonstrated high values for traits such as days to 50% flowering, plant width, and 100-seed weight, while maintaining



X2	X3	X5	X1	X4	X6	
3	1	2	2	1	1	SKI-397 (16)
3	2	1	1	1	1	VP-1 (4)
2	2	1	1	1	1	JI 436 (10)
2	1	1	1	3	1	SKI-327 (13)
1	1	1	1	1	1	JI 424 (8)
1	1	1	2	2	2	RG-3073 (19)
1	2	3	3	3	3	SKI-215 (12)
2	2	3	3	3	1	SKI-392 (15)
3	2	2	1	1	3	JI 244 (5)
3	2	2	1	2	3	JI 390 (6)
3	2	2	2	2	3	JI 426 (9)
3	1	2	1	2	3	JI-437 (11)
3	3	3	1	3	3	RG-3041 (18)
2	1	2	1	3	3	JC-24 (20)
2	1	2	1	3	3	500-2 (22)
3	1	2	2	3	3	SKI-405 (17)
2	2	2	2	3	3	PCS-124 (21)
3	2	1	3	3	2	SKP-84 (3)
2	3	2	2	2	2	JP-96 (1)
2	3	2	2	2	2	JI 398 (7)
3	3	2	1	3	1	JP-106 (2)
3	3	2	1	2	1	SKI-343 (14)

Fig. 2. Visualizing index score and clustering: A graphical analysis.

medium values for seeds per pod and days to maturity. These results aligned with our research, providing additional support.

Moreover, Sasipriya *et al.* (2022) employed Metroglyph analysis in a study conducted after 2022 to classify genotypes into six groups. Among these, Group IV was the largest, encompassing 20 genotypes. Notably, Cluster VI showcased a remarkable combination of high seed yield and a significant number of seeds per pod, including three genotypes, namely Julang Sesame and NI8-8316. This contemporary research further reinforced our findings, emphasizing the consistency of our results.

These findings are like a treasure map for future breeders and researchers, revealing promising combinations of traits hidden within the gene pool. Armed with this knowledge, crossing programs can be designed to harness the full potential of this captivating diversity, unlocking the secrets of favorable trait combinations and paving the way for an exciting new era of agricultural exploration.

Conclusions

In summary, castor is a highly adaptable and resilient crop, particularly well-suited for arid regions facing water scarcity and environmental challenges. This study's Metroglyph analysis revealed significant morphological diversity among castor genotypes. This diversity, along with castor's wide distribution and diverse uses, makes it a valuable genetic resource for breeding programs and potential bioactive

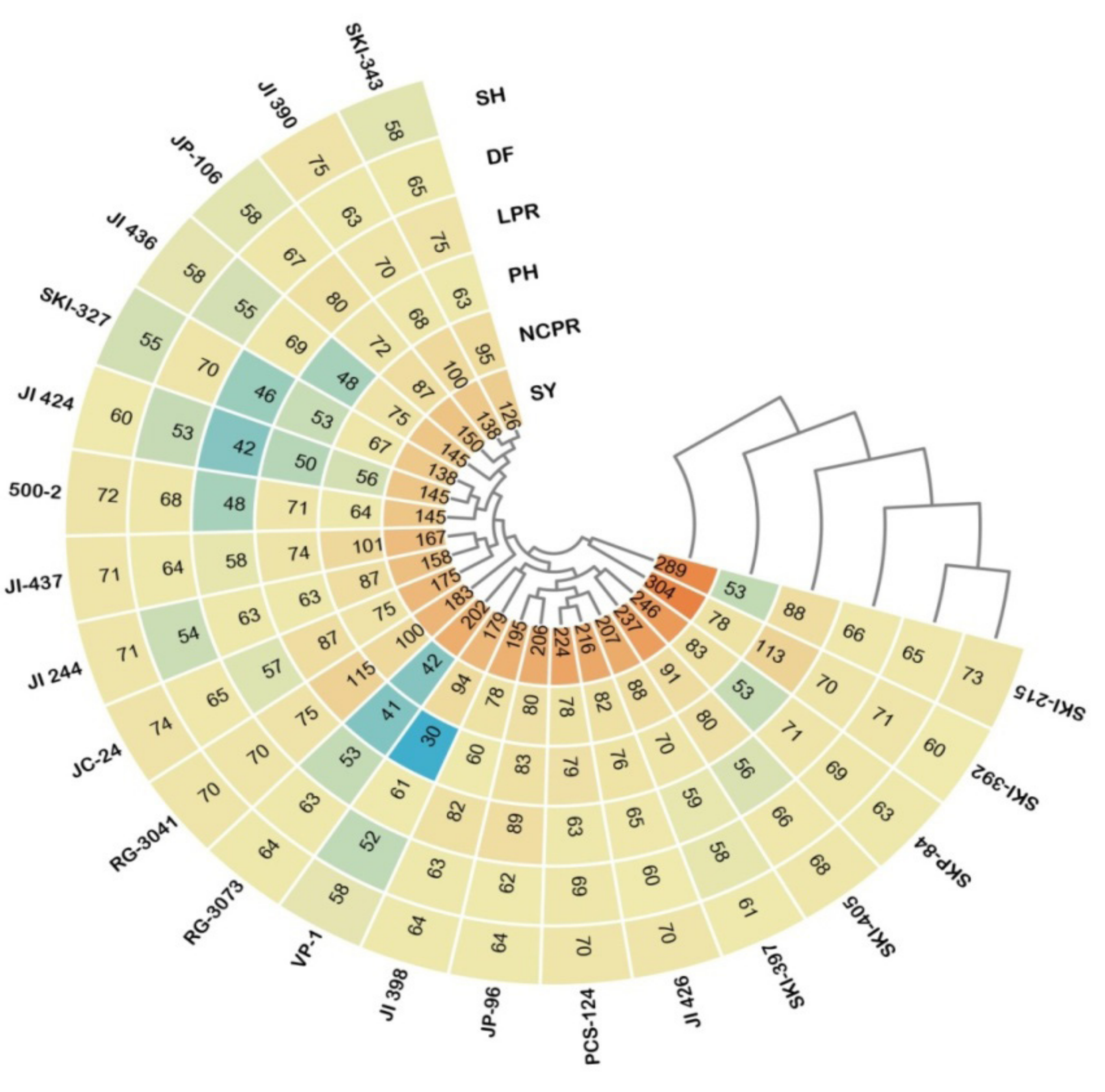


Fig. 3. Genotype diversity and clustering: A comprehensive graphical analysis.

compounds. These findings provide a roadmap for breeders and researchers, offering insights into promising trait combinations within the gene pool. This knowledge has the potential to drive advancements in plant breeding and sustainable agriculture, particularly in arid zones where castor's adaptability is valuable.

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