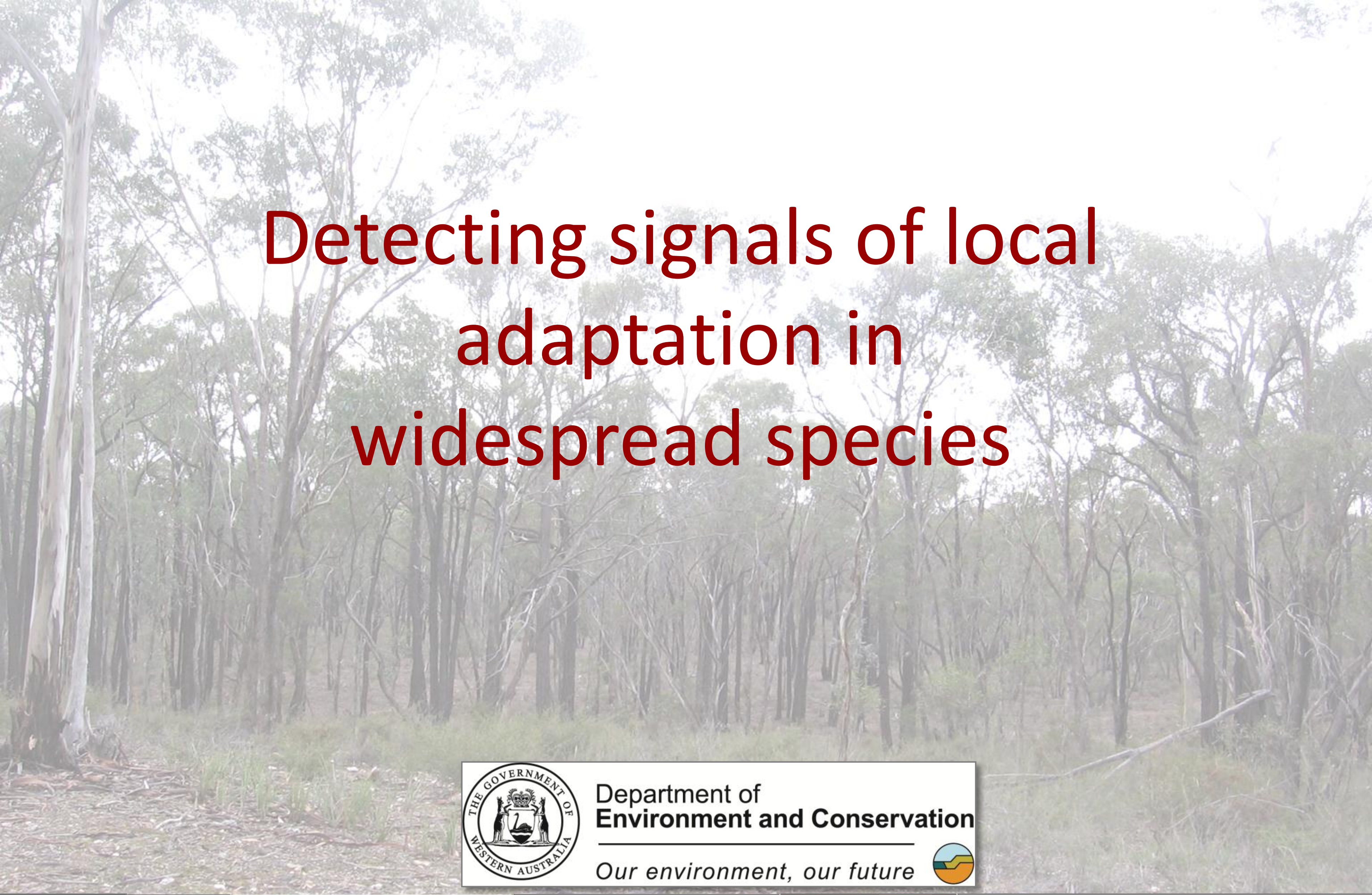


# Detecting signals of local adaptation in widespread species

Department of
**Environment and Conservation**

*Our environment, our future*

CSIRO

UTAS

NCCARF
National
Climate Change Adaptation
Research Facility

CENTRE *for*
ECOSYSTEM
MANAGEMENT
EDITH COWAN UNIVERSITY

AUSTRALIA
ECU
EDITH COWAN
UNIVERSITY

University of the
Sunshine Coast
The best of both worlds

# What should we plant?

Current paradigm for revegetation projects:

Use locally sourced seed to:

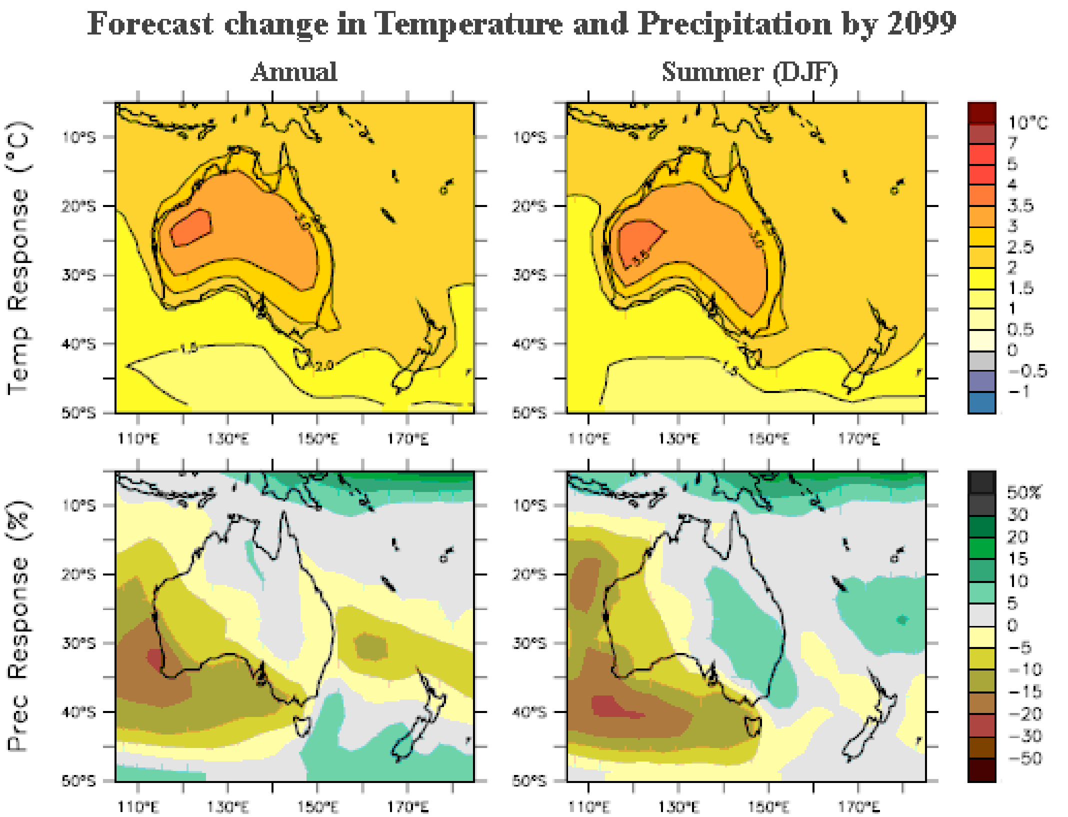
- ➢ maintain current patterns of genetic variation
- ➢ avoid problems of:
    - ❖ poorly adapted germplasm
    - ❖ genetic contamination of local populations
    - ❖ outbreeding depression

Image: P Tilyard

# But is this appropriate when environmental conditions are changing?

Models of climate change in Australia predict shifts in geographic and temporal patterns of:

- Rainfall
- Temperature
- Drought
- Flooding
- Fire frequency



Annual mean and summertime (December-January-February) changes for the period 1980-1999 vs. 2080-2099. Image credit: [2007 IPCC report](#).

