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Cluster analysis of floral traits in Asian *Coelogyne* spp. for germplasm selection and breeding strategy

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Abstract. *Coelogyne spp*. are orchids with high aesthetic and exclusive value. However, environmental degradation and climate change threaten its populations in their natural habitats. A total of 12 *Coelogyne* orchid species from Asia were evaluated based on 24 qualitative floral traits to assess variation and determine potential parent combinations for hybridization. The analysis revealed that 87.5% of the characters were variable, with an average Shannon–Wiener diversity index (H') of 0.905, indicating overall high of floral traits variation. Floral traits, particularly color, labellum, and floral scent, showed the highest variation and contributed significantly to species differentiation. Cluster analysis using the UPGMA method grouped the species into two main clusters with nine sub-clusters, highlighting distinct patterns of similarity and divergence. The similarity coefficient ranged from 0.29 to 0.75, where the lowest value indicated substantial divergence (e.g., *C. pandurata* and *C. ovalis*), while the highest value reflected close similarity (e.g., *C. parishii* and *C. celebensis*). Species with high similarity are predicted to have higher hybridization success but limited phenotypic variation, whereas those with low similarity offer greater potential for generating novel traits despite lower compatibility. These findings provide a objective quantitative basis for selecting parent combinations in *Coelogyne* breeding and conservation.

1 Introductions

Orchids are one of the ornamental plant commodities that have high aesthetic and economic value. With this potential, the opportunity for development is very strategic and promising, especially through the plant breeding. *Coelogyne* is a particularly notable genus, that represents one of the important ornamental orchid groups valued for its diverse and distinctive floral characteristics, including variation in flower size, shape, color (including patterns), labellum structure, and fragrance [1]. *Coelogyne* has a wide distribution of species on the Asian continent, especially in various tropical forests of Southeast Asia with specific microclimate conditions. The uniqueness of orchids from this genus makes them popular and expensive.

In orchids, flowers are an essential part, because they have high artistic value, but also an important indicator that supports plant breeding programs and characterization. In floriculture, the selection of appropriate parents is a critical step to obtain superior hybrids with desirable and stable floral traits [2]. To increase genetic variation in orchids, especially those that have an impact on interesting variations in flower morphology, this can be done through interspecific crossing. Flower traits that represent morphological identity in the parent plant, influence the success of orchid hybridization and the results of the offspring, because it reflects genetic distance. Variability in floral traits provides an opportunity to identify genetically divergent parents, which can enhance heterosis and broaden phenotypic variation in progenies.

The initial step that can be taken to differentiate the genotype of a species based on phenotype is to carry out morphological characterization. The morphological characters that are more accurate in describing the genotype is the qualitative character, because the qualitative character is only regulated by one or a few major genes which are generally not strongly influenced by the environment [3]. A database on the qualitative morphological characteristics of orchids, especially in the flower section, is fundamental information for determining orchid parents based on the desired floral traits.

Plants with high morphological similarity (genetically close) tend to exhibit higher hybridization success but result in limited variation among the offspring. Conversely, crosses between morphologically distinct parents may have lower success rates but can generate offspring with greater morphological variation. This also works on floral traits produced through the crossing process, so that diversity between species is an important resource for creating new hybrid orchids. However, the selection of parent candidates is often conducted subjectively based on visual assessment, this subjectivity can lead to inefficient hybridization strategies and suboptimal utilization of genetic resources. Therefore, a more systematic and quantitative approach is required to evaluate the diversity and relationships among species.

Accuracy of predictions in orchid breeding is something that need to be considered, because they are

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related to resources used, time, and success rates. Selection of cross-breeding results usually takes quite a long time, because orchids tend to have slow growth until they enter the generative/flowering phase, so it is very important to increase the chances of successful crossing. One of the main reasons for orchid crossing failure or inappropriate results is caused by selecting parents that do not consider relevant traits.

Cluster analysis has been extensively applied as a multivariate statistical method to classify plant germplasm based on qualitative morphological characters [4]. This method enables the grouping of species according to their similarity levels, thereby facilitating the identification of genetically distant parents for hybridization. Previous studies on orchid diversity have largely emphasized morphological variation without interpreting these findings into practical breeding strategies.

