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STUDY OF THE GENETIC DIVERSITY AND CONSERVATION OF DENDROBIUM SPECIES

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Abstract

Genetic diversity, which shows potential of evolution of a species is an important parameter in the proper management and conservation of the species. Therefore, the preservation of the genetic variation is necessary for carrying out the species conservation and choosing and breeding different varieties of new plants which are appropriate for a variety of environment conditions. The dendrobium is one of the biggest groups in the family of the Orchidaceae consisting nearly 1500 species all around the world and it is mostly found in the equatorial and surrounding areas of Asia, Europe and Australia and the surrounding islands of Oceania. In the last few years, different types of molecular methods such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), simple sequence repeat (SSR), and amplified fragment length polymorphism (AFLP) are employed to study the genetic diversity and structure of endangered plants which are within species and among species, allowing the researchers to find the reasons behind the dangers and also to find possible conservation strategies. Tissue culture, gives us a method by which we can produce a huge amount of genetically similar plants, healthy and physiologically superior quality plantlets in a short amount of time. In the production of the plants by this method, there is a very high amount of survival percentage, which is accompanied by a good quality of acclimatized plantlets, which are in great demand in commercial levels and orchid production by the process of micropropagation.

Keywords: genetic diversity, orchidaceae, restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), simple sequence repeat (SSR), amplified fragment length polymorphism (AFLP), micropropagation

Introduction

Genetic diversity is considered as a key of biological diversity, and it shows the ability, a given species can undergo so as to adjust to the surroundings and the ability of the species to survive for the long-term and undergo evolution as the changes occurs in the environment constantly (Tripathi et al., 2012;Chen et al., 2013). Normally, the population mean genetic diversity, mean fitness, and the size of the population are related to each other positively (Rao and Hodgkin, 2002). But, orchids are known to show a distinct nature in relation with these characteristics. For instance, under normal conditions, a rare and endangered plants normally shows little amount of genetic diversity (Swensen et al., 1995), however some of the rare orchids such as *D. nobile* (Bhattacharyya et al., 2013), *D. officinale* (Ding et al., 2008; Li et al., 2008), and *Calanthe tsoongiana* T. Tang et F.T. Wang (Qian et al., 2013) shows higher amount of genetic diversity. Generally, a common species shows high genetic diversity (Yu et al., 2011).

The Orchidaceae family constitutes about 10% of all flower plants, it contains a big reserve of 25,000 species (Dressler, 1993), and so the biologists and the people are very interested in these plants (Cozzolino and Widmer, 2005). Unfortunately, many of these species which possess great conservation and economic value are threatened to extinction because of the excessive exploitation, and therefore proper study and conservation of these species are very. The genetic diversity and phylogenetic study of Orchidaceae are directly connected to the effective study and proper use of the available resources and also more important to the production of improved-quality new varieties and therefore growth of the ornamental industry. Morphological and anatomical analysis are normally used to study of the relationship among orchid species. However, these methods are often afflicted by plant variability and growth habitats (Morris et al., 1996; Stern, 1997a,b; Stern and Whitten, 1999). In the last few years, a quick improvement in the biotechnology field at the molecular level has equipped modern plant taxonomists with important tools to trace out accurate evolutionary history Orchidaceae (Cozzolino and Widmer, 2005; Hsiao et al., 2011). In the last few years, the fast improvement of biotechnology at the molecular level has provided the plant taxonomists with important resources to study the precise evolutionary trends of the Orchidaceae (Cozzolino and Widmer, 2005; Hsiao et al., 2011).

Microsatellites also known as simple sequence repeats are short, DNA tandem repeats (2–6 bp motifs), and they are mostly dinucleotide or trinucleotide repeats spread all over the plant genomes. Microsatellite markers are multiple allelic, they are codominant, which are highly reproducible and polymorphic. They are known to be used in a large amount of fields, which includes identification of the individual, research of the genetic diversity, structure of population and mapping of genome (Riaz et al., 2004; Song et al., 2004; This et al., 2004; Silfverberg et al., 2006; Gu et al., 2007; Ma et al., 2009; Zhang et al., 2009;). In Dendrobium genus, microsatellite markers are developed in the species Dendrobium officinale and D. fimbriatum (Gu et al., 2007; Fan et al., 2009; Xie et al., 2010). But, there are no materials available in relation to the isolation and growth of microsatellite markers for D. loddigesii.

Genetic diversity

Genetic diversity, which shows potential of evolution of a species is an important parameter in the proper management and conservation of the species. Therefore, the preservation of the genetic variation is necessary for carrying out the species conservation programs (Avise and Hamrick, 1996) and choosing and breeding different varieties of new plants which are appropriate for a variety of environment conditions (Rice and Emery, 2003). The Dendrobium is one of the biggest groups in the family of the Orchidaceae consisting nearly 1500 species all around the world and it is mostly found in the tropical and subtropical areas of Asia, Europe and Australia (Burke et al., 2008). The Dendrobium species can produce pollen and dust-like seeds which can travel a very long distance by various pollinators and the winds, and as a result is generally believed to help the regular gene flow among the populations (Arditti and Ghani, 2000a,b). In China, the genus Dendrobium comprised of 74 species and two varieties (Tsi, 1999), and about 50 species are used as traditional medicines for hundreds of years because of their pharmacological properties, which includes nourishing yin, purifying the "evilheat,", improving immune system, lowering blood sugar levels, checking cancer, and elongating life (Bao et al., 2001; Bulpitt etal., 2007). For example, "Tongpi Fengdou," a popular traditional Chinese tonic medicine, is prepared from the stems of Dendrobium moniliforme (Linnaeus) Swartz (Hu, 1970; Zhang et al., 2011). Because of the large amount of uses of the flower in horticulture and traditional medicine, all Dendrobium species are classified as critically endangered species in China, on the other hand the information of the genetic diversity of the Dendrobium genus is very little and the measures taken to conserve are limited. Until now, the genetic diversity has been studied for conservation purposes in a few Dendrobium species, such as Dendrobium officinale Kimura et Migo (Ding et al., 2008, 2009; Li et al., 2008; Hou et al., 2012), Dendrobium loddigesii Rolfe (Cai et al., 2011, 2012), and Dendrobium nobile Lindley(Bhattacharyya et al., 2013); but the study has not been done not yet in D. moniliforme, a popular traditional Chinese medicinal plant.

