GOVERNMENT OF WESTERN AUSTRALIA
Department of **Biodiversity, Conservation and Attractions**

Moving plants – revealing the past and informing the future

Margaret Byrne

Biodiversity and Conservation Science

Biotic responses - genetic signatures

Changes in climate and environment → Changes in size, distribution and interactions → Changes in genetic diversity and structure

Genetic signatures differ for

- localised persistence – high haplotype diversity, high population differentiation
- contraction to macro refugia – high diversity
- range expansion – low haplotype diversity, low population differentiation

Phylogeography –

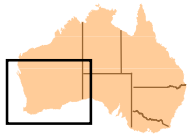
geographical distribution of genealogical lineages

inference of biotic responses

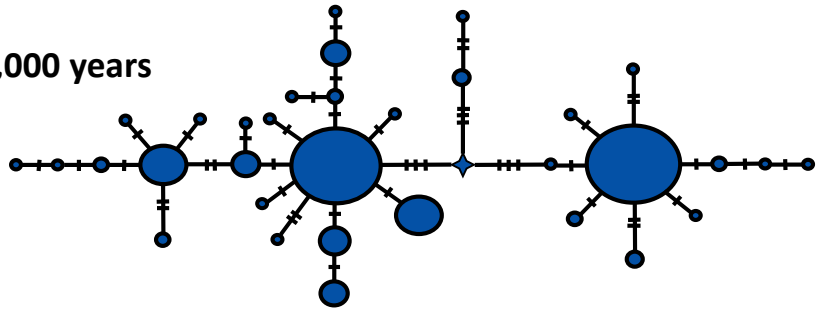
Plants – chloroplast DNA – slowly evolving, evolutionary history

Localised persistence

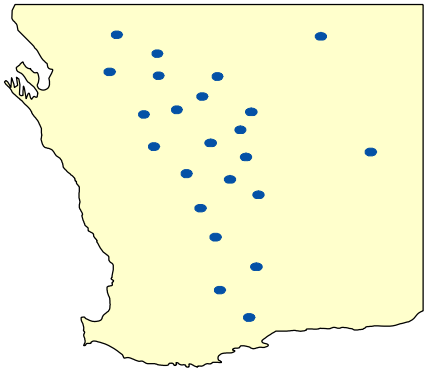
High diversity, high pop differentiation