# Widespread foundation species live in diverse environments

Is there adaptive genetic variation across environmental gradients?

If so, can we exploit it to:

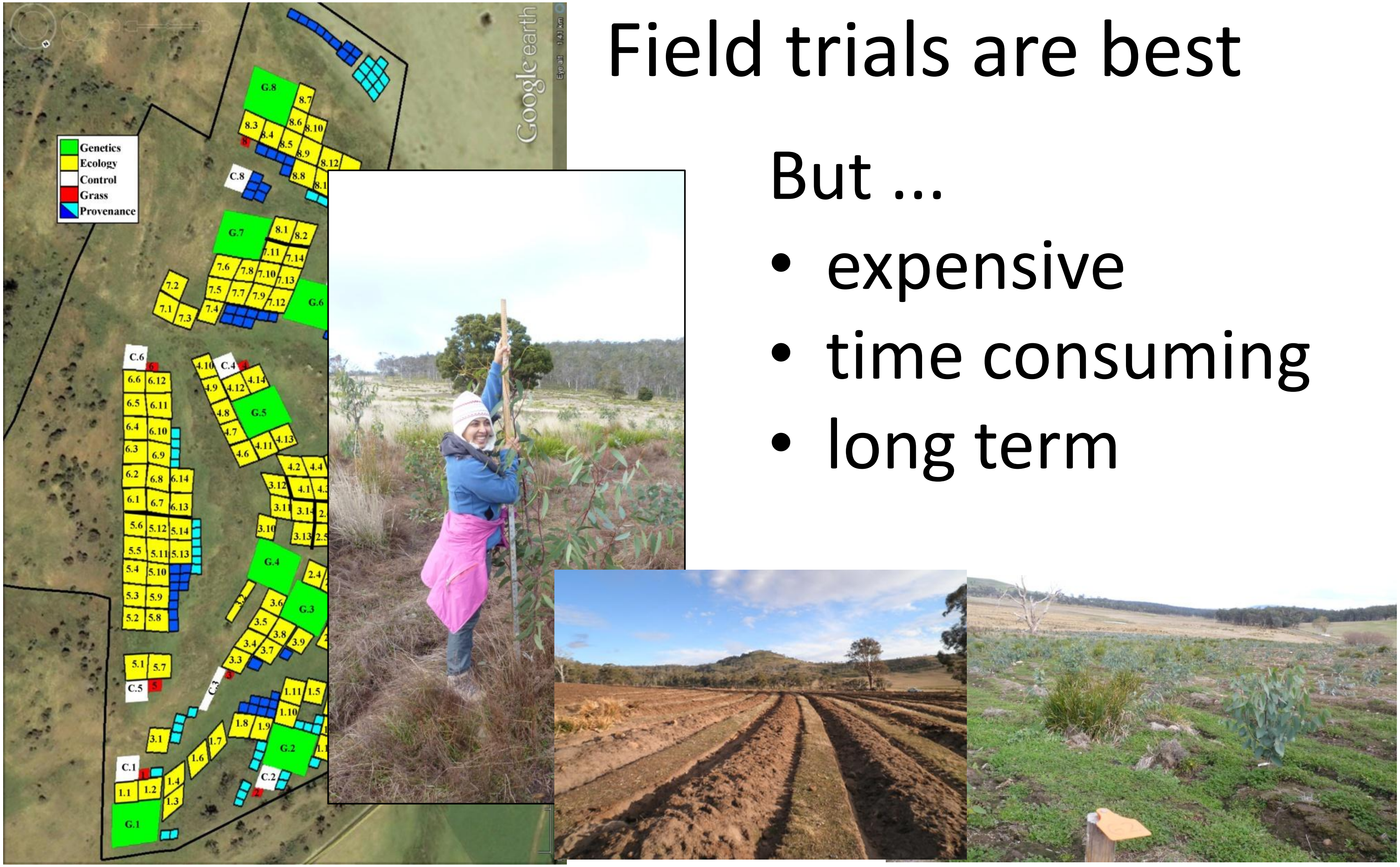
- facilitate the persistence of plantings?
- maintain ecosystem functions?

*Eucalyptus tricarpa*, Victoria

Mean annual rainfall 440-1200 mm
Mean annual temperature 11-17°C

Images: E. Mclean

# Detecting adaptive variation



Field trials are best

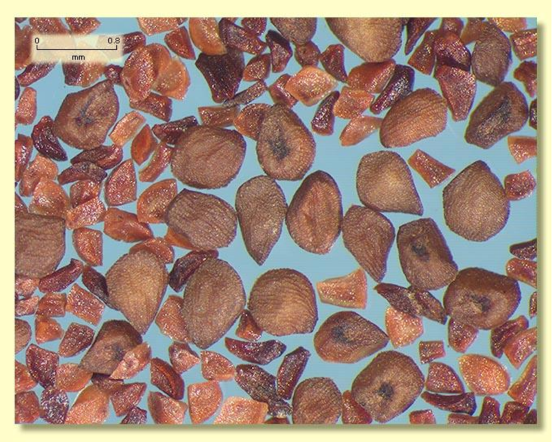
But ...

- expensive
- time consuming
- long term

# A genomic approach to:

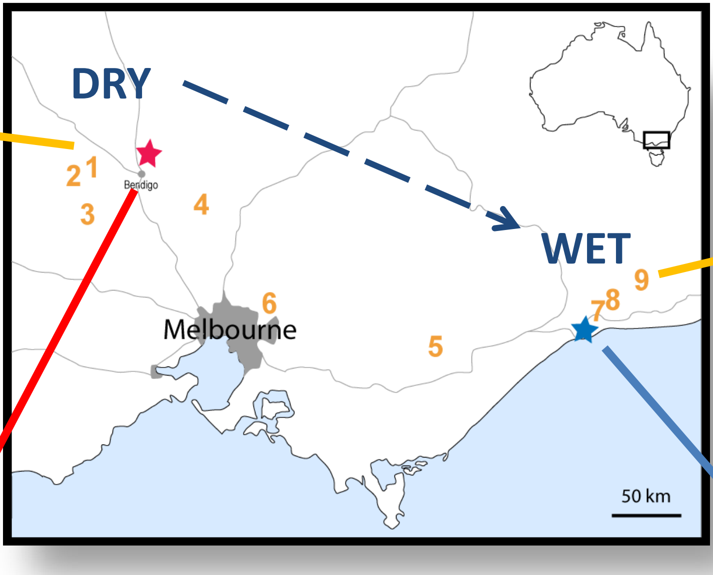
- studying adaptation in restoration species
- developing seed transfer guidelines