Because of the habitat loss, overexploitation, pollution, and climate change, a large number of species has become extinct in the last few decades (Frankham et al., 2014). The conservation genetics studies rare and endangered species which has important genetic resources and they have become very important and extensive (Al-Qurainy et al., 2013). An important reason for the conservation of threatened and endangered species is to preserve the genetic diversity of these species, an important factor which is crucial for their adaptation to changing environments, survive long-term, and evolution (Avise and Hamrick, 1996; Swarts et al., 2009; Munoz et al., 2010; Frankham, 2012). Therefore, the study of the genetic diversity in endangered species is very important for building an effective and efficient conservation ways (Geet al., 1998; Gale et al., 2010). For example, by studying the population genetics of the endangered plant *Narcissus pseudonarcissus L*., Colling et al. (2010) suggested that many of its populations in the different regions should be preserved to save the overall genetic variation. Chen et al. (2013) established that the current genetic content of the natural populations of *Dipsacus chinensis* (Miq.)Maxim was strongly affected by harvesting and habitat fragmentation. These studies gave us useful knowledge for protecting critically endangered species.

Molecular Markers

The research instruments used by the plant taxonomists to study the precise evolutionary trends of the Orchidaceae are biochemical marker isozymes, plastid and nuclear sequences of ITS, matK, rbcL, psbA-trnH (Cameronet al., 1999; Chemisquy and Morrone, 2012; Cisternas et al., 2012;Górniak et al., 2010; Lau et al., 2001; Sharma et al., 2012; Xianget al., 2013), DNA markers such as RFLP are also used (restriction fragment length polymorphism), RAPD (random amplified polymorphic DNA), ISSR (inter-simple sequence repeat) and AFLP(amplified fragment length polymorphism) markers. Microsatellites, which are also called as simple sequence repeats (SSRs), are repetitive DNA sequences with repeat motifs of 1–6 nucleotides at a given locus. Although other DNA markers are sensitive to PCR amplification environments, or requires a large amount of labor with difficult procedures, SSR markers are multiallelic, co-dominantly inherited, found commonly, spread around the genome, and they are simpleand even automatically scored (Powell et al., 1996). SSR genotyping are commonly used for genetic identification and to assess the parentage (Buteler et al., 2002; Malysheva et al., 2003), study of the genetic diversity and phylogenetic studies (McCouch et al., 2000; Zhu et al., 2000), building of the genetic maps (Temnykhet al., 2000), etc.. Therefore, when compared to the other ways, competitive genomic mining of SSR markers between the closely related species is considered as one of the most efficient and useful way for the discovery of novel DNA marker. Sequence data that we obtain from several crop plant species that are studied shows that enough homology are seen among genomes of two or more closely related genera/species. Hence, the primer pairs obtained from a species can be used to sense the SSRs in similar species and sometimes among other genera which are of the same family (Kalia et al., 2010).

On the contrary, if little amount of SSR marker resources is available, it delays the study of genetics in the Orchidaceae family. Until now, a proper study on the detailed phylogenetic relationships of the orchids in China at molecular level is not available. A large amount of SSR markers are found in several orchid genus such as Phalaenop-sis (Hsu et al., 2011), Vanda (Teh et al., 2011), Doritis (Jantasuriyaratet al., 2012), and Cymbidium (Huang et al., 2010), and the cross-taxon transferability of SSR markers are commonly seen in the genus Dendrobium (Gu et al., 2007; Lu et al., 2012a,b, 2013; Xie et al., 2010). As Dendrobium is one of the biggest genera in the Orchidaceae family(Baker and Baker, 1996), exchange of the Dendrobium SSR markers to the other Orchidaceae plants are possible with a large potential in both basic and applied orchid studies.

Out of all the molecular tools, RFLP needs a large amounts of DNA, however it produces little information; RAPD results are most of the times very hard to reproduce; and SSRs results are known to produce medium amount of results both in abundance and reproducibility (Garcia et al., 2004;Agarwal et al., 2008). However, AFLP is a highly powerful and consistent technique that can be used for finding the polymorphisms and study of genetic diversity of species, especially when used together with fluorescent DNA sequencing equipment (Huangand Sun, 1999; Bonin et al., 2007). Therefore, AFLP markers are often used to find the genetic diversity of rare and endangered plant species and they are used to design effective ways for protection and conservation (Damasceno et al., 2011; Vanden-Broeck et al., 2011).

Sequence-related amplified polymorphism (SRAP), is a recent molecular marker first showed by Li and Quiros (2001), which targets to amplifying of open reading frames (ORFs). SRAP are known to have many advantages such as simplicity, reproducibility, high throughput rate, easy to isolate the bands for sequencing and it aims at open reading frames (ORFs). SRAP are used often in molecular identification, construction of the genetic linkage map, gene tagging, genomic and cDNA fingerprinting, analysis of genetic diversity and comparative genetics of different species (Wang et al., 2009a,b; Li and Quiros, 2001; Ferriol et al., 2003; Budak et al., 2004; Ding et al., 2008; Li et al., 2010).

