The genetic and ecological basis of adaptation and speciation

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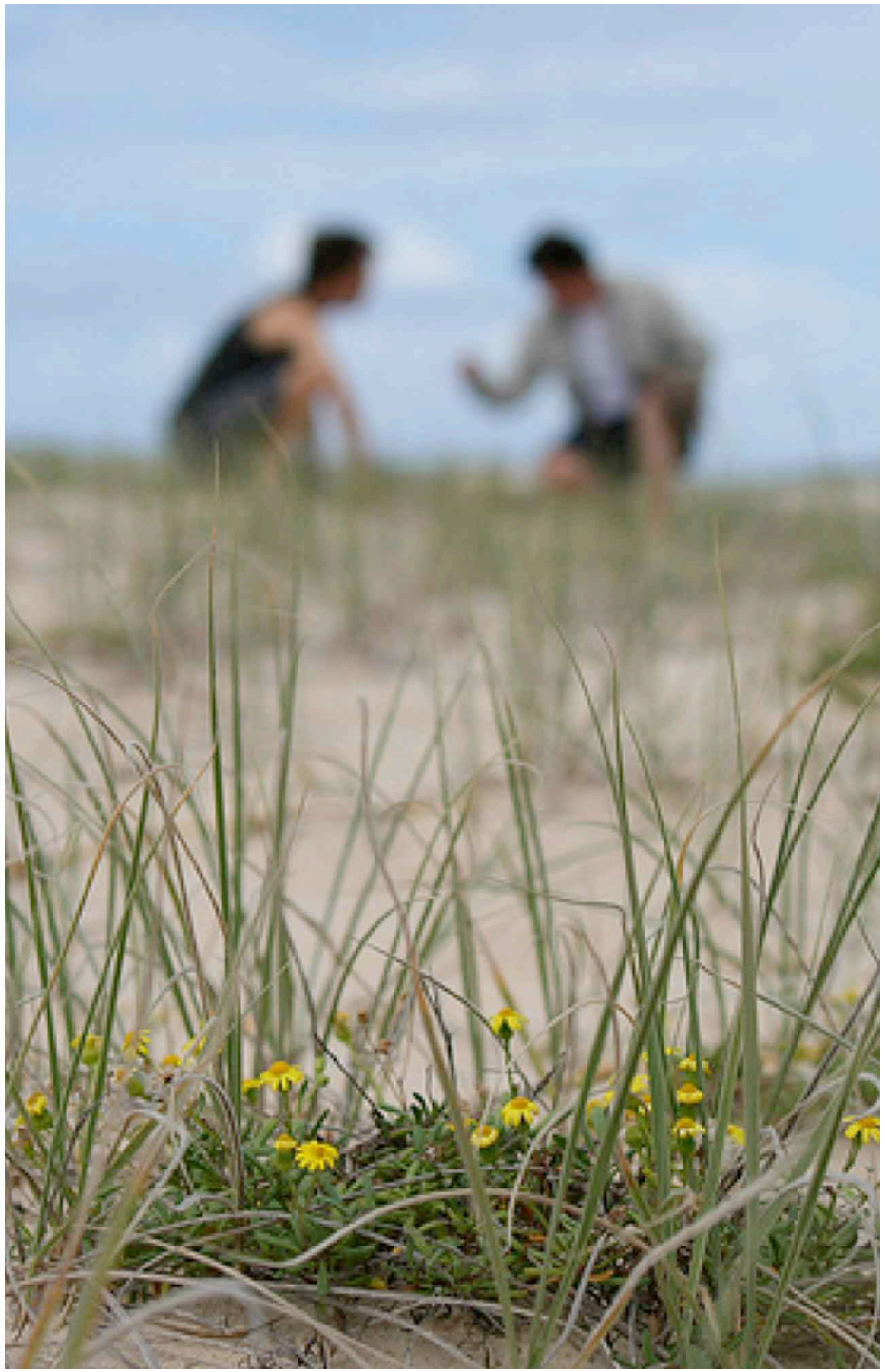


Research program

1) Does divergent natural selection drive the early stages of speciation?

2) What is the genetic architecture of speciation with gene flow?

3) What genes contribute to the origins of reproductive isolation?

4) Does gene flow constrain or promote divergence?