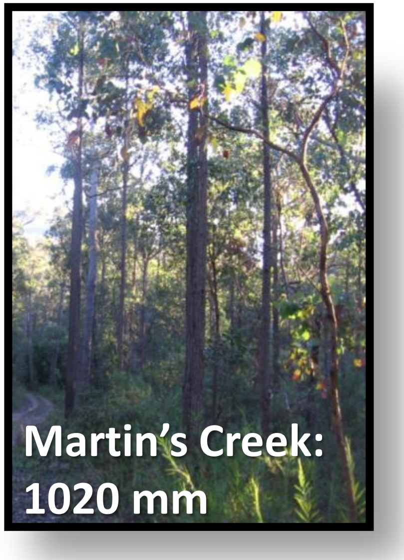
mage: P Tilyard



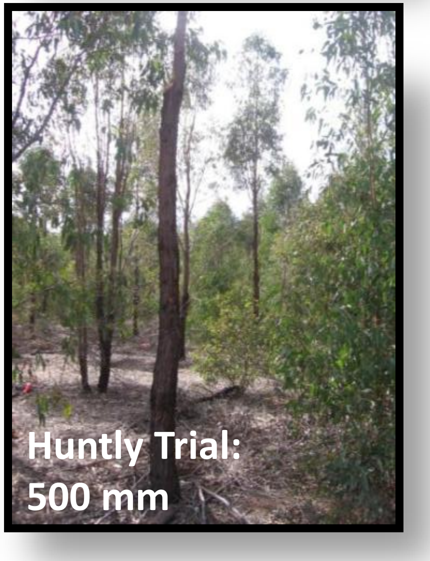
# *Eucalyptus tricarpa* grows across a rainfall gradient in southeastern Australia

Tarnagulla: 460 mm



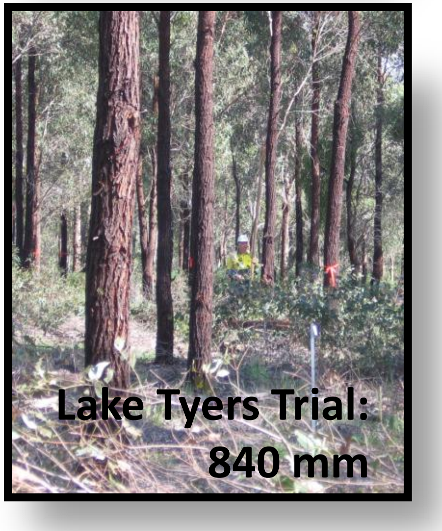


Martin's Creek: 1020 mm



Huntly Trial: 500 mm

- **Nine provenances**
- **Genomic Analysis:**
  30 trees/provenance
  DArTseq markers
- **Functional Trait analysis:**
  10 trees/provenance in the wild and in 12 y.o field trials.



Lake Tyers Trial: 840 mm

# Functional trait measurements

Plant, Cell & Environment

*Plant, Cell and Environment* (2014) **37**, 1440–1451

doi: 10.1111/pce.12251

**Original Article**

**Plasticity of functional traits varies clinally along a rainfall gradient in *Eucalyptus tricarpa***

Elizabeth H. McLean[1,2], Suzanne M. Prober[2], William D. Stock[3], Dorothy A. Steane[4,5], Brad M. Potts[4], René E. Vaillancourt[4] & Margaret Byrne[1]

**Morphology**

Leaf size

Leaf thickness

Leaf density

Specific leaf area

Circumference of main stem

Total cross-sectional area

Tree height

Trait plasticity

**Physiology**

Cellulose $^{13}$C

Leaf $^{13}$C

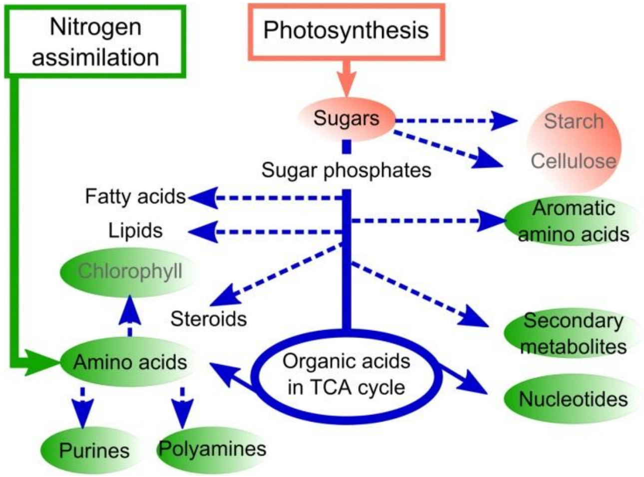
Leaf $^{15}$N

$C_{mass}$

C/N ratio

Leaf $N_{area}$

Leaf $N_{mass}$



# Genomic analysis

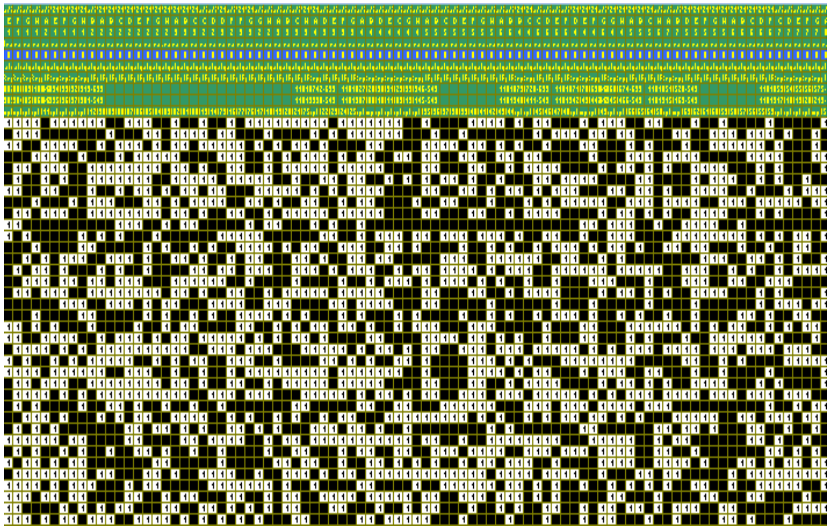
**DArTseq**

Genome-wide genotyping using next generation (short-read) sequencing of a set of restriction fragments from whole genome

(1) Presence/absence data

(2) Sequence data (70 bp)

