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ORIGINAL ARTICLE



Morphological variation, species delimits, and phylogenetic relationships of four important *Ipomoea* species in Sri Lanka

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Abstract

Genus *Ipomoea* is the largest of the family Convolvulaceae. It is a highly diverse genus distributed all around the world. In Sri Lanka, 13 members have been identified in *Ipomoea*; however, most of them have not been morpho-genetically characterized. In the present study, we selected I. batatas, I. aquatica, I. nil, and I. pes-caprae for the assessment based on certain criteria viz., food security, leafy vegetable, emergent weed, and coastal conservation capabilities. The morphological variation, species delimits, and phylogenetic relationships among these four species were assessed. The DNA was extracted from young leaf samples using CTAB method and subjected to PCR using *ITS* and *rbcL* as markers. The PCR products were subjected to sequencing. The DNA sequences were analyzed, and phylogenetic trees were generated by using PAUP to define the species delimits, identify the speciation and evolutionarily relationships in comparison to the homologous *Ipomoea* sequences available in GenBank. The tuber bearing ability, flower colour, and leaf shape are the key morphological descriptors that can be used to delimit the selected species. Both *rbcL* and *ITS* markers could be used to identify the four species studied distinctively. However, among the two markers, ITS provides a greater variation to identify the four species and their evolutionary relationships. Thus, the present study provides a key platform with usable morphological traits and DNA barcoding markers to characterize all *Ipomoea* species in Sri Lanka.

Keywords: Convolvulaceae, I. aquatica, I. batatas, I. nil, I. pes-caprae

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1. Introduction

Ipomoea is a plant genus containing a group of warm climate trees, vines, and shrubs that are distributed mostly in the tropical and temperate zones in the world. Ipomoea is a highly diverse genus comprising of more than 500 different species. Hence, it is the largest the flowering plant genus in family Convolvulaceae, which predominantly consists of 1650 tropical species grouped into 50-60 genera (Austin and Huáman 1996). Most species in Convolvulaceae are climbing or twinning woody or herbaceous plants that frequently possess heart-shaped leaves and funnel-shaped flowers (Lobin 1986). Except for the flowers and leaves, these plants exhibit different morphological features and variations their distribution within different in environmental and geographical locations. Sri Lanka is one of the tropical countries with very high diversity, which includes 13 species of the genus Ipomoea (Table 1). Among them, four species, I. batatas, I. aquatica, I. nil, and I. pes*caprae*, were selected for the assessment in the present study based on food and medicinal values, weed properties and ecological and soil conservation properties respectively.

I. batatas (sweet potato) is the most abundantly found Ipomoea species in Sri Lanka. It is a herbaceous creeping plant with smooth green leaves with purple pigmentation along the veins (Wickramasinghe et al. 2009). I. batatas contains both tuberous roots and fibrous roots. The former is considered as a root vegetable, a major food source, where people consume the sweet-tasting, large, starchy tuberous roots. The tubers are rich in minerals such as sodium, potassium, calcium, and vitamin D (Izawa and Okamoto 1959). The tuber also contains 12% of the dietary fibre. The leaves of *I. batatas* are also consumed occasionally. The leaves contain appreciable levels of important nutrients such manganese, potassium, zinc, sodium, as magnesium, calcium, iron, and vitamin C (Antial et al. 2006). In addition to serving as an indispensable constituent of the human diet, I. batatas is used to treat cancer, diarrhea, nausea, and asthma in Ayurvedic medicine its antimicrobial, utilizing antioxidant. demulcent, and astringent properties (AMPSL 2020).