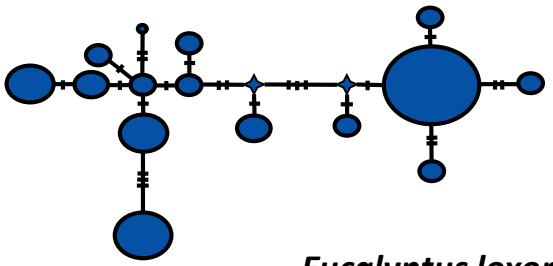
800,000 years



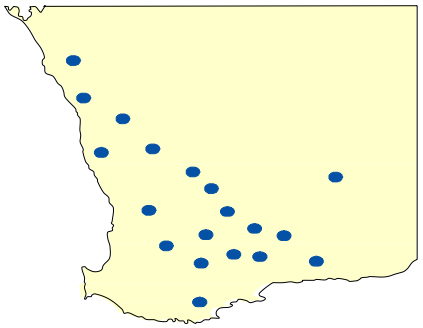
Acacia accuminata



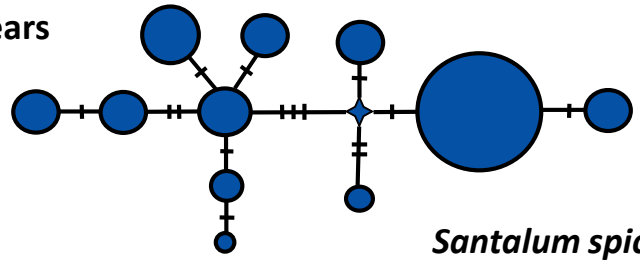
700,000 years



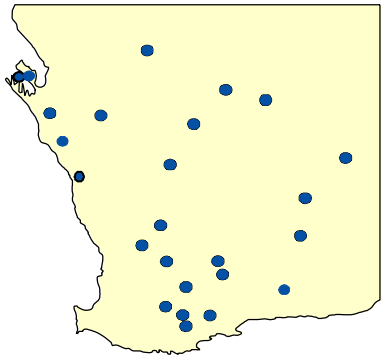
Eucalyptus loxophleba



1 million years



Santalum spicatum

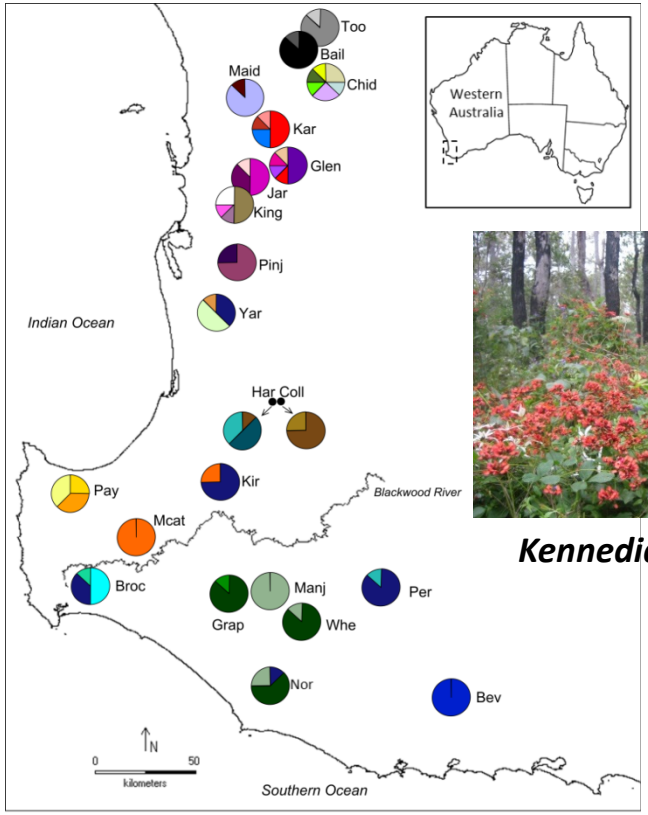


Byrne 2008 QSR

Byrne et al. 2002, 2003; Byrne & Hines 2004

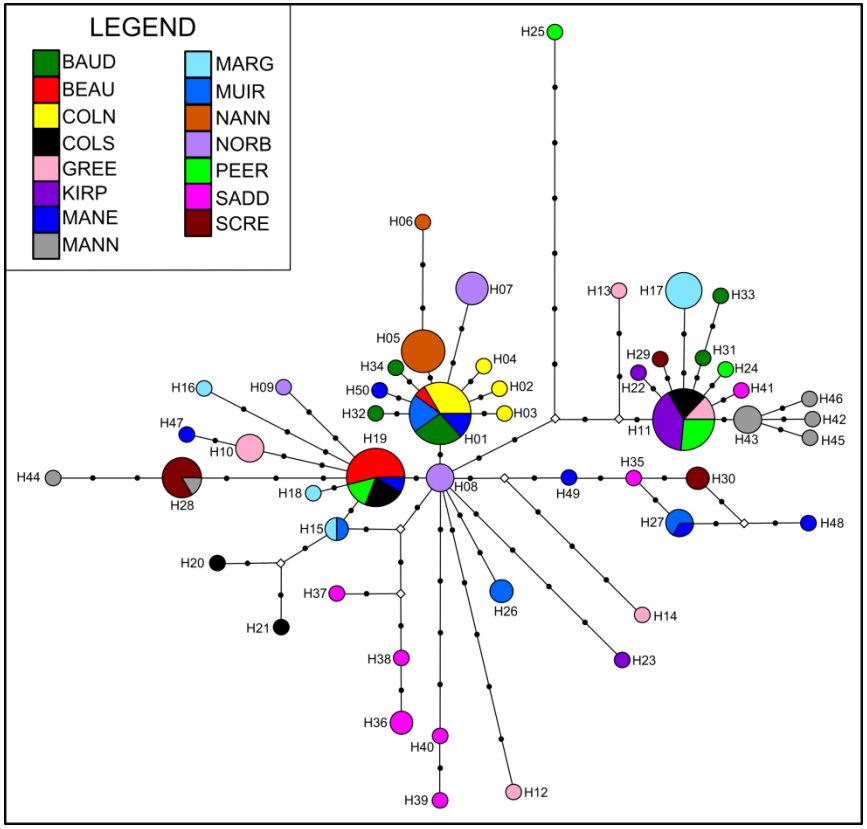
Localised persistence

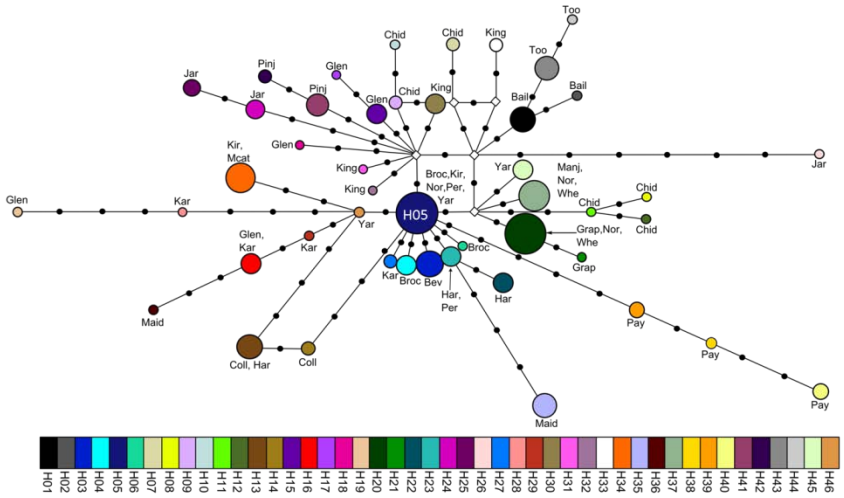
High diversity, high pop differentiation