Thousands of markers distributed across genome



274 individual trees

6,544 DArTseq markers

35 climatic variables -> 15 climatic variables

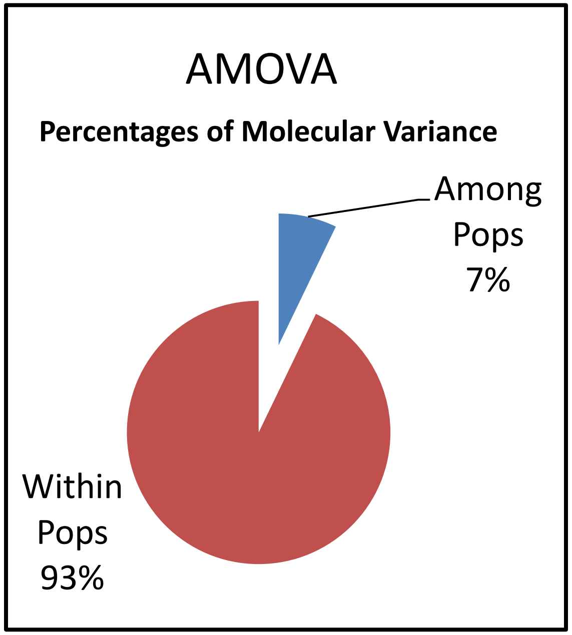
15 functional traits

# There is genetic structure across populations

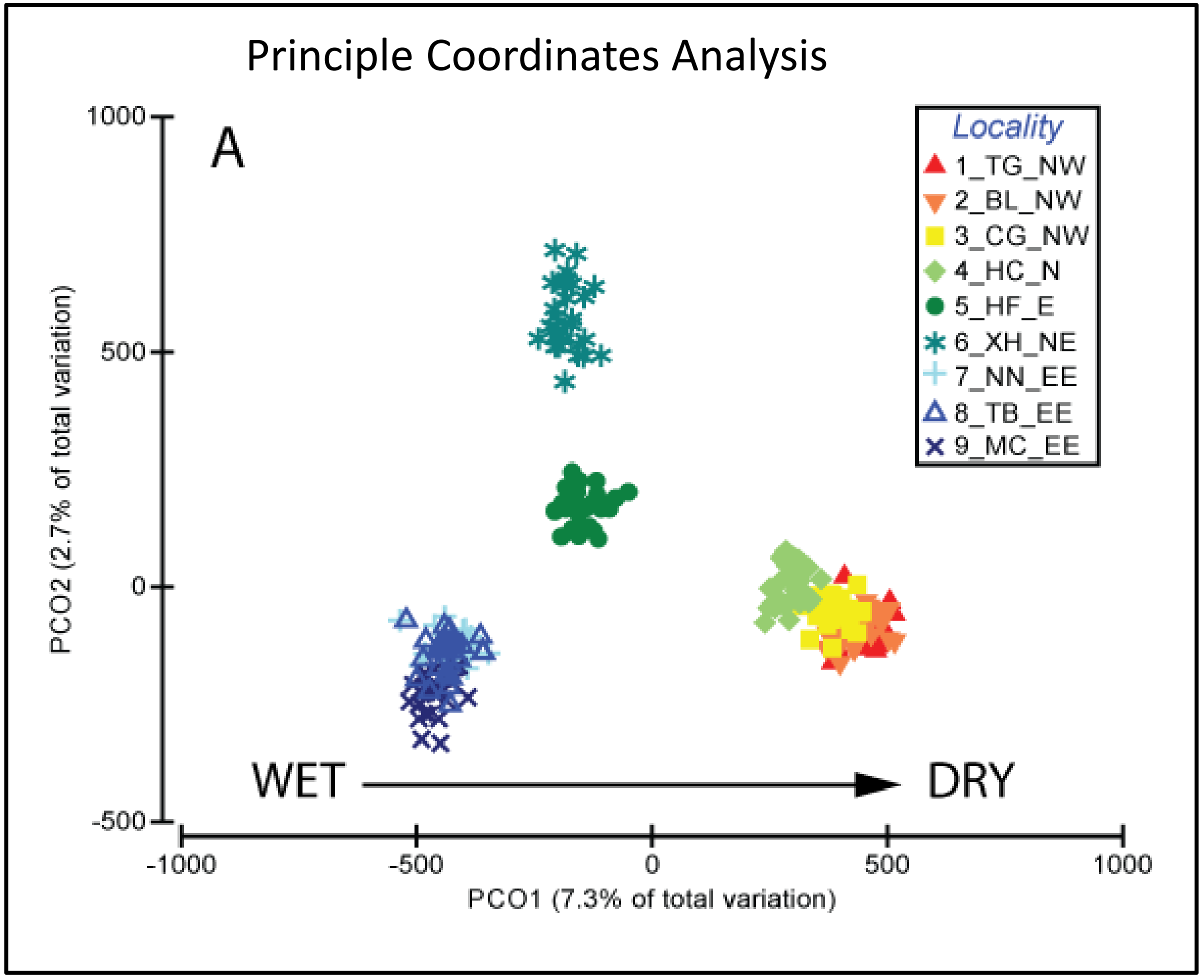
274 trees

9 populations

6,544 markers

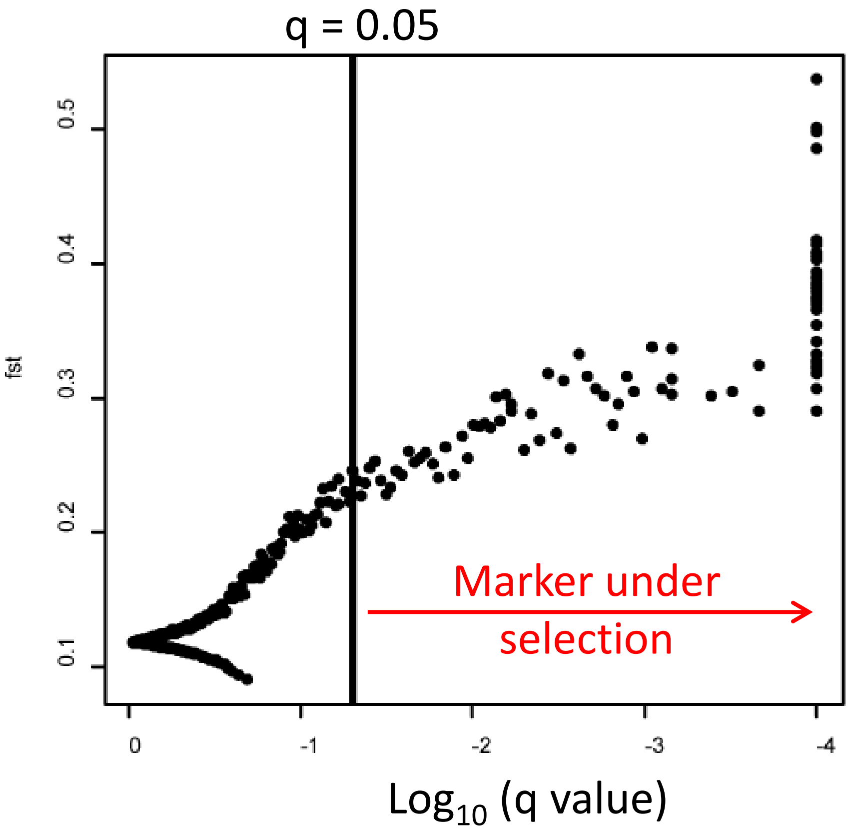

AMOVA

**Percentages of Molecular Variance**


Principle Coordinates Analysis

… but how much of it is adaptive?

# Fst outlier analysis identifies markers that may be under selection



Fst – degree of inbreeding within sub-populations relative to the whole population (based on allele frequencies)

Outlier analysis – plots marker Fst values against the probability that the allele frequency of a marker differs more among subpopulations than would be expected from chance (drift).

Bayescan 2.1 (Foll & Gaggiotti 2008)