I. aquatica (water spinach) is a semiaquatic leafy vegetable grown as a green vegetable in Sri Lanka. The shoot-tops (i.e. leaves and young,

Scientific name	English name	Local Name
I. alba	Moon vine	Alanga / Kalu alanga
I. aquatica	Water morning glory	Kankun
I. asarifolia	-	Ela binthamuru
I. batatas	Sweet potato	Batala
I. littoralis	• ·	Thel kola
I. mauritiana	Giant potato	Kiri badu
I. nil	Blue morning glory	Kaladana / Kalamaruva
I. obscura	Obscure morning glory	Maha madhu / Tel kola
I. pes-caprae	Goat foot vine, Bayhops	Muhudu binthamburu
I. pes-tigridis	Tiger foot morning glory	Divipahuru
I. quamoclit	Cypress vine	Rata pamba / Rathingna mal
I. sepiaria	Purple heart glory	Rasa thel kola
I. triloba	Little bell	Wasa thella

(Ayurveda Medical Plants of Sri Lanka 2020)

floating stems) are harvested to make delicious dishes for consumption (Kailasapathy and Koneshan 1986). Water spinach is also rich in minerals such as vitamin C, vitamin A, iron, potassium, and manganese. This crop can be easily grown and harvested at irregular intervals. The water spinach cultivation requires low labor and is immune to various natural pressures (Edie and Ho, 1969; Umar et al. 2007). It is also known to control the water quality due to its ability to accumulate heavy metals (Gothberg et al. 2002). The bioaccumulation of heavy metal ions greatly hinders the food value of water spinach (Ranathunga et al. 2019).

I. nil (Japanese morning glory) is an annual climbing herb, which is capable of producing self-pollinating, ephemeral blue flowers. This is largely cultivated as an ornamental plant in many parts of the world, and there are many named varieties (Huxley 1992). Currently, in Sri Lanka, a large number has been spread in the up-country regions, which includes many tea estates and abundant lands. Due to the recent ban on using glyphosate, I. nil is prominently emerging as a weed causing problems such as blocking sunlight, interrupting plucking and other operations, and harboring pests and diseases in tea lands. The seeds of this plant have some rare medicinal value. I. nil is used to treat conditions like constipation, ascariasis, oliguria, and edema.

I. pes-caprae (beach morning glory) is a creeping vine that is restricted and abundantly distributed in the sandy shores of Sri Lankan oceans and throughout the tropical coastal

areas. It is salt tolerant, and the seeds of this plant disperse through oceans by floating in the seawater. *I. pes-caprae* is also a known primary sand stabilizer and successfully grows in sandbanks. The extensive runners of this kind appear from large, thick, and woody rootstock, and the stems could extend up to 30 cm along with root at the nodes. This spreading pattern often results in a dense net of low growth vines covering the whole coastal line (Das and Mukherjee 1997). These mesh-like covering could protect the soil from erosion. This plant also has various uses in medicine as well as in agroforestry. The boiled roots are used to treat bladder related diseases. The leaves are used to provide relief during chickenpox conditions, dropsy, and urethral discharges; also, the stems are known to have anti-tumor properties as well (Bragadeeswaran et al. 2010).

The members of the genus *Ipomoea* of the family Convolvulaceae must be morphogenetically characterized to harness the food, agricultural, and ecological values. To our knowledge, no studies have been conducted to characterize and identify species delimits of *Ipomoea* spp. in Sri Lanka. Therefore, the present study was undertaken to assess *I. batatas, I. aquatica, I. nil,* and *I. pes-caprae,* in Sri Lanka, using morphological and phylogenetic approaches.

2. Materials and Methods

Plant material

Initially, the distribution of the members of the *Ipomoea* genus and their diversity were recorded throughout the country. Then the variation of their morphological features based

on the islandwide distribution and diversity was assessed and four important species were chosen. Based on these observations, a total of 10 representative samples referring to four selected *Ipomoea* species, including *I. batatas, I. aquatica, I. nil,* and *I. pes-caprae* were collected in the natural range of Sri Lanka (Table 2). Then the voucher specimens used in this study were preserved, and their morphological features were studied.

Table 2: Locations of the collected plant materials

Species	Voucher	Location	GPS
	Number		Coordinates
I. batatas	DMB09	Peradeniya	7.271748
			80.598761
	DMB10	Galle	6.053842
			80.225386
I. aquatica	DMB06	Peradeniya	7.271748
			80.598761
	DMB07	Dambulla	7.884588
			80.667958
	DMB08	Digana	7.298066
			80.737409
I. nil	DMB192	Nuwara-Eliya	7.035686
			80.517982
	DMB193	Pussellawa	7.109321
			80.639426
I. pes-	DMB500	Pasikuda	7.929618
caprae			81.560875
	DMB501	Moratuwa	6.753961
			79.888277
	DMB502	Negombo	7.231338
			79.842457

DNA extraction, PCR and sequencing

Fresh leaf samples from each selected species were collected to extract DNA using the cetyltrimethylammonium bromide (CTAB) method (Doyle and Doyle 1990), and the extracted DNA samples were stored at -20 ^oC.

