Progress Report SP 2006-008

Identification of seed collection zones for rehabilitation

Ecosystem Science

Project Core Team

Supervising Scientist

Margaret Byrne

Data Custodian Site Custodian

Project status as of July 27, 2018, 3:58 p.m.

Update requested

Document endorsements and approvals as of July 27, 2018, 3:58 p.m.

Project TeamgrantedProgram LeadergrantedDirectoraterequired



Identification of seed collection zones for rehabilitation

M Byrne, D Coates, S Mcarthur

Context

The Forest and Ecosystem Management Division of the Department provides guidelines to the Forest Products Commission on seed collection zones for forest rehabilitation. Rehabilitation of sites through revegetation requires knowledge of the genetic adaptation of species to sites in order to manage in an ecologically sustainable fashion. This requires an understanding of the genetic structure and local adaptation of species.

Aims

Identify appropriate seed collection zones (provenances) for species being used for rehabilitation. Initial work is focused on species in the jarrah and karri forest where seed is used for rehabilitation after logging.

Progress

- A paper has been published in *Biological Journal of The Linnean Society* on the analysis of nuclear genetic variation and cpDNA variation in marri (*Corymbia calophylla*). There was little genetic structure across the species range consistent with a strong influence of pollen dispersal in maintaining connectivity among populations, but some evidence of effects of current environment (aridity). Phylogeographic analysis revealed population persistence in mesic habitats but unexpected episodic range expansion from the early Pleistocene, probably in association with progressive drying and major climatic changes.
- A paper is in preparation on the genetic relationships among *Corymbia calophylla*, *C. haematoxylon* and *C. ficifolia*,that show distinct genetic separation in the nuclear genome and shared cpDNA haplotypes, consistent with shared evolutionary history.
- Analysis of microsatellite variation and cpDNA variation in 28 eight populations of Banksia sessilis revealed
 two major genetic clades, one on the Darling range and plateau, and another on coastal limestone
 that exhibited both higher genetic diversity and greater structure. The patterns of genetic diversity
 and phylogeographic structure suggest the ancestor to these clades originated in the northern coastal
 environment and diversified through the Darling Plateau during the mid Pleistocene. A paper is in
 preparation.

Management implications

• Knowledge of genetic structure and local adaptation will enable identification of appropriate seed collection zones for rehabilitation of forest areas, in order to maintain the genetic integrity of the forest on a sustainable basis. Current data on *Kenedia coccinea, Bossiaea ornata* and *A. humilis* indicate that seed collected from the same landscape management unit as the area to be rehabilitated would be an acceptable seed-sourcing strategy. Alternatively, where seed is not readily available from the relevant landscape management unit then use of seed from nearby areas in adjacent landscape management units would also suffice. This information has been used to update seed collection zones for forest rehabilitation in the *Forest Management Plan 2014-2023*.

Future directions

• Complete publication of genetic analysis of phylogeographic patterns and genetic structure, and seed sourcing strategies for *B. sessilis*.