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Genomic Resources of a Neotropical Orchid Opens New Avenues for Evolutionary Research of Endangered Flora in Brazil

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Abstract

Next-generation sequencing (NGS) technologies have greatly reduce the cost and difficulty of sequencing partial genomes. Genome datasets are a promising approach to generate genomic resources to further support population genomic and association genetic studies. In a recent study da Rocha Perini *et al.* describe the complete chloroplast genome of the endangered *Cattleya crispata,* the first genome from the Neotropical orchid subtribe Laeliinae. The development of genomic resources of *Cattleya* species adds to the genomic toolbox for conservation genetics and allows new approaches to better understand the complex evolutionary history of Neotropical orchid species.

Keywords: *Cattleya*, conservation, genome, next-generation sequencing, genome, Orchidaceae

Increased genome-wide resolution in population genomics and association genetics has been greatly facilitated by the emergence of next-generation sequencing (NGS) technologies, such as 454 (Margulies *et al.*, 2005; Moore *et al.*, 2006; El Mujtar *et al.*, 2014) and Illumina platforms (Cronn *et al.*, 2008; Parks *et al.*, 2009; Straub *et al.*, 2012). These technologies reduced the cost and difficulty of sequencing partial genomes and assembling complete organellar genomes. The chloroplast (*cp*) genome has been widely used in phylogenetic and evolutionary studies in plants (Chaw *et al.*, 2004; Ruhfel *et al.*, 2014). Plastid genomes are a result of co-evolution of the cellular genetic compartments that together constitute an integrated genetic system (Herrmann *et al.*, 2003; Rand *et al.*, 2004). Thus, *cp* genome divergence might encode mutations that are able to cause Dobzhansky–Muller incompatibilities responsible for reproduction barriers and speciation (Turelli & Moyle, 2007; Greiner *et al.*, 2011; Pinheiro *et al.*, 2013; Prosdocimi, 2014).

The fast and extensive diversification observed in Orchidaceae has imposed a great challenge for taxonomists and evolutionary biologists. Genetic studies with orchid species have mainly relied on *cp* genome to resolve phylogenetic uncertainties and date the evolution of groups (Cameron *et al.*, 1999; Freudenstein *et al.*, 2004; van den Berg *et al.*, 2009; Antonelli *et al.*, 2010; van den Berg, 2014). However, little is known about the major evolutionary patterns of genome evolution in Orchidaceae and its consequences for speciation. The recent publication of the nuclear orchid genome (Cai *et al.*, 2015), transcriptomic resources (see OrchidBase 2.0, Tsai *et al.*, 2013) and the fast increase in available plastid genomes (Wu *et al.*, 2010; Delannoy *et al.*, 2011; Logacheva *et al.*, 2011; Barrett & Davis, 2012; Pan *et al.*, 2012; Yang *et al.*, 2013; Luo *et al.*, 2014; Perini *et al.*, 2015) build up a set of genomic resources able to improve evolutionary studies of Orchidaceae.

The complete *cp* genome of *Cattleya crispata*, contributed by da Rocha Perini *et al.*, 2015, allows new genomic studies to improve the understanding of the implications of genome evolution for adaptation, reproductive barriers and the speciation processes in the highly diverse Neotropical Laeliinae subtribe. The assembled genome contained 148,343 bp in length and conserved the quadripartite structure following the typical pattern observed in photosynthetic orchids (Jheng *et al.*, 2012; Luo *et al.*, 2014). In addition to the complete *cp* genome, the partial nuclear genome dataset of *C. crispata* opens new possibilities to (i) identify genes or groups of genes with accelerated evolutionary rates, (ii) develop tools to study the expression levels of genes and (iii) develop both neutral and potentially functional gene-based markers (SSRs and SNPs). The advance of genomic toolbox for Neotropical orchids will allow association studies that may reveal important evolutionary mechanisms of *Cattleya* adaptation to Neotropical environments, as the one suggested for rock outcrop adaptation (Leles *et al.*, 2015). This knowledge is of prime importance for the proper management of endangered *Cattleya* in the face of continuous treats by anthropogenic pressure and climate change (Dirnböck *et al.*, 2011; Sonter *et al.*, 2014).

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