# Outliers provide an 'adaptively enriched genetic space'

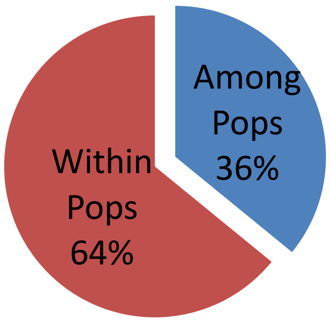
274 trees

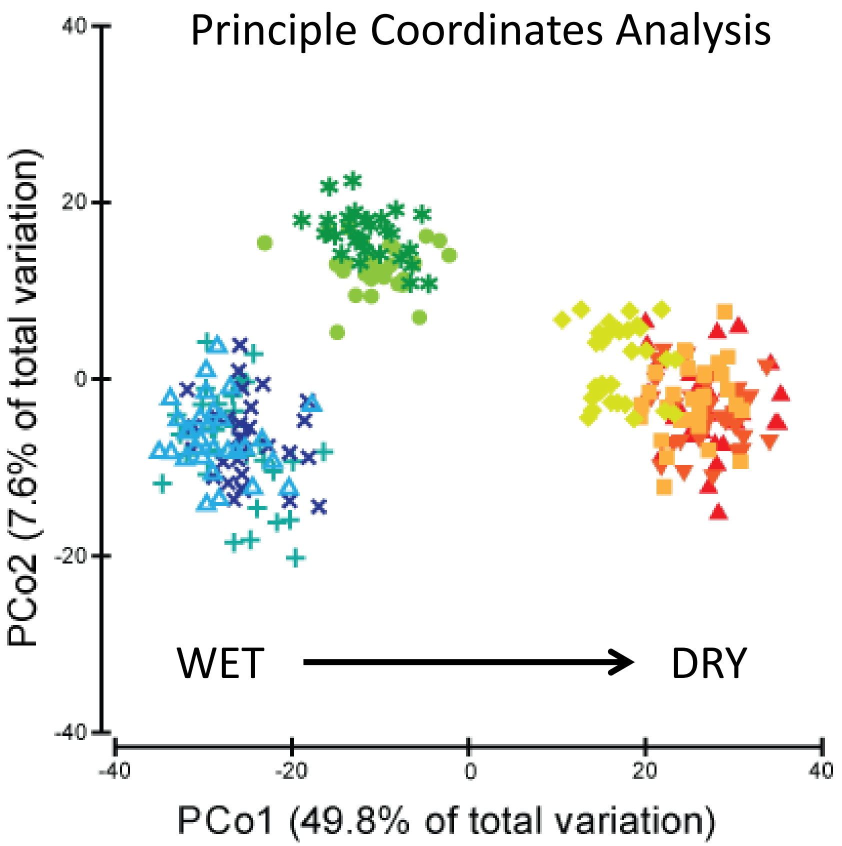
9 populations

94 outlier markers

AMOVA

**Percentages of Molecular Variance**




Principle Coordinates Analysis

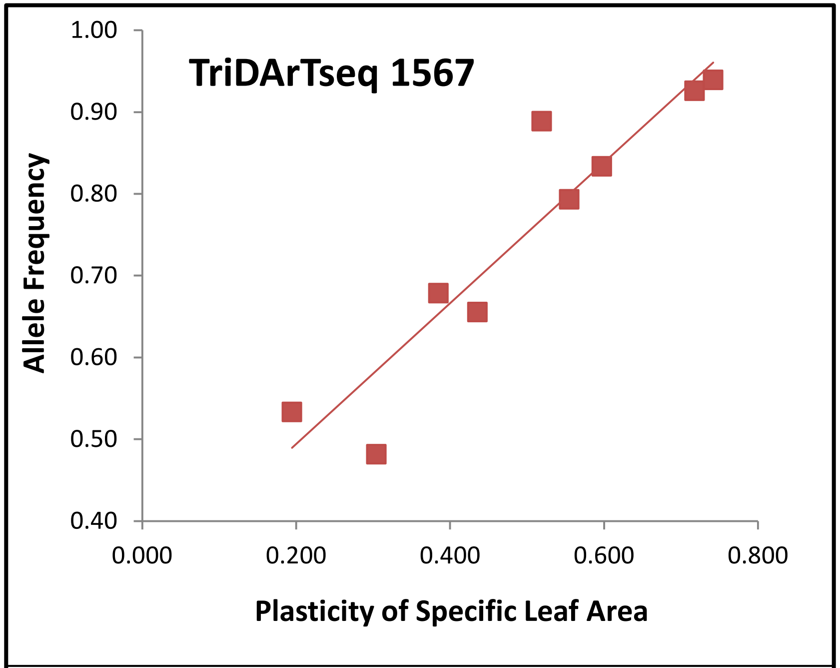
# But what evidence is there that the outlier markers are ‘adaptive’?

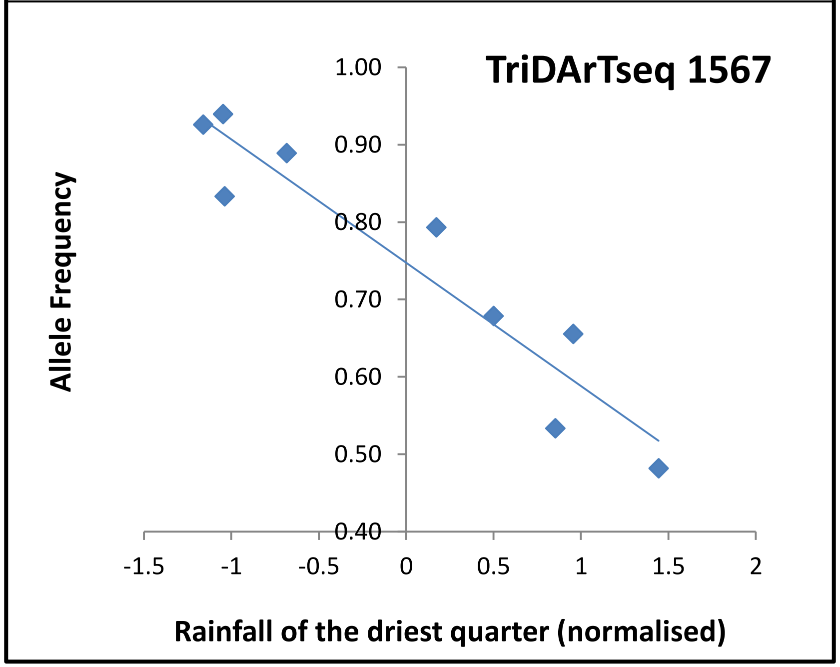
*Are allele frequencies across populations correlated with*
*(i) functional trait variation, or*
*(ii) changes in an environmental variable?*

We did LOTS of linear regressions!

| | **94 outliers** | **3,590 neutral** |
|---|---|---|
| **35 Climatic variables** | 3,290 | 125,650 |
| **15 Soil variables** | 1,410 | 53,850 |
| **14 Wild population traits** | 1,316 | 50,260 |
| **28 Common garden traits** | 2,632 | 100,520 |

… correcting for multiple testing using a ‘Dependent False Discovery Rate’ (DFDR) of 5%





# All outlier loci were correlated with climate and/or functional traits

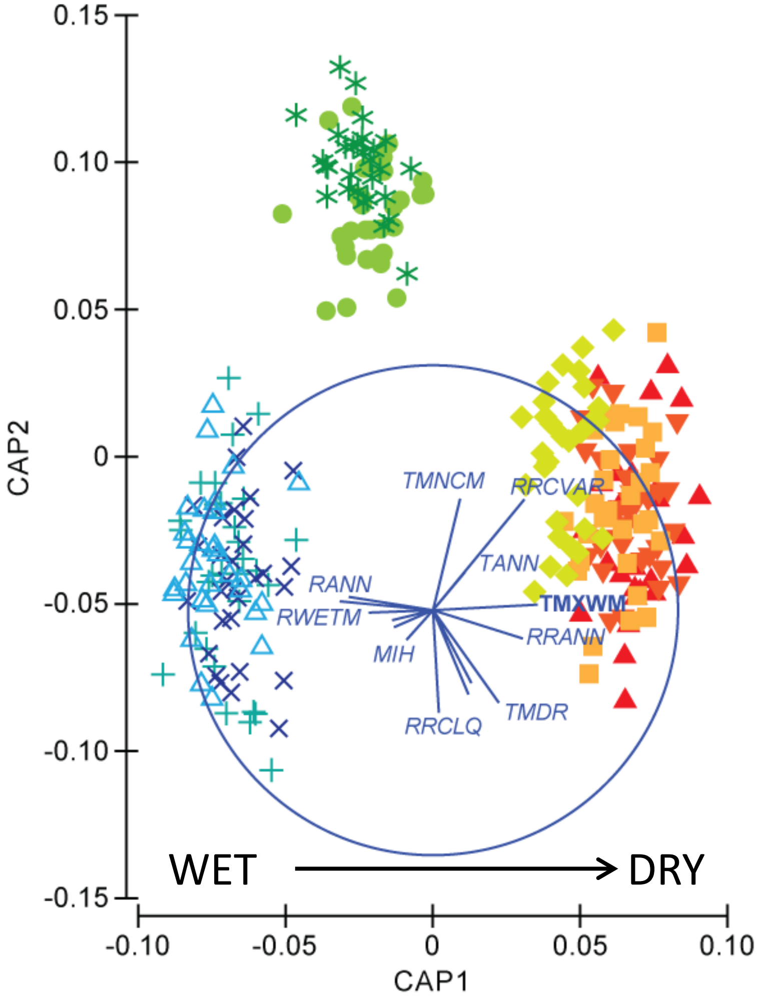
100% associated with at least one climate variable (8X*)