Kennedia coccinea

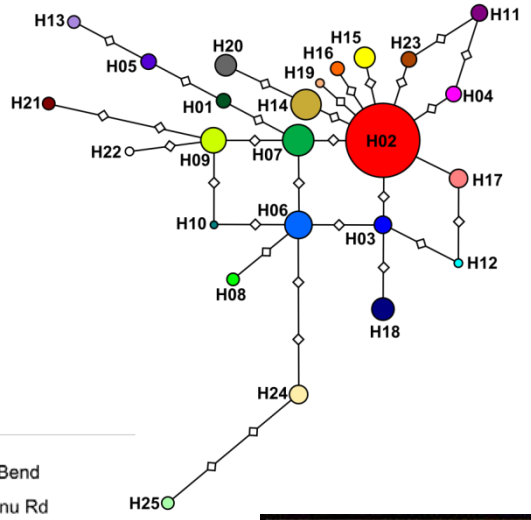
Bossiaea ornata

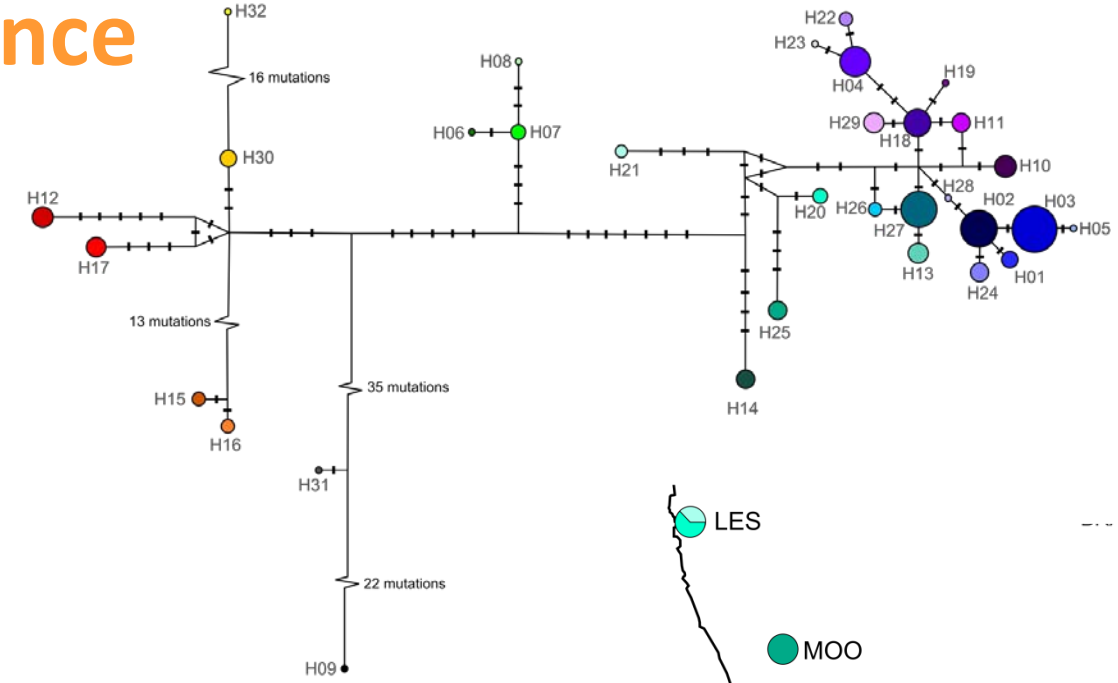


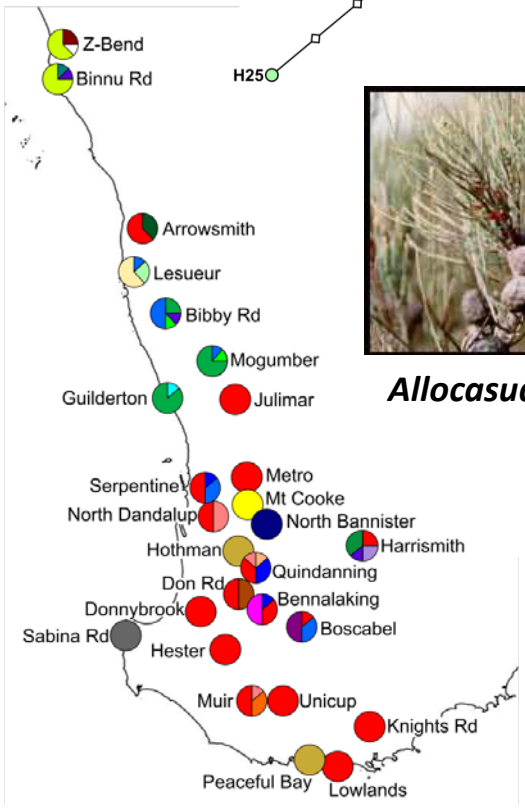


Bradbury et al. 2015a, b

Localised persistence

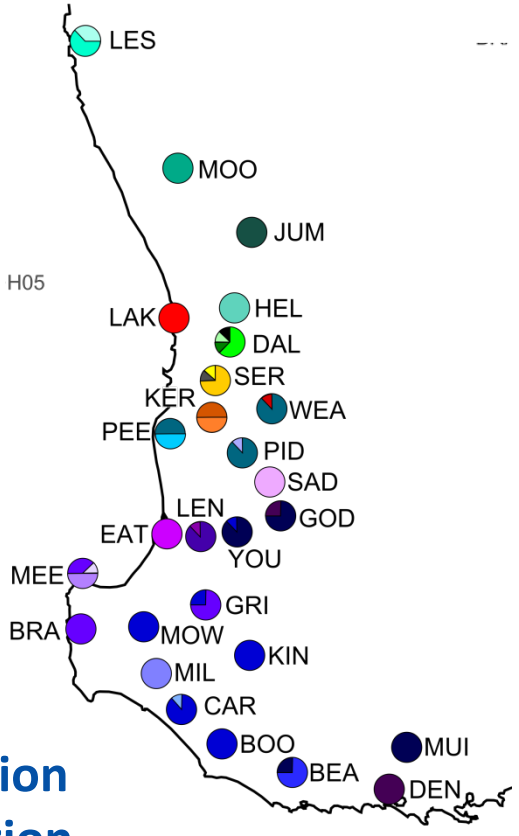






Allocasuarina humilis

Corymbia calophylla



