Low Genetic Structure in an Epiphytic Orchidaceae (*Oncidium hookeri*) in the Atlantic Rainforest of South-eastern Brazil

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Received: 10 May 2006 Returned for revision: 5 July 2006 Accepted: 7 August 2006 Published electronically: 28 September 2006

- **Background and Aims** *Oncidium hookeri* is a neotropical species of epiphytic Orchidaceae found in the Brazilian Atlantic rainforest at the top of the Mantiqueira Range of mountains. The genetic variation of *O. hookeri* was studied to assess the distribution of genetic variability within and among six populations localized in Atlantic rainforest remnants. Gene flow among populations and the occurrence of recent bottlenecks were investigated in order to infer the degree of isolation of these populations.
- **Methods** Thirteen polymorphic loci were used for allozyme electrophoresis. The data were analysed by means of standard statistical approaches, to estimate gene diversity and the genetic structure of the populations.
- **Key Results** The mean gene diversity and allelic richness were *H* = 0.099 and *A* = 1.75, respectively. *F*-statistics revealed high heterozygote deficiencies in all populations (*F* < 0.43–0.82). Several rare alleles were found in all the populations, and three populations presented private alleles. Low genetic differentiation among *O. hookeri* populations was detected (*F*ST = 0.029); natural selection may be involved in PGM locus differentiation among populations. The genetic differentiation between paired populations was low, bearing no correlation with geographic distance (Mantel test: *r* = −0.34, *P* = 0.72). Only two populations showed signs of recent bottlenecks.
- **Conclusions** The heterozygote deficiency found seems to be caused by pollinator behaviour; the low frequencies of several alleles of different loci can be maintained due to clonal propagation. Despite the stochastic nature of the wind-dispersal of seeds to long distances, this process may promote an effective gene flow among populations, thus avoiding genetic differentiation.

**Key words:** Orchidaceae, *Oncidium hookeri*, allozyme, genetic variability, genetic structure, tropical Atlantic rainforest, wind-dispersed seeds, vegetative propagation, insect-pollination.

**INTRODUCTION**

During the last two decades, several studies have concentrated on the distribution of genetic variability in orchid populations (see Hanrick and Godt, 1996; Forrest et al., 2004). This family represents an excellent example for adaptive radiation and rapid diversification, facilitating research on a myriad of ecological and evolutionary aspects (Nilsson, 1992; Dressler, 1993; Tremblay et al., 2005). In this context, the evolution of floral morphology, the dynamics of plant–pollinator interactions, the effects of habitat fragmentation on the genetic diversity of species, and the effectiveness of gene flow in natural conditions are some of the relevant points highlighted (Sun, 1996; Ackerman and Ward, 1999; Wong and Sun, 1999; Tremblay and Ackerman, 2001; Trapnell and Hamrick, 2005; Tremblay et al., 2005).

In general, breeding systems are regarded to be the main factor in determining the organization of genetic variability in plant populations (Loveless and Hamrick, 1984; Lande and Shemskem, 1985). In orchids, the population level of genetic structure is greatly influenced by pollinator behaviour and, under natural conditions, the fruit set is predominantly pollinator-dependent (Neiland and Wilcock, 1985; Cozzolino and Widmer, 2005; Tremblay et al., 2005). In some cases, seeds may be even more important than pollen for interpopulational gene flow (Peakall and Beattie, 1991; Rasmussen, 1995; Cozzolino et al., 2003; Brzosko et al., 2004). In general, it is predicted that Orchidaceae seeds, which are very small and light, can be wind-dispersed over long distances (Dressler, 1981, 1993; Ackerman and Ward, 1999; Chung et al., 2004), promoting genetic homogeneity among populations. However, recent studies have shown that most orchid seeds settle down near to the maternal plant (Murren and Ellison, 1998; Machon et al., 2003), causing a spatial genetic structure on a small scale (among individuals within populations) (Peakall and Beattie, 1996; Chung et al., 2004; Trapnell et al., 2004).