Experimental approaches

1) Classical and quantitative genetics in glass house conditions

2) Reciprocal transplants of targeted genotypes to native habitats

3) Reconstruction experiments

4) Population genomic analyses

The system

1) *Senecio pinnatifolius*, one of ~90 Australian endemics

2) n=20 chromosomes, genome size ~ 2.4pg

3) Multiple varieties, annual to short lived perennials

4) Parapatric and allopatric populations

5) Continental-wide distribution

6) ~8 weeks seed to seed

High alpine meadows in Victoria Kosciusko National Park

Coastal beach and sand dunes in Eastern Australia

Exposed coastal rocky headland in Eastern Australia

Tableland habitat on the Great Dividing Range in New South Wales

Individuals of Dune and Headland types in glasshouse and natural conditions

HEADLAND

DUNE

Leaf shape variation in F2 populations

Serrated

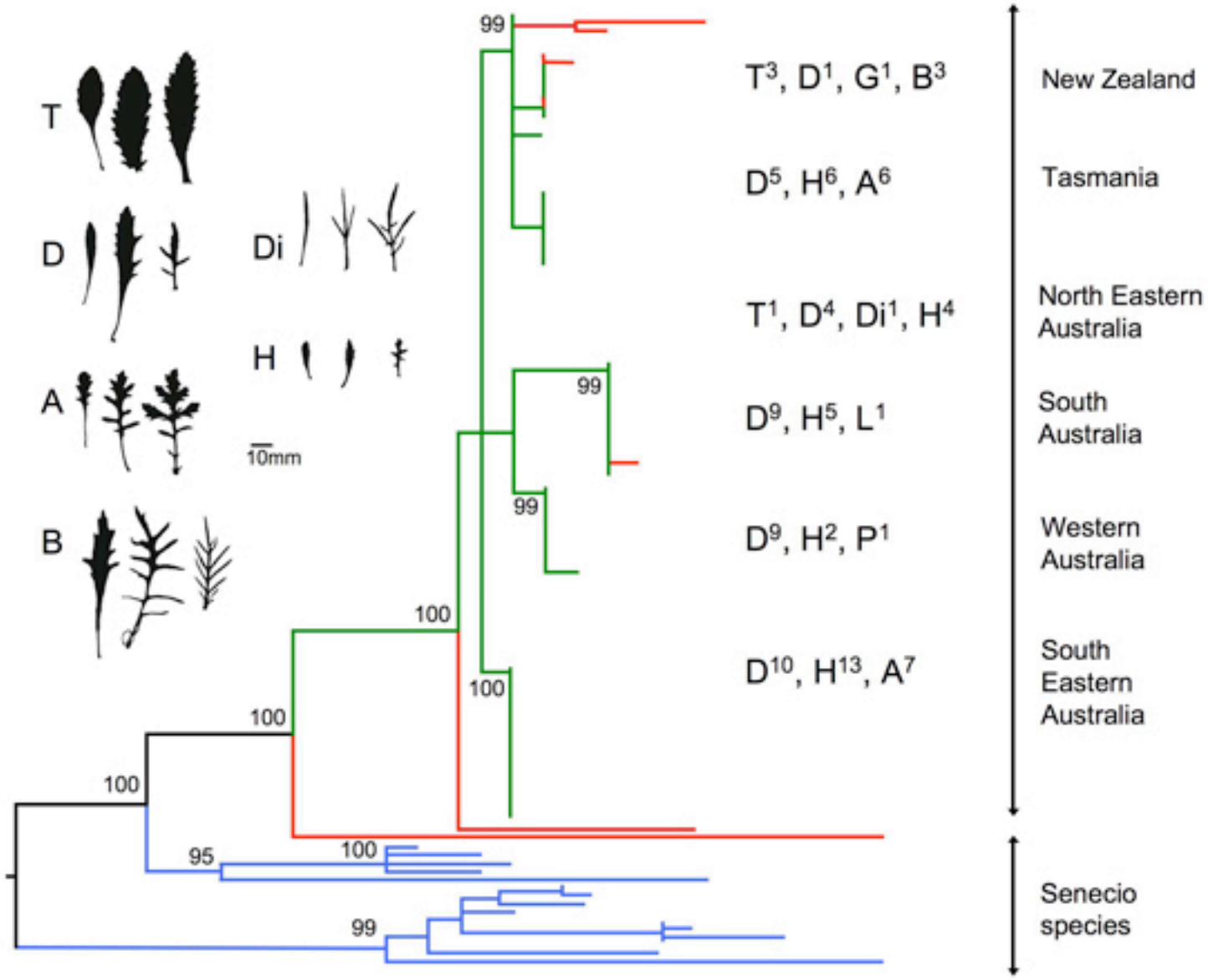
Wide

Smooth

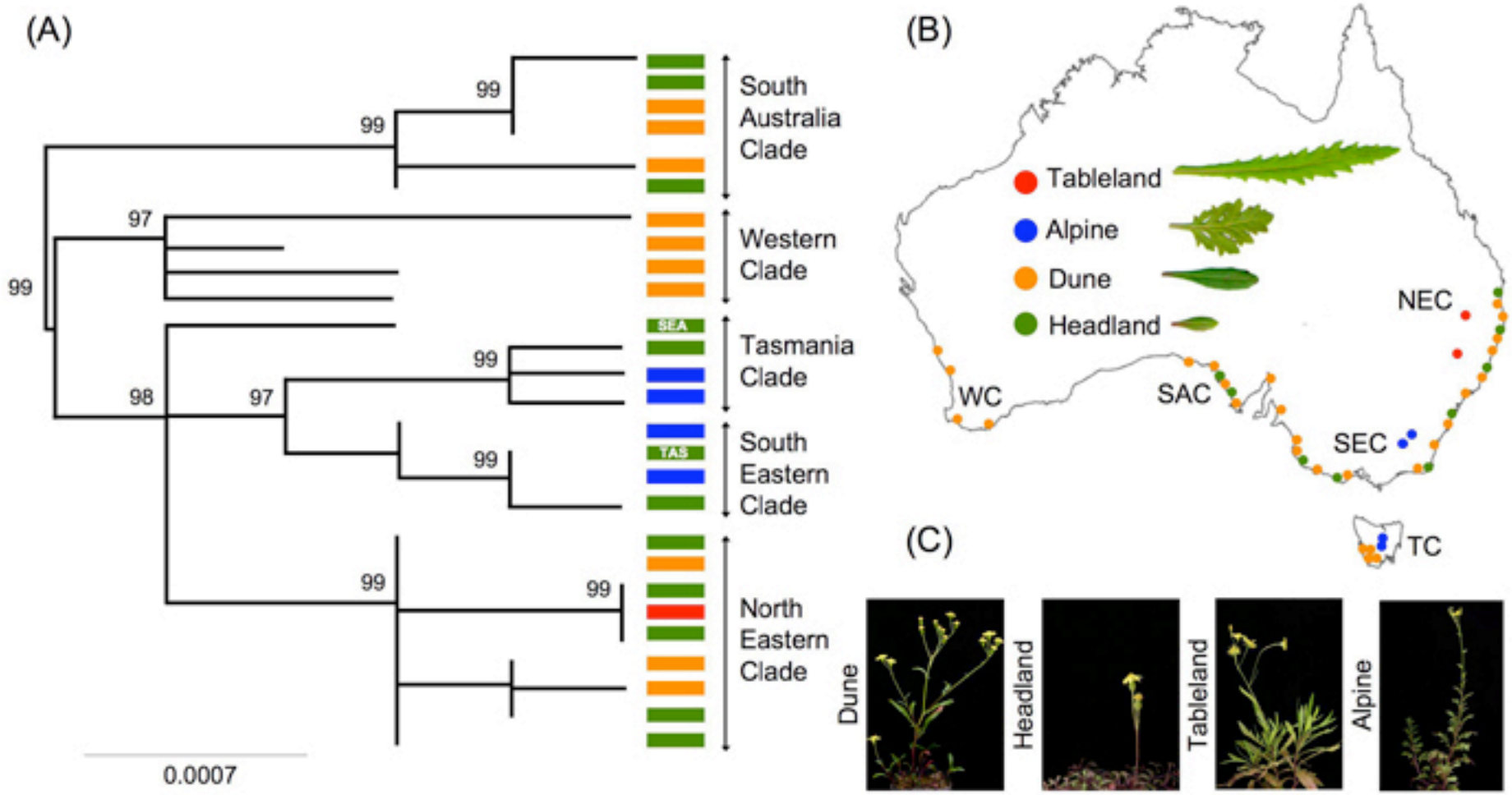
Mendelian segregation of growth habit

Cross	% Tall	n
Dune	95	51
Headland	7	52
F1	92	56
Backcross	53	384
F2	73	307

Rapid evolution of Senecio ecotypes



Parallel evolution of Senecio ecotypes



Ecological selection in *Senecio pinnatifolius*