High diversity, high pop differentiation

Some low diversity, low differentiation

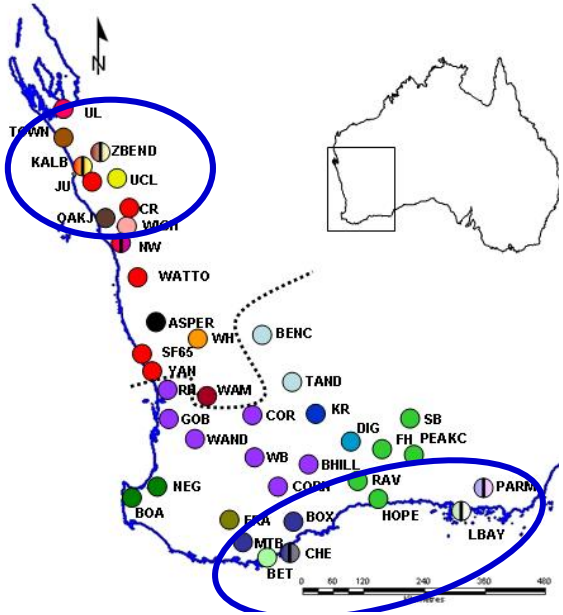
Llorens et al. 2017; Sampson et al. 2018

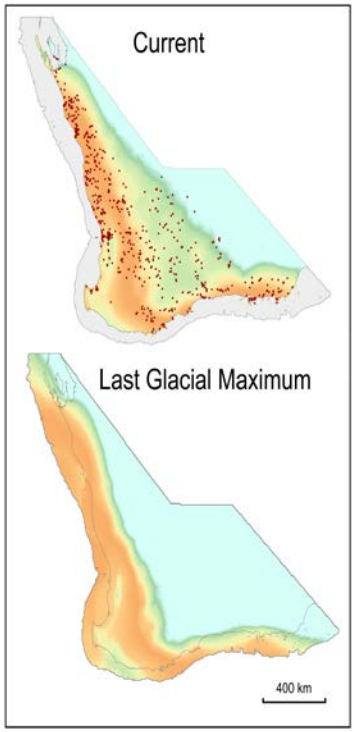
Refugia and expansion

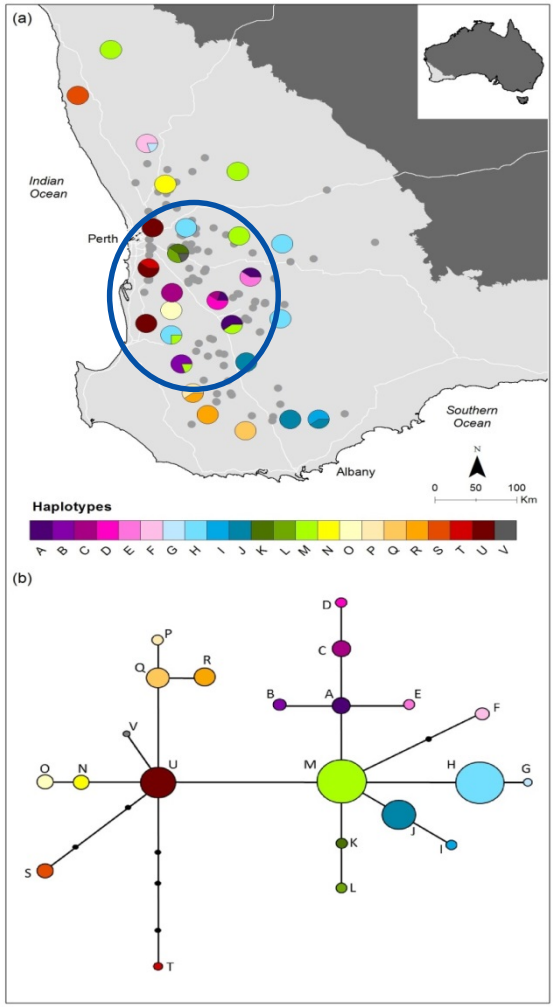
High diversity / Low diversity, low pop differentiation

