Genetic variability, heritability, genetic advance and multivariate analysis studies in New Guinea Impatiens cultivar

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Abstract. Genetic diversity is essential for any plant breeding program to produce a superior cultivar. Genetic parameters, which include genetic variability, heritability, and correlation between characters, are essential factors in the selection process. The objective of this study was to evaluate the genetic diversity and investigate the association between the various quantitative parameters of the New Guinea cultivars of Impatiens. The experiment was carried out in Screen House Garden of BRIN in Palasari Cipanas West Java, Indonesia (1000 above sea level), from September 2022 to May 2023. Fifteen Impatiens accessions were evaluated in a Randomized Complete Block Design with three replicates. Fourteen morphological descriptors were measured to determine the variability and correlation coefficients. The analysis of variance showed a highly significant variation for all characters, which indicates greater variability in the accession. The analysis of variance revealed a highly significant variation for all characters, indicating increased variability in the accession. The genotypic coefficient of variance ranged from 0 (dorsal petal width) to 71.28 flower number per plant). The phenotipic coefficient of variance ranged from 10.01 (flower width) to 80.13 (flower number per plant). High heritability in broad sense estimates were obtained for the majority of the traits examined. High heritability in broad sense (0.61 - 1.00) estimates were obtained for all the traits examined. Leaf length, ventral petal length, and flower number showed high genetic advance. The range of correlation between characters was from -0.01 - 0.96. Genotype NGP01, NGP02, NGP03, and PLS33.3 are potential candidates for breeding programs.

Keywords: Impatiens, heritability, correlation, character, biodiversity

1. Introduction

Impatiens is a semi-succulent herbaceous plant, some types of which are half shrubs [1]. Impatiens plants can be found mainly at high altitudes in the tropics and subtropics. The main centers of diversity of the Impatiens genus are in Africa, Madagascar, India, Sri Lanka, the Himalayas and Southeast Asia [2]. Impatiens are either annuals or evergreen perennials, with fleshy stems bearing simple, serrated leaves and single or clustered, spurred, 5-petalled blooms. *Impatien hawkeri* is ideal for pots, hanging baskets and garden borders. Also for landscaping, fast growing and large flowers. New Guinea Group Impatiens are Impatiens plant hybrids with a wide range of flower and leaf colors that are offered in nurseries and garden centers as summer bedding and patio plants. *Impatiens hawkeri* hybrids are commonly known as New Guinea. Impatiens are the product of hybridization of three Impatiens species [3].

The species *'hawkeri'* is frequently crossed with *Impatiens aurantiaca* and *Impatiens platypetala* to improve features such as drought resistance and floriferousness, as well as to broaden the colour range and improve plant habit and compactness. New Guinea Impatiens is an ornamental species used as a garden and pot plant [4]. The estimation from [5] that the world demand for Impatiens cuttings is more than 100 million plants each season. New Guinea Impatiens

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is native from the Papua highlands to the Australian sub-tropics with average daily day and night temperatures of 25-30 and 18-21°C respectively [6].

Impatiens plants desired by the American market have characteristics mainly in flower size and flower color intensity; leaf size; color on the uppermost part and variegation as an effect of coloring and leaf shape and disease resistance. New Guinea Impatiens is characterized by large flowers with a variety of flower and leaf colors [7]. Studies reveal that brighter flower colors like red-violet, bi-colors (e.g., lavender-purple star patterns), and dark pink are highly preferred by consumers. Over 60% of surveyed participants ranked these colors in their top three choices, making them key targets in breeding programs for enhanced market appeal [8]. Impatiens New Guinea (Impatiens x *hawkerii*) is mostly propagated through cuttings and hardly through seeds [7].

Studies of genetic diversity using appropriate genetic criteria are therefore required for an effective breeding programme [9]. The genetic variety of New Guinea Impatiens (*Impatiens hawkeri*) is crucial for the long-term sustainability of breeding programs for several reasons: genetic diversity allows breeders to select and develop cultivars that can adapt to changing environmental conditions such as temperature, resistance to various diseases and pests [10, 11]. Maintaining high genetic diversity can help species adapt to avoid inbreeding [12]. In flowering plants, self-incompatibility is a mechanism that can prevent inbreeding. The yield is a very complicated unit impacted by a number of yield components that are susceptible to environmental changes [13]. Thus, choosing based on income components has a larger likelihood of success. As a result, it is vital to understand the types and nature of yield components, as well as their interrelationships.

Impatiens accessions are being conserved in BRIN's working collection and the potential of this Impatiens diversity in our collection can only be fully realized when properly characterized. The evaluation of Impatiens genetic resources using agronomic descriptors will help us to understand the variations between accessions and choose those with the desired characteristics for the breeding programme.

Information on the extent of genetic variability in genetic stocks, heritability, and genetic advance of specific traits would be extremely useful for future breeding programs. With these facts in mind, this study examined the genetic diversity and correlation between all characters and related variables in our Impatiens collection.

In addition, the character information obtained can be used as a basis for conducting genetic resource enrichment activities in order to increase the genetic diversity of the Impatiens collected accessions. This study aimed to characterize the genetic variability in New Guinea Impatiens accessions from BRIN's collection through multivariate analysis of quantitative traits and evaluate the genetic diversity and investigate the correlation between the various quantitative characters of the New Guinea cultivars of Impatiens.