82% associated  with at least one functional trait (3X*)

75% associated with both functional traits and climate variables

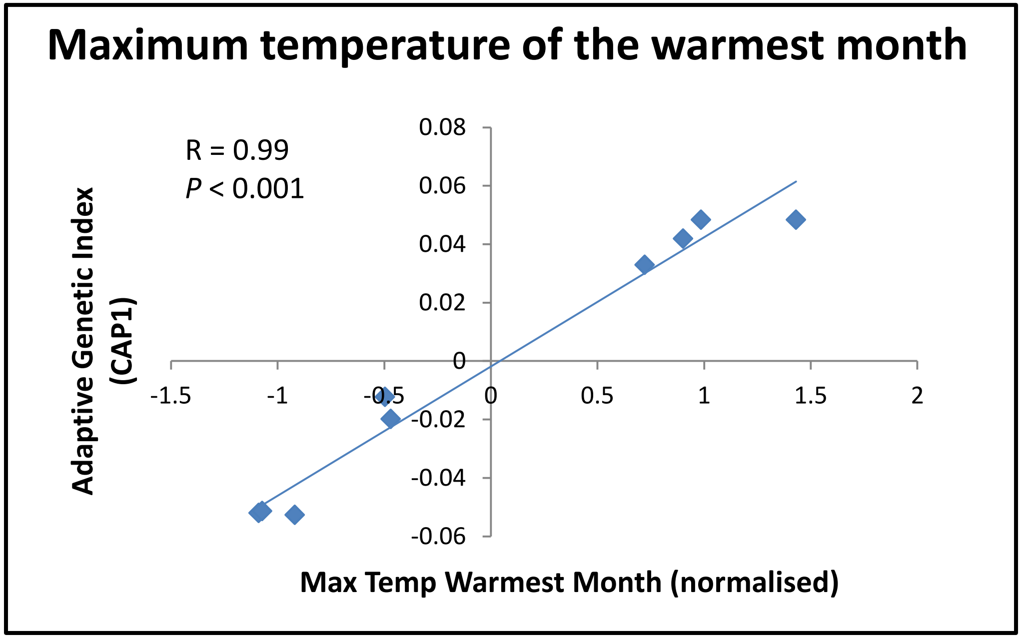
*increase in number of marker-trait associations ($P$<0.001) relative to neutral markers

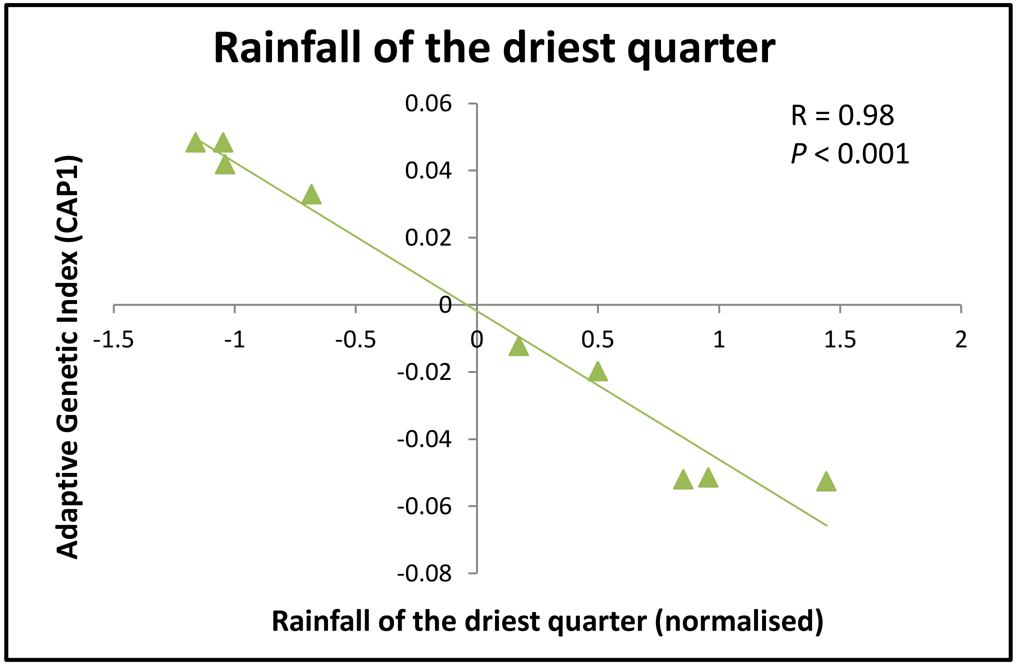
# Canonical Analysis of Principle Coordinates provides a ‘climate-aligned adaptive genetic index’



PERMANOVA software (Anderson *et al.* 2008)

CAP1 represents the direction of molecular change most closely associated with change in climate.