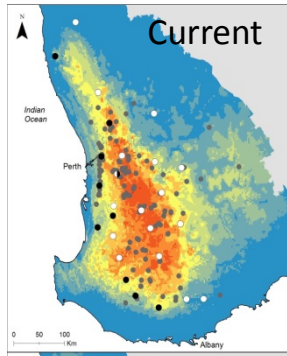
Calothamnus quadrifidus

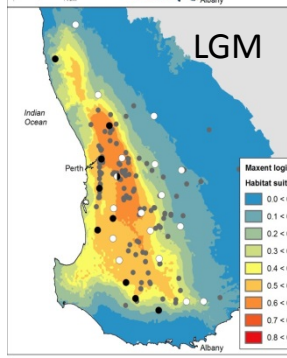
Eucalyptus wandoo

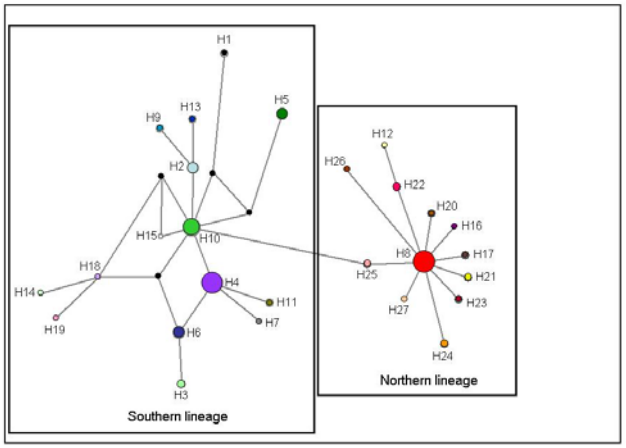












Nistelberger et al. 2014; Dalmaris et al. 2015

Inferences

Localised persistence – major response

local climate conditions, broad fundamental niche/adaptation

importance of mosaic of habitats in heterogeneous landscapes

Some evidence for 'major' refugia and expansions

Refugia – reservoirs of genetic diversity,

important for response to future changing climates

Persistence of the biota through future climate change facilitated by

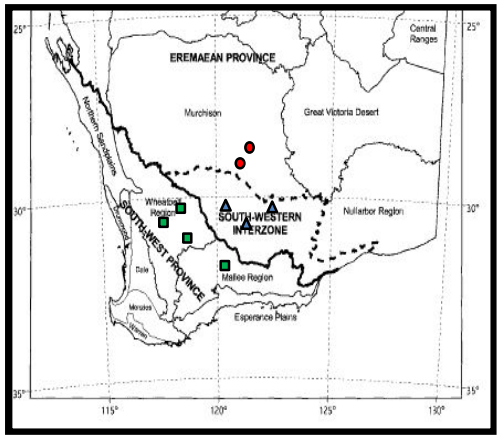
- **maintenance of dynamic evolutionary processes**
- **mosaic of habitats in heterogenous landscapes**
- **conservation of genetic variability & adaptive potential**

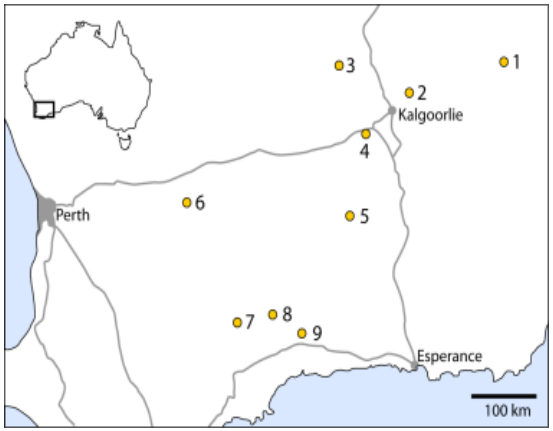
Adaptation to climate

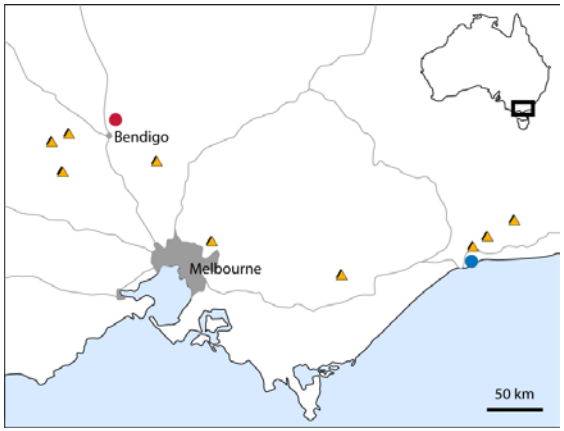
E. loxophleba ssp. lissophloia

E. salubris

E. tricarpa







Genome wide screening - DArTseq markers and outlier analysis

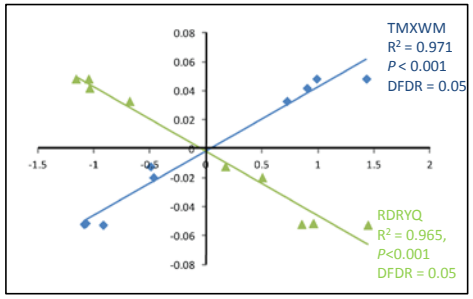
Morphological traits - leaf size, thickness, tissue density

Ecophysiological traits - C isotope ratio, N content, water use efficiency

Widespread eucalypts

E. tricarpa

6544 SNPs
94 outlier markers
correlated with climate



TMXWM = maximum summer temp
RDRYO = rainfall in driest quarter

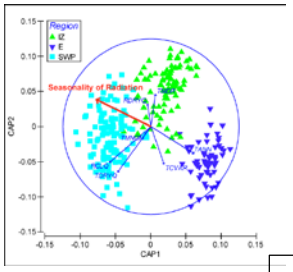
Genetic variation positively correlated with high temperatures and radiation negatively correlated with summer rainfall and seasonality

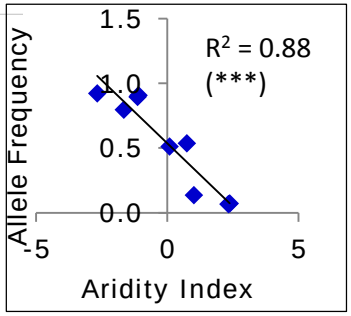
Morphological traits adaptive
Physiological traits plastic