2. Materials and Methods

2.1 Material

Research materials in the National Research and Innovation Agency Republic of Indonesia (BRIN) collections consist of 15 cultivars of New Guinea *Impatiens* genotype (Figure 1) propagated from cuttings planted in 30 cm plastic pots. Fifteen genotypes originated from Bina Usaha Flora nurseries and all were Divine series and its derivatives. Plants were cultivated in a screen house at temperatures ranging from 17°C to 28°C.

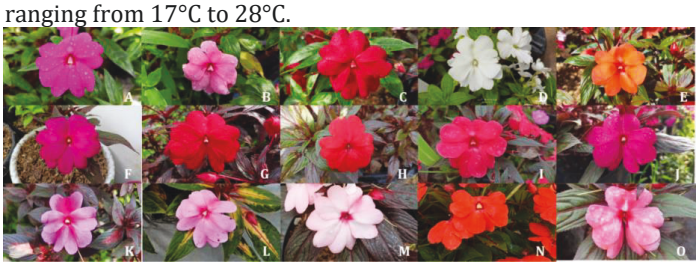

Figure 1. Genotypes of Impatiens flower. (A) NGP03, (B) NGP05, (C) NGP08, (D) NGP06, (E) NGP02, (F) NG230, (G) PLS33.3, (H) PLS36, (I) PLS236, (J) PLS46.1, (K) NGP01, (L) NGP228, (M) NGP227, (N) NGP61, (O) NGP60

2.2 Method

The study was carried out at BRIN's field and screen house facility in Palasari, West Java from September 2022 to March 2023, at an elevation of 1,000 meters above sea level. The experiment used a randomized complete block design (RCBD) with 3 replication was used in this study, applying 15 cultivar of New Guinea *Impatiens* as the genotype treatment. The quantitative characters measured were leaf length (*LL*), and leaf width (*LW*), flower length (*FL*), flower width (*FW*), eye zone width (*EZW*), dorsal petal length (*DPL*), dorsal petal width (*DPW*), lateral petal length (*LPL*), lateral petal width (*LPW*), ventral petal length (*VPL*), ventral petal width (*VPW*), spur length (*SL*) (Figure 2), flower number per bud (*FNPB*) and flower number per plant (*FNPP*). Observations were made on 4 months old plants.

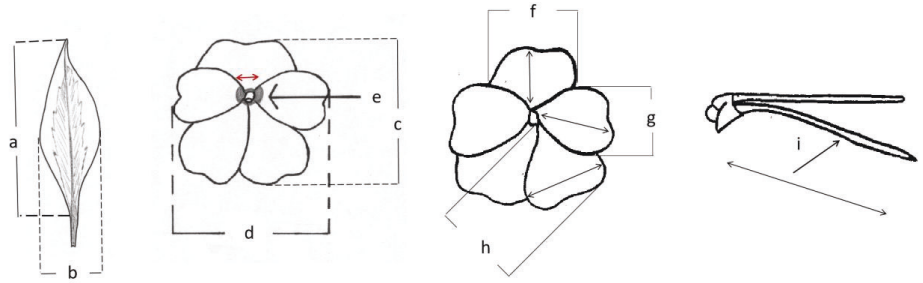

Figure 2. The quantitative characters measured: (a) leaf length (*LL*), (b) leaf width (*LW*), (c) flower length (*FL*), (d) flower width (*FW*), (e) eye zone width (*EZW*), (f) dorsal petal length (*DPL*) and dorsal petal width (*DPW*), (g) lateral petal length (*LPL*) and lateral petal width (*LPW*), (h) ventral petal length (*VPL*) and ventral petal width (*VPW*), (I) spur length (*SL*).

Table 1 shows the analysis of variance, performed using SAS software version 9.1 (SAS® 9.1, SAS Institute Inc., NC, USA). The mean value separation test was carried out by an HSD test (Honesty Significant Difference) with a probability level of 5%. Analysis of variance was used to calculate genotypic and phenotypic variations, which were then reported as variances and wide heritability estimates.

Table 1. Analysis of variance

Source of variance	Df	SS	MS	Expected MS
Replication	r−1	SS replication	MSr	
Treatment	t−1	SS genotypes	MSt	$\sigma^2_e + r\,\sigma^2_g$
Error	t (r−1)	SS error	MSe	σ^2_e

Description: Df = the degrees of freedom; SS = the sum square; MS = the mean square; r = the number of replications; t = the number of treatments.

The genotypic and phenotypic variance component (σ^2_g and σ^2_p) were calculated according to equation 1 and 2 [14]:

$$\text{Estimation of } \textit{phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_{e/r} \text{ or } (\sigma 2_p) = \frac{MSt}{r} \quad (1)$$

$$\text{Estimation of } \textit{genotypic variance } (\sigma^2_g) = (\text{MSt} - \text{MSe})/r \text{ or } (\sigma^2_g) = \frac{MSt - MSe}{r} \quad (2)$$

where, *r* is the number of replications, *MSt* is the mean square of treatments, and MSe is the mean square of error.

Determination of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation GCV) was made based on equation 3 and 4:

$$\textit{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{\mu} \times 100 \quad (3)$$

$$\textit{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{\mu} \times 100\% \quad (4)$$

where σ^2_p = phenotypic variance; σ^2_g = genotypic variance and μ = sample mean [15].

