

Progress Report SP 2018-068

Conservation genetics

Kings Park Science

Project Core Team

Supervising Scientist	Siegfried Krauss
Data Custodian	Siegfried Krauss
Site Custodian	

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S Krauss, J Anthony, E Sinclair, B Ayre

Context

The conservation, restoration and horticultural development of Western Australia's unique biodiversity is informed by an understanding of patterns of genetic diversity at multiple hierarchical levels (individuals, populations, species, communities), as well as the key ecological and evolutionary drivers of this genetic diversity, such as adaptation, mating and dispersal. Conservation genetic research seeks to understand the impacts on genetic diversity and the key drivers of this diversity from environmental stressors such as habitat fragmentation, climate change, and introduced species, and identify solutions based on genetic data and theory.

Aims

- Experimentally assess seed sourcing strategies for improved restoration outcomes.
- Assess the conservation and evolutionary consequences for plants pollinated by vertebrates.
- Assess reproductive functionality in restored plant communities.
- Experimentally assess the resilience of plant populations to environmental stressors.
- Assess responses of the soil microbiome through ecological restoration.

Progress

- Monitoring of large-scale, multi-species, field-based provenance trials continue to assess best practise seed sourcing strategies under current and future climates for ecological restoration of *Banksia* woodlands. Fully reciprocal provenance trials with 3,200 seedlings of *Eucalyptus tottiana* from four sites from across the Swan Coastal Plain show little effect of provenance for seedling growth and mortality, but a strong effect of trial site on seedling performance. Analysis of mating systems in these source populations show equivalent parameters of genetic quality of seed.
- Pollinator exclusion experiments showed that exclusion of birds as pollinators for *Banksias* and kangaroo paws significantly impacts plant fitness. For catspaws, the predicted high mate diversity for bird pollinated plants was not found, highlighting that herbaceous species may differ from tree species.
- Multiple natural and restored plant populations have been sampled for an ecological genetic assessment of reproductive functionality following ecological restoration.
- Long-term reciprocal transplant experiments, *ex situ* controlled stress experiments and stress-related gene expression analysis of seagrass in Shark Bay continues. Survival and growth rates at 2.5 years following establishment of a long-term replicated reciprocal transplant experiment for *Posidonia* in Shark Bay (four sites, two different establishment seasons) show strong plastic, rather than local adaptation, responses to environmental variability in salinity and temperature, with site specific responses associated with variable predation. An *ex situ* controlled stress experiment was conducted and data are being analysed.
- The diversity and composition of soil microbial communities following post-impact rehabilitation in the jarrah forest were assessed using eDNA, and contrasted to plant community transition patterns. While restored soil bacterial communities quickly returned to the pre-disturbance state, soil fungal communities closely tracked plant community trajectories toward the pre-disturbance state, but were short of targets even after 30 years.

Management implications

- Provenance trials continue to suggest that diverse local provenance seed provides resilience to current and future climates for restored plant communities of *Banksia* woodlands. Consequently, genetically diverse seed for restoration should continue to be sourced locally, but ongoing experiments embedded in restoration sites should continue to assess provenance effects where possible, and especially test for benefits from climate-adjusted provenancing.

- Seagrass meadows, although impacted by extreme climate events, show a resilience to climate change that suggests local diverse sourcing of propagules provides for effective restoration.
- Refined understanding of the critical importance of vertebrates for pollination indicates control of feral honeybees (*Apis mellifera*) may reduce negative pollination impacts on native flora.
- Enhanced knowledge of soil biota trajectories through post-disturbance restoration shows soil management needs to be improved to enhance the return to pre-disturbance communities, and identifies key missing elements that may suit inoculation.

Future directions

- Continue to assess conservation genetic consequences of vertebrate pollination through molecular and ecological studies. Pollinator exclosures erected on *Banksia menziesii*, *B. attenuata*, *B. ilicifolia* and *Adenanthos cygnorum* plants in diverse *Banksia* woodland sites will manipulate access to flowers by pollinators, and resulting seed production and genetic diversity assessed using microsatellites.
- Continue to assess the resilience of seagrass to environmental stressors through *in situ* reciprocal transplant trials in Shark Bay, transcriptome population genomic analysis, and controlled *ex situ* stress manipulative experiments.
- Continue to assess seed sourcing for restoration strategies through large scale provenance trials, glasshouse trials, and seed germination trials for key species for ecological restoration of *Banksia* woodlands. Seed to be collected from 20 source populations for *Banksia menziesii*, *B. attenuata*, *Eucalyptus tottiana* and *Adenanthos cygnorum*, processed and prepared for glasshouse germination (*E. tottiana* and *A. cygnorum*) or *in situ* sowing into each of four provenance trial sites. Plants to be sampled for population genomic analysis, and soils sampled for soil microbiome assessment. Glasshouse seedling growth and seed germination trials to be established for *E. tottiana*, where provenance responses to water and temperature manipulation will be assessed.
- Continue to assess delivery of vertebrate pollinator services as a measure of restoration success for key species in ecologically restored plant communities, through genotyping of 800 *Lambertia multiflora* seedlings from restoration and natural populations.
- Continue to assess the post-disturbance restoration of the soil microbiome through eDNA, and above-ground/below-ground linkages. Soil microbiomes across post-mining restoration chronosequences at four sites (in northern Jarrah forest, Swan Coastal Plain and Eneabba sandplain) to be assessed for bacterial and fungal community composition and diversity and contrasted to natural soils.