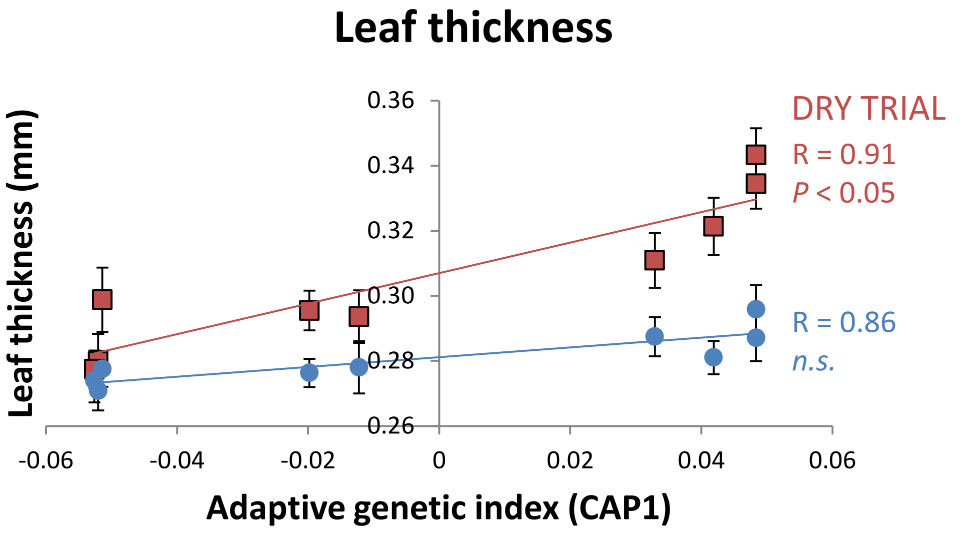




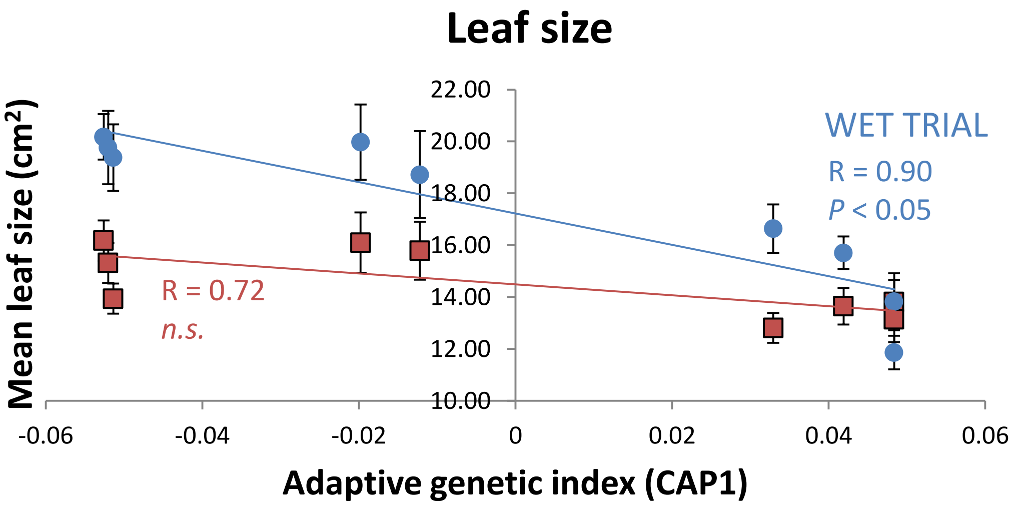
# Population-level variation in outlier markers, as described by CAP1, is strongly associated with climate variation.

23/35 climatic variables were significantly (P<0.05) associated with change in CAP1.

Strongest associations were with factors that contribute to summer aridity.



Higher CAP1 = genetically thicker leaves (dry site)



Higher CAP1 = genetically smaller leaves (wet site)

# Population-level variation in outlier markers (CAP1) is correlated with quantitative genetic changes in functional traits.

# CAP1 describes molecular genetic change associated with adaptation of *E. tricarpa* populations to increasing aridity.

# CAP1 forms the foundation of a management metric

Aridity Index (AI) = $\Sigma a_i b_i$

$a$ = normalised climatic variable, $x$

$b$ = the weighting of the climatic variable on the canonical eigenvector aligned with CAP1

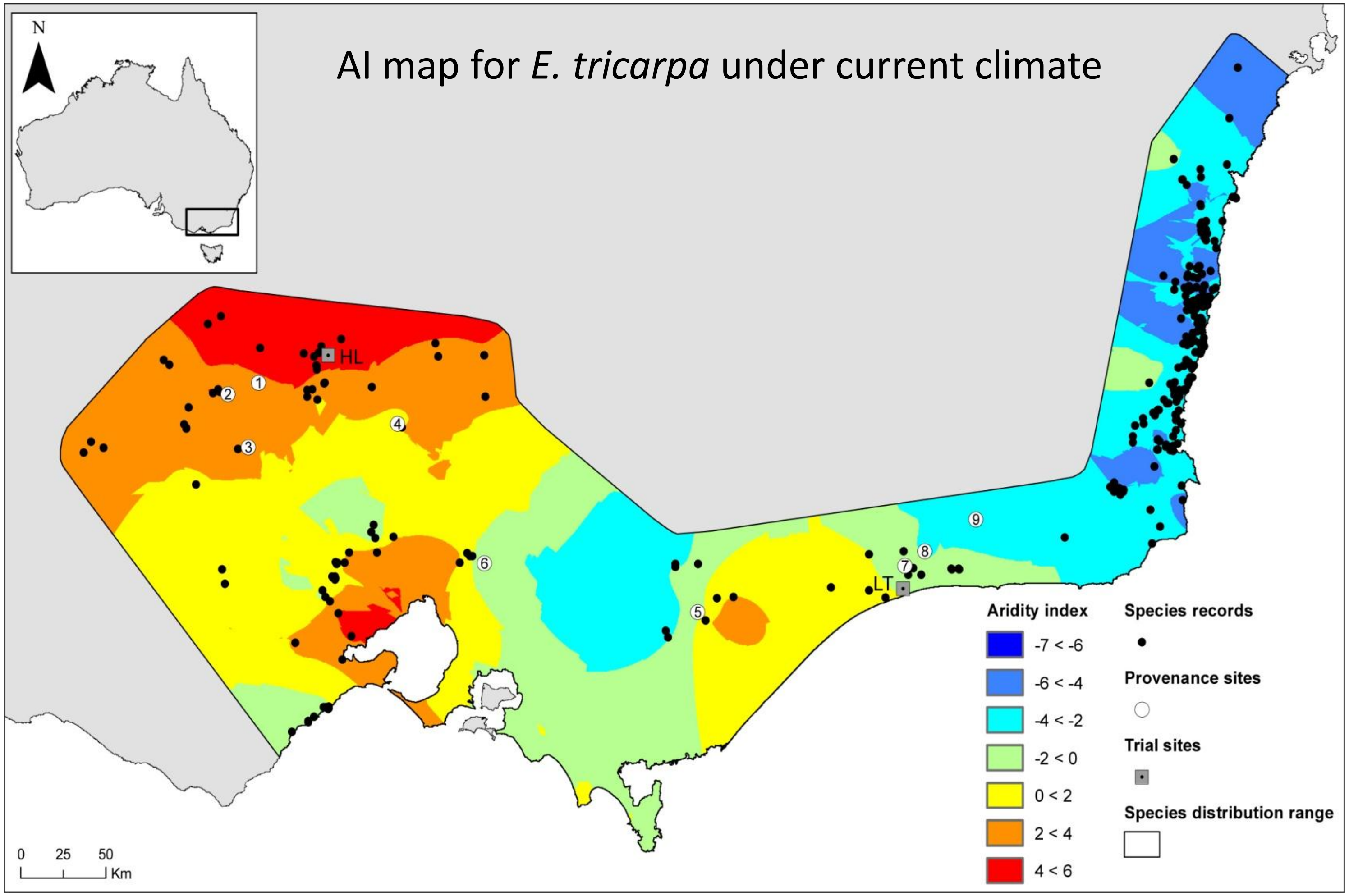
EXAMPLE

$AI_{TARNAGULLA} = (TMXWM_{TARN} \times CAP1_{TMXWM}) + (RANN_{TARN} \times CAP1_{RANN}) + (TMNCM_{TARN} \times CAP1_{TMNCM})$