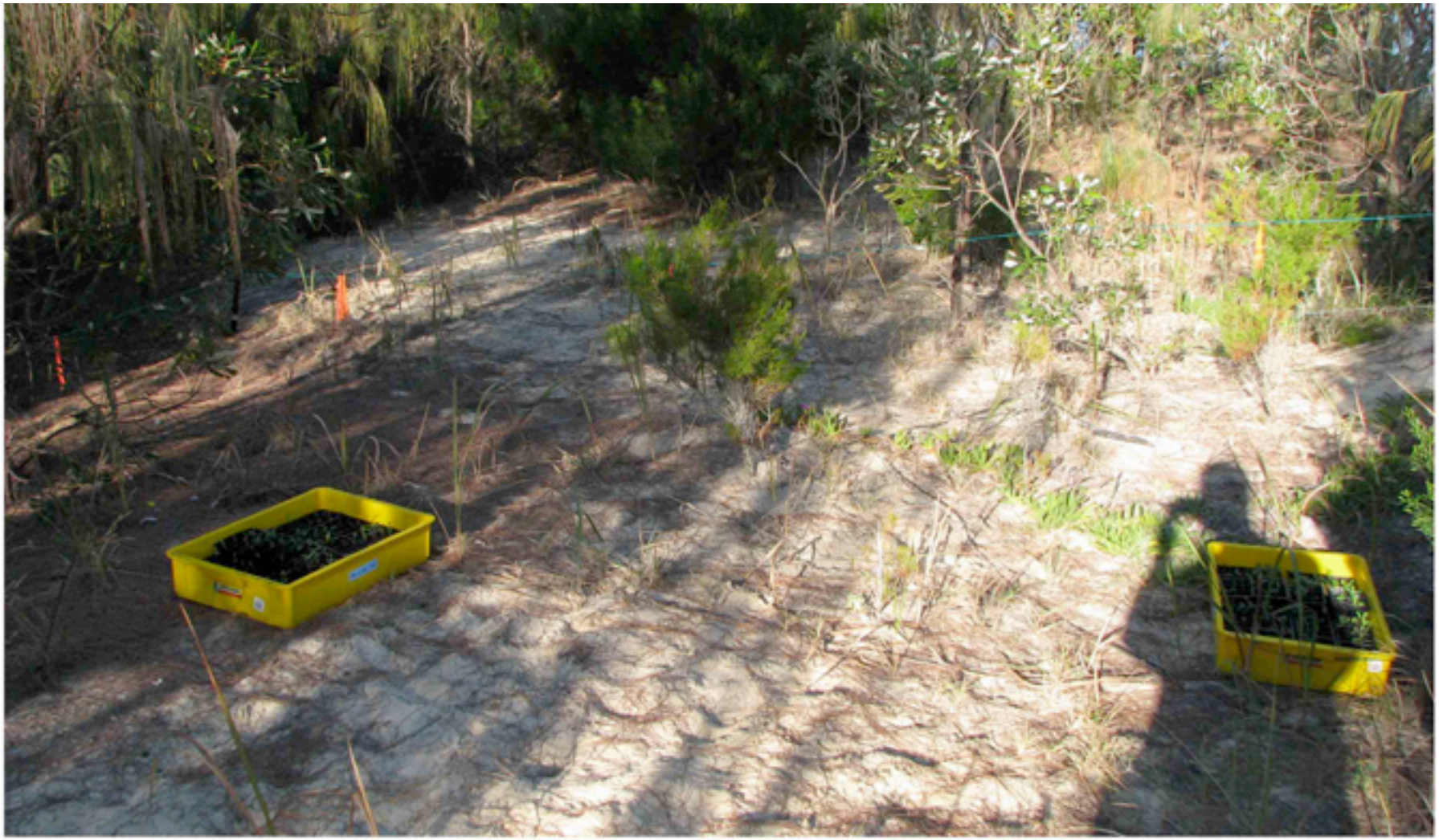
Field experiment in Stradbroke Island

Ecological selection in *Senecio pinnatifolius*

Field experiment in Stradbroke Island

Headland environment

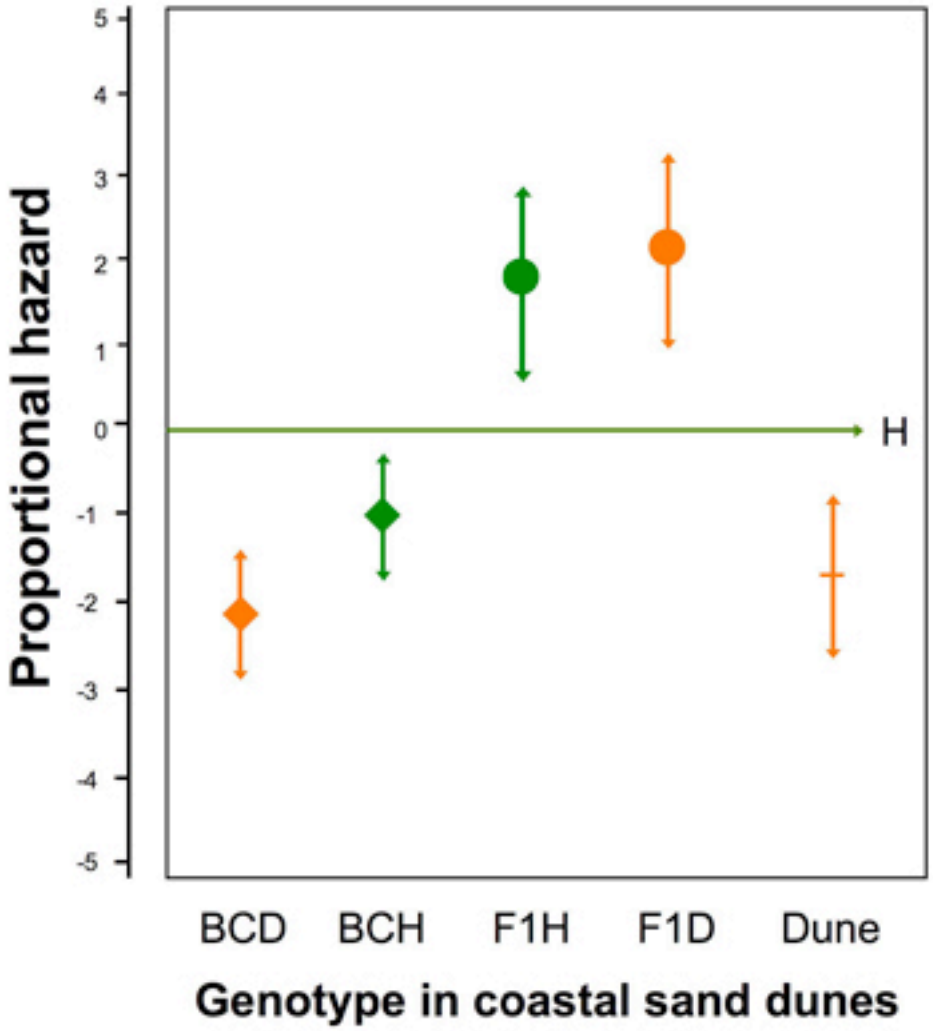
Field experiment in Stradbroke Island



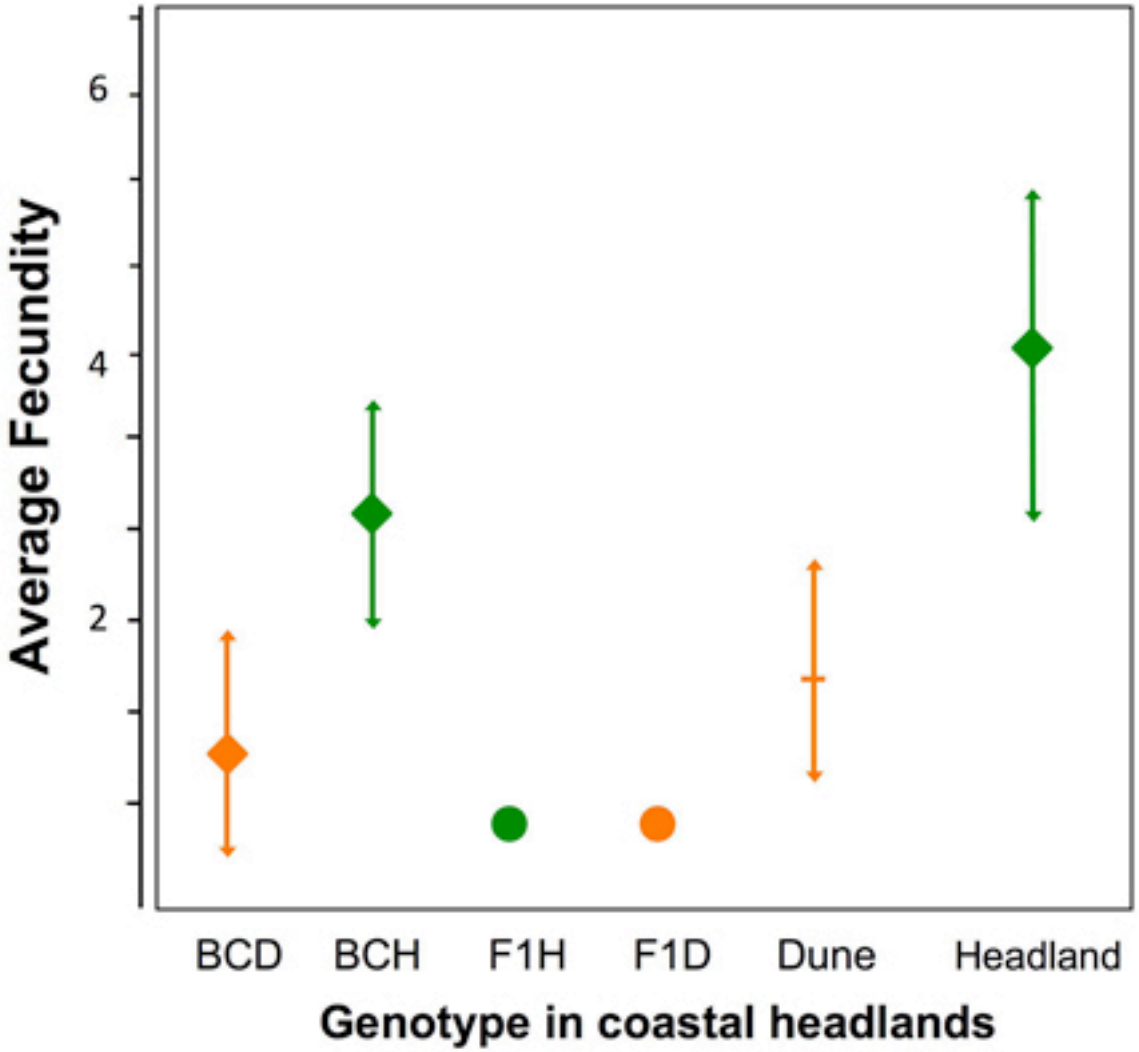
Sand dune environment

Field experiment in Stradbroke Island