Recently, many types of new marker techniques are developed along with the fast growing genomic research (Gupta and Rustgi, 2004). Because of the tremendous growth in public biological databases, the growth of the functional markers which are found in or near the candidate genes are very easy (Andersen and Lubberstedt, 2003). Starting a way, away from random DNA markers towards gene-targeted markers, a novel marker system known as Start Codon Targeted (SCoT) Polymorphism (Collard and Mackill, 2009) was built which is based on the short conserved region flanking, the ATG start codon in plant genes. SCoT markers are primarily reproducible, and is known that the primer length and annealing temperature are not the only factors used to determine the reproducibility. They are major markers like random amplified polymorphic DNA (RAPD) and inter simple sequence repeats (ISSR) and can be used for genetic analysis, quantitative trait loci (QTL) mapping and bulk segregation analysis (Collard and Mackill, 2009). The different uses of these markers such as in the diversity analysis and diagnostic fingerprinting are successfully showed in peanut, potato and grape (Gorji et al., 2011; Guo et al., 2012; Xiong et al., 2011).

Here, we make three tables on genetic diversity of dendrobium species using various marker genes.

Species	DNA	Development	Potential	Referenc
	Markers	Methods	Applications	es
Dendrobium chrysotoxum Lindl.	ISSR Markers, SCoT markers	using 20 different inter- simple sequence repeats (ISSR) and 9 start codon targeted (SCoT)	different conservation strategies suited for effectively managing the endangered orchid	Leimapokpa m Tikendra et al. (2021)
44 species of 15 Orchidaceae genera	simple sequence repeat (SSR) markers	SSR markerswere applied to test their transferability and polymorphism	microsatellite markers enrich the available resource ofmolecular markers, which would facilitate further evolution and genetic diversity studies, germplasmappraisal and molecular breeding of Orchidaceae species	Jie Yu Kang et al. (2015)
Dendrobium moniliforme	fluorescent amplified fragment length polymorphism (AFLP)	Dendrobium moniliforme (Orchidaceae) from different regions of Asia were collected to investigate itsgenetic diversity, using fluorescent amplified fragment length polymorphism (AFLP)	isolation by distance (IBD) did exist in D. moniliforme and some useful conservation strategies were proposed for theeffective and sustainable exploitation of D. moniliforme.	Meirong Ye et al. (2015)
Dendrobium loddigesii Rolfe	simple sequence repeats (SSR)	12 new microsatellite markers of D. loddigesii were developed	will contribute to research on individual identification, genetic diversity, population structure, genome mapping and conservation biology of D. loddigesii.	Xiaoyan Cai et al. (2012)

Table 1

	1			
Dendrobium	sequence-	SRAP markers were	Recommendations for	Xiaoyan Cai
loddigesii	related	applied to assess the	conservation of the	et al. (2011)
Rolfe	amplified	level and pattern of	endangered species	
	polymorphism	genetic diversity in	resources are	
	(SRAP)	seven	proposed.	
	markers	populations of D.		
		loddigesii	•	D 11
Dendrobium	Start Codon	sixty individuals	it can	Paromik
nobile Lindl.	Targeted	comprising	be seen as a	Bhattacharyy
	(SCoT) marker	of six natural	preliminary point for	a et al. (2012)
		populations were investigated for the	future research on the population and	(2013)
		existing natural genetic	evolutionary genetics	
		diversity.	of this	
		diversity.	endangered orchid	
			species of medicinal	
			importance	
31	inter-simple	inter-simple sequence	demonstrated the	Hui-Zhong
Dendrobium	sequence	repeats (ISSRs) to	utility of ISSR marker	Wang et al.
species	repeats (ISSRs)	evaluate genetic	for	(2009)
species		diversity and	species diagnosis and	(200))
		phylogenetic	genetic diversity study	
		relationship among 31	of the genus	
		Dendrobium species	Dendrobium	
Dendrobium	AFLP markers	phenolics, flavonoids	can be utilized for	Paromik
thyrsiflorum		and alkaloid	conservation strategy	Bhattacharyy
		contents alongwith	formulation of this	a et al.
		antioxidant activity	important medicinal	(2017)
		measured by 1, 1-	orchid with high	2
		diphenyl-2-	antioxidant	
		picrylhydrazyl (DPPH)	activity	
		and ferric reducing		
		antioxidant power		
		(FRAP) assays		
		revealed		
Dendrobium	single	investigated	the SNPs and KASP	Jaihyunk
plants	nucleotide	genetic diversity and	assay sets are an	Ryu et al.
	polymorphism	variations among 7	economically efficient	(2018)
	(SNP) markers	Dendrobium mutant	tool for mutant	
		genotypes and 11	screening and for	
		commercial	selection of elite	
		Dendrobium cultivars	genotypes in	
		using single nucleotide	Dendrobium breeding	
		polymorphism (SNP) markers	programs.	
D. catenatum	simple sequence		valuable for constin	T.M. Zhao et
D. calenalum	simple sequence repeats (SSR)	simple sequence repeats (SSR) were	valuable for genetic studies and molecular	al. (2019)
	repeats (SSK)	identified from 3814	breeding in	al. (2017)
		genomic scaffolds in D.	Dendrobium	
		catenatum		
Dendrobium	SCoT and	start codon targeted	SCoT and	Shangguo
species.	TRAP markers	(SCoT) and target	TRAPmarkers are	Feng et al.
Species.		region amplification	informative	(2015)
		region ampinication	intornative	(2010)