Even though most species (approx. 70 %) of Orchidaceae are epiphytic (Dressler, 1993), data on genetic diversity are biased towards terrestrial species. Some studies have shown high genetic diversity and low differentiation in populations of Brazilian rupicolous orchids; these findings are thought to be the consequence of self-incompatibility and seed dispersal by wind in an open environment (Borbé et al., 2001). It has been proposed that the gene flow of epiphytes could be more susceptible to environmental changes than other species due to the habitat, patchy distribution and specific pollination strategies of these species (Ackerman and Ward, 1999; Tremblay and Ackerman, 2001; González-Astorga et al., 2004; Trapnell et al., 2004). Furthermore, changes in pollinator dynamics affect small populations restricted to remnants of
vegetation more intensely than they affect large ones (Ellstrand and Ellam, 1993; Young et al., 1996; Lande, 1999; Oostermeijer et al., 2003).

In this study, the genetic variability of *Oncidium hookeri* populations in an Atlantic rainforest area of south-eastern Brazil is analysed. *Oncidium* is a neotropical orchid genus, including more than 600 epiphytic, terrestrial and epipetric species (Chase, 1986; Dressler, 1993). The pollinators reported are several genera of native bees (Apidae, which gather oils produced by specialized glands); however, fruit setting in the field is rare, despite the reward offered by the flowers (Singer and Cocucci, 1999; Reis et al., 2000; Singer, 2003). Although uncommon in orchids, there is a suggestion that the Subtribe Oncidiinae is self-incompatible, due to frequencies of abortion in geitonogamic breeding (i.e. between flowers of the same individual) (Singer and Koehler, 2003). A large number of *Oncidium* populations are currently restricted to remnants of the tropical Atlantic rainforest and the aim of the present study was to determine whether the populations of *O. hookeri* in these vegetation fragments are genetically structured. To do this, inbreeding and intrapopulational genetic variability of six populations of *Oncidium hookeri* were estimated, and the genetic differentiation and gene flow among these populations evaluated. The genetic variability of the species was assessed by means of allozyme electrophoresis. The results may highlight the processes that influence the distribution of genetic variability in a tropical epiphytic orchid.

**MATERIALS AND METHODS**

**Species studied**

*Oncidium hookeri* Rolfe is a perennial, long-lived, small, epiphytic orchid, occurring in the mountains of the south-eastern and southern regions of Brazil. Species identification followed the criteria of Pabst and Dungs (1977). The leaves are inserted into pseudobulbs, and the inflorescence is lateral, ramified, with a high number of flowers. The pendant inflorescence possesses 15–30 small flowers (approx. 1 cm) with yellow petals and elaiophores (glands which produce floral lipids). Floral morphology, lipid-oil production (gathered by several genera of Apidae) and field observations have shown that *Oncidium* species are pollinated mainly by native bees (Singer and Cocucci, 1999; Reis et al., 2000; Singer, 2003). However, the fruits are rare because the behaviour of the pollinators promotes some degree of geitonogamy, and the self-incompatibility (abortion) may be responsible for the low pollination success in this group (Singer, 2003; Singer and Koehler, 2003). *Oncidium* species can also grow clonally through pseudobulbs, which are capable of maintaining clones for many generations.

**Sampling sites**

Specimens were collected in six rainforest fragments located in the Southern Mantiqueira Range in Minas Gerais state (22°28′16″/W46°08′42″) (Fig. 1). The area is situated above 1400 m a.s.l., and was originally characterized as evergreen vegetation (Rizzini, 1979). The region’s climate is classified as Cwb (Köppen, 1948), where the mean temperature of the hottest month is below 22 °C. The area contains a high number of forest fragments of various sizes in an agricultural matrix. In general, the fragments are isolated and occur at the top of the mountains.