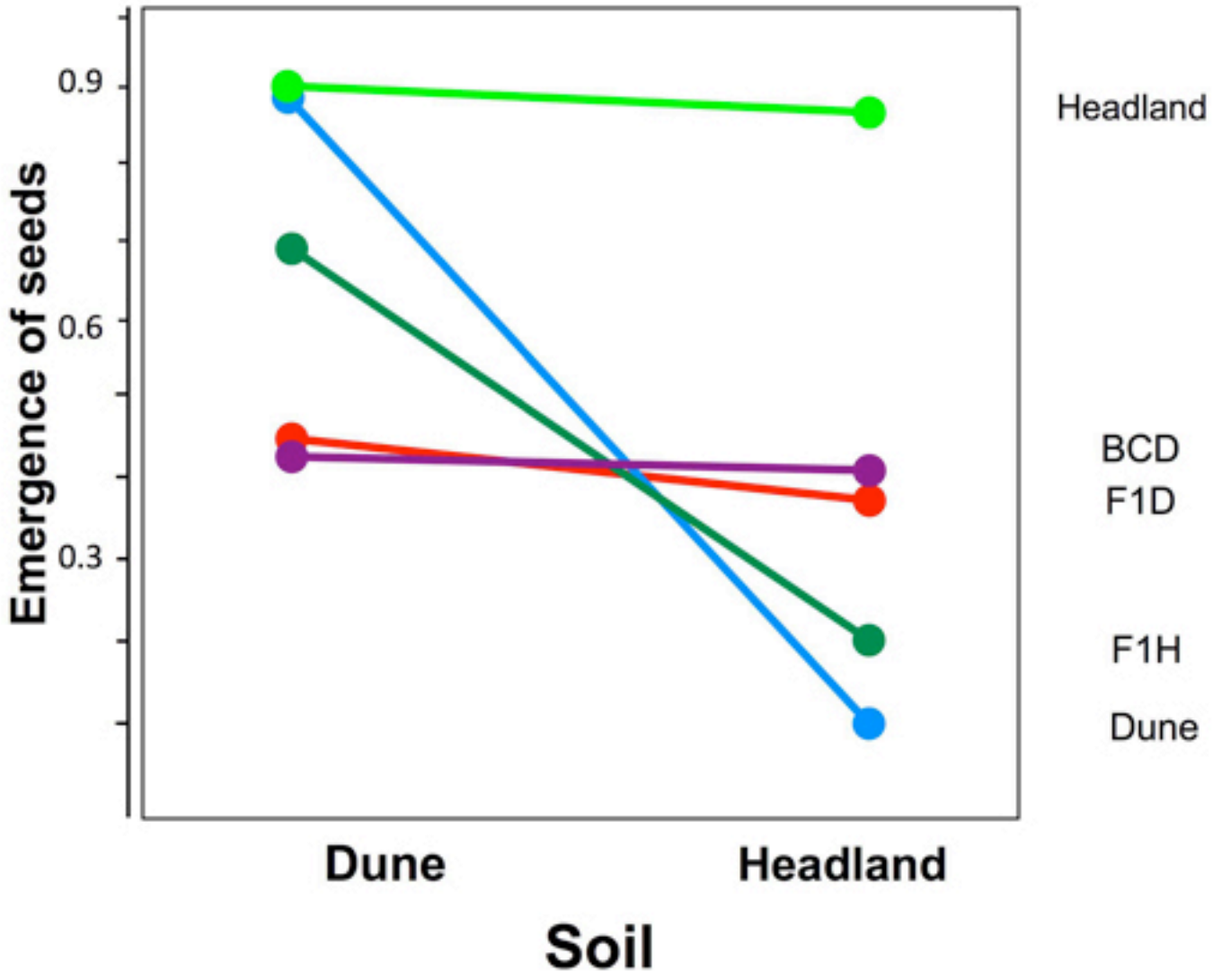
Extrinsic reproductive isolation



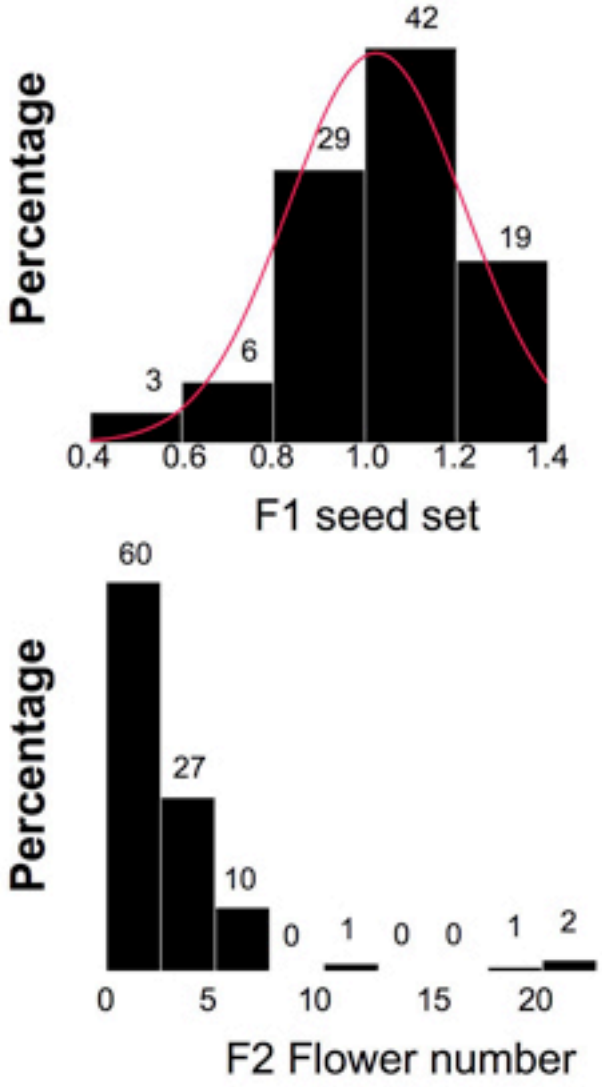
Extrinsic reproductive isolation



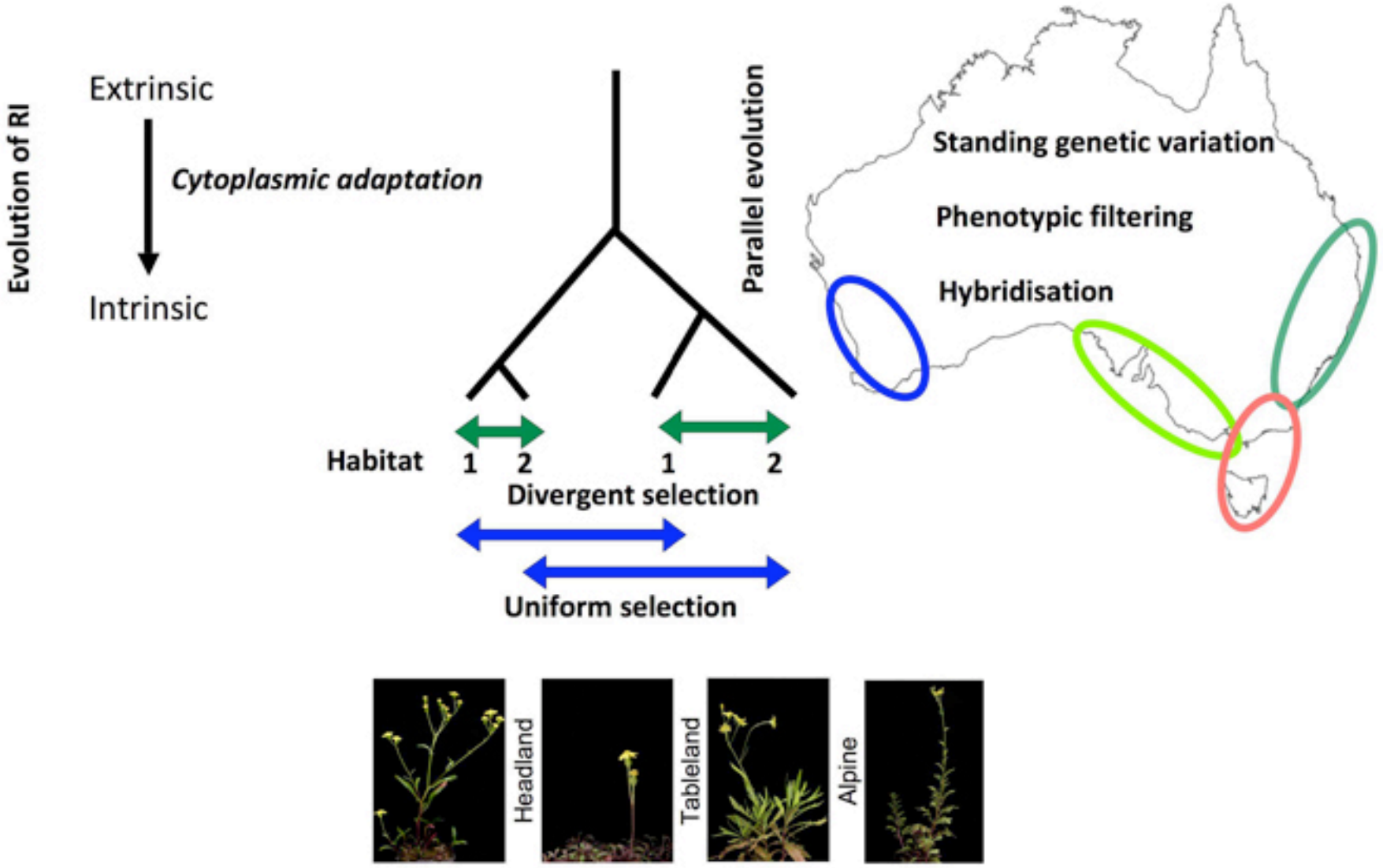
Extrinsic reproductive isolation



Intrinsic reproductive isolation



Evolving reproductive isolation



Population Genomics

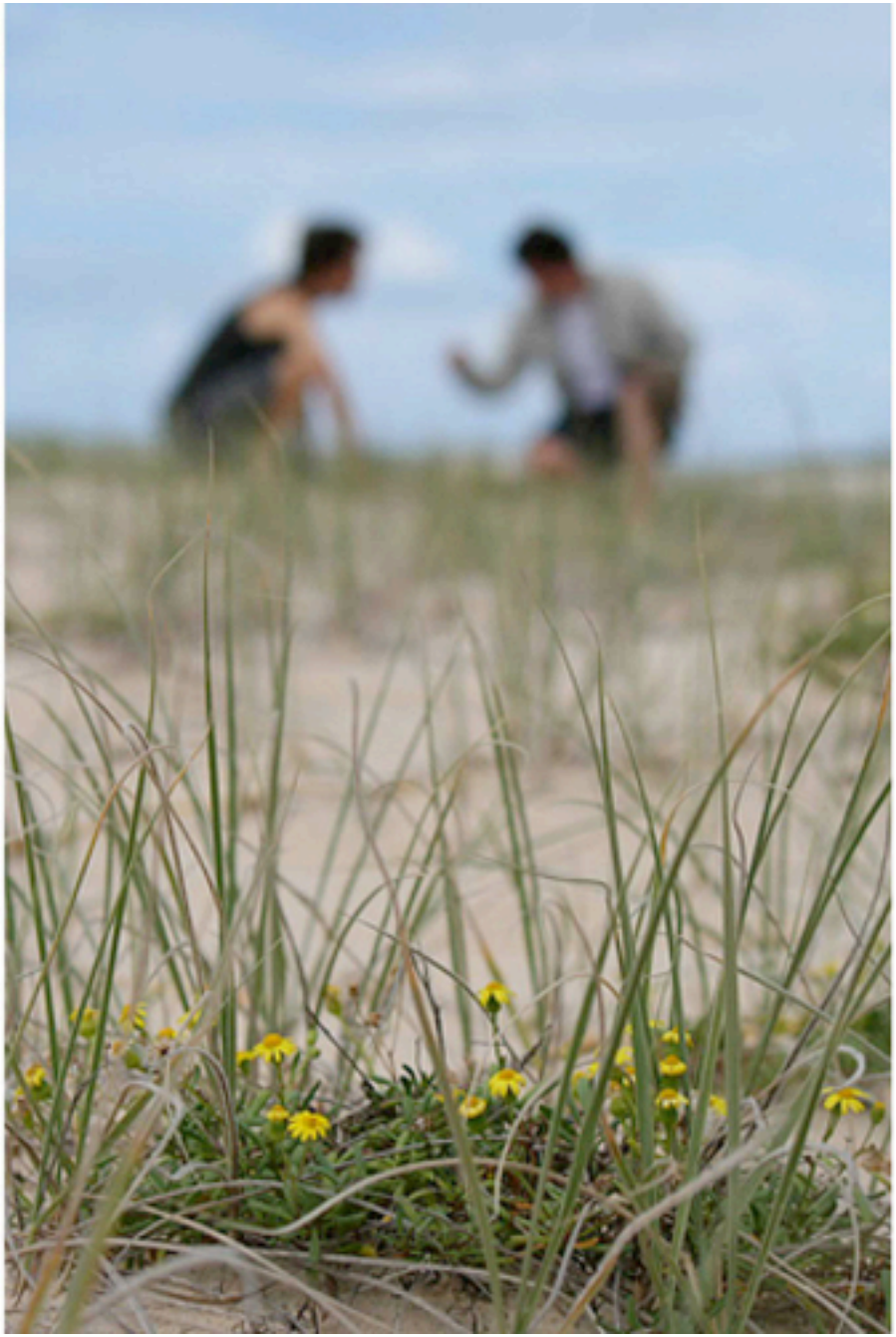
1) 454 Transcriptome sequencing - cDNA and RNAseq