	1		1 1 1	
		polymorphism	and can be used to	
		(TRAP), were used for	evaluate genetic	
		genetic relationship	relationships between	
		analysis of 36	Dendrobium species	
		Dendrobium species		
Dendrobium	EST-SSR	generate new EST-SSR	would facilitate further	Jiang-Jie Lu
nobile Lindl.	markers	markers and to evaluate	evolution and	et al.(2013)
		their potential	genetic diversity	
		for cross-species	studies, germplasm	
		utilization in phylogeny	appraisal, genetic	
		study of genus	mapping, and	
		Dendrobium	molecular breeding of	
			D. nobile and	
			other congeneric	
			species.	
Dendrobium	polymorphic	polymorphism of the	useful tool for the	Wen Xu et al
moniliforme	chloroplast	nine chloroplast	study of genetic	(2011)
(L.) Sw. and	microsatellite	microsatellite primers	diversity, population	
Dendrobium	primers	was tested across	genetic structure,	
loddigesii	-	Dendrobium	evolution of D.	
Rolfe		moniliforme	officinale and	
		(L.) Sw. and	establishment of	
		Dendrobium loddigesii	effective conservation	
		Rolfe	strategies	
Dendrobium	ISSR and	genetic and chemical	the cumulative marker	Paromik
nobile	DAMD markers	diversity existing	approach could be	Bhattacharyy
		amongst 6 natural	the best suited for	a et al.
		populations of D.	assessing the genetic	(2015)
		nobile were assessed	relationships with high	
		using molecular	accuracy amongst	
		markers	distinct D. nobile	
			accessions	
Dendrobium	Amplified	analyses of Amplified	contributes to our	Lalita
speciosum	Fragment	Fragment Length	understanding of the	Simpson et
complex	Length	Polymorphism (AFLP)	factors shaping	al. (2017)
(Orchidaceae	Polymorphism	profiles for D.	biodiversity patterns in	
	(AFLP)	speciosum sampled	Australia's mesic	
'	()	from across its	biome.	
		distribution showed		
		that the complex		
		consists of two highly		
		supported main groups		
Dendrobium	single	Plastomewide	we recommend using	Ludan Li et
species of	nucleotide	comparison showed the	large single-copy	al. (2020)
"Fengdou"	polymorphisms	co-occurrence of single	(LSC)for accurate	
(DSFs)	(SNPs) and	nucleotide	authentication of DSFs	
	insertions/	polymorphisms (SNPs)		
	deletions	and insertions/		
	(indels)	deletions (indels),		
		which can be explained		
		by both the repeat-		
		associated and indel-		
		associated mutation		

hypotheses.

Species	DNA Markers	Development Methods	Potential Applications	Reference s
Dendrobium officinale Kimur a et Migo (D. officinale)	start codon targeted (SCoT) polymorphis m molecular markers	Using 13 selected SCoT primers, 181 bands were generated, 157 (86.86%) of which were polymorphic	provides guidelines for D. officinale 'Ruishen No.2' identification, for the breeding of D. officinale plants with a high content of active ingredients, and for industrial production	Qingguo Liet al. (2018)
Dendrobium	inter-simple	Genetic diversity was	a novel	G. Ding
officinale	sequence	examined within and	evolutionary unit	et al.
	repeat	among nine natural	should also be paid	(2009)
	(ISSR) and	populations using inter-	more attention to	
	random	simple sequence repeat	during D.	
	amplifi <mark>ed</mark>	(ISSR) and random	officinale conservati	1
	polymorphic	amplified polymorphic	on practi <mark>ce</mark>	
	(RAPD)	(RAPD)		
Dendrobium	amplified	Data of 12 populations	Keeping a stable	Xuexia Li
officinale	fragment	were used to assess its	environment is	et al
	length	genetic diversity and	critical for the in situ	(2007)
	polymorphis	population structure,	conservation and	
	m (AFLP)	employing the method of	management of this	
		amplified fragment length	rare and endangered	
		polymorphism (AFLP)	plant, and for ex situ	
			conservation it is	
			important to design	
			an integrated	
Dendrobium	15	15 polymorphic	germplasm bank The 15 new	Beiwei
officinale	polymorphic	trinucleotide	microsatellite loci	Hou et al.
officinate	trinucleotide	microsatellite loci of D.	may be used as a	(2012)
	microsatellit	officinale were developed	powerful tool for	(2012)
	e loci	to examine the genetic	further evaluation	
		diversity and structure of	and conservation of	
		three D.	the genetic diversity	
		officinale germplasm	of D.	
		collections	officinale germplas	
			m resources	
Dendrobium	sequence-	84 individuals from nine	In situ conservation	Ge Ding
officinale	related	wild populations of D.	is the first advocated	et al.
	amplified	officinale were analyzed	and ex situ should be	(2009)
	polymorphis	using the method of	proposed at the same	