Moreover, the use of qualitative floral traits as a primary basis for quantitative clustering and parent selection remains underexplored, particularly in *Coelogyne* spp. Based on these considerations, this study aims to analyze the variation in floral traits among several *Coelogyne* species from Asia, using cluster analysis to identify potential germplasm or parental candidates that can be utilized in strategies and future breeding programs.

2 Research method

The research was conducted from January to March 2026 at an orchid screenhouse located in Temanggung Regency and Surakarta City, Central Java. The tools used in this study were a magnifying glass, tweezers, digital camera (Nikon D90) with a macro lens (Nikon AF-S 105 mm f/2.8G VR Micro IF-ED N), and orchid morphology observation guidebook/descriptor [5]. The materials used in this study were explained in Table 1

Table 1. Origin of the *Coelogyne* orchid

Species	Media	Origin (wide)	Average Age (month) and height
C. pandurata	E (m), L, and T	Southest Asia	±14/46 cm
C. brachyptera	E	Southest Asia	±9/21 cm
C. sulphurea	E	Southest Asia	±11/28 cm
C. ovalis	E	Southest Asia and Himalayas	±15/21 cm
C. usitana	E and L	Philppines	±11/25 cm
C. pulverula	E and L	Southest Asia	±26/53 cm
C. viscosa	E and L	Southest Asia	±8/31 cm
C. odoardi	E and L	Borneo	±12/31 cm
C. speciosa	E (m), L, and T	Southest Asia	±8/27 cm
C. tenasserimensis	E	South Indo-China	±10/25 cm
C. parishii	E	Southest Asia	±8/33 cm
C. celebensis	E	Celebes	±12/37 cm

Description: E: epiphytes, L: lithophytic, T: terrestrial, and (m): mostly.

Observation of floral traits/flower morphology was carried out directly on orchids that have been moved into the screenhouse. Observations were carried out for 5 days (especially in the morning or evening) and all orchids were in flowering condition. Before observations were carried out, the orchids were first left in the screenhouse for 7 days to adaptation. To increase the accuracy of morphological character observations, a replication was carried out with 3 plants per species used. Referring to the ornamental plant characterization guide, especially orchids, published by the Center for Horticultural Research and Development, Agricultural Research and Development Agency, Indonesian Ministry of Agriculture, there are 24 qualitative characters of floral traits used to characterize the 12 species of *Coelogyne* orchids studied, including shape, color, variation of flower organs, and flower scent (Table 2).

Table 2. Qualitative morphological characters of flower, sub-character, and scoring values

No.	Character	Sub-characters and scoring
1.	Flowering position	[1] base, [2] side, and [3] shoot/axillary
2.	Flowering type	[1] single, [2] limited, [3] nail-biting, [4] bunch, [5] panicle, [6] scars, and [7] umbrella
3.	Resupination	[0] non-resupinant and [1] twisted
4.	Spur	[0] absent or [1] present
5.	Flowes shape	[1] round, [2] star, [3] curly, and [4] horned
6.	Sepal shape	[1] lanceolate, [2] ribbon/straight, [3] oblong, [4] rhomboid, [5] breech-ovate, [6] spoon-shaped, [7] void, and [8] slightly rouned
7.	Petal shape	[1] ribbon/straight, [2] oval, [3] oblong, [4] rhomboid, [5] breech-ovate, [6] spoon-shaped, [7] oval, and [8] slighty rounded
8.	Petal arrangement	[1] open, [2] touching, and [3] overlapping
9.	Sepals and petals tips shape	[1] sharp, [2] tapering with sharp edges, [3] pointed-tipped shallow-tipped, [4] sharp-boned, [5] blunt, [6] flat-shaped, [7] rumpled, [8] torn, [9] three-toothed, [10] serrated, [11] brush-shaped, and [12] tailed
10.	Cross section of sepals and petals	[1] convex, [2] flat, and [3] concave
11.	Labellum	[1] constricted triangle, [2] triangle, [3] trapezoid, [4] round, [5] oval, and [6] spoon-shaped
12.	Labellum curve	[1] tip, [2] base, and [3] middle
13.	Cross-section of labellum	[1] curved in with turned tips, [2] curved very deeply, [3] curved rather deeply, [4] flat, [5] turned rather deeply, [6] turned very deeply, [7] turned out with curved tips
14.	Curvature of side plate	[1] U-shaped, [2] C-shaped facing up, and [3] flat C-shaped
15.	Callus type	[1] equipped with plates, [2] complex, and [3] simple

