



# Genetic diversity of willows in southeastern Australia

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1. Quantify level of genetic differentiation among catchments
2. Determine the power of molecular fingerprinting to track seed movement across the landscape
3. Assess relative importance of vegetative versus seed reproduction
4. Quantify the spatial scale of seed dispersal
5. Revisit the appropriate landscape scale for effective willow eradication and invasion risk assessment

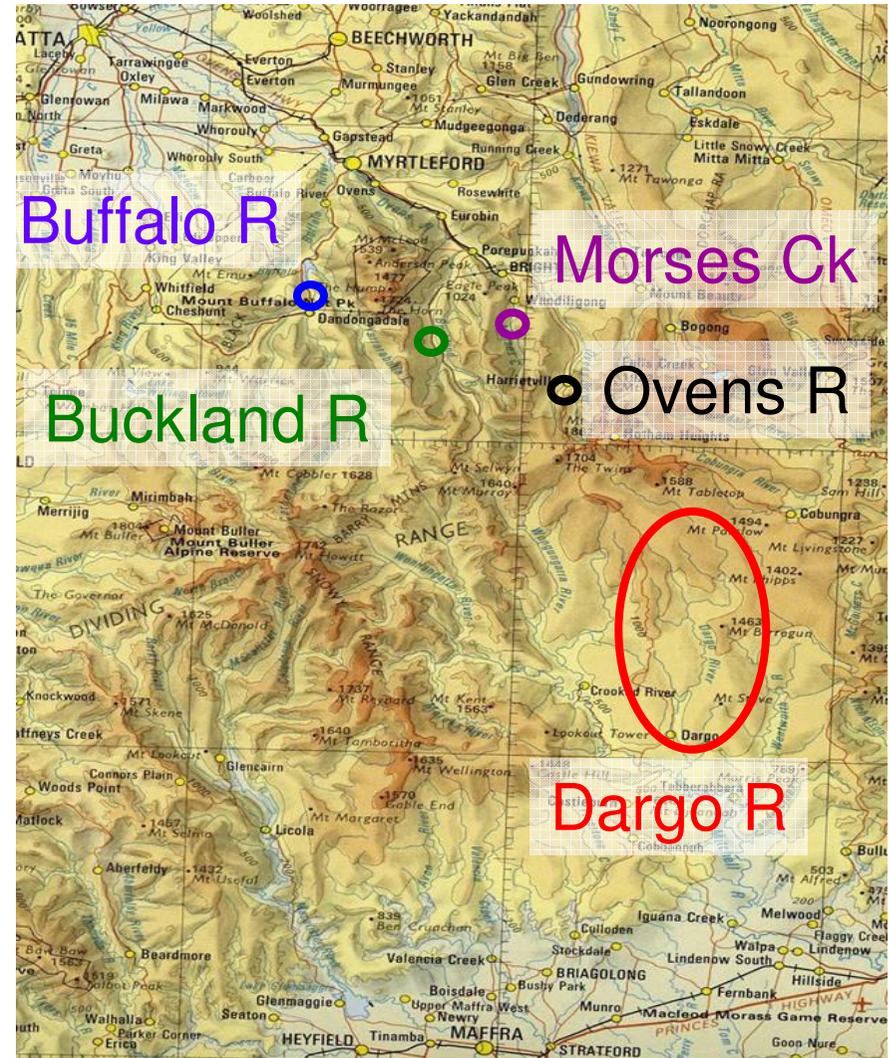


## Sampling

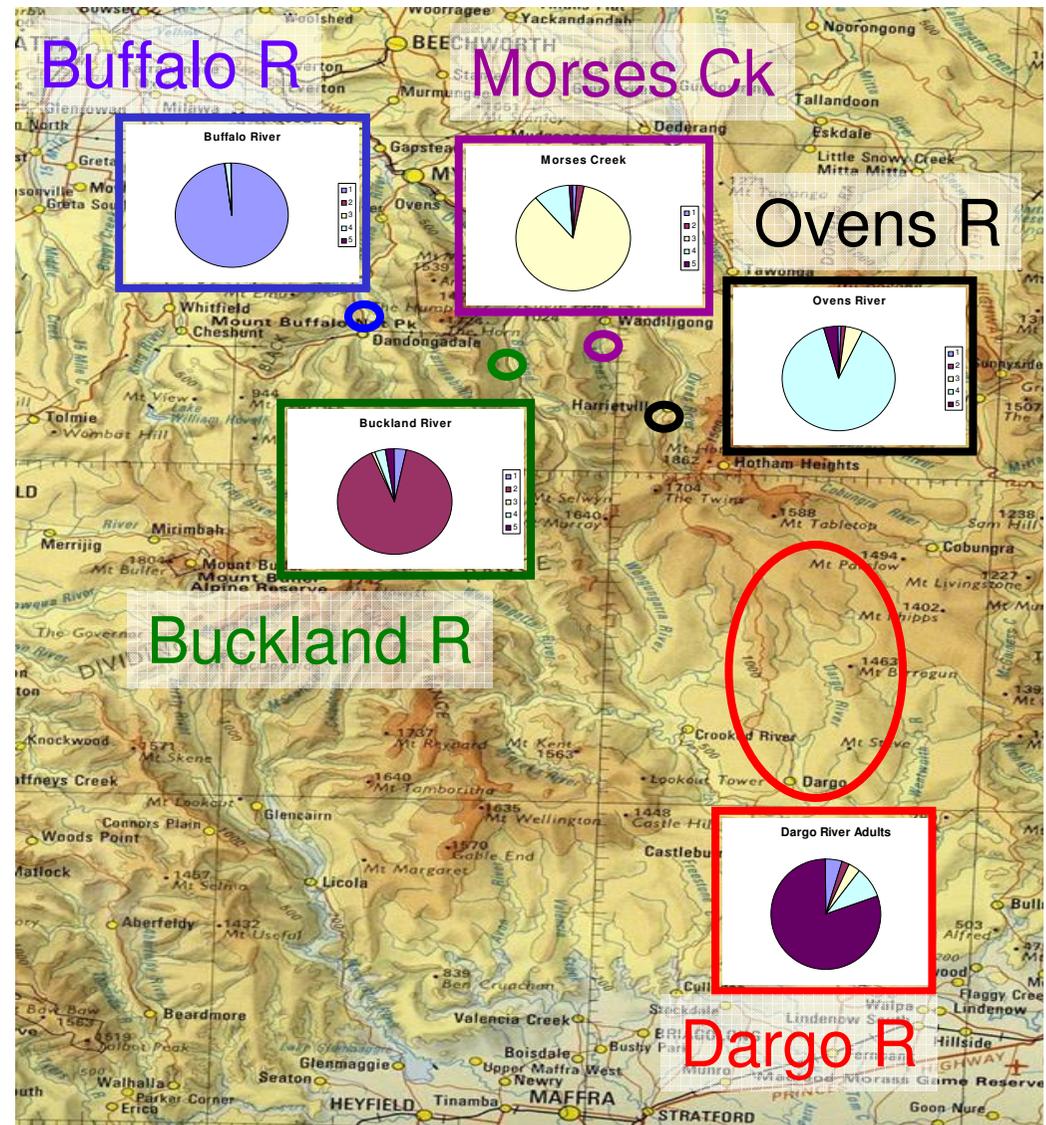
- 50 mature trees in four putative source catchments
- 30 mature trees and 38 seedlings in one target catchment (Dargo River)