Steane et al. 2014 Plant, Cell, Environ

E. loxophleba

4851 SNPs
58 outlier loci





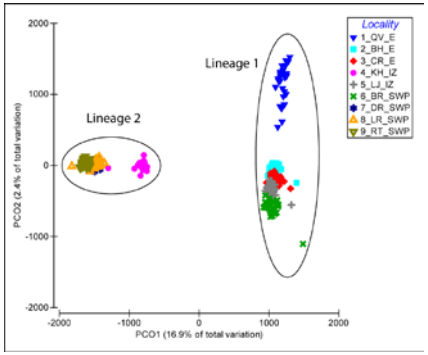
correlation –
9 environmental variables
mainly moisture and rainfall indices, but also radiation

Morphological traits adaptive
Physiological traits plastic

Steane et al. 2017 Biol J Linn Soc

E. salubris

14,949 SNPs
Significant genetic structure
2 lineages – F_{ST} 0.11
Phenotypic differences –
leaf thickness, SLA, leaf N



Lineage 1
24 outlier markers
correlated with climate variables (temp and rainfall)

Steane et al. 2015 Tree Gen Genom

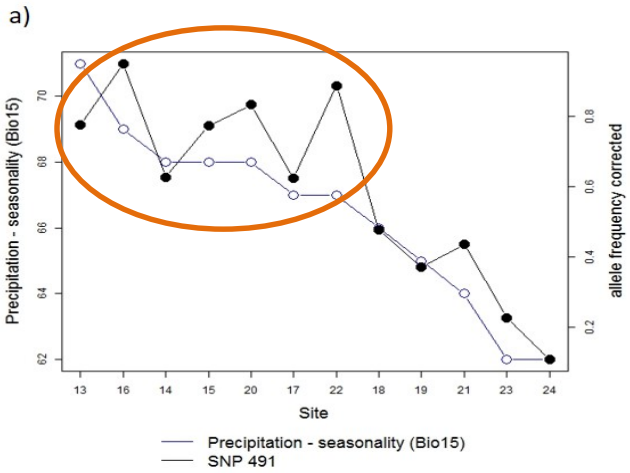
Riparian systems

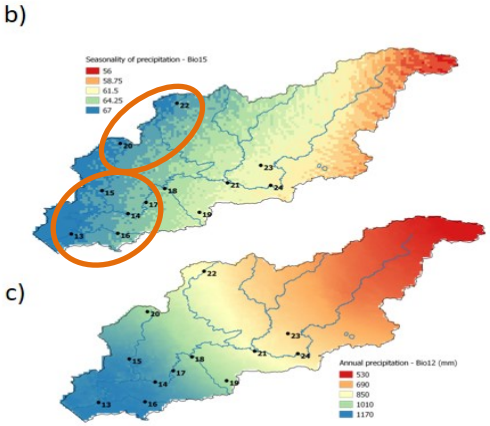
Callistachys lanceolata

Widespread, not restricted to wet areas,
Restricted to lower/wetter/cooler $^{2}/_{3}$ catchment
High levels of genetic structure / low gene flow

2488 SNPs (BayPass, BayEnv2, BayeScan, Arlequin)
39 directional outliers
70 balancing outliers

8 SNPs associated - at least one climate variable
30 significant SNP-climate variable associations





Astartea leptophylla

Restricted to main river,
wind / water dispersed seed
Greater range – cool/wet to hot/dry
Low genetic structure / high gene flow

7971 SNPs
(BayPass, BayEnv2, BayeScan, Arlequin)
74 directional outliers
93 balancing outliers

Few environmental correlations
1 SNP significantly associated
2 climate variables (BF >20)