The estimation of heritability in the broad sense (h^2) can be determined using equation 5 [16]:

$$\textit{Broad sense heritability } (h^2_{bs}) = \frac{\sqrt{\sigma^2 \text{g}}}{\sigma^2 g + \sigma^2 e/\text{r}} \times 100 \quad (5)$$

The criteria for classification of heritability values were low heritability was indicated by a value of

$h^2 < 0.2$, medium heritability by $0.2 \leq h^2 \leq 0.5$, and high heritability by $h^2 > 0.5$ [17]. The genetic advance of mean is considered high if it is greater than 20%, moderate if it was between 10–20%, and low if it is less than 10% [18].

The genetic advancement (*GA*) and the value of genetic advance (*GAM*) of the mean using Equations 6 and 7.

$$\textit{Genetic advancement (GA)} = 2 \times \sigma^2 p \; x \; k \quad (6)$$

$$\textit{Genetic advance of Mean (GAM)} = \frac{\text{GA}}{\mu} \times 100 \quad (7)$$

where *k* is the standardized selection differential at 5% selection intensity (*k=2.063*), μ is the character's average mean value, and $\sigma^2 p$ is the square root of phenotypic variance. The genetic advance of the mean is deemed high if it exceeds 20%, moderate if it falls between 10% and 20%, and low if it falls below 10% [18].

Data calculations of genetic parameters were conducted with Microsoft Excel program. Correlation between variables were analyse with R Program software (version R4.1.2) to calculate Pearson correlation. Biplot Principal Component Analysis (*PCA*) was used to visualize the genotype-characters connection. The biplot diagram was analyzed and visualized using R Programme software (version R4.1.2) using the *factoextra* package.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance, Genetic variability, Heritability and Genetic advance

The analysis of variance showed that there was significant variance in all characteristics throughout the 15 New Guinea Impatiens (Table 2). The number of flowers per plant varies greatly in number both per cluster and per plant. After transformation the data, the new analysis for coefficient variation has decreased from 63.38 to 27.06.

Table 2. Means Square, mean value, standard deviation, and coefficient of variation for 16 characters among 15 genotypes of New Guinea Impatiens

Character	Mean Square of Treatment		Mean value (± SD)	Cv (%)
leaf length (cm)	10.75	**	8.53 ± 2.01	11.31
leaf width (cm)	1.08	**	2.91 ± 0.70	16.36
Flower length (cm)	1.27	**	5.76 ± 0.79	8.77
Flower width (cm)	1.03	**	5.85 ± 0.75	10.24
Eye zone width (cm)	0.05	**	0.65 ± 0.13	8.76
dorsal petal length (cm)	0.34	**	0.24 ± 0.40	12.11
dorsal petal width (cm)	0.92	**	3.82 ± 0.62	10.00
lateral petal length (cm)	0.47	**	2.83 ± 0.46	10.53
lateral petal width (cm)	0.62	**	2.99 ± 0.54	11.96
ventral petal length (cm)	1.59	**	3.00 ± 0.76	10.79
ventral petal width (cm)	0.47	**	3.31 ± 0.48	10.97
Spur length (cm)	1.95	**	5.43 ± 0.87	8.09
flower number per cluster	1.22	*	1.89 ± 0.86	36.10
flower number per plant	490.33	**	15.96 ± 15.11	27.06

Description : **: Significant F test at 0.01 level of probability; *: Significant F test at 0.05 level of probability

Genotype PLS33.3 had the widest leaf (3.63 cm) and eye zone (1.03 cm) as well as the longest spur (6.80 cm). For the characters related to leaf growth, the most extended leaf length in PLS236 and the widest diameter in PLS33.3 genotype. The average size of flower ranged from 4,40-6,97 cm length and 4.60-6.80 cm width. Meanwhile the genotype with the largest flower size was NG228 followed by PL46.1. The longest of dorsal petal, lateral petal and ventral petal was belongs to genotype NG228, but the widest of those characters was belongs to PLS46.1 genotype. The smallest flower size was PL61. Genotype PLS236 had the most flower per cluster (3.67) but the most flower per plant was achieved by PLS36 (53) (Table 3). The character differences might come from environmental and genetic factors [16]. To determine whether the difference is due to genetic or environmental factors, the analysis was continued by manipulating the variance components.

The genetic parameters of genotypes were shown in Table 4. The heritability estimates for all characters ranged from 0.61 (flower number per cluster) to 1.00 (eye zone width). All observed characters showed high heritability. The highest broad sense heritability estimate was shown by eye zone width (1.00), then followed by ventral petal length, leaf length and spur length i.e., 0.93, 091 and 0.90 respectively. Similar research was reported by [19, 20] in which the the spur length has high heritability (0.90). Spur length and curvature varies among plants within one population. According to [21] spur is important traits because it is associated with flower evolution, and the length of the spur influences the success of plant reproduction. The nectar spur is a important element of pollination and ecological adaptability in flowering plants, and it is a key innovation for promoting species diversity in specific plant lineages [22]. Impatiens is a *protandrous* plant, so it requires pollinators for pollination. Long spurs often drive specialization and speciation, while short spurs provide flexibility and adaptability in pollination [23].