16.	Fruit/pod shape	[1] capsules or [2] berries
17.	Labellum pattern	[0] absent or [1] present
18.	Petal color	[1] white, [2] yellowish white, [3] yellow, [4] orange, [5] light brown, [6] brown, [7] black, [8] light green, and [9] green
19.	Sepal color	[1] white, [2] yellowish white, [3] yellow, [4] orange, [5] light brown, [6] brown, [7] black, [8] light green, [9] green, and [10] yellowish green
20.	Labellum color	[1] white, [2] yellowish white, [3] yellow, [4] orange, [5] light brown, [6] brown, [7] black, [8] light green, [9] green, and [10] yellowish green
21.	Dorsal sepal color	[1] white, [2] yellowish white, [3] yellow, [4] orange, [5] light brown, [6] brown, [7] black, [8] light green, [9] green, and [10] yellowish green
22.	Column color	[1] white, [2] yellowish white, [3] yellow, [4] orange, [5] light brown, [6] brown, [7] black, [8] light green, and [9] green, and [10] yellowish green
23.	Labellum pattern color	[1] red, [2] yellow, [3] orange, [4] brown, and [5] black
24.	Floral scent	[0] odorless, [1] mild, [2] moderate, and [3] pungent

Description: The absence of sub-character is expressed in a score of 0.

Floral traits in orchids will be scored using a nominal model (1, 2, 3...etc.) to represent each existing sub-character. The scoring obtained will be the main data in conducting cluster analysis. Cluster analysis was performed using the NTSYSpc 2.02i series program with the UPGMA, hierarchical grouping algorithm based on group averages through the SimQual sub-program procedure. Phenograms and similarity matrices will be presented to show the degree of similarity and difference between species based on floral traits.

The variability of floral traits is an important component in providing the choice of traits desired by breeders. Variability is also an individual's genetic identity both genotype and phenotype. To analyze the variability of floral traits that are important for parent selection in all observed species based on the frequency and distribution of each character category, Shannon-Wiener (H') analysis was used with the following equation:

$$H' = -\sum_{i=1}^{s} \quad Pi \ ln \ (pi) \qquad (1)$$

Pi is the relative abundance of each observed character, Ni is the number of species per character, and ln(pi) is the natural logarithm of the proportion of (i) species. Characters with high variability, especially those that contribute to variation, are worth considering in orchid breeding because they have many options/variations. If H' < 0.5 then the variability is low, 0.5 ≤ H' 0.75 is medium, and > 0.75 is high [6].

3 Results and discussion

3.1 Variability of floral traits

The variability that exists in the collection of genetic resources is an advantage in plant breeding programs. The more character variations in the collection of species owned, the higher the opportunity to create new variations in the offspring resulting from breeding. Especially in this context, is to obtain *Coelogyne* orchid hybrids with diverse flower variations. Floral traits evaluation and characterization of existing parent species are very important in order to obtain initial information. Character variations in floral traits of the 12 orchid species observed can be seen in Table 3.