Hopley and Byrne submitted

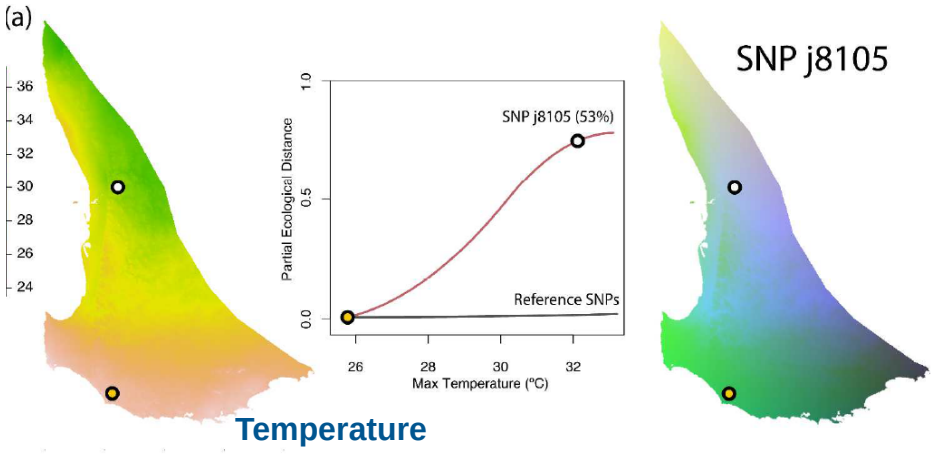
Corymbia calophylla

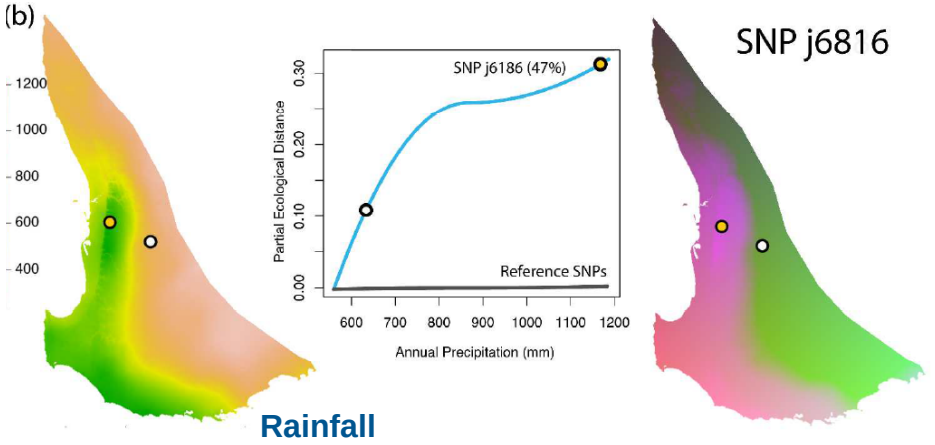
Widespread – forest
Insect pollinated tree

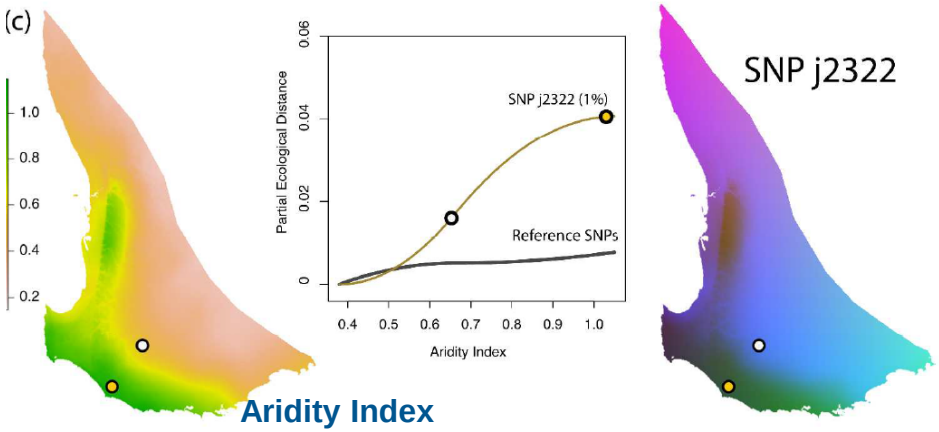
Nuclear diversity, no structure
Low differentiation F_{ST} = 0.055

9,560 SNPs
609 SNPs significantly associated with environment variables
(LFMM, BayEv2, Baypass)