Table 3. The means of leaf and flower characters of 15 New Guinea Impatiens

GENOTYPES	LL	LW	LT	FL	FW	FT	EZW	DPL	DPW	LPL	LPW	VPL	VPW	SL	FNPB	FNPP
NGP03	6.22^{fg}	2.24^{bcd}	0.29^{abcd}	4.60^{bc}	4.98^{bc}	0.24^{abc}	0.60^{bcd}	2.02^{abc}	3.44^{bc}	2.36^{cd}	2.79^{abc}	2.21^{f}	2.98^{abc}	4.67^{cd}	2.00^{ab}	20.33^{b}
NGP05	8.36^{abcdef}	3.39^{abc}	0.33^{ab}	5.70^{abc}	5.69^{abc}	0.24^{abc}	0.68^{bc}	2.41^{abc}	4.11^{ab}	2.49^{bcd}	3.48^{ab}	2.60^{f}	3.57^{ab}	4.76^{cd}	1.67^{ab}	13.00^{b}
NGP08	7.60^{cdefg}	2.59^{abcd}	0.32^{abc}	6.09^{abc}	6.13^{abc}	0.22^{abc}	0.60^{bcd}	2.47^{abc}	4.20^{ab}	2.60^{bcd}	3.61^{a}	2.61^{ef}	3.27^{abc}	5.93^{abc}	1.33^{b}	16.67^{b}
NGP06	6.87^{defg}	2.53^{abcd}	0.34^{a}	5.58^{abc}	5.60^{abc}	0.20^{bc}	0.62^{bcd}	2.68^{ab}	3.91^{abc}	2.71^{abcd}	2.97^{abc}	2.34^{f}	3.42^{abc}	5.08^{bcd}	2.00^{ab}	7.67^{b}
NGP02	10.51^{abc}	3.71^{a}	0.25^{bcd}	5.63^{abc}	5.42^{abc}	0.24^{abc}	0.61^{bcd}	2.46^{abc}	3.32^{bc}	2.68^{abcd}	2.46^{bc}	2.92^{cdef}	2.83^{bc}	5.12^{bcd}	1.67^{ab}	6.00^{b}
NG230	8.99^{abcdef}	3.18^{abcd}	0.26^{bcd}	6.33^{ab}	6.21^{abc}	0.23^{abc}	0.57^{cd}	2.79^{a}	4.11^{ab}	3.21^{abc}	3.07^{abc}	3.71^{abcd}	3.23^{abc}	5.81^{abc}	2.67^{ab}	3.33^{b}
PLS33.3	10.83^{ab}	3.63^{ab}	0.26^{bcd}	6.27^{ab}	6.37^{abc}	0.27^{ab}	1.03^{a}	2.53^{abc}	3.50^{bc}	3.13^{abc}	2.93^{abc}	3.97^{ab}	3.27^{abc}	6.80^{a}	1.67^{ab}	15.33^{b}
PLS36	6.70^{efg}	2.10^{cd}	0.29^{abcd}	5.53^{abc}	5.73^{abc}	0.21^{bc}	0.70^{bc}	2.33^{abc}	3.30^{bc}	2.73^{abcd}	2.83^{abc}	2.83^{def}	3.23^{abc}	4.23^{d}	2.00^{ab}	53.00^{a}
PLS236	11.30^{a}	3.20^{abcd}	0.25^{cd}	6.00^{abc}	6.30^{abc}	0.27^{ab}	0.67^{bc}	2.50^{abc}	4.43^{ab}	3.20^{abc}	3.50^{ab}	3.93^{abc}	3.67^{ab}	5.77^{abc}	3.67^{a}	32.00^{ab}
PLS46.1	9.70^{abcd}	3.47^{abc}	0.32^{abc}	6.37^{ab}	6.53^{ab}	0.30^{a}	0.60^{bcd}	2.73^{a}	4.83^{a}	3.33^{ab}	3.73^{a}	4.00^{ab}	3.97^{a}	6.13^{ab}	2.33^{ab}	19.33^{b}
NGP01	7.43^{defg}	3.13^{abcd}	0.25^{bcd}	5.80^{abc}	5.67^{abc}	0.21^{bc}	0.47^{d}	2.32^{abc}	3.53^{bc}	2.75^{abcd}	2.27^{c}	3.02^{bcdef}	3.01^{abc}	5.64^{abc}	1.67^{ab}	9.33^{b}
NG228	10.70^{ab}	3.57^{ab}	0.23^{d}	6.97^{a}	6.80^{a}	0.21^{abc}	0.60^{bcd}	2.90^{a}	4.43^{ab}	3.57^{a}	3.07^{abc}	4.13^{a}	3.63^{ab}	6.73^{a}	1.67^{ab}	8.00^{b}
NG227	9.37^{abcde}	2.60^{abcd}	0.25^{bcd}	5.60^{abc}	6.13^{abc}	0.22^{abc}	0.77^{b}	2.20^{abc}	4.00^{ab}	3.00^{abcd}	3.03^{abc}	3.63^{abcde}	3.70^{ab}	5.70^{abc}	1.67^{ab}	3.00^{b}
PLS60	8.33^{bcdef}	2.50^{abcd}	0.22^{d}	5.60^{abc}	5.67^{abc}	0.16^{c}	0.63^{bcd}	1.83^{bc}	3.37^{bc}	2.47^{bcd}	3.00^{abc}	2.50^{f}	3.40^{abc}	4.83^{bcd}	1.33^{b}	19.00^{b}
PLS61	4.97^{g}	1.87^{d}	0.32^{abc}	4.40^{c}	4.60^{c}	0.17^{c}	0.63^{bcd}	1.73^{c}	2.77^{c}	2.17^{d}	2.23^{c}	2.03^{f}	2.40^{c}	4.27^{d}	1.00^{b}	13.33^{b}
Mean value (μ)	8.53	2.91	0.28	5.76	5.85	0.23	0.65	2.39	3.82	2.83	3.00	3.10	3.31	5.43	1.89	15.96
F test	**	**	**	**	**	**	**	**	**	**	**	**	**	**	*	**
cv (%)	11.31	16.36	8.77	10.24	9.89	12.15	8.76	12.11	10	10.53	11.96	10.79	10.97	8.09	36.1	63.38

