Genomic Resources Note

Transcriptome Sequencing and Simple Sequence Repeat Marker Development for Three Macaronesian Endemic Plant Species

Olive W. White1,2, Bethany Doo2, Mark A. Carine2, and Mark A. Chapman2,3

1Plants Division, Natural History Museum, London SW7 5BD, United Kingdom; and 2Centre for Biological Sciences, University of Southampton, Southampton SO17 1BJ, United Kingdom

• Premise of the study: Oceanic islands offer unparalleled opportunities to investigate evolutionary processes such as adaptation and speciation. However, few genomic resources are available for oceanic island endemics. In this study, we publish transcriptome sequences from three Macaronesian endemic plant species (Argyranthemum broussonetii [Asteraceae], Descurainia bourgaeana [Brassicaceae], and Echium wildpretii [Boraginaceae]) that are representative of lineages that have radiated in the region. In addition, the utility of transcriptome data for marker development is demonstrated.

• Methods and Results: Transcriptomes from the three plant species were sequenced, assembled, and annotated. Between 1972 and 2282 simple sequence repeats (SSRs) were identified for each taxon. Primers were designed and tested for 30 of the candidate SSRs identified in Argyranthemum, of which 12 amplified well across three species and eight were polymorphic.

• Conclusions: We demonstrate here that a single transcriptome sequence is sufficient to identify hundreds of polymorphic SSR markers. The SSRs are applicable to a wide range of questions relating to the evolution of island lineages.

Key words: Argyranthemum broussonetii; Descurainia bourgaeana; Echium wildpretii; Macaronesia; marker development; simple sequence repeats (SSRs); transcriptomics.

The availability of next-generation sequencing (NGS) technology for nonmodel organisms in prime ecological scenarios has revolutionized evolutionary biology (Egan et al., 2012). An exciting prospect of NGS is the potential to improve our understanding of the genetic basis of processes such as adaptation and speciation (Stapley et al., 2010; Kelley et al., 2012; Chapman et al., 2013; Sousa and Hey, 2013; Rius et al., 2015; Twyford et al., 2015). Volcanic oceanic islands have long served as model systems for the study of such evolutionary processes (Emerson, 2002); however, the capabilities of NGS for oceanic island endemics are only starting to be realized (Kueffer et al., 2014). For example, NGS approaches have been employed to investigate the radiation of Darwin’s finches from the Galápagos Islands (Lamichhaney et al., 2015) and to untangle the complex phylogenetic relationships of Tolpis Adans., a genus of flowering plants from Macaronesia (Mort et al., 2015). NGS has also been successfully applied to other “island-like” scenarios such as the radiation of cichlid fishes in African and Neotropical lakes (Fan et al., 2012).

While NGS is becoming more affordable, the cost of obtaining genome-level sequences from multiple individuals or population sampling is still high. However, a large genetic resource from just a single or a few individuals (e.g., a transcriptome sequence or an expressed sequence tag [EST] library) offers the ability to produce highly cost-effective PCR-based molecular markers that can be amplified in many individuals at a fraction of the cost (Ellis and Burke, 2007). To generate further interest in this area and to develop a novel genetic resource, we have sequenced and assembled transcriptome sequences for three plant species (Argyranthemum broussonetii [Pers.] Humphries [Asteraceae], Descurainia bourgaeana [E. Fourn.] Webb ex O. E. Schulz [Brassicaceae], and Echium wildpretii H. Pearson ex Hook. f. [Boraginaceae]) that belong to three endemic radiations of Macaronesia (Fig. 1).

Isolated oceanic archipelagos are botanically diverse and rich in endemic species, making them ideal systems to investigate the origin and evolution of plant diversity (Losos and Ricklefs, 2009; Kueffer et al., 2014). These taxa have been selected because they belong to genera that offer exceptional “natural laboratories” in the Macaronesian archipelagos with which to investigate a range of evolutionary phenomena.

Argyranthemum Webb is the largest endemic genus found in Macaronesia with at least 23 species (Fig. 2A) (Humphries, 1976, 1979; Francisco-Ortega et al., 1996), including a rare putative example of homoploid hybrid speciation (Brochmann et al., 2000; Fjellheim et al., 2009). There are seven species of Descurainia Webb & Berthel. endemic to the Canary Islands where they exhibit multiple independent adaptations to high-altitude habitats.