2) 454 bulk segregant analyses

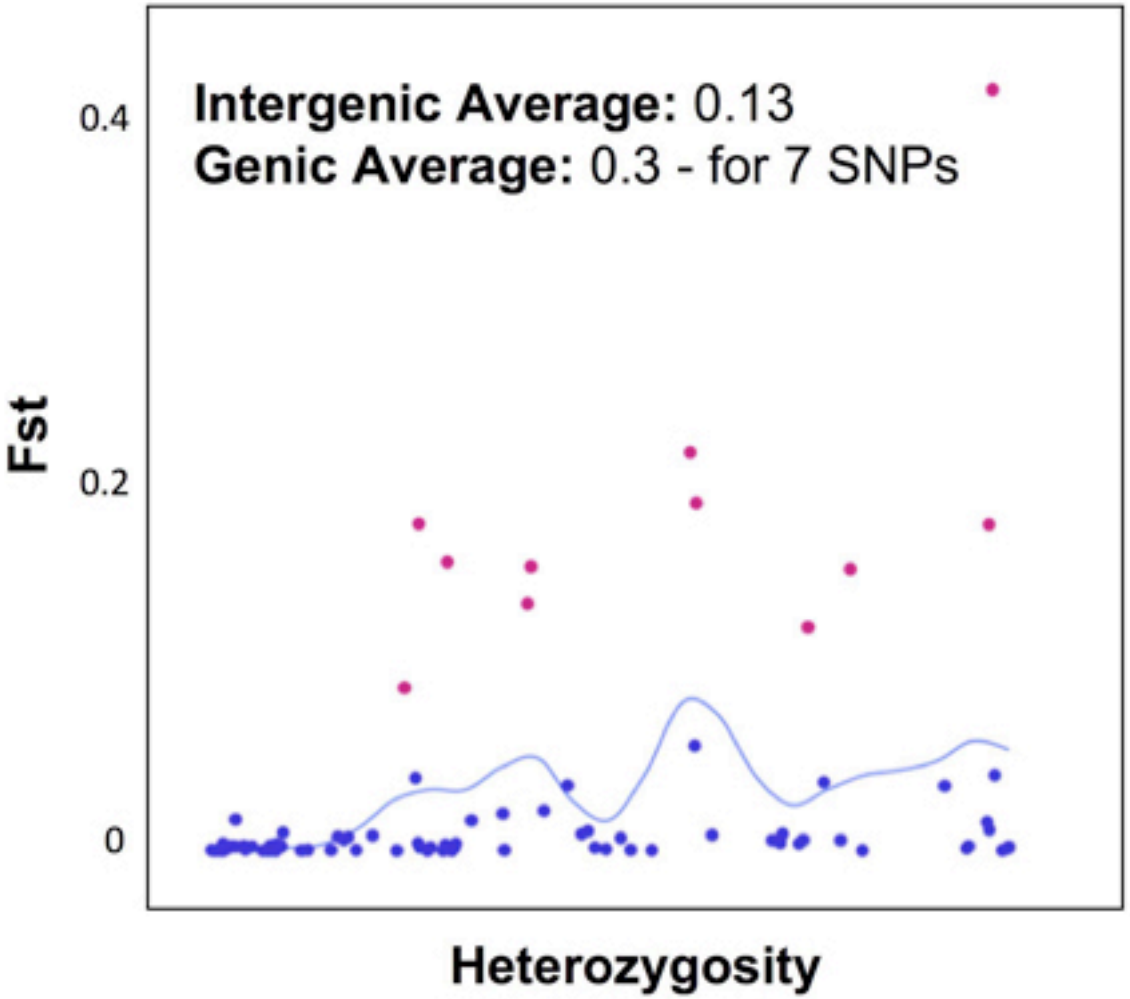
3) RADs 24 populations, production of gene space with Illumina (4 lanes)