Description: LL=leaf length, LW=leaf width, FL= flower length, FW = flower width, EZW = eye zone width, DPL = dorsal petal length, DPW=dorsal petal sith, LPL=lateral petal length, LPW=lateral petal width, VPL=ventral petal length, VPW=ventral petal sidth, SL = spur length, FNPB= flower number per cluster, FNPP = flower number per plant. Mean followed by different supperscript letters on the same row indicated significant different (p<0.05)

Table 4. Estimation of genetic parameters of quantitative variables of 15 New Guinea Impatiens

	Mean	σ_g	σ_p	h^2_{bs}	Category	GCV (%)	Category	PCV (%)	Category	GA	GAM (%)	Category
LL	8.53	3.27	3.58	0.91	high	21.22	Broad	22.20	Broad	3.60	33.26	high
LW	2.91	0.28	0.36	0.79	high	18.26	moderate	20.59	Broad	0.31	2.66	low
FL	5.76	0.31	0.42	0.72	high	9.61	Narrow	11.29	moderate	0.34	16.68	moderate
FW	5.85	0.23	0.34	0.67	high	8.19	Narrow	10.01	moderate	0.25	23.76	high
EZW	0.65	0.02	0.02	1.00	high	19.78	Broad	19.78	moderate	0.02	5.70	low
DPL	2.39	0.09	0.11	0.76	high	12.30	moderate	14.06	moderate	0.10	27.22	high
DPW	3.82	0.26	0.31	0.84	high	0.00	Narrow	14.50	moderate	0.28	183.61	high
LPL	2.83	0.13	0.16	0.81	high	12.59	moderate	14.01	moderate	0.14	34.18	high
LPW	3.00	0.16	0.21	0.79	high	13.48	moderate	15.17	moderate	0.18	68.97	high
VPL	3.10	0.49	0.53	0.93	high	22.69	Broad	23.51	Broad	0.54	190.93	high
VPW	3.31	0.11	0.16	0.72	high	10.19	moderate	11.98	moderate	0.12	63.12	high
SL	5.43	0.59	0.65	0.90	high	14.10	moderate	14.84	moderate	0.65	183.68	high
FNPB	1.89	0.25	0.41	0.61	high	26.47	Broad	33.76	Broad	0.28	20.37	high
FNPP	15.96	129.35	163.44	0.79	high	71.28	Broad	80.13	Broad	142.43	6056.44	high

Description: σ^2_g = genotypic variance; σ^2_p = phenotypic variance; h^2_{bs} = broad-sense heritability; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation, GA = genetic advance, GAM = genetic advance of mean. LL=leaf length, LW=leaf width, FL= flower length, FW = flower width, EZW = eye zone width, DPL = dorsal petal length, DPW=dorsal petal sith, LPL=lateral petal length, LPW=lateral petal width, VPL=ventral petal length, VPW=ventral petal sidth, SL = spur length, FNPB= flower number per cluster, FNPP = flower number per plant.

The Genotypic Coefficient of Variance (*GCV*) of New Guinea Impatiens was ranged from 0.00% (dorsal petal width) to 71.28 % (flower number per plant). Four parameters, leaf length, ventral petal, flower number per cluster and flower number per plant showed a wide range of genotypic diversity across the 15 examined genotype. The phenotypic coefficient of variation (*PCV*) followed a similar trend as the *GVC*, indicating that these four characters (flower number per cluster, eye zone width, dorsal petal width, and flower number per plant) were less influenced by the environment. High heritability indicates that most of the observed variation in a specific trait within a population is due to genetic factors rather than environmental influences [16; 24]. This is important in plant breeding because it suggests that the trait can be reliably passed on to the next generation through selective breeding. Broad-sense heritability values can be used as a baseline for running an effective breeding programme since they suggest that a population has enough genetic variation to respond to selection pressure [25]. Furthermore, the combination of a high estimate of broad-sense heritability, genetic advance as a percentage of the mean, and genotypic coefficient of variation yields the most precise estimates of the amount of expected improvement through phenotype selection [18]. Traits with high heritability (>0.5), are largely determined by genetics and respond well to selection [14, 16, 17]. In this case all traits had high heritability. Breeders can confidently select plants with desirable traits knowing that offspring will inherit these traits consistently.

Except for leaf width, flower length, and eye zone width, all traits revealed a high Genetic Advance of Mean (Table 4). Broad-sense heritability was linked to high Genetic Advance and Genotypic Coefficient of Variance in the cases of leaf length, ventral petal length, flower number per cluster, and flower number per plant (Table 4), indicating the presence of additive gene action and thus a high genetic gain from phenotype selection. In the former study in *Impatiens platypetala*, a high genetic advance was observed for leaf length (37.2), leaf width (21.51), and flower width (36,81) [19].

3.2 Correlation between quantitative characters

Quantitative characters data were derived from leaf and flower measurements of 15 characters to perform correlation between character. In Figure 2A it can be seen that a high positive correlation is depicted with orange colour that gets darker with higher correlation, while purple colour depicts a negative correlation that gets darker with higher negative correlation. In order to clearly see which characters have a high positive and negative correlation, it can be seen in Figure 2B. A high positive correlation is indicated by the colour blue, whereas a high negative correlation is indicated by orange.