A ramet from each individual was collected and cultivated in the greenhouse of the Genetics and Evolution Department of the State University of Campinas, from September 2002 to February 2003. Special care was taken in order to collect individuals isolated in different trees to avoid sampling clones. At least 17 individuals from each fragment were collected and considered as one sample (Pop. 1, 24 individuals sampled; Pop. 2, 18; Pop. 3, 21; Pop. 4, 26; Pop. 5, 28; Pop. 6, 17).

**Allozyme electrophoresis**

A small portion of fresh leaf tissue (approx. 5 mg) was crushed in 0.5 mL of grinding buffer [0.1 mol L\(^{-1}\) Tris, 0.2 mol L\(^{-1}\) sucrose, 0.6 % PVP (w/v), 1 mmol L\(^{-1}\) EDTA, 0.15 % BSA, 0.03 mol L\(^{-1}\) DIECA, 0.03 mol L\(^{-1}\) sodium tetraborate and 0.2 % mercaptoethanol; pH 7.0], modified from Sun and Ganders (1990). The extracts were absorbed in pieces of Whatman paper no. 3 and loaded onto an 8.5 % starch gel (Sigma). Different buffer systems and running conditions were employed: System 1, 0.026 mol L\(^{-1}\) LiOH, 0.095 mol L\(^{-1}\) boric acid and 0.0033 mol L\(^{-1}\) EDTA, with electrode diluted 1:10, 15 mA; System 2, 0.04 mol L\(^{-1}\) citric acid, pH 6.1 adjusted with N-(3-aminopropyl)morpholine and electrode diluted 1:20 (Clayton and Tretiak, 1972), 20 mA; System 3, 0.047 mol L\(^{-1}\) LiOH,
1.91 mol L\(^{-1}\) boric acid, pH 8.4, and electrode of 0.008 mol L\(^{-1}\) citric acid, Tris 0.015 mol L\(^{-1}\), pH 8.1, diluted 1:20, 24 mA.

Standard electrophoreses were performed until the inner marker (bromophenol blue) reached 8 cm from the application site. The gels were stained for 11 enzymatic applications, according to Alfenas et al. (1991): System 1 was used to analyse alcohol dehydrogenase (ADH1, ADH2 and ADH3; EC 1.1.1.1), diophorase (DIA; EC 1.8.1.4), malic enzyme (ME; EC 1.1.1.40), phosphoglucoisomerase (PGI; EC 5.3.1.9) and phosphoglucomutase (PGM1; EC 5.4.2.2).

System 2 was used to analyse glyceraldehyde-3-phosphate dehydrogenase (G3PDH; EC 1.2.1.12), isocitrate dehydrogenase (IDH; EC 1.1.1.42), malate dehydrogenase (MDH; EC 1.1.1.37) and shikimate dehydrogenase (SKDH; EC 1.1.1.25.). System 3 was used to analyse fumarase (FUM; EC 1.1.1.37) and shikimate dehydrogenase (G6PDH; EC 1.1.1.49). Alleles were identified by their mobility in relation to the alleles of the same Oncidium hookeri reference individual applied in all gels.

**Data analysis**

Allele frequencies were determined by visual interpretation of gels. The genetic variability for each population was estimated according to the mean number of alleles per locus (A), the proportion of polymorphic loci (P: 95% criterion), and the observed (\(H_o\)) and expected (\(H_e\)) mean heterozygosity per locus in each populations. Analyses were performed using the BIOSYS 1.0 software package (Swofford and Selander, 1981).

Departures from frequencies expected under Hardy–Weinberg equilibrium were tested by randomization using the software Genetix (Belkhir et al., 1996–2001). The \(F_{IS}\) values obtained were compared using a \(\chi^2\)-test. \(F\)-statistics (Wright, 1978) were calculated in order to determine the levels of allelic variation within and among populations of *O. hookeri*. The confidence interval of \(F\)-coefficients was estimated through bootstrap procedures (Manly, 1997).