Table 3. Character variation and H' index

Charater	Sub-characters	H'
Flowering position	[1]: 2 and [3]: 10	0.451
Flowering type	[4]: 8 and [6]: 4	0.637
Resupination	[0]: 1 and [1]: 11	0.287
Spur	[1]: 12	0.000
Flowes shape	[2]: 11 and [4]: 1	0.287
Sepal shape	[1]: 3, [2]: 1, [3]: 6, [4]: 1, and [6]: 1	1.314
Petal shape	[1]: 9, [2]: 2, and [3]: 1	0.721
Petal arrangement	[1]: 12	0.000
Sepals and petals tips shape	[1]: 7, [2]: 4, and [3]: 1	0.888
Cross section of sepals and petals	[1]: 1, [2]: 1, and [3]: 10	0.566
Labellum	[1]: 2, [3]: 1, [4]: 5, [5]: 3, and [6]: 1	1.424
Labellum curve	[1]: 1, [2]: 5, and [3]: 6	0.918
Cross-section of labellum	[1]: 2, [2]: 1, [3]: 1, [4]: 3, [5]: 3, and [6]: 2	1.705
Curvature of side plate	[1]: 9, [2]: 2, and [3]: 1	0.721
Callus type	[1]: 2, [2]: 8, and [3]: 2	0.868
Fruit/pod shape	[1]: 12	0.000
Labellum pattern	[0]: 1 and [1]: 11	0.287
Petal color	[1]: 3, [2]: 3, [4]: 1, [5]: 1, and [8]: 4	1.474
Sepal color	[1]: 2, [2]: 1, [4]: 1, [5]: 2, [6]: 1, [8]: 3, [9]: 1, and [10]: 1	1.979
Labellum color	[1]: 8, [4]: 1, [5]: 1, [6]: 1, and [8]: 1	1.099
Dorsal sepal color	[1]: 2, [2]: 1, [4]: 1, [5]: 2, [6]: 1, [8]: 3, [9]: 1, and [10]: 1	1.979
Column color	[1]: 2, [3]: 4, [4]:1, [6]: 1, [8]: 2, [9]: 1, and [10]: 1	1.792
Labellum pattern color	[0]: 1, [3]: 1, [4]: 4, and [5]: 3	1.127
Floral scent	[0]: 1, [1]: 6, [2]: 3, and [3]: 2	1.199

Description: Sub-characters that are not present in the species are not listed.

Based on Table 3, there are characters with high, medium, low, and even no diversity categories. There are 21 of the 24 characters that show variation (87.5%) with an average H' index of 0.905, which is in the high category. Characters with medium to high levels of diversity can be used to produce new variations in offspring resulting from cross-breeding [7]. Greater character diversity among the 12 *Coelogyne* species, when combined through appropriate crossing schemes, can produce offspring with novel traits or even exhibit heterosis. Orchid flower accessories such as petals, sepals, labellum and non-accessory parts such as callus show moderate to high character diversity. All color characters in the flower accessories and floral scent show high variation (H' > 0.75). making them an important option for determining parent plants. Based on appearance (Figure 1), the flowers of each species show different shapes and colors.

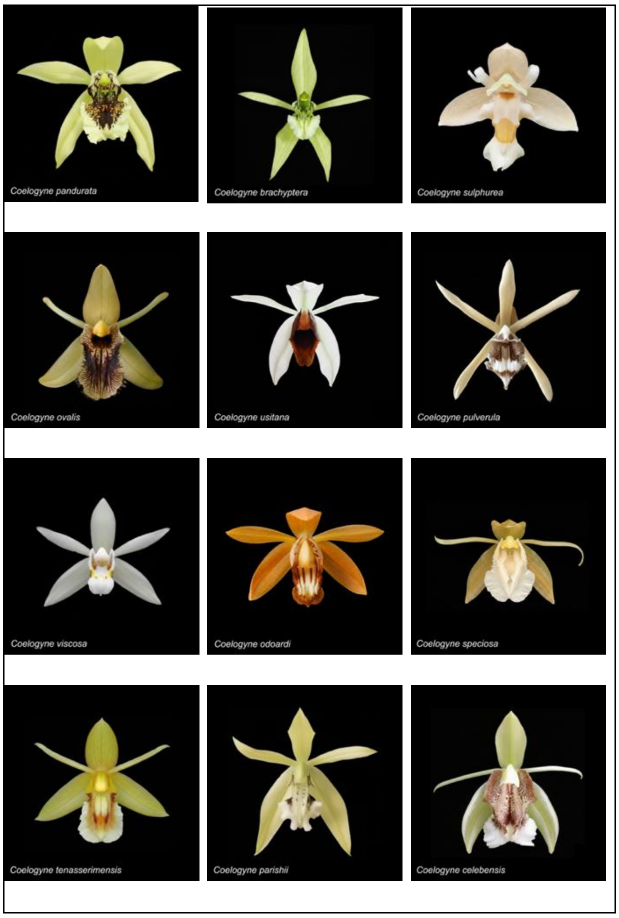

Fig. 1. Flower appearance of 12 *Coelogyne* spp.