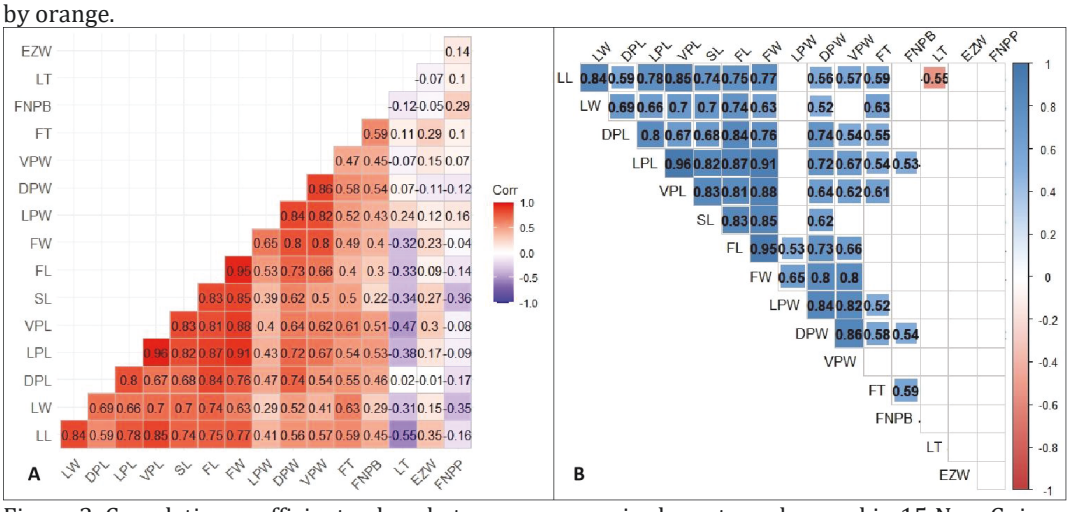

Figure 3. Correlation coefficient values between agronomic characters observed in 15 New Guinea Impatiens cultivar. *LL*=leaf length, *LW*=leaf width, *FL*= flower length, *FW* = flower width, *EZW* = eye zone width, *DPL* = dorsal petal length, *DPW*=dorsal petal width, *LPL*=lateral petal length, *LPW*=lateral petal width, *VPL*=ventral petal length, *VPW*=ventral petal width, *SL* = spur length, *FNPB*= flower number per cluster, *FNPP* = flower number per plant.

Correlations between quantitative characters ranged from no correlation (r=0.02) to a high positive correlation (r=>0.50 to 0.96) and low negative correlation (r=-0.01 to <0.38) to a high negative correlation (r=-0.55). Most high and medium correlations between characters had significant differences (P<0.05) (Figure. 3). The majority of the significant positive and strong correlation were discovered among quantitative leaf or floral characteristics. *LL* was positive correlated with *LW, DPL, LPL, VPL, SL, FL, FW, DPW, VPW,* and *FT* (*r=0.80, r=0.59, r=0.78, r=0.86, r=0.74, r=75, r=0.77, r=0.56, r=0.57, and r=0.59 respectively; all P<0.01*); *LW* was correlated with *DPL, LPL, VPL, SL, FL, FW, DPW* and *FT* (*r=0.69, r=0.66, r=0.70, r=0.70, r=0.74, r=63, r=0.52, and r=0.63 respectively; all P<0.01*); *DPL* was correlated with *LPL, VPL, SL, FL, FW, DPW, VPW* and *FT* (*r=0.80 r=0.67, r=0.68, r=0.84, r=0.76, r=74, r=0.54, and r=0.55 respectively; all P<0.01*); *LPL* was correlated with *VPL, SL, FL, FW, DPW, VPW, FT, FNPB* (*r=0.96 r=0.82, r=0.87, r=0.91, r=0.72, r=74, r=0.67, R=0.54and r=0.53 respectively; all P<0.01*); *VPL* was correlated with *SL, FL, FW, DPW, VPW* and *FT,* (*r=0.83 r=0.81, r=0.88, r=0.64, r=0.62, and r=0.61 respectively; all P<0.01*); *SL* was correlated with *FL, FW,* and *DPW* (*r=0.83, r=0.85, and r=0.62 respectively; all P<0.01*); FL was correlated with *FW, LPL, DPW* and *VPW* (*r=0.95, r=0.53, r=0.73, and r=0.66 respectively; all P<0.01*); *FW* was correlated with *LPL, DPW* and *VPW* (*r=0.65, r=0.80, and r=0.80 respectively; all P<0.01*); *LPW* was correlated with *DPW, VPW* and *FT* (*r=0.84, r=0.82, and r=0.52 respectively; all P<0.01*); *DPW* was correlated with *VPW, FT,* and *FNPB* (*r=0.86, r=0.58, and r=0.54 respectively; all P<0.01*); *FT* was correlated with FNPB (*r=0.59*). There is intriguing data showing that *LL* is negatively linked with *LT* (*r=-0,55, P<0.01*), implying that the longer the leaf, the thinner the leaf thickness. Eye zone width and flower number per plant were not correlated with all characters.