Pairwise \(F_{ST}\) were estimated according to Weir and Cockerham (1984) for six populations of *O. hookeri* and the confidence interval calculated with 5000 permutations using the Fstat software (Goudet, 1995). A Mantel test (Mantel, 1967) was used to test the correlation between pairwise \(F_{ST}\) and geographical distance matrices with Genetics software.

A bottleneck test (Cornuet and Luikart, 1996) was carried out to determine signs of excess expected heterozygosity (\(H_e\)) in relation to heterozygosity expected under mutation-drift equilibrium (\(H_{eq}\)).

**RESULTS**

**Genetic variability within populations**

The genetic variation observed in *O. hookeri* was high. The mean number of alleles per locus was 1.75 (s.d. = 0.1), whereas the percentage of polymorphic loci was between 15.4 and 61.5 (Table 1). The allelic frequencies did not fit those expected by the Hardy–Weinberg equilibrium \((P < 0.05)\), with a much lower observed heterozygosity \((H_o = 0.034, s.d. = 0.01)\) than expected \((H_e = 0.099, s.d. = 0.02)\); \(F_{IS}\) values ranged from 0.43 to 0.824.

Four loci were monomorphic in all populations, and most showed one allele with a frequency of near to 1.0 (Table 2). The number of alleles in polymorphic loci

**TABLE 1. Genetic variability in six populations of Oncidium hookeri**

<table>
<thead>
<tr>
<th>Populations</th>
<th>(N)</th>
<th>(A)</th>
<th>(P) ((95%))</th>
<th>(H_o)</th>
<th>(H_e)</th>
<th>(F_{IS})</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>23.2</td>
<td>1.86</td>
<td>15.4</td>
<td>0.031</td>
<td>0.06</td>
<td>0.503*</td>
</tr>
<tr>
<td>2</td>
<td>16.4</td>
<td>1.61</td>
<td>46.1</td>
<td>0.019</td>
<td>0.11</td>
<td>0.824*</td>
</tr>
<tr>
<td>3</td>
<td>20.5</td>
<td>1.77</td>
<td>46.1</td>
<td>0.023</td>
<td>0.09</td>
<td>0.755*</td>
</tr>
<tr>
<td>4</td>
<td>26</td>
<td>1.77</td>
<td>38.6</td>
<td>0.038</td>
<td>0.1</td>
<td>0.617*</td>
</tr>
<tr>
<td>5</td>
<td>22.1</td>
<td>1.85</td>
<td>61.5</td>
<td>0.033</td>
<td>0.13</td>
<td>0.748*</td>
</tr>
<tr>
<td>6</td>
<td>15.7</td>
<td>1.61</td>
<td>38.5</td>
<td>0.062</td>
<td>0.01</td>
<td>0.43*</td>
</tr>
<tr>
<td>Mean (± s.d.)</td>
<td>20.6</td>
<td>1.75</td>
<td>41.03 ± 13.8</td>
<td>0.034</td>
<td>0.09</td>
<td>0.66*</td>
</tr>
</tbody>
</table>

* Significant at the 0.05 level.

\(N\), average number of individuals with sampled loci; \(A\), mean of alleles per locus; \(P\), percentage of polymorphic loci; \(H_o\), observed mean heterozygosity; \(H_e\), expected mean heterozygosity and \(F_{IS}\), inbreeding coefficient.

**FIG. 2.** Allele frequencies of PGM loci in six populations of *Oncidium hookeri*. A, B, C and D represent the four different alleles. Pop. 1, ‘Mata dos Damários’; Pop. 2, ‘Mata Campo Alegre’; Pop. 3, ‘Mata dos Garcias’; Pop. 4, ‘Mata Alto Caxambu’; Pop. 5, ‘Morro Alto do Serro’; Pop. 6, ‘Pedreira dos Garcias’.
ranged from two to four. Among the six populations, Pop. 2 and Pop. 6 (the populations with the lowest number of individuals found in the field) showed signs of recent bottlenecks ($P$-values: 0.048 and 0.029, respectively).