Characters that shows no to low levels of variation (H' = 0.00-0.49) such as flowering position, resupination, spur, flower shape, petal arrangement, fruit shape, and labellum pattern will have the consequence of minimal variation produced when cross-breeding is carried out, although there is still the possibility for intermediate. Flower character diversity is an important resource in parent selection to produce superior hybrids with high aesthetic value, unique color combinations, attractive symmetry, flower size, and attractive aroma are the primary targets in crossbreeding programs. Each qualitative character in orchid flowers represents the genotypic differences in each species [8]. However, when the target flower traits is a quantitative character such as size, then the right environmental conditions will also influence it [9], apart from genotype factors.

There are several unique flower morphologies in the 12 species observed. Resupination is the process of rotating the orchid flower 180º during its development, from bud to bloom. Only *C. usitana* is non-resupinant, whereas the majority of *Coelogyne* species are resupinant . The majority of observed *Coelogyne* flower shapes are star-shaped, but *C. ovalis* is actually a bunch-shaped flower. Apart from petal and sepal coloration, the color and morphology of the labellum also exhibit distinct variations. Unique or species-specific traits are particularly important in plant breeding, as hybridization can generate novel floral characteristics that are not present in existing hybrids.

Floral aroma in orchids, particularly its intensity and qualitative profile, represents an important trait for study, as one of the main attractions of *Coelogyne* orchids is their distinctive and often fragrant scent. This aroma is composed of volatile compounds produced in floral tissues, especially in the labellum, where specialized structures known as osmophores function as scent glands that play a key role in attracting pollinators [10].

Most of the osmophores (scent glands) in orchids are located in the labellum and a small number in the column [11]. In *Coelogyne* spp., differences in labellum shape and pattern provide different aroma profiles and intensities. This also occurs in the genus *Ophrys*, where the structure of the osmophore and the micromorphology of the labellum, form variations in the profile and intensity of different aromas in flowers [12]. Genetically, the genes that express labellum shape vary between species, as do those that regulate the complexity of volatile compounds. Differences in the labellum give different aromas, so if cross-breeding is carried out, it is predicted that it will produce different variations.

To assess the floral fragrance profile and aroma intensity, organoleptic test and sensory evaluation were conducted using 15 testers familiar with orchids. Aroma intensity was assessed using a four-point scale (odorless, mild, moderate, and pungent), while the fragrance profile evaluation was determined by collecting information on what type of aroma can be described. The description and intensity score reported by the majority of the 15 testers were used to characterize the floral aroma of each *Coelogyne* species.

Among the 12 species examined, all flowers exhibited distinct scent profiles, including sweet, musky, mandarin, and jasmine aromas. Two species showed the most intense fragrance, *C. pandurata* emitted a very strong scent resembling a combination of honey and musk, while *C. odoardi* has a strong smell combination of subtle sweetness and apricot jam with a slightly fruity smell.

3.2 Cluster analysis of floral traits

Genetic diversity reflected through character variations is an important resource in orchid breeding. However, there is a trade-off between the success rate of crosses and the genetic distance between the parents. Crosses between species with large morphological differences can produce wide phenotypic variation, but often have lower success rates. Greater morphological differences among individuals indicate greater genetic distance, which may reduce genetic compatibility during hybridization [13].

Cluster analysis is an important approach in plant breeding, particularly for determining parent selection strategies in hybridization programs based on floral traits. Through this analysis, species are grouped based on the degree of similarity or difference in traits, allowing breeders to obtain an objective description of phenotypic relationship patterns in the context of orchids, which exhibit extremely high floral diversity, this approach is crucial for simplifying the complexity of morphological variation into structured, easily interpretable information, for example in the form of a phenogram (Figure 2).