Table 2

	m (SRAP)	sequence-related amplified polymorphism	time to protect the endangered plant	
			and to preserve germplasm resources	
Dendrobium nobile	SSR primers	Seven pairs of genomic SSR primers were newly designed, and two pairs were chosen from the EST-SSRs	seven new microsatellite loci may be informative for further evaluation and conservation of the genetic diversity of D. nobile	Wenjin Yan et al. (2015)
Dendrobium nobile Lindl.	randomly amplified	The genetic structure of D. nobile from	The present findings are useful outcomes	Paromik Bhattacha
nobile Linai.	polymorphic DNA	Northeast India was investigated using	for germplasm conservation and	ryya et al. (2014)
	(RAPD)	randomly amplified polymorphic DNA (RAPD)	formulation of new breeding strategies for this extremely	
			important medicinal orchid species	
Dendrobium pla	sequence-	sequence-related	the SRAP marker	Shang-
nts	related	amplified polymorphism	system is	Guo Feng
	amplifi <mark>ed</mark>	(SRAP) markers were	informative and	et al.
	polymo <mark>rphis</mark>	applied to molecular	would facilitate	(2013)
	m (SRAP)	phylogeny analysis and	further application in	
	markers	species identification of 31	germplasm	
		Chinese Dendrobium spe	appraisal, evolution, and genetic diversity	
		cies	studies in the	
			genus Dendrobium	
Dendrobium	75 EST-	81 D.	the D.	Xiankun
officinale K.	SSRs	officinale individuals	officinale germplas	Xie et al.
Kimura et Migo		including wild-collected,	m resources from	(2020)
		market-collected, and two	Jiangxi was	
		germplasm resources	recommended for	
		from Zhejiang and	hybridization in	
		Jiangxi province was	order to develop	
		scanned with 75 EST- SSRs	superior cultivars	
D.	random	genetic linkage maps	provide an important	Shangguo
nobile and D.	amplified	were constructed using	basis for genetic	Feng et
moniliforme	polymorphic	90 F1 progeny	studies and further	al. (2013)
	DNA	individuals derived from	medicinal and	
	(RAPD) and	an interspecific cross	horticultural traits	
	intersimple	between D. nobile and D.	mapping and marker-assisted	
	sequence repeat	moniliforme using RAPD and ISSR	selection	
	(ISSR)		in Dendrobium bree	
			ding programmes	
Dendrobium,	NGS based	Genetic diversity was	signifying that	Subhas
Geodorum, Cy	ddRAD	assessed in the four	selection might have	Chandra

mbidium and Rhynchostylis	sequencing	orchid species using NGS based ddRAD sequencing data	played a role in evolution of these genes in these four	Ray et al. (2016)
Dendrobium nobile	ten novel polymorphic microsatellit e markers	ten novel polymorphic microsatellite markers were isolated by a modified biotin- streptavidin capture method	groups of orchids highly informative for further genetic diversity studies and could be used to evaluate the conservation of D.	Wenjin Yan et al. (2014)
Dendrobium off icinale	13 novel microsatellit e makers	isolated and developed 13 novel microsatellite makers from expressed sequence tag sequences of endangered Chinese endemic herb Dendrobium officina le	nobile efficiently potential for application in germplasm appraisal, genetic diversity study, genetic mapping, and molecular breeding in D. officinale and other	Jiang-Jie Lu et al. (2012)
Dendrobium sp ecies	rDNA ITS region sequence analysis	the rDNA ITS region sequence analysis was developed for rapid and accurate identification of	congeneric species can be used as an effective tool for molecular identification and	Hongmei Liu et al. (2019)
		thirteen wild and cultivated Dendrobium sp ecies belonging to two sections Formosae and C hrysotoxae	classification, as well as the reconstruction of the phylogeny of wild and cultivated Dendrobi um species belonging to different sections	
36 Dendrobium species	sequence analysis of the internal transcribed spacer (ITS) region of ribosomal DNA	sequences of the complete ITS region obtained from the 36 Dendrobium species and 2 outgroup species by using PCR amplification and direct DNA sequencing	phylogenetic relationships revealed by ITS DNA analysis partially supported previously published morphological data	Z-Q Yuan et al. (2009)
Dendrobium officinale	allele- specific PCR primers based on SNPs	Two pairs of allele- specific PCR primers based on SNPs were designed to authenticate two genuine populations	methods based on SNPs of rDNA ITS region and AS-PCR are simple, practical and effective for genuine germplasm authentication of D. officinale during the process of GAP and hygienic food quality control	Ge Ding et al. (2008)

Dendrobium officinale	simple sequence repeats (SSRs)	8527 potential genic simple sequence repeats (SSRs) were identified from 7332 (18.15%) unigene sequences, of which 1023 (2.53%) unigenes contained more than one SSR	these genic SSR markers are valuable tools not only for germplasm conservation of this species but also for phylogenetic studies of Dendrobium	Meng Xu et al. (2017)
Limonium speci es (Limonium sinense, L. bicolor, L. aureum and L. wrightii)	single nucleotide polymorphis m (SNP), amplification refractory mutation system (ARMS), Inter simple sequence repeat (ISSR)	single nucleotide polymorphism (SNP) and amplification refractory mutation system (ARMS) have been applied to authenticate Limonium sp ecies, Inter simple sequence repeat (ISSR) was used to assess genetic diversity and population structure of L. sinense and a high level of genetic diversity was detected	SNP and ARMS could be used to authenticate not only Limonium spec ies but related herbs on rDNA internal transcribed spacer region	G. Ding et al. (2013)
Dendrobium so nia-28 Phytophthora palmivora	protocorm- like bodies (PLBs) rep-PCR (BOX, ERIC, REP and M13)	selection of F. proliferatum-tolerant protocorm-like bodies (PLBs) was carried out by assessing the effects of differing concentrations of fusaric acid (FA) genetic diversity among 81 isolates of P. palmivora from various host plants and	showing different banding patterns for each FA concentration and specific bands for selected and control plants possible explanations for the results and suggested strategies	Rahaleh Dehgahi et al. (2015) Masanto et al. (2019)
	and microsatellit e markers	geographical regions in Indonesia and Japan was evaluated using rep-PCR (BOX, ERIC, REP and M13) and microsatellite markers	for disease management are discussed	
Habenaria edgeworthii Ho ok. f. ex Collett	Inter-simple sequence repeat (ISSR)	variations among morphological, phytochemical and molecular markers were assessed	can be useful for breeding programme of the species when no other genetic information, such as linkage maps and quantitative trait loci, is available	Lalit Giri et al. (2016)