$= (1.431 \times 0.421) + (-1.251 \times -0.343) + (0.068 \times 0.134)$

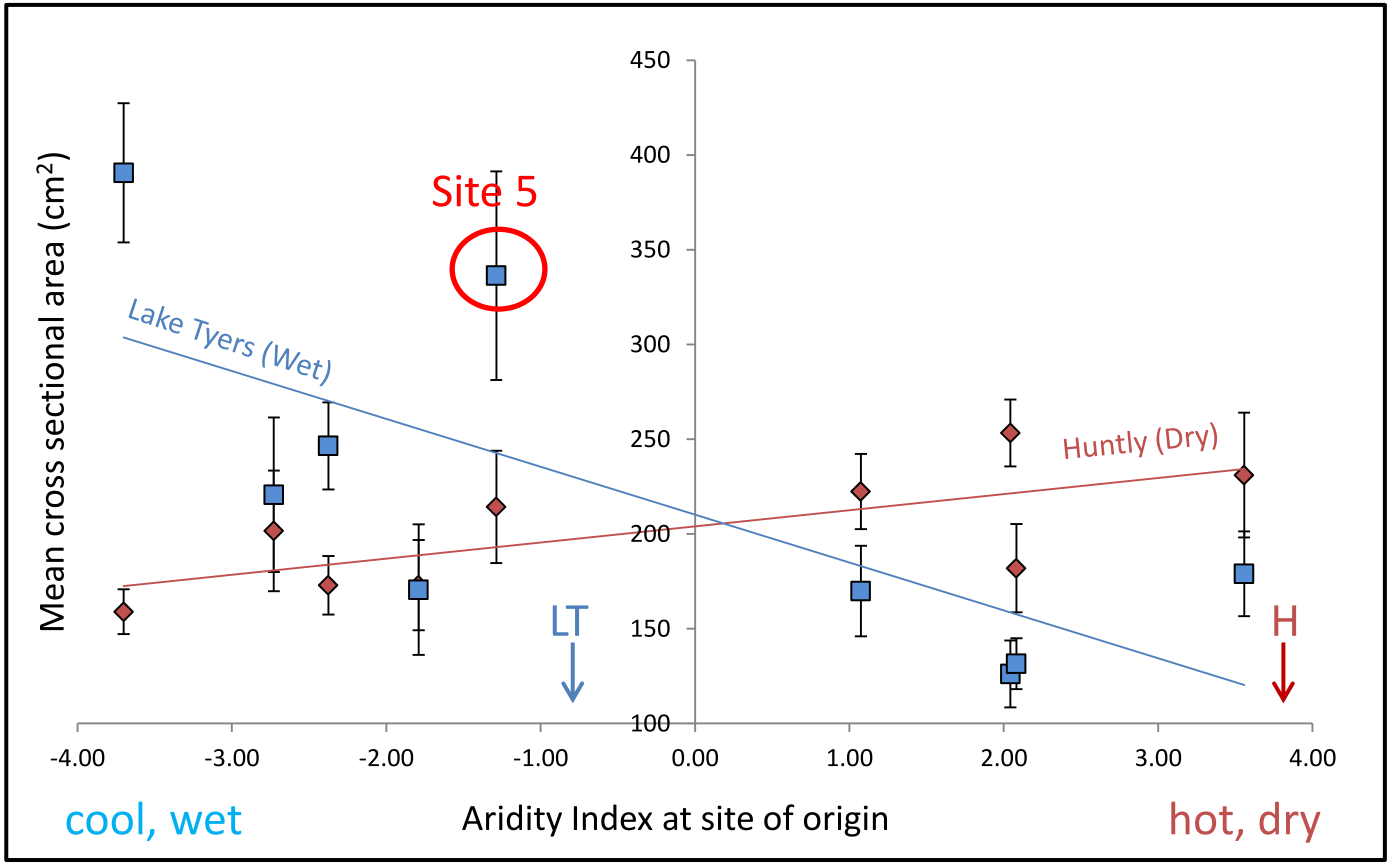
$= 2.290$

# Seed transfer guidelines?



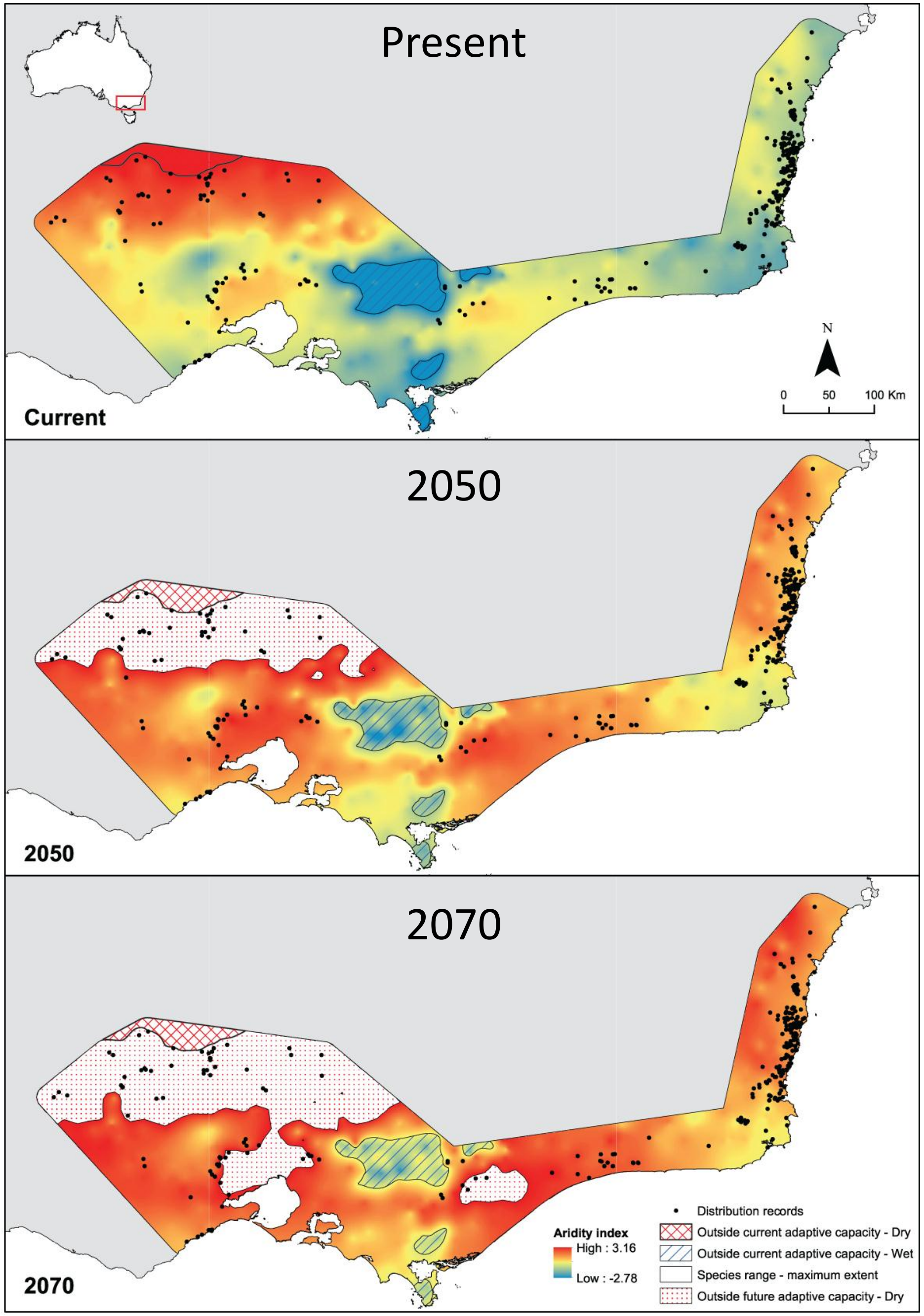
AI map for *E. tricarpa* under current climate

# But does it work?



Seed from drier areas (higher AI) grew better at drier trial
Seed from wetter areas (lower AI) grew better in wetter trial

# Guidelines for assisted migration?



CSIRO global climate model for 2050 and 2070

# The Team

Dr Margaret Byrne
Plant Conservation Geneticist
Dept. Conservation and Environment, WA

A/Prof René Vaillancourt
Plant Geneticist
University of Tasmania

Prof Brad Potts
Forest Geneticist
University of Tasmania

Dr Dorothy Steane
Plant Geneticist
University of Tasmania and
University of the Sunshine Coast

Dr Elizabeth McLean
Plant Physiologist
DEC WA/CSIRO

Prof William Stock
Plant Physiologist
Edith Cowan University, WA

Dr Suzanne Prober
Plant Ecologist
CSIRO Ecosystem Science, WA

Peter Harrison
GIS expert
University of Tasmania