## Fingerprinting

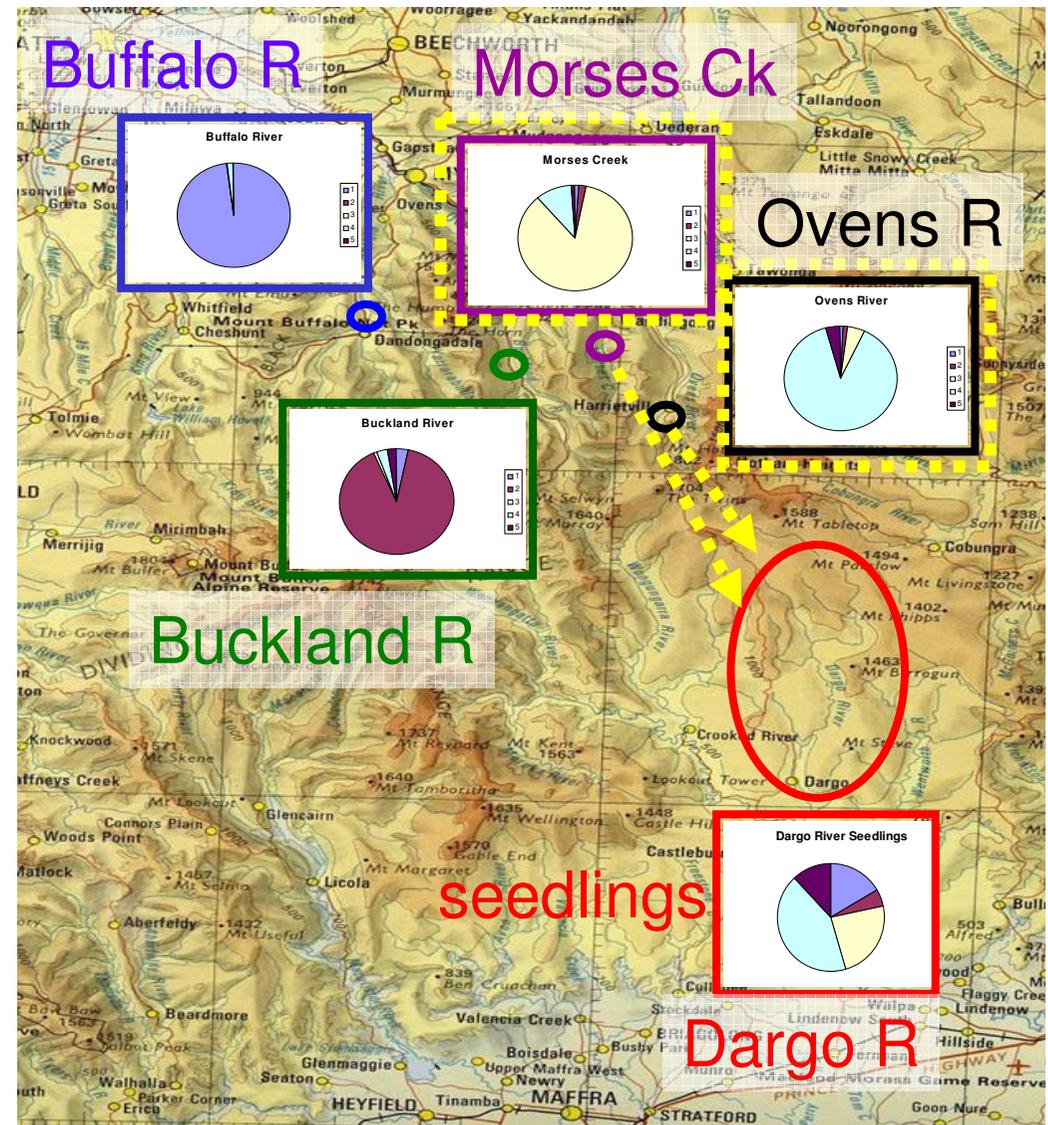
- Individuals genotyped with two marker systems (SSRs and AFLPs)