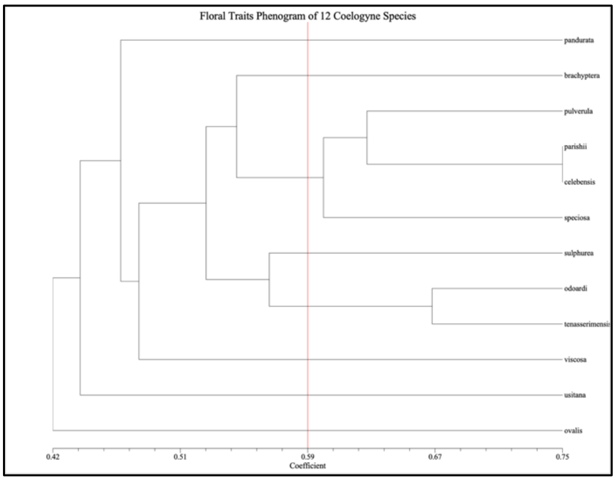

Fig. 2. Phenogram of 12 *Coelogyne* orchid species based on qualitative floral traits.

The visual result of cluster analysis in the form of phenogram, serves to show the close relationships between species in the form of a branching diagram. Branches that are close together indicate a high degree of similarity in traits, while branches that are far apart reflect greater differences. This information is very useful in parent selection. In some cases, orchid breeders cross-breed orchids with close genetic distances to maintain certain characteristics that are considered useful as in *Vanilla* spp., but some also cross-breed orchids with large genetic distances to obtain high genetic variability as in *Dendrobium* and *Phalaenopsis* spp.. The phenogram helps orchid breeders visualize complex morphological diversity data [14], thus facilitating decision-making in the development of new superior varieties.

Based on the phenogram in Figure 2, it can be understood that two large clusters were formed, and there is one cluster that is only filled by 1 species, namely *C. ovalis*, so that it can be interpreted as the species with the highest differences. There are 9 sub-clusters, sub-cluster 1 consists of *C. pandurata*, sub-cluster 2 consists of *C. brachyptera*, sub-cluster 3 consists of *C. pulverula*, *C. parishii*, and *C. celebensis*, sub-cluster 4 consists of *C. speciosa*, sub-cluster 5 consists of *C. sulphurea*, sub-cluster 6 consists of *C. odoardi* and *C. tenasserimensis*, sub-cluster 7 consists of *C. viscosa*, sub-cluster 8 consists of *C. usitana*, and sub-cluster 9 is the second large cluster which only consists of *C. ovalis*.

The similarity coefficient formed in the similarity matrix from 0.29 to 0.75, which means that there are several species with a very low level of similarity, with a coefficient of 0.29 and several species with high similarity with a coefficient of 0.75. An example of a species with low similarity is *C. pandurata* with *C. ovalis* (0.29) and an example of a species with high similarity is *C. parishii* with *C. celebensis* (0.75), this is based on the similarity of floral traits.

Comparison of similarity coefficients between the studied species can be observed in the form of similarity matrix as can be observed in Figure 3. Low similarity values indicate a high level of divergence among accessions, reflecting substantial differences in their morphological or genetic characteristics.

Species	1	2	3	4	5	6	7	8	9	10	11	12
1	1.00											
2	0.50	1.00										
3	0.42	0.46	1.00									
4	0.29	0.42	0.38	1.00								
5	0.42	0.42	0.46	0.33	1.00							
6	0.50	0.50	0.50	0.42	0.38	1.00						
7	0.42	0.50	0.42	0.46	0.46	0.46	1.00					
8	0.50	0.54	0.54	0.33	0.42	0.50	0.50	1.00				
9	0.33	0.50	0.54	0.58	0.50	0.58	0.46	0.46	1.00			
10	0.50	0.50	0.58	0.50	0.46	0.58	0.46	0.67	0.58	1.00		
11	0.54	0.58	0.50	0.42	0.42	0.67	0.50	0.54	0.54	0.58	1.00	
12	0.50	0.58	0.46	0.54	0.50	0.58	0.54	0.54	0.67	0.54	0.75	1.00

Fig. 3. Similarity matrix of 12 *Coelogyne* orchid species based on qualitative floral traits.

Description: 1 : *C. pandurata*, 2 : *C. brachyptera*, 3 : *C. sulphurea*, 4 : *C. ovalis*, 5 : *C. usitana*, 6 : *C. pulverula*, 7 : *C. viscosa*, 8 : *C. odoardi*, 9 : *C. speciosa*, 10 : *C. tenasserimensis*, 11 : *C. parishii*, and 12 : *C. celebensis*

Comparison between species as in Figure 3, there are 6 pairs of species which when compared with each other have a low similarity index of < 0.40, so it can be assumed that the genetic or phenotypic distance is large. There is a difference in the minimum similarity value between the phenogram and the matrix, the minimum value in the phenogram is 0.42, while the matrix is 0.29. The minimum value of 0.42 is the lowest level of similarity when two large clusters are combined, while in the matrix it is the original pairwise value of each species being compared.