**Genetic structure and gene flow among populations**

Estimated $F_{IS}$ values were high for most loci (Table 3), and a great heterogeneity of values per locus among populations was observed. A low, but significant, genetic structure was observed among populations ($F_{ST} = 0.029$).

According to Wright (1978), the $F_{ST}$ of PGM locus indicates a moderate structure (0.073; Table 3).

Populations 1, 3 and 4 showed private alleles. However, only one in a total of six alleles had a frequency $>0.05$ (on SKDH locus in Pop. 3; Table 2). There was no correlation between $F_{ST}$ values and the geographical distances matrices (Mantel test: $r = -0.34$, $P = 0.72$; Table 4). The lowest genetic differentiation ($0.001$) was estimated between populations 2 and 5 (5.6 km apart) and the highest differentiation ($0.096$) occurred between populations 3 and 6 (2.12 km apart).

### DISCUSSION

#### Genetic variability within Oncidium hookeri

There was a higher genetic variability within *Oncidium hookeri* compared with other plant species, be they herbaceous or perennial (Hamrick and Godt, 1990). However, the $A$ and $P$ values reported here are similar to those observed in other insect-pollinated orchids (Scacchi et al., 1990, 1991; Sharma et al., 2000; Borba et al., 2001; Sun and Wong, 2001; Trapnell et al., 2004). It is generally agreed that wind-dispersed seeds can reach long distances (Dressler, 1981; Ackerman and Ward, 1999), which could maintain enough gene flow to counterbalance losses due to genetic drift (Sharma et al., 2000, 2003). However, the few available studies of seed dispersal and genetic variability in orchids show a significant fine-scale structure (Peakall and Beattie, 1996; Chung et al., 2004). According to Trapnell et al. (2004), this pattern is caused mainly by highly

### Table 3. $F$-statistics of nine polymorphic loci of six populations of Oncidium hookeri

<table>
<thead>
<tr>
<th>Loci</th>
<th>$F_{IS}$</th>
<th>$F_{ST}$</th>
<th>$F_{IT}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADH1</td>
<td>0.83</td>
<td>0.83</td>
<td>0.01</td>
</tr>
<tr>
<td>ADH3</td>
<td>0.07</td>
<td>0.07</td>
<td>0.003</td>
</tr>
<tr>
<td>DIA</td>
<td>0.68</td>
<td>0.68</td>
<td>0.014</td>
</tr>
<tr>
<td>G3PDH</td>
<td>1</td>
<td>1</td>
<td>0.01</td>
</tr>
<tr>
<td>IDH</td>
<td>0.23</td>
<td>0.22</td>
<td>0.008</td>
</tr>
<tr>
<td>MDH</td>
<td>0.33</td>
<td>0.32</td>
<td>0.006</td>
</tr>
<tr>
<td>ME</td>
<td>0.92</td>
<td>0.92</td>
<td>0.05</td>
</tr>
<tr>
<td>PGM</td>
<td>0.64</td>
<td>0.66</td>
<td>0.073</td>
</tr>
<tr>
<td>SKDH</td>
<td>1</td>
<td>1</td>
<td>0.02</td>
</tr>
</tbody>
</table>

Mean±s.d. Confidence: 0.40 – 0.83, 0.41 – 0.84, 0.004 – 0.05 interval (95%)

### Table 4. Genetic differentiation and geographical distance for pairwise Oncidium hookeri populations

<table>
<thead>
<tr>
<th>Pop. 1</th>
<th>Pop. 2</th>
<th>Pop. 3</th>
<th>Pop. 4</th>
<th>Pop. 5</th>
<th>Pop. 6</th>
</tr>
</thead>
<tbody>
<tr>
<td>$F_{ST}$ above diagonal; spatial distance (km) among populations, below diagonal.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Significant at the 0.05 level; Mantel test, $r = -0.34$ and $P = 0.72$. 