Species	DNA Marker types/ Methods used	Development Methods	Potential Applications	Referen ces
Dendrobium moniliforme	DNA (cpDNA) markers (<i>trnC-pet</i> N and <i>trnE-trn</i> T)	One hundred and thirty-five samples were collected from 18 natural populations of <i>D</i> . <i>moniliforme</i> coverin g the entire range of the Sino-Japanese Floristic Region (SJFR) of East Asia	results supported the hypothesis that glacial refugia were maintained on different spatial- temporal scales in the SJFR during the last glacial maximum or earlier cold periods, suggesting that Quaternary refugial isolation promoted allopatric speciation of <i>D. moniliforme</i> in East Asia	Meiron g Ye et al. (2016)
D. officinale	Near-infrared spectroscopy coupled	Near-infrared spectroscopy	the results show that coupling of near-	Yangch ao Wei
	to chemometrics	coupled to chemometrics was used to develop a method to discriminate <i>D</i> .	infrared spectroscopy to chemometric techniques is a valuable tool for	et al. (2014)
		<i>officinale</i> , fr <mark>om non-</mark> <i>D. officinale</i>	rapid, inexpensive, and non-invasive authentication of <i>D</i> . <i>officinale</i>	
Dendrobium officinale	Infrared and Ultraviolet-Visible Spectroscopies with Data Visualization and Mining	two types of spectra combined with unsupervised and supervised pattern recognition were investigated for authentication of 17 Dendrobium spec ies	the data visualization and mining strategy are effective approaches for original plant authentication of Fengdou materials in the herbal market	Ye Wang et al. (2020)
D. naungmunge nse	used the next- generation sequencing technology and assembled a complete plastid genome	A total of 123 genes were predicted, including 38 tRNA genes, 8 rRNA genes, and 77 protein-coding genes	suggested <i>D</i> . <i>naungmungense</i> to be sister to <i>Dendrobium</i> <i>wardianum</i>	Min- Hua Wang et al. (2019)
<i>Dendrobium</i> <i>hancockii</i> Ro lfe	the first complete chloroplast genome sequence of <i>D. hancockii</i> was reported and characterized	It encodes 106 genes, consisting of 72 unique protein- coding genes, 30 unique tRNA gene, and 4 unique rRNA genes	The phylogenetic analysis indicated that <i>D. hancockii</i> is basal-most species for the sect. <i>Dendrobium</i>	Zhenyu Hou et al. (2019)

Table 3

Dendrobium wattii	The complete chloroplast (cp) genome sequence and the genome features of <i>D. wattii</i> were reported for new data on the phylogeny of <i>Dendrobium</i>	The complete cp genome sequence of <i>D. wattii</i> is 159,366 bp in length, including a large single-copy region (LSC, 87,192 bp), a small single-copy region (SSC, 18,422 bp), and two inverted repeat sequences (IRs, 26,876 bp, each)	suggested that <i>D.</i> <i>wattii</i> be closely related to other species of <i>Dendrobium</i>	Yan- Ping Wang et al. (2020)
Dendrobium pseudotenell um	we report the complete chloroplast (cp) genome sequence and its genome features of <i>D. pseudotenellum</i>	The cp genome encoded 125 genes, including 80 protein- coding genes, 37 tRNAs, and 8 rRNAs	helpful for the phylogeny and conservation of <i>Dendrobium</i>	Quing- Qin Tan et al. (2020)
Dendrobium harveyanum	we report the complete chloroplast (cp) genome sequence and the cp genome features of <i>D</i> . <i>harveyanum</i>	The cp genome encoded 138 genes, of which 120 were unique genes	show that <i>D</i> . <i>harveyanum</i> is closely related to other species in <i>Dendrobium</i>	Zhi- Cong Huang et al. (2019)
Dendrobium strongylanth um	the complete chloroplast genome was constructed from whole-genome Illumina sequencing data	A total of 130 chloroplast genes were successfully annotated, including 84 protein coding genes, 38 tRNA genes, and eight rRNA genes	showed that the chloroplast genome of <i>Dendrobium stron</i> gylanthum is related to that of the <i>Dendrobium offi</i> cinal	Jing Li et al. (2015)
Dendrobium chrysocrepis	we report the complete chloroplast (cp) genome sequence and the cp genome features of <i>D</i> . <i>chrysocrepis</i>	The cp genome encoded 130 genes, of which 115 were unique genes	indicated that <i>D.</i> <i>chrysocrepis</i> was closely related to other species in <i>Dendrobium</i>	Jin Zhang et al. (2010)
Dendrobium wangliangii	the complete chloroplast (cp) genome sequence and the genome features of <i>D</i> . <i>wangliangii</i> were analyzed	The cp genome contains 129 genes, consisting of 124 unique genes (78 protein-coding genes, 38 tRNAs, and 8 rRNAs)	showed that <i>D</i> . <i>wangliangii</i> nested with other <i>Dendrobium</i> s pp. and was closely related to <i>D</i> . <i>ellipsophyllum</i> , <i>D</i> . <i>wattii</i> and <i>D</i> . <i>longicornu</i>	Shi- Cheng Shao et al. (2010)
Dendrobium longicornu L ind	we report the first complete chloroplast genome of <i>D</i> . <i>longicornu</i>	The cp genome encoded 142 genes, of which 110 were unique genes (80	showed that <i>D</i> . <i>longicornu</i> clustered together with <i>D</i> . <i>ellipsophy</i>	Xin-Yi Wu et al. (2019)