The extracted genomic DNA samples were PCR amplified using two standard plant DNA barcoding markers; rbcL and ITS (Table 3). The PCR mixture was prepared of 15 µl volume, consisting of 2× GoTaq® Green Master Mix, 0.3 pmol of forward and reverse primers, and 50 ng of template DNA. The PCR program consisted of an initial denaturation at 95 °C for 5 min, 35 cycles with denaturation at 95 °C for 30 s, primer annealing at 55 °C for 1 min and synthesis at 72 °C for 90 s, final extension at 72 °C for 4 min. The PCR products were purified using the QIAquick® PCR Purification Kit (Catalog No: 28104, Qiagen, Hilden, Germany). The purified PCR products were cycle sequenced using the Genetic Analyzer 3500 (Catalog number: 622-0010, Applied Bio System).

Table 3: The primer details for the DNA barcodingDNA markerSequence (5'-3')

what *	F: ATGTCACCACAAACAGAGACTAAAGC
TDCL	R: GTAAAATCAAGTCCACCRCG
ITC1 /**	F: TCCGTAGGTGAACCTTGCGG
1151-4	R: TCCTCCGCTTATTGATATGC

*Wang et al. (2001); gene for the large subunit of the ribulose-bisphosphate carboxylase in chloroplast genome

**White et al. (1990); internal transcribed spacer of *rRNA* genes in nuclear genome

Phylogenetic analysis

The raw sequences resulted from automated sequencing were checked for the quality and accuracy by reading the electropherogram. The 3× sequence reads were then aligned, trimmed, and concatenated to a consensus sequence using the software MEGA 7 (Kumar et al. 2016). The datasets of Ranathunga et al. (2019) and Xu et al. (2018) were used with the sequences

Spacias	Vouchor No	Country	GenBan	k Ac. No.	Deference
species	voucher No.	Counti y	rbcL	ITS	
Ipomoea pes-caprae	DMB500	Sri Lanka	MN563135	MN559534	This study
	DMB501		MN563136	MN559535	
	DMB502		MN563137	MN559536	
I. batatas	DMB09	-	MH796547	MH792117	Ranathunga et al. (2019)
	DMB10		MH796548	MH792118	
I. aquatica	DMB06	-	MH796544	MH792114	-
	DMB07		MH796545	MH792115	
	DMB08		MH796546	MH792116	
I. triloba	201509146	China	MF135366	KY968868	Xu et al. (2018)
	13365		MF135405	KY968904	
	201509156		MF135374	KY968875	
	201509190		MF135384	-	
	201509143		MF135365	KY968867	
	201509172		MF135377	KY968878	
I. lacunose	201509150	-	MF135368	KY968870	-
	201509210		MF135389	KY968889	
I. nil	201509152	-	MF135370	KY968871	-
	201509208		MF135388	KY968888	
I. purpurea	201507092	-	MF135354	KY968856	-
I. hederfolia	13516	-	-	KY968940	-
Solanum pseudocapsicum	201509147	-	MF135367	KY968869	-
(outgroup)	201507061		MF135342	KY968847	

Table 4: The *rbcL* and *ITS* sequences assessed

generated in the present study (deposited in GenBank) to create a multiple sequence alignment to assess the species delimits and phylogenetic relationships of Ipomoea spp. which got sequences in GenBank (Table 4). Solanum pseudocapsicum was used as the outgroup in the phylogenetic analysis. The ITS and *rbcL* sequence datasets were analyzed separately. A model test was performed to assess the evolutionary process of the nucleotide substitutions. Thus, the model fitting for the datasets can be conducted in the phylogenetic analysis. The model test was performed using Akaike Information Criteria (AIC) (Akaike 1974), Modified Akaike