Pop., Population; paired $F_{ST}$ above diagonal; spatial distance (km) among populations, below diagonal.
localized (on a scale of centimetres) seed dispersal within the population. Other studies also show that, in the great majority of orchids, seeds are dispersed short distances, near to the maternal plants (Murren and Ellison, 1998; Machon et al., 2003).

In contrast with the high variability found, there were four monomorphic loci (ADH2, FUM, G6PDH and PGI), and most of the polymorphic loci showed only one allele at a frequency of close to 1 and some rare alleles. The absence of allozyme diversity has already been reported in highly inbred orchids, such as the terrestrial Cephalanthera damasonium (Scacchi et al., 1991), Eulophia sinensis and Zeuxine gracilis (Sun and Wong, 2001) and the epiphyte Spiranthes hongkongensis (Sun, 1997). However, assuming the self-incompatibility observed in Oncidium species (Singer, 2003), including O. hookeri (see next paragraph), the absence of variability in four loci is surprising. Chung et al. (2004) found a similar pattern in one population of Cephalanthera longifolia, a predominantly outcrossing orchid species, and suggested that it was genetically isolated and had drifted to fixation, or had undergone a recent bottleneck. In O. hookeri, there are signs of recent bottlenecks in two out of six populations, suggesting that other processes may also be influencing genetic variability. A long generation time due to vegetative propagation, as well as the overlapping generations, can also mitigate the loss of genetic variation by drift and maintain alleles in low frequencies (Ellstrand and Rose, 1987; Gustafsson, 2000; Borba et al., 2001). During the sampling of plant material, more individuals were observed at the limits of the forest than inside, suggesting that the environmental conditions at the boundaries of the fragments (Murcia, 1995) are suitable for O. hookeri. Furthermore, tests for genetic bottlenecks, revealing a putative effect of habitat fragmentation, were significant for only two of the populations studied.

There are no previous reports on the mating system of O. hookeri. Although orchids are usually self-compatible (van der Pijl and Dodson, 1966; Dressler, 1993), hand self-pollination carried out on several individuals maintained in the greenhouse (approx. 40 flowers of different individuals) was not successful (S. Alcantara et al., unpubl. data). Additionally, fruits were rarely observed in the field, suggesting the rarity of natural matings (both cross- and self-), as was also observed in other Oncidium species (Singer and Cocucci, 1999; Singer, 2003; Singer and Koehler, 2003). The rarity of self-pollination contrasts with the high fixation indices and the heterozygote deficiencies observed. Studies on the genetic variability of orchids showed different patterns of heterozygosity, probably reflecting various life histories, pollination systems, geographical distributions and bottlenecks, as well as fragmentation events (Scacchi et al., 1990; Sun, 1996; Wong and Sun, 1999; Ehlers and Pedersen, 2000; Gustafsson, 2000; Borba et al., 2001; Sharma et al., 2003). In some cases, pollinator behaviour promotes inbreeding in plant populations (Levin and Kerster, 1969; Schmitt, 1980; Fritz and Nilsson, 1994; Kearns et al., 1998). It is well established that the foraging strategies of food-seeking pollinators can lead to high levels of pollen transfer within the same plant and mean pollen dispersal distances are typically less than several metres (Richards, 1997). The pollinators reported for Oncidium species are, in general, solitary bees (Trigona, Tetrapedia, Centris), with short flight ranges, that exhaust the feeding sources in an area before moving on to another (Dodson, 1962; Singer and Cocucci, 1999; Parrat Tabla et al., 2000; Singer and Koehler, 2003), promoting inbreeding and a low numbers of heterozygotes. Thus, the high inbreeding coefficients found could be attributed to pollinator behaviour in these rewarding orchids (Dressler, 1981; Peakall and Schiestl, 2004).