D. densiflorum	the first complete chloroplast genome sequence of <i>D</i> . <i>densiflorum</i> was reported and characterized	protein-coding genes, 26 tRNAs and 4 rRNAs) The complete cpDNA of <i>D</i> . <i>densiflorum</i> is a circular molecule of 153,122 bp, which contains 76 protein- coding genes, 30 tRNA genes, and	indicated that the newly sequenced cpDNA of <i>D</i> . <i>densiflorum</i> could be used for the phylogenetic study of <i>Dendrobium</i> speci es	Liu Wei et al. (2020)
Dendrobium nobile	The complete chloroplast (cp) genome sequence of <i>Dendrobium nobile</i> is studied	four rRNA genes 130 unique genes were annotated and they were consisted of 76 protein-coding genes, 30 tRNA genes and 4 rRNA genes	Fourteen genes contained one or two introns are shown	Wenjin Yan et al. (2015)
Dendrobium thyrsiflorum Rchb.f.	the complete chloroplast (cp) genome of <i>D</i> . <i>thyrsiflorum</i> was deciphered by high- throughput sequencing	A total of 126 genes were <i>de</i> <i>novo</i> assembled in this cp genome, including 78 protein genes, 40 tRNA genes and 8 rRNA	provides molecular information for future evolution, genetic and molecular biology studies of <i>Dendrobium</i>	Bin Zhu et al. (2019)
Dendrobium zhenghuoens e	we reported the complete chloroplast genome of <i>D</i> . <i>zhenghuoense</i>	genes The genome contained 130 genes, including 75 protein- coding genes, 38 tRNA genes and 8 rRNA genes	indicated that <i>D</i> . <i>zhenghuoense</i> was the sister to the rest 11 species of <i>Dendrobium</i> teste d	Yuan- Zhen Huang et al. (2019)
Dendrobium officinale	The complete chloroplast sequence of <i>Dendrobium officin</i> <i>ale</i> was reported and characterized	The complete cp DNA contains 83 protein-coding genes, 39 tRNA genes and 8 rRNA genes	Fourteen genes contained one or two introns	Pei Yang et al. (2014)
<i>Dendrobium</i> <i>bellatulum</i> R olfe	we reported the complete chloroplast (cp) genome sequence and the cp genomic features of <i>D</i> . <i>bellatulum</i>	The genome was 152,107 bp long with 129 genes comprising 83 protein-coding genes, 40 tRNA genes, and 6 rRNA genes	indicated that <i>D</i> . <i>bellatulum</i> is clustered with other species in <i>Dendrobium</i>	Yun- Jiao Zhang et al. (2018)
<i>Dendrobium</i> officinale' zhong ke IV hao	we reported and characterized the complete chloroplast (cp) genome sequence of <i>Dendrobium</i> <i>officinale</i> [•] zhong ke	the complete cp DNA contains 89 protein-coding genes, 30 tRNA genes, and 8 rRNA genes	showed that the chloroplast genome of <i>D officinale</i> <i>'zhong ke IV hao'</i> is related to that of the traditional <i>D.officina</i>	Zhimin Zhong (2016)

IV hao', a new variety	le	
from self-cross plants		
of imported		
Sichuan D. officinale		

Tissue Culture

Even though there is a very big demands in the market, propagation of Dendrobium orchids by means of sexual hybridization are not used for commercial purposes as there is not much profit because of the long amount of time in the generation period which normally takes 3 years to produce the seeds of the flowers and also because of the absence of functonal genetic variability (Kuehnle and Sugii, 1992; Yin et al., 2011; Poobathy et al., 2012). The production of the Dendrobium orchids by means of tissue culture propagation by both in-vitro and agricultural cultivation methods are developed for mass production to control this problem. Hence it is a key factor to build an efficient way in preservation of Dendrobium orchids (Kuehnle and Sugii, 1992; Bustam et al., 2013). There are two methods by which the endangered plant species are preserved, in situ conservation method, where the plants are conserved in their natural habitat, and by the method of ex situ conservation, in which the plants are kept in an artificial surrounding (Hirano et al., 2005; Bustam et al., 2013).

Tissue culture is also used as a method to get new *Dendrobium* cultivars (Cardoso, 2012; Teixeira da Silva et al., 2015a) and the process of the production of the *in vitro* environment gives us a chance for producing seedlings obtained by symbiotic method (Teixeira da Silva et al., 2015b) or asymbiotic (Teixeira da Silva et al., 2015c) growing in an aseptic surrounding following the proper instructions (Teixeira da Silva et al., 2016a). The plants that are grown by the method of tissue culture needs a great amount of treatments to harden the plants and also to avoid the plant death after the are brought in the *ex vitro* conditions (Pospišilová et al., 1999; Ziv and Chen, 2008). Plantlets which are grown in *in vitro* are sometimes not able to produce resistance for some small or big microbial pathogens or stresses both biotic and abiotic as a result of the *in vitro* controlled environment, they are recognized by an aseptic conditions with little differnces in the temperature, the high amount of the air humidity, high nutrients available and a little amount of light intensity and carbon dioxide (CO2) (Teixeira da Silva et al., 2015b). The conditions mentioned give a photomixotrophic growth and the requirement of the carbohydrate to be used in the culture medium. After the survival, they are then transferred to greenhouse or the artificial environment, and it greatly affected by physiological and anatomical requirements. There are no studies available that links the responses that are produced by *Dendrobium* as a result of the biotic stresses. Some of the pests that are known to feed on *Dendrobium* plants during acclimatization are slugs, snails, *Dendrobium* beetles, thrips, mealybugs, and many others during acclimatization (MM Hossain, personal observation).

