## Diversification analysis of a songbird lineage within a remote archipelago suggests a role for intra-island speciation

Maëva Gabrielli\*<sup>1</sup>, Benoit Nabholz<sup>2</sup>, Thibault Leroy<sup>2</sup>, Borja Milá<sup>3</sup>, and Christophe Thébaud<sup>4</sup>

<sup>1</sup>Laboratoire Evolution et Diversité Biologique (EDB) – CNRS : UMR5174, Université Paul Sabatier (UPS) - Toulouse III, Institut de recherche pour le développement [IRD] : UMR5174, ENSFEA – Bâtiment 4R1 118 Route de Narbonne 31062 TOULOUSE CEDEX 4, France
<sup>2</sup>Institut des Sciences de lÉvolution de Montpellier (ISEM) – Centre de Coopération Internationale en Recherche Agronomique pour le Développement : UMR116-2015, Université de Montpellier, Institut de recherche pour le développement [IRD] : UR226, Centre National de la Recherche Scientifique : UMR5554 – Place E. Bataillon CC 064 34095 Montpellier Cedex 05, France
<sup>3</sup>Museo Nacional de Ciencias Naturales – Consejo Superior de Investigaciones Científicas (CSIC), Madrid 28006, Spain

<sup>4</sup>Laboratoire Evolution et Diversité Biologique (EDB) – CNRS : UMR5174, Université Paul Sabatier (UPS) - Toulouse III, Institut de recherche pour le développement [IRD] : UMR5174, ENSFEA – Bâtiment 4R1 118 Route de Narbonne 31062 TOULOUSE CEDEX 4, France

## Abstract

Island endemic congeners can be sister species that have arisen through intra-island speciation following initial colonization by a common ancestor, or they may represent multiple independent colonization events. These two contrasting scenarios provide different expectations regarding the relative roles of natural selection and geographic isolation in driving speciation. However, discriminating between the two scenarios has proven difficult and demonstrating intra-island differentiation has remained elusive. The Reunion grev whiteeye (Zosterops borbonicus) is a species complex that harbours four geographically structured forms with abutting ranges on a small and remote volcanic island, providing an interesting system to test for intra-island divergence. We generated genome-wide SNP loci using GBS (Genotyping-By-Sequencing) data from a large sample of individuals and a high-quality genome sequence for the species. Using a population genomic framework as well as phylogenetic inferences, we reconstructed the evolutionary histories of the different forms on Reunion island. We first confirmed the monophyly of the species relative to its sister species Zosterops mauritianus. Then, we show that the paraphyly and basal position of one of the lowland forms strongly argues in favour of intra-island divergence. Expansion analyses suggest sequential colonisations from the North to the South of the island. The marked genomic structure found indicates that gene flow between forms is limited and suggests that these forms may be reproductively isolated.

<sup>\*</sup>Speaker

**Keywords:** Intra island speciation, Phylogeography, Expansion, Spatial structure, Hybrid classes, La Réunion