Information Criteria (AICc) (Cavanaugh 1997), and Bayesian Information Criteria (BIC). A total of seven substitution schemes were considered alongside with the proportion of invariants and gamma shape parameters. The complete analysis was carried out using the software, Jmodel test (Posada 2008), in CIPRES science gateway (Miller et al. 2010). The phylogenetic trees were constructed in PAUP 4.0a (Swofford 2002). The Neighbour Joining trees were drawn considering an uncorrected pairwise genetic distance matrix, and the best tree was constructed in a heuristic search implementing the tree bisection and reconstruction method. A parsimonious bootstrap analysis was

performed for 1000 iterations to validate the tree topologies. The final 50% consensus tree was constructed using the total trees created. The resulting trees were further modified and visualized in Figs. 1.4.3 (Rambaut 2014).

3. Results

Morphological features of the selected Ipomoea spp.

Vernacular name: sweet potato

Botanical name: I. batatas

Stems: greenish or red-purplish, thin stems with or without hair and contain latex, prostate, and slender. Lateral stem branches arise from the short stem and usually unbranched, height can vary from 1 m - 5 m. Leaves: light green to deep purple, simple, spirally arranged, the shape can be rounded, retiform, triangular, lobbed and almost divided, margins are entire, toothed or lobed, length varies from 5 cm - 15 cm, width varies from 5 cm - 15 cm. Inflorescence: solitary flowers or in fewflowered cymes, glabrous. (Fig. 1a). Flowers: lavender, pale purple or white, darker in colour inside the tube, trumpet shape, up to 4 cm - 7 cm long. Fruits: dry dehiscent fruit capsule and ovoid, each capsule consists of one to four seeds, glabrous. Seeds: brown to black, irregular, slightly angular to a rounded shape. Root: fibrous roots, pentarch or hexarch. Tuberroot: skin color varies from purple, cream to brown, round or longish shape, pulp varies from white to yellow, placed closely or far from Seedlings: deeply bi-lobed the main root. cotyledons, subacute or obtuse lobes, prominent rounded auricles (Figs. 2a, 3a, and 4a) (Purseglove 1974; Lebot 2009; Hue et al.2010).

Vernacular names: water ipomoea, storage cabbage, water spinach

Botanical name: I. aquatica

Stems: round, hollow or spongy in shape, free branching, long trailing, herbaceous, have a milky sap, length varies from 2 m – 3 m. Leaves: greenish. simple, alternatively arranged. arrowhead, or lanceolate in shape, margins are entire or with few irregular serrations or small lobes near the base, length varies from 5 cm -15 cm, width varies from 2 cm - 8 cm. Inflorescence: contain solitary flowers in leaf axis, thin corolla with a broadly funnelform, free, sub-equal, five stamens, two locular and elliptic anthers, and two globose shaped stigma (Fig. 1b). Flowers: white to pale pink or lilac in colour with a mauve centre, trumpet-shaped, diameter varies from 3 cm – 5 cm, the length is about 5 cm. Fruits: ovoid to globose shaped capsules, 4 seeded, 1 cm long, 0.5 inches wide. Seeds: brown, densely pilose, 7 mm in length, 4 mm wide. Root: adventitious roots, formed at nodes. Seedlings: cotyledons are petiolated, bi-lobed with V-shape (Figs. 2b, 3b, and 4b) (Jayeola and Oladunjoye 2012; Madhvi et al. 2014).

Vernacular names: beach morning glory, goats foot

Botanical name: I. pes-caprae

Stems: greenish or red-purplish, succulent with a milky latex, glabrous, occasionally twinning, angular or flattened branches, hairless or with hair, length varies from 1 m - 3 m. Leaves: simple, thick and robust, alternate leaf arrangement, variable in shape, lobed margin, 3 cm - 14 cm in length, 2.5 cm - 12 cm wide. Inflorescence: axillary, ovate or elliptic outer sepals and broader outer sepals, glabrous ovary, stamens and styles are surrounded by petals (Fig. 1c). Flowers: pink, reddish, purple or violet, large, trumpet-shaped, 3 cm - 5 cm in length. Fruits: spherical shape, 4-locular capsule, 12 mm - 17 mm in diameter. Seeds: brownish, four suborbicular seeds, densely hairy, 7 mm – 12 mm in length, 6 mm – 8 mm in diameter. Root: long, deep taproot, and small adventitious roots, 20 feet in depth. Seedlings: Each pair of cotyledons is deeply lobed and folded (Figs. 2c, 3c, and 4c) (Devall 1992; Bach 1998).