The high genetic variability and high $F_{IS}$ values observed can be explained by the life history of the species, with most seed dispersal occurring within populations, self-incompatibility mechanisms and pollinators with restricted foraging areas. In this scenario, a high genetic variability and a high number of alleles at low frequencies can be maintained by clonal propagation, since each genotype can remain for many generations (Ellstrand and Rose, 1987; Borba et al., 2001).

**Genetic structure and gene flow**

Despite the fact that populations were sampled in small, isolated fragments, they presented a modest genetic structure ($F_{ST} = 0.029$). This differentiation is low, as reported by Hamrick and Godt (1996), who noted a very low differentiation in orchids, compared with other perennial herbaceous, due to species-specific pollinators and wind-dispersed seeds. Other studies on recently fragmented orchid populations found contrasting patterns in perennials and allogamous species (Sun, 1996; Wong and Sun, 1999; Ehlers and Pedersen, 2000; Gustafsson, 2000; Tremblay and Ackerman, 2001; Forrest et al., 2004; Trapnell and Hamrick, 2004). Although wind-dispersal of seeds may be highly localized, generating a fine scale genetic structure, Trapnell and Hamrick (2004) pointed out that some seeds can enter the air column and be dispersed over long distances (kilometres), as predicted for small and light seeds. The long-distance tail of the seed dispersal distribution (Murren and Ellison, 1998) is also important because even small amounts of gene flow have significant consequences for the homogenization of genetic variation among populations (Chung et al., 2004; Trapnell and Hamrick, 2004), minimizing the effects of isolation and population differentiation. Assuming the scenario that the majority of the seeds settle near the maternal plant, the high $F_{IS}$ values reported here indicate low pollinator mobility. On the other hand, the open matrix may promote efficient seed exchange, hindering the differentiation of populations. The moderate value of $F_{ST}$ in the PGM locus and its different allele frequencies among populations suggest the action of selection on this locus or nearby loci (hitchhiking effect; Maynard Smith and Haigh, 1974). For the remaining loci, there are no differences in population frequencies or significant structure to suggest non-neutral dynamics.

In Oncidium hookeri, seeds seem to play a more important role in gene flow between populations than pollen. A comparative analysis of nuclear and organellar DNA markers in natural populations would help in testing this hypothesis. Despite the small number of fruits, the
large number of seeds per fruit and the proximity of the populations seem to promote sufficient gene flow to avoid the structuring of populations, independently of the spatial distance between them. The differentiation observed between Pop. 3 and Pop. 6 and the other populations could be due to their location in isolated, inclined fragments, surrounded by stone formations. The private alleles observed in Pops 1, 3 and 4 could either have appeared recently or represent a transitory polymorphism, which could be maintained due to clonal propagation.

Conclusions

The low differentiation among Oncidium hookeri populations, the absence of correlation between genetic structure and spatial distance among populations, the high genetic variability, the weak evidence for bottlenecks, and the high number of individuals at the boundaries of the fragments indicate that the isolation of these populations within remnants of the Atlantic rainforest apparently does not directly threaten this species. The heterozygote deficiency found seems to be caused by the pollinator behaviour coupled with mechanisms of self-incompatibility, in a situation where the majority of seed dispersal occurs near to the maternal plants, and the low frequencies of several alleles at different loci may be maintained by vegetative propagation. Despite the stochastic nature of the wind-dispersion of seeds over long distances, this process may promote effective gene flow among populations, as in other orchid species, thus, preventing the build-up of genetic differentiation.

ACKNOWLEDGEMENTS

We thank J. M. Alcantara, G. H. Aguirre and M. C. Crevellaro for their help with field work, and J. José, F. N. Ramos, C. F. Verola, the handling editor Dr Christian Lexer, and the anonymous referees for valuable comments and suggestions on the manuscript. This work was supported by CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico 587959736203248).

LITERATURE CITED