3.3 Implications for germplasm selection (potential parents) and breeding strategy

Parent selection is a crucial activity in breeding programs, particularly in hybridization strategies for developing orchid hybrids. In *Coelogyne* spp., the choice of parental genotypes should consider both genetic compatibility and trait complementarity. Furthermore, the assignment of male and female roles in reciprocal crosses can significantly affect progeny performance, resulting in variation in offspring characteristics. Relatively, crossing between two individuals with high character similarities will increase the potential for offspring with homozygous alleles, but the success rate will be relatively higher. Crosses between individuals with low character similarities will increase the potential for offspring with heterozygous alleles, but the success rate is low because the genetic distance is too far.

The flower characteristics that will be expressed by the offspring resulting from crossbreeding also depend on the inheritance mechanism of traits from the parents, especially those bound by sex (role as pollen donor or recipient). Male orchid parents have the greatest possibility of carrying traits regulated by genes found in the cell nucleus (nuclear inheritance), such as general appearance/morphology, and follow the concept of Mendel's law of balanced contributions. Meanwhile, maternal inheritance in female orchids occurs in several characters regulated by genes outside the cell nucleus, such as in mitochondria and chloroplasts, such as quantitative characters and plant resistance. However, both can also combine to form new traits.

Parent selection in orchid breeding, also should be aligned with the target traits of the desired progeny, particularly floral characteristics such as shape, color, and fragrance. In contrast, vegetative organs in the *Coelogyne*, including leaves, pseudobulbs, and growth habit, generally exhibit relatively high similarity with limited variation. Meanwhile, the morphological characters of flowers are significantly more diverse than vegetative organs, so they can be used to differentiate between species, as well as to differentiate characters.

Compatibility is a very important factor in crossbreeding, especially its ability to produce pods containing seeds with good viability and vigor [15]. Several orchid species with similar floral traits will relatively increase the potential for successful crossbreeding. In this study, 3 pairs with high similarity were taken, namely *C. parishii* with *C. celebensis* (0.75), *C. speciosa* with *C. celebensis* (0.67), and *C. viscosa* with *C. tenasserimensis* (0.67), but with minimal predicted variation in the offspring. Meanwhile, 3 pairs of species with the lowest similarity were *C. pandurata* with *C. ovalis* (0.29), *C. pandurata* with *C. speciosa* (0.33), and *C. ovalis* with *C. odoardi* (0.33), but were able to produce high character variations in the results/offspring, although the success rate is lower. The results of the scheme will be different if each pair is reciprocal.

This study provides essential baseline information for pre-hybridization, particularly in informing parent selection. As each trait reflects the unique identity of a species, thorough characterization is crucial for maintaining species integrity. While breeding outcomes are inherently influenced by breeder objectives, the results of this study objectively elucidate patterns of similarity and divergence among traits, thereby offering a framework to predict the potential success of hybridization among the 12 species examined. The findings of this study are expected to contribute to the development of more efficient and targeted breeding strategies in ornamental orchids, particularly in generating hybrids and help maintain the sustainability of *Coelogyne* spp. orchids by increasing genetic diversity.

4 Conclusion and recommendation

Floral traits in *Coelogyne* orchids exhibit high variability and serve as key characters for species differentiation and parent selection. Cluster analysis revealed clear patterns of similarity and divergence among species, with similarity coefficients ranging from 0.29-0.75. Crosses between closely related species are likely to yield higher success rates but limited variation, whereas crosses between more divergent species offer greater potential for novel trait combinations despite lower compatibility. Therefore, effective parent selection requires balancing genetic similarity and trait diversity to optimize hybridization outcomes. Future studies should integrate molecular markers to complement morphological data and improve the accuracy of genetic relationship analysis. Additionally, experimental hybridization is needed to validate predicted cross compatibility and offspring performance.

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