Vernacular names: Japanese morning glory, ivy morning glory Botanical name: *I. nil* Stems: slender wine, cylindrical or angular shaped, covered with hairs, 2 m – 5 m in length. Leaves: simple, alternately arranged, 3-lobed, ovate to sub-orbicular shaped, entire margin, 4 cm – 15 cm in length, 4.5 cm – 14 cm in width. Inflorescence: solitary or cymes, sub-equal funnel-shaped, glabrous sepals, corolla, globular stigma, slender style and a superior ovary with 2 – 5 cells (Fig. 1d). Flowers: blue or pink with whitish tubes, funnel-form, 5 cm – 6 cm in length. Fruits: ovoid to a globose shaped, glabrous capsule. Seeds: black or brown, puberulous, ovoid-trigonous shaped, 5 mm - 6 mm in length. Root: taproot system. Seedlings: bi-lobed cotyledons, and cordate base (Figs. 2d, 3d, and 4d) (Der Marderosian et al. 1964; Kajita and Nishino 2009).

Morphological key for selected Ipomoea species

A key to identify the most abundant species within the genus *Ipomoea* in Sri Lanka is given below.

Tuberous root system; tuberous roots-purple to brown skin color, round or longish shape, placed closer to main root, pulp cream to white. *I. batatas*

1 Roots tap root system; I. aquatica, I. nil and I. pes-caprae

2 Flowers blue; pink with whitish tubes, funnel-form, 5 cm – 6 cm in length. *I. nil*2 Flowers pink; reddish; purple or violet, large, trumpet shaped, 3 cm – 5 cm in length. *I. aquatica, I. pes-caprae*

3 Leaves simple; thick and robust, alternate leaf arrangement, variable in shape, lobed margin, 3 cm - 14 cm in length, 2.5 cm - 12 cm wide. *I. pes-caprae*3 Leaves simple; spirally arranged, sagittate to lanceolate, margins are entire, toothed or lobed, length vary from 5 cm - 15 cm, width varies from 5 cm - 15 cm. *I. aquatica*



Figure 1: The morphological features of the selected *Ipomoea* species. A: *I. batatas*, B: *I. aquatica*, C: *I. pes-caprae*, D: *I. nil*. 1: Line diagram of the top view of flower, 2: Top view of flower, 3: Line diagram of the mature leaf, 4: Mature leaf, 5,6,7: The line diagrams of the stages of fruit development. Scale bar represents 1 cm.



Figure 2: Line diagrams of the *Ipomoea* species in their natural habitats. A: *I. batatas*, B: *I. aquatica*, C: *I. pes-caprae*, D: *I. nil*. Scale bar represents 1 cm.

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Figure 3: The morphology of the *Ipomoea* species in their natural habitats. A: *I. batatas*, B: *I. aquatica*, C: *I. pes-caprae*, D: *I. nil*. Scale bar represents 1 cm.



Figure 4: The selected Ipomoea species in their natural habitats. A: I. batatas, B: I. aquatica, C: I. pes-caprae, D: I. nil. Scale bar represents 1 cm.