3.3 Principal component and bi-plot analysis.

To investigate the association between the quantitative characters and genotype, Principal Component Analysis (PCA) bi-plots and cluster plots were undertaken for all data sets, combining PCA of characters and genotype. Principal component analysis (*PCA*) was performed using characters: leaf length (*LL*), and leaf width (*LW*), flower length (*FL*), flower width (*FW*), eye zone width (*EZW*), dorsal petal length (DPL), dorsal petal width (*DPW*), lateral petal length (*LPL*), lateral petal width (*LPW*), ventral petal length (*VPL*), ventral petal width (*VPW*), spur length (*SL*), flower number per bud (*FNPB*) and flower number per plant (*FNPP*). For this *PCA* analysis, we added 2 characters that were not included in the variance analysis, namely leaf thick and flower thick. (Table 5).

Table 5. Result of principal component analysis based on 16 characters. PC1 first principal component, PC2 second principal component, PC3 third component and PC4 fourth component.

No.	Characters	PC1	PC2	PC3	PC4
1	leaf length (LL)	0.864	-0.292	0.215	0.008
2	leaf width (LW)	0.780	-0.317	-0.108	0.133
3	Leaf thick (LT)	-0.285	0.704	-0.320	0.466
4	flower length (FL)	0.909	-0.138	-0.162	-0.047
5	flower width (FW)	0.950	-0.013	0.003	-0.013
6	Flower thick (FT)	0.678	0.290	0.221	0.239
7	eye zone width (EZW),	0.211	-0.143	0.657	0.659
8	dorsal petal length (DPL)	0.824	0.082	-0.291	-0.003
9	dorsal petal width (DPW)	0.841	0.397	-0.306	-0.056
10	lateral petal length (LPL)	0.931	-0.127	0.037	-0.153
11	lateral petal width(LPW)	0.643	0.626	-0.062	0.156
12	Ventral petal length (VPL)	0.917	-0.204	0.199	-0.072
13	Ventral petal width(VPW)	0.778	0.375	-0.008	-0.003
14	Spur length (SL)	0.850	-0.316	-0.103	0.184
15	Flower number per cluster (FNPB)	0.545	0.386	0.282	-0.459
16	Flower number per plant (FNPP)	-0.115	0.529	0.665	-0.259
	Eigenvalue	8.82	2.09	1.42	1.10
	Variance %	55.11	13.06	8.89	6.85
	Cumulative variance %	55.11	68.17	77.06	83.92

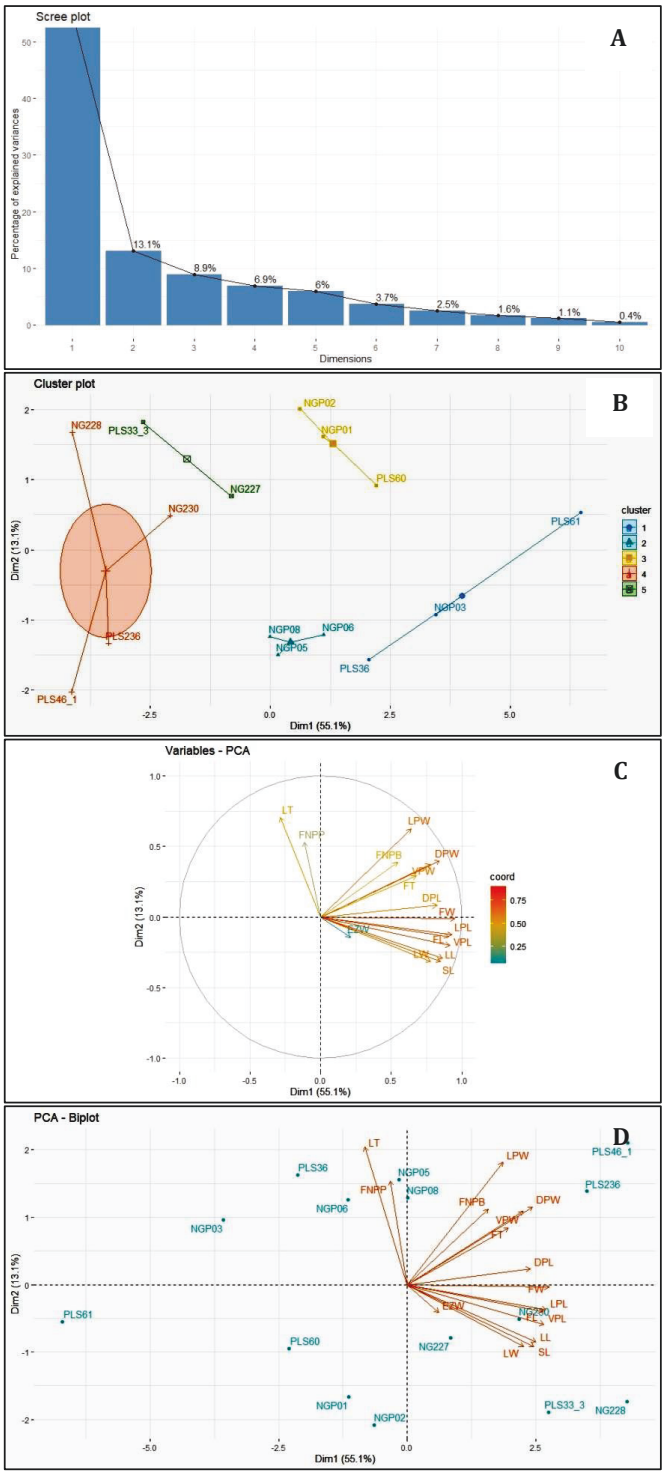

Figure 4. (A) Scree Plot explaining the contribution of 10 various principal components, (B) PCA Cluster Plot, (C) PCA Variables Plot, (D) PCA bi-plots explaining the contribution of 16 traits to the total variation in the 15 New Guinea Impatiens genotypes. Note; leaf length (*LL*), and leaf width (*LW*), leaf thick (*LT*), flower length (*FL*), flower width (*FW*), flower thick (*FT*), eye zone width (*EZW*), dorsal petal length (*DPL*), dorsal petal width (*DPW*), lateral petal length (*LPL*), lateral petal width (*LPW*), ventral petal length (*VPL*), ventral petal width (*VPW*), spur length (*SL*), flower number per cluster (*FNPB*) and flower number per plant (*FNPP*).