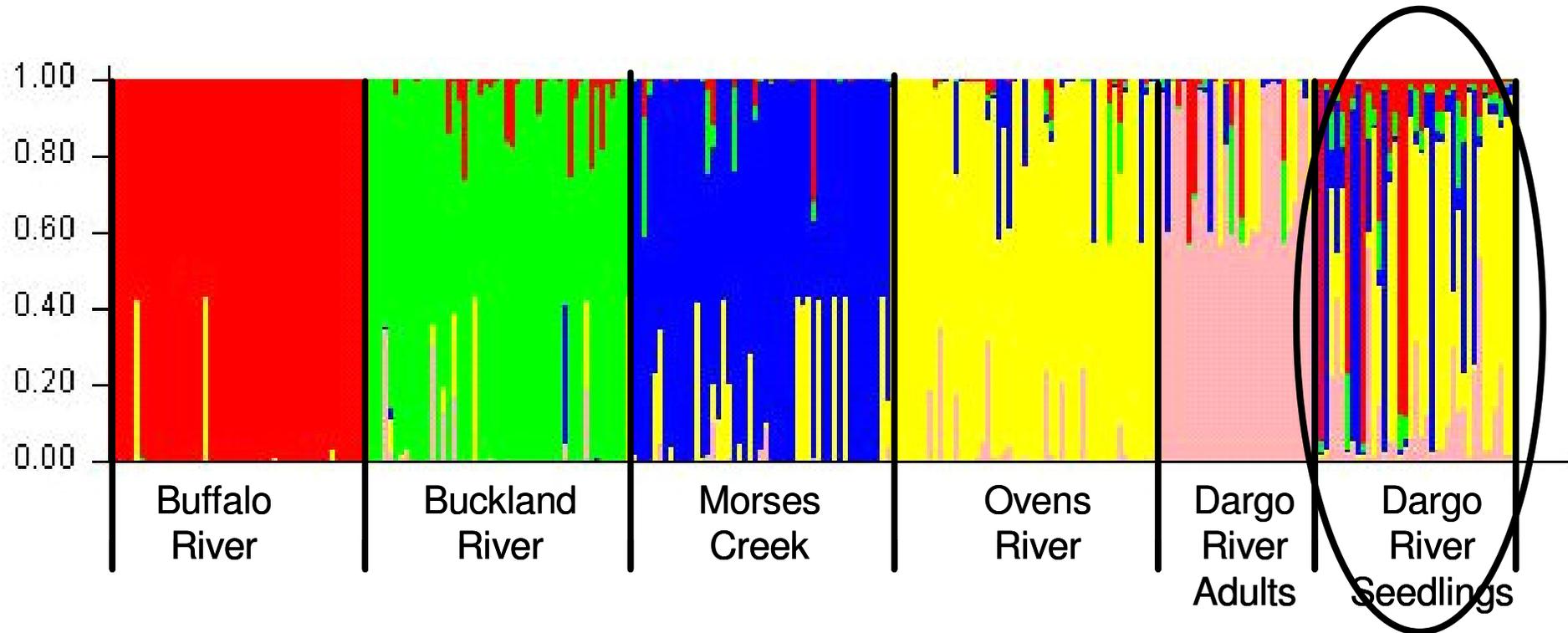


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  - adults fall into five genetic groups
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- Model I: no *a priori* information
  - adults fall into five genetic groups
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  - Dargo seedlings mixed assignments
  - >70% not local origin
  - Ovens R and Morses Ck (>50km)





- Model II: *a priori* population assignments
- Apparent pollen and seed movement across catchments is evident

# Conclusions of pilot study

- AFLPs work well as genetic markers in *Salix cinerea* for measuring gene flow.
- Levels of genetic diversity are high
- Significant seed and/or pollen movement across the landscape (>70% Dargo seedlings have immigrant genes)
- Ovens River and Morses Creek contribute most seed/pollen to the Dargo River catchment > 50km!
- Need to scale up eradication efforts and coordinate across multiple catchments simultaneously

- Scale of movement
  - Seed
  - Pollen
- Differences between species in relation to reproductive strategies
- Potential for spread
- Management implications



## Sexual reproduction

- Millions of seeds produced
- Seeds are wind and water dispersed
- Seeds only last for 2 weeks
- Germination can occur within 24 hours
- Many seedlings die within months of germination