Species delimits and phylogenetic relationships: The GTR+I+G model resulted in the best representation of the substitution schemes in both datasets for all three model evaluation criteria. Both NJ trees constructed for rbcL and ITS datasets had almost similar topologies. Particularly, both trees retained the main phylogenetic relationships between each *Ipomoea* spp. However, the tree constructed for the *rbcL* dataset had a low resolution at the nodes near the operational taxonomic units (Fig. 5). Especially the clade containing I. batatas, I. triloba and I. lacunose was not

separated in *rbcL* phylogeny. Moreover, the *rbcL* phylogeny had low node support at many branches showing the low resolvability of the *rbcL* marker. Contrastingly the *ITS* phylogeny was well separated with higher node support, validating the phylogenetic relationships (Fig. 6). *I. pes-caprae* was clade sister to *I. aquatica* in both phylogenies. This clade was well supported in *rbcL* (bs = 76) and *ITS* (bs = 100). *I. pes-caprae* and *I. aquatica* had 1% and 5% mean uncorrected pairwise genetic distance for *rbcL* and *ITS* markers separately.



Figure 5: The NJ tree constructed for the marker *rbcL* showing the phylogenetic relationships between *lpomoea* spp. The black dots indicate the nodes that have bootstrap values over 70. The scale bar represents the uncorrected pairwise genetic distance.



Figure 6: The NJ tree constructed for the marker *ITS* showing the phylogenetic relationships between *Ipomoea* spp. The black dots indicate the nodes that have bootstrap values over 70. The scale bar represents the uncorrected pairwise genetic distance.

Haplotype analysis

For *ITS and rbcL* markers, all four *Ipomoea* spp.; *I. aquatica, I. batatas, I. nil,* and *I. pes-caprae* shared unique haplotypes (Figs. 7 and 8). The *ITS* region of the four *Ipomoea* species contains a high degree of SNPs in comparison to the *rbcL* region. A large INDEL of 24 nucleotides for *ITS* marker is present in *I. batatas* and *I. nil*, which can be helpful to distinguish *I. batatas* and *I. nil* form others. Whereas 14 SNPs can in the *ITS* region can be efficiently used to distinguish all four *Ipomoea* spp. from each other.



Figure 7: The *rbcL* haplotypic polymorphism for the Ipomoea spp. assessed in the present study. There were 9 SNPs/indels detected among four species. The sequence alignment is shown with the base positions of the PCR products of *rbcL* shown in the top. The UPGMA tree is placed in parallel to the sequence alignment to depict the interspecies variation.

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Figure 8: The *ITS* haplotypic polymorphism for the *Ipomoea* spp. assessed in the present study. There were 129 SNPs/indels detected among four species. The sequence alignment is shown with the base positions of the PCR products of *ITS* shown in the top. The UPGMA tree is placed in parallel to the sequence alignment to depict the interspecies variation.

4. Discussion

The identification of *Ipomoea* species based on morphological analysis is somewhat challenging in scientific assessments. Many species share common features so that often, they can be misidentified and wrongly classified (Wilkin 1999; Taia 2005). However, some of the morphological characteristics are highly distinct in the four species studied (Figs. 1, 2, 3, and 4). Hence, for the general use the morphological key presented in this paper could be particularly useful. Further studies are needed to establish a comprehensive key for all the species given in Table 1.

The phylogenetic analysis revealed much information about the relatedness of these species. According to the results, the *rbcL* marker is capable of delimiting *I. nil, I. aquatica*, and I. pes-caprae. I. aquatica is clustered sister to *I. pes-caprae* indicating that there was a close evolutionary similarity between the two species. This similarity further implies that the important genes could be transferred between I. aquatica and I. pes-caprae without much of a difficulty. However, *rbcL* marker cannot delimit *I. batatas* species along with *I. triloba* and I. lacunosa. Moreover, the rbcL marker makes a crown group which cannot be further delimited (Figs. 5 and 7). On the other hand, the ITS marker polymorphism can delimit I. nil, I. aquatica, and I. pes-caprae as in rbcL based tree. Moreover, it can discriminate against the crown group I. triloba, I. batatas, and I. lacunosa into individual species. According to ITS polymorphism, I. batatas is clustered as a sister group to I. triloba (Figs. 6 and 8). Due to the

greater similarity among the members in *Ipomoea* genus, morphology-based identification is less accurate on certain occasions. Hence, the utilization of the DNA barcoding markers such as *ITS*, and *rbcL*, enhances the accuracy of species identification than morphology-based classical methods (Thorne 1992).