The results showed that the data had four PCA factors. Out of 10 principal components (PCs)(Figure 4A), the first four components with an *eigen* value > 1.0 contribute maximum variation, i.e. 83.92% (Figure 3A). The first (PC1), second (PC2), third (PC3) and fourth (PC4) principal components contributed to the total variations by 55.11%, 13.06%, 8.89% and 6.85% (Table 5). The first principal component (PC1) exhibited a high positive associated with leaf length (0.864), flower length (0.909), flower width(0.950), dorsal petal length (0.824), dorsal petal width (0.841), lateral petal length (0.931), ventral petal length (0.917) and spur length (0.850). The second PCA was positively associated with leaf thick (0.704) and lateral petal width (0.626). The third PCA was positively associated with flower number per plant (0.665). The fourth PCA was negatively associated with flower number per cluster (Table 5).

Cluster analysis based on quantitative data resulted in the successful classification of the 15 genotypes into five groups (Figure 4B). The First group consist of 4 genotipes (PLS46.1; PLS236; NG230 dan NG228), second group consist of 2 genotypes (PLS33.3 and NG227), third group consist of 3 genoytpes (NG05, NG06 and NG08), fourth group consist of (PLS60, NG01, NG02) and the last group consist of 3 genotypes (PLS36, PLS61 and NG03). The genotype in group 4 all have similar values for Dim1 and Dim2. It suggests that these genotype are similar to each other. In contrast, the genotypes in group 1 have very different values for Dim1 and Dim2. This suggests that these genotypes are quite different from each other.

The variables LPL, VPW, FNPB, DPW, LPW, LT and FNRP (Figure 4C) are strongly positively correlated with Dim1. The variables SL, LL, LW, FW, and DPL are strongly negatively correlated with Dim1. The variable EZW is the least correlated with Dim1. The variables SL, LL, LW, FW, and DPL are strongly positively correlated with Dim2. The variables LPL, VPW, FNPB, DPW, LPW, LT and FNRP are strongly negatively correlated with Dim2. The variable EZW is the least correlated with Dim2. This bi-plot can be used to identify the variables that are most important in explaining the variation in the data, as well as to identify the genotype that are most similar and different.

The bi-plot (Figure 4D) showed the relationship between the genotype(represented by the blue dots) and the variables (represented by the arrows). The genotypes are plotted along the two principal components, which are the directions of greatest variance in the data. The arrows represent the variables, and their length and direction indicate their correlation with the principal components. The genotypes that are close to each other are more similar, while the samples that are far apart are more different. The variables that are pointing in the same direction are positively correlated, while the variables that are pointing in opposite directions are negatively correlated. In this particular bi-plot: genotypes NG227, NG230, PLS33.3 and NG228 are closer to each other than the rest of the genotypes, so we choose genotype PLS33.3 among that four closer genotype. The genotype NGP01 and NGP02 are the most different from the rest.

Bi-plot PCA has been widely utilized to reveal the association between traits [26]. The bi-plot provides a useful starting point for selecting samples for breeding, but a comprehensive analysis considering all relevant traits and factors is necessary for a successful breeding program. The bi-plot showed that genotype NGP01, NGP02 and NGP03 are located at the left side of the plot, indicating they have lower values for the first principal component (Dim1). Based on this observation, we can consider NGP01, NGP02, and NGP03 as potential candidates for breeding programs, as they are distinct from the other samples. However, it's crucial to consider the specific traits represented by Dim1 before making a final decision. First, correlations between variables: the arrows in the bi-plot showed the correlation between variables and principal components. This information can help us understand which traits contribute most to the differences between the genotype. Second, genetic diversity: It's essential to consider the genetic diversity of the selected samples to prevent inbreeding and maintain genetic variability in the breeding program.

The distribution of New Guinea Impatiens in Indonesia is still very limited because the nursery industry has not received any seed from outside since 2015 (Widaningsih, personal communication). This means that existing of this plants did not develop or limited in variety. The plants degrade over time due to vegetative propagation. Additionally, New Guinea Impatiens is less resilient to environmental stress including drought and heat [27].

Conclusion

All characters observed were highly significant variation, indicating increased variability in the accession. The genotypic coefficient of variance was ranged from 0 (dorsal petal width) to 71.28 flower number per plant). The phenotipic coefficient of variance was ranged from 10.01 (flower

width) to 80.13 (flower number per plant). High heritability in broad sense estimates were obtained for the majority of the traits examined. High heritability in broad sense (0.61 - 1.00) estimates were obtained for all of the characters examined. Leaf length, ventral petal length, and flower number showed high genetic advance. The range of correlation between characters was from -0.01 - 0.96. Character flower thick influencing the flower number per plant, so that a direct selection through this trait will be effective. The largest data diversity is described by four components, with a total variance of 83.92%. Genotype NGP01, NGP02, NGP03 and PLS33.3 are potential candidates for breeding programs.

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