Ahrens et al. submitted

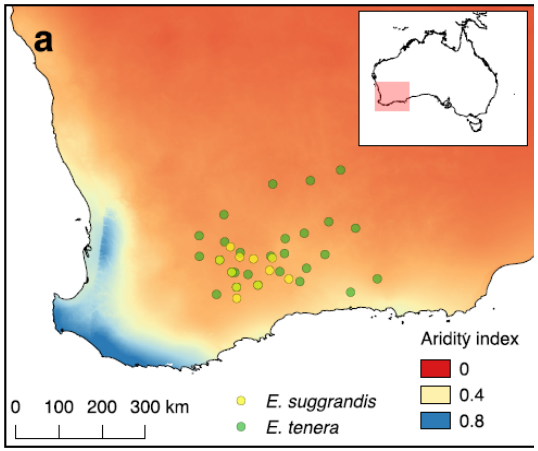




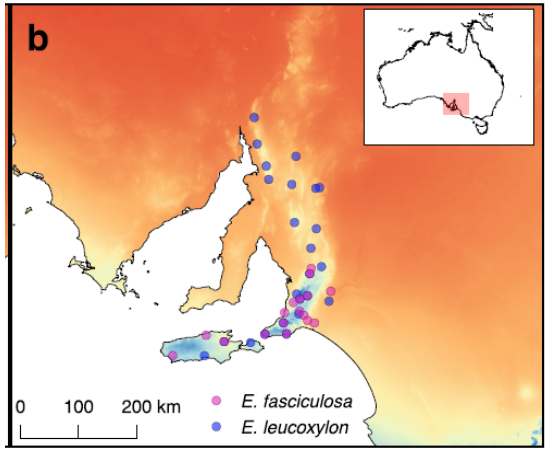


Restricted vs widespread eucalypts

E. tenera vs *E. surgrandis ssp surgrandis*

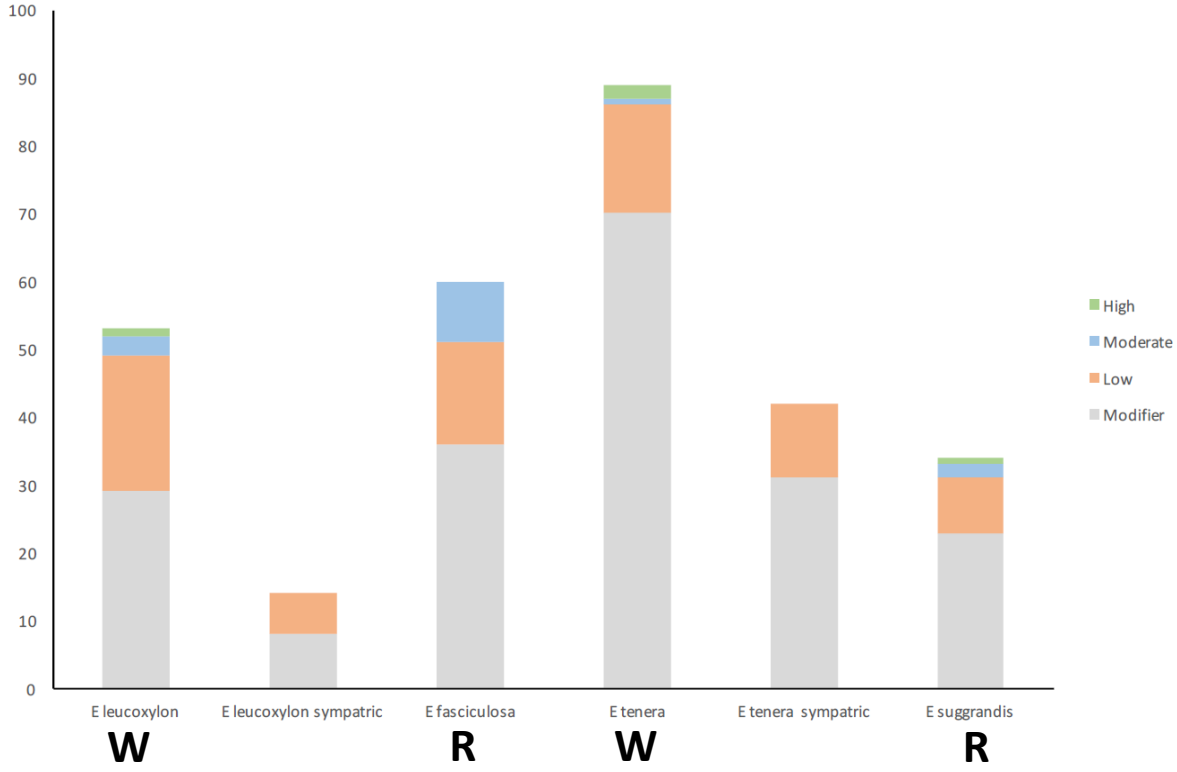


E. leucoxylon vs *E. fasticulata*



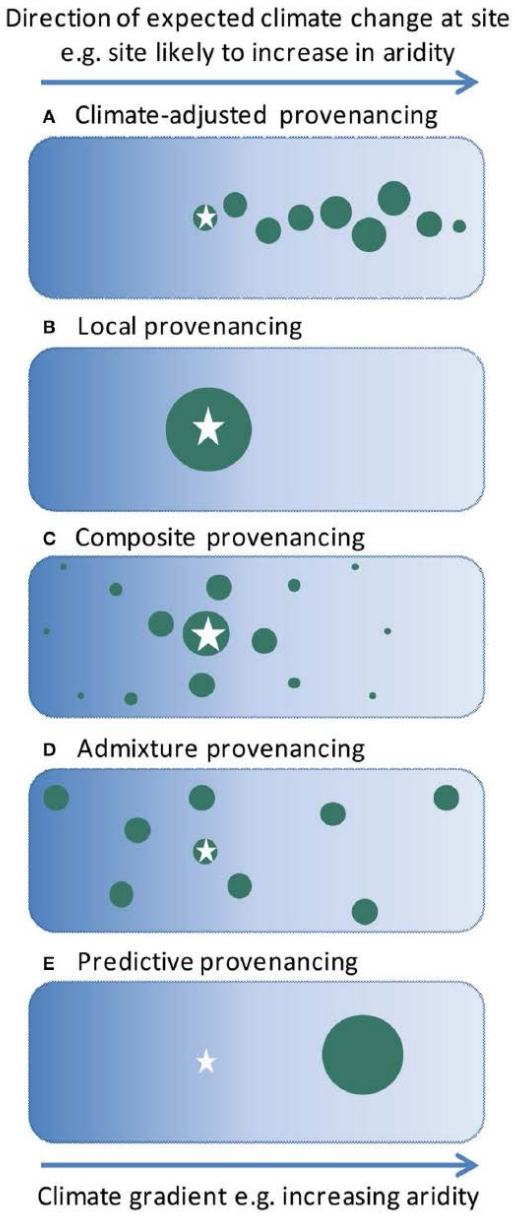
EUChip 60K (Bayescan, PCAdapt, Samßada)

E. tenera	14,009 SNPs	(association climate 89)
E. surgrandis	10,257 SNPs	(association climate 34)
E. leucoxylon	18,942 SNPs	(association climate 53)
E. fasticulata	9,164 SNPs	(association climate 60)



Christmas, Lowe, Breed, Hopley Byrne unpubl data

Assisted gene migration



Climate-adjusted provenancing

Capture the adaptive variation and capacity for plasticity in ecophysiological traits in advance of changing climates

frontiers in Ecology and Evolution

OPINION
published: 23 June 2015
doi: 10.3389/fevo.2015.00065

Climate-adjusted provenancing: a strategy for climate-resilient ecological restoration

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Keywords: climate adaptation, ecological restoration, genomics, plasticity, widespread species

Acknowledgements

Phylogeography projects

Sarah Tapper

Donna Bradbury

Tanya Llorens

Jane Sampson

Heidi Nistelberger

Eleftheria Dalmaris

David Coates

Bronwyn Macdonald

Shelley McArthur

Forest Products Commission

Climate adaptation projects

Dot Steane

Suzanne Prober

Liz McLean

Will Stock

Brad Potts

Rene Vaillancourt

Tara Hopley

Paul Rymer

Collin Ahrens

Andrew Lowe

Martin Breed

Matthew Christmas

NCCARF

Biodiversity Fund

ARC Linkage

ARC Discovery