The most straightforward and powerful tool of the species differentiation is haplotype identification (Liu et al. 2008). According to the haplotype analysis, it is evident that all four Ipomoea species studied could be identified easily by using either *rbcL* or *ITS* barcoding markers. The *rbcL* haplotype contains only nine SNPs, while *ITS* haplotype is consisting of the 129 variations along with the indel. The haplotype analysis results obtained from 14 SNPs in the ITS regions can be used to distinguish all the four species separately (Figs. 7 and 8). Moreover, all the samples of the same species that are collected from different locations do not show any variation among their DNA sequences. This finding suggests that all the *Ipomoea* species within Sri Lanka share the same genetic architecture, although some of them are shown different morphologies. These variations may be due to phenotypic plasticity as a response to various geographical and climatic changes (Oostra et al. 2018). Therefore, this method of identification is crucial because these selected four species have a significant agricultural, economic, and ecological value compared to the other members of the Ipomoea genus.

Tuber crops and leafy vegetable production in the world play a significant role in fighting against global hunger (Scott and Suarez 1992). Sweet potato is considered as the seventhlargest food crop grown in warm temperate, tropical, and sub-tropical regions around the world. Even though it is consumed in many south Asian countries, the commercial production of these crops remains at a meager rate (Tortoe et al. 2010; Ezin et al. 2018). Moreover, *I. aquatica* also holds a high degree of nutritional and medicinal value. It is considered as a leafy vegetable and consumed in many parts of the country. But no commercial cultivation can be seen in Sri Lanka. Therefore *I. batatas* and *I. aquatica* are classified as under-utilized crop plants in Sri Lanka despite their uses in diverse fields (Arachchi and Wijerathne 2007). Many far eastern and western countries have used I. nil (morning glory) as an ornamental plant (Shibuya 2012). However, in Sri Lanka, the growers are not aware of its ornamental value, so that the commercial cultivation is less common. The plant can only be seen in unused or abandoned lands. This plant is also highly invasive; hence proper control measures are needed to be taken (Hou et al. 2015). *I. pes-caprae* is widely found in the coastal line as a natural barrier against sea erosion. Its salttolerant property is highly valuable. It thrives through high salinity by expressing genes responsible for salt tolerance (Zhang et al. 2018) via biochemical tolerance mechanism related to osmotic stress and water deficiency. I. pes-caprae has a higher growth rate and grows rapidly into large beds covering the

entire land area, which is ideal for preventing soil erosion.

However, considering the high range of abundance as well as the preference of the consumers. farmers could enhance the production of *I. batatas* because the sweet potatoes which are rich in carotenoids, which improvise the vitamin A component in children, especially in developing countries (van Jaarsveld et al. 2005). Also, it contains a lot of dietary fibre, vitamins, and minerals. Moreover, these crops provide supplementary food in rural areas (Burri 2011), whereas *I. nil* could be grown commercially to use as an ornamental plant. Moreover, any breeding attempt could be planned to introduce the genes responsible for salt-tolerance in *I. pes-caprae* into *I. batatas.* The activity and expression of ion channels responsible for this property are relatively higher in *I. pes-caprae* compared to other species in the *Ipomoea* genus (Venkatesan and Chellappan 1999). The salt tolerance ability could be further investigated using different marker alleles. Thereby, the identified genes could be used in marker-assisted breeding programs for the generation of novel and improved Ipomoea varieties.

5. Conclusions

The genus *Ipomoea* of family Convolvulaceae is one of the most diverse plant genera in the world. There are about 13 *Ipomoea* spp. documented in Sri Lanka. In an attempt to morpho genetically characterize the genus Ipomoea, we assessed four important members *I. batatas, I. aquatica, I. nil,* and *I. pes-caprae. I.* *batatas* and *I. aquatica* based on the food, medicinal, agricultural, and ecological values. Morphologically tuber bearing ability, flower color, and leaf shape can be used to delimit the selected species. Furthermore, out of the standard plant DNA barcoding markers *ITS* and *rbcL*, the sequence polymorphism in *ITS* can be used to define the species delimits in comparison to the world-wide *Ipomoea* germplasm.

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