Dendrobium in Traditional Chinese Medicine (TCM)

A huge number of species with its origin in China of Dendrobium genus are known to use as a traditional medicine for the last 2300 years. The different parts of the plants can be used as a very high quality tonic in Traditional Chinese Medicine (TCM). These plants carry different types of medicinal qualities such as maintaining a healthy kidney, lungs, enhance the stomach, maintaining the production of various body fluids.

About 40 species of Dendrobium genus are known to be used in TCM. And the development of the Dendrobium industry can be described by the three main phases. (a) the phase in which the Dendrobium is collected from the wild, (b) the phase of large scale commercial cultivation in an artificial-sheltered environment, (c) the phase in which the cultivation is done in an ecologically-friendly way. Advancement in the field of seed technology helps in improving the quality of the products and the involvement of the farming technology helps in increased production of the Dendrobium in TCM industry. Both methods of cultivation i.e. cultivation in an artificial-sheltered environment and cultivation in an ecologically-friendly environment helps in conserving the dendrobium species. They use the seedlings that are grown from the seeds which are produced by sexual reproduction and clonal propagation based on meristematic are not used.

The development fields of the Dendrobium industry

The advancements in the technology has improved the Dendrobium industry. Technologies such as the mycorrhizal technology and fertilizers by using microorganism eases the production of seed and also helps in germination of the seed. Its survival and the growth rates (Teixeira et al. 2015). Technology such as sowing directly along with symbiotic fungi are known to use ecological cultivation,

and the resulting culture substrates which are mixed along with fungi are known to develop stronger root systems, thicker stems and improve the yield (Xu et al., 2014).

And these methods are low cost and can be easily operated and the technique fully relies on natural conditions from the very beginning i.e. sowing to harvest and there is no need for chemical fertilizer or pesticides (Zhang et al.,2012).

Big improvements are seen in the pharmacological research of the Dendrobium species. Polysaccharides, the substanceThe main substance that we get from the Dendrobium, polysaccharides shows the properties of resistance to oxidization, tumor resistance and increased immunity (Kang et al., 2011). Recently, the polysaccharide of *D. officinale* is known to decrease the blood glucose (Sun et al., 2016). But, a lot research is very much needed to properly know the pharmacologic effect, action mechanism and the extreme effect of the Dendrobium species for medicinal uses.

The relationship between Dendrobium industry and species conservation

The demand for the Dendrobium species is rising rapidly because of its distinct medicinal properties of the medicinal Dendrobium species, and it has caused a big pressure on the wild population (Hinsley et al., 2018). However, to conserve and revive the wild resources to prevent species extinction, and at the same time continue giving the opportunities, especially in regions of low economic development is a very big problem (Ding et al., 2009; Hinsley et al., 2019). It is said that the cultivation of the Dendrobium provides the opportunity to connect both the commercial TCM industry as well as develop the steps for biodiversity conservation, and also to provide the sustainable development of the Dendrobium industry can be achieved in the very nar future.

Conclusion

The main function of the conservation genetics is to study the variation in the genetics and structure of population of the vulnerable and high risk species to obtain the knowledge on genetics critical for developing useful conservation strategies. Maintaining the genetic diversity is very important in making sure of the continued survival of the species and continue to keep the evolutionary potential (Zhang et al., 2005; Wu et al., 2006). Both in-situ and ex-situ conservation methods can be used to conserve the orchids properly. The in-situ conservation way is mostly used for preserving the total gene pool of those particular species in the original habitats for these organisms and they are most useful in preserving the vulnerable and endangered species (Zhao et al., 2017). Habitat conservation is very important as orchids normally have particular habitats that they thrive and also depend a lot on the pollination, and hence these species these species exists together with other organisms like fungi and various pollinating agents and their life cycle cannot be complete without these organisms (Li and Ge, 2006). Habitat destruction and decrease in the population of a species highly increases the chance of extinction. The reason is because of the loss of genetic diversity due to random genetic drift and inbreeding depression (Reed and Frankham, 2003; Li and Ge, 2006). Hence, the main aim of conservation should be immediate preservation of the natural habitats consisting genetically different orchid species which are very sensitive to the destruction of the habitat and exploitation of the germplasm by both humans and animals.

Keeping a high population genetic diversity is very important for the survival as every population is its own distinct gene pool, and destruction of the population may cause irreparable loss of genetic diversity (Pinheiro et al., 2012). We can increase the genetic diversity by transferring the pollen or mature seeds taken from other populations. We can also get genetically stable orchids that are micropropagated obtained from healthy orchid populations can be introduced to enhance genetic diversity and conserve diverse gene pools. In situ conservation plan should be implemented with a prime focus on protecting the core areas with vulnerable populations to preserve and maintain the prevailing genetic diversity. The ex-situ approach of conservation should involve the establishment of germplasm or seed bank for D. chrysotoxum.

Orchid seed collection, plant transfer to different suitable habitats, and micropropagated plants re-introduction to increase population size and genetic heterozygosity level can be some of the crucial works associated with ex situ orchid conservation.

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