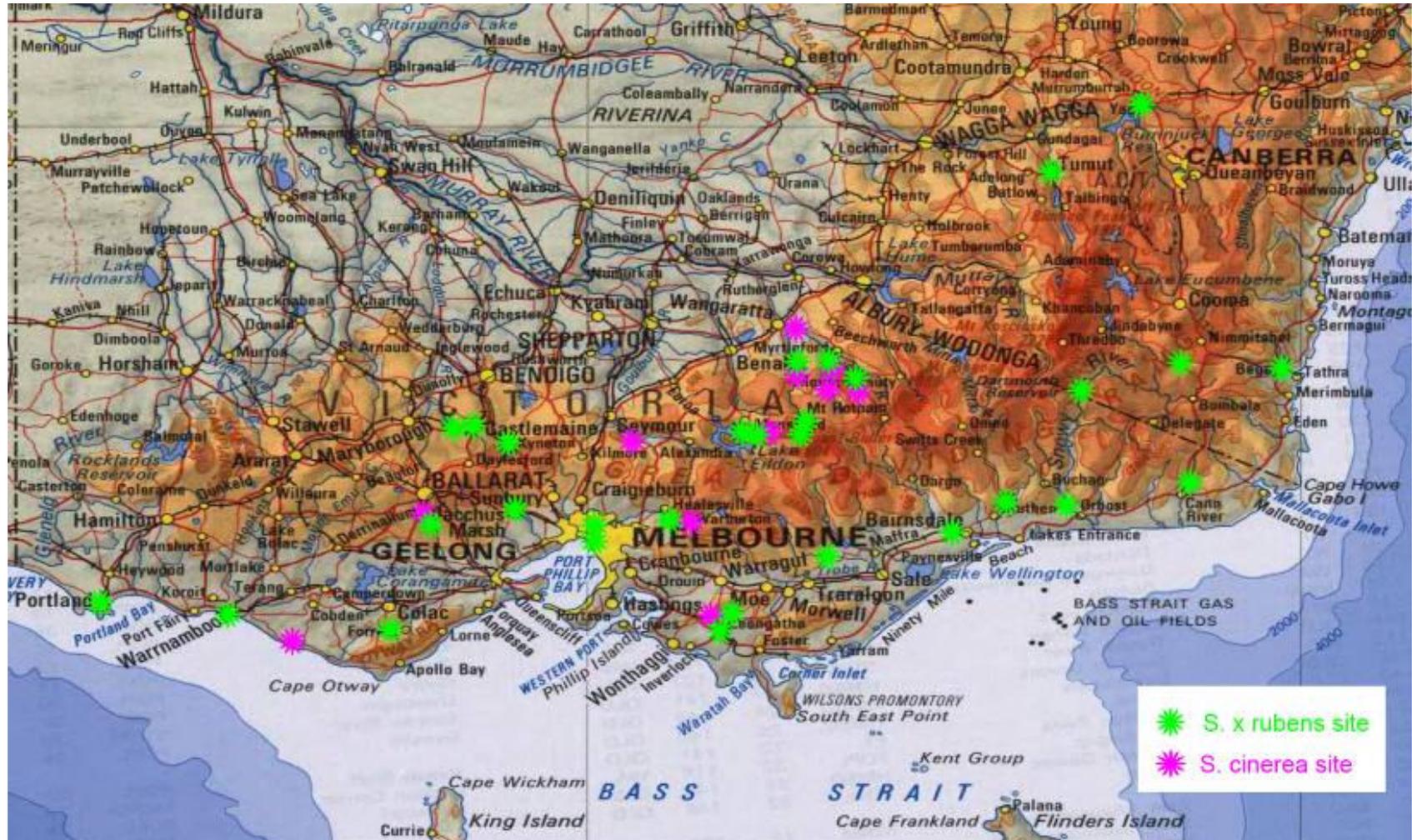
## Asexual reproduction

- Fragility or brittleness
- Abscission point at base of twigs
- Spreads mainly downstream



- State wide sampling of *S. cinerea* and *S. x rubens* complex
- Genetic structure using SSR markers
  - Across the state
  - Within CMA regions
  - Within catchments
- Compare any structure with breeding strategies of species
- Implications for scale of management

# 45 sites, 1350 samples



- Intensive sampling along a river system
- Genetic structure along the river
- Any difference in structure between reproductive strategies



- Historical invasion patterns
- Current reproductive strategies
- Dispersal patterns of willow in terms of the scale of seed and pollen movement
- Identifying the most efficient geographical scale of control that will minimise the likelihood of reinfestation
- Providing more quantitative analysis of catchments that are most at risk of invasion in the future



# Acknowledgments

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