4) RAD-based association mapping + Linkage map

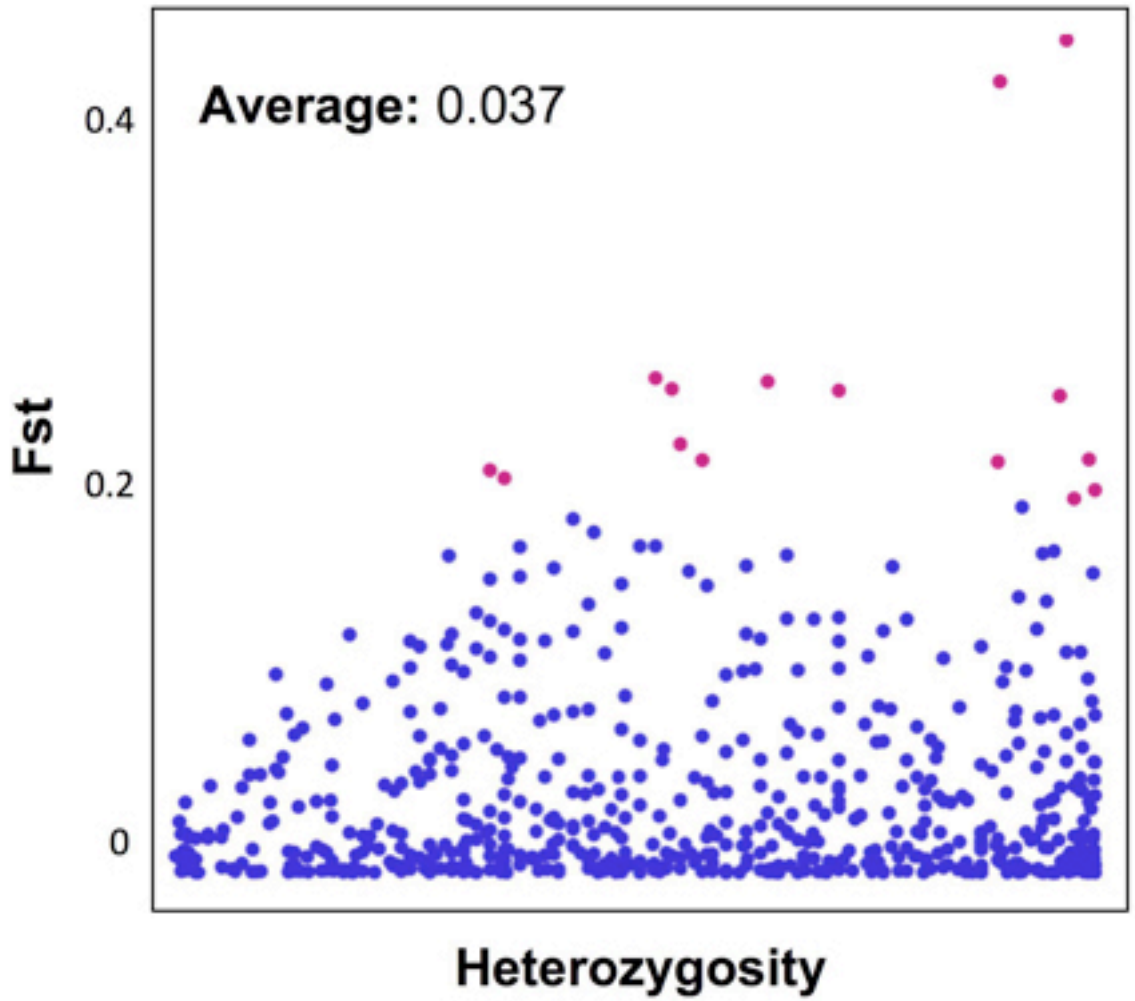
5) Pipeline construction



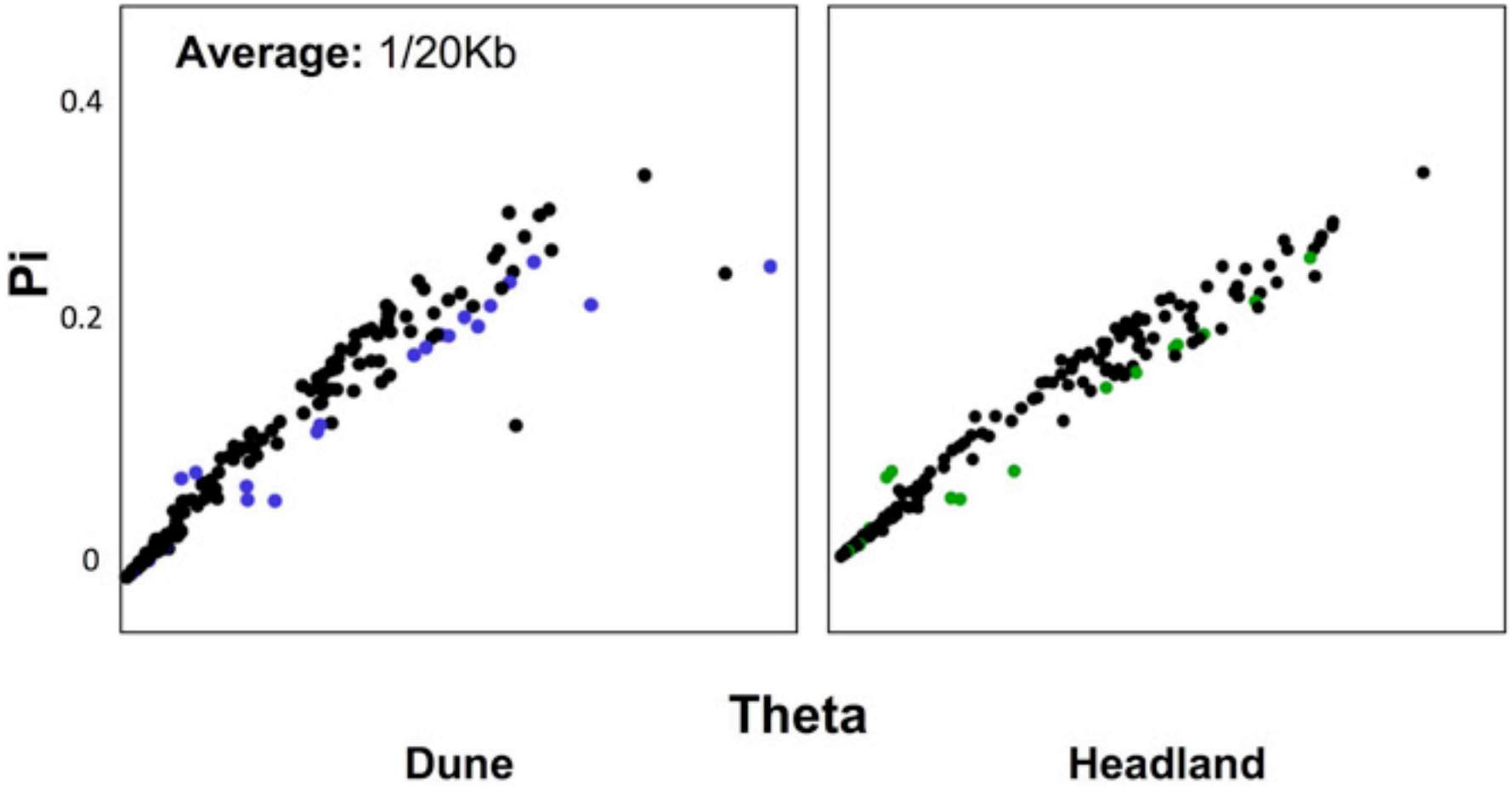
Intergenic chDNA genetic differentiation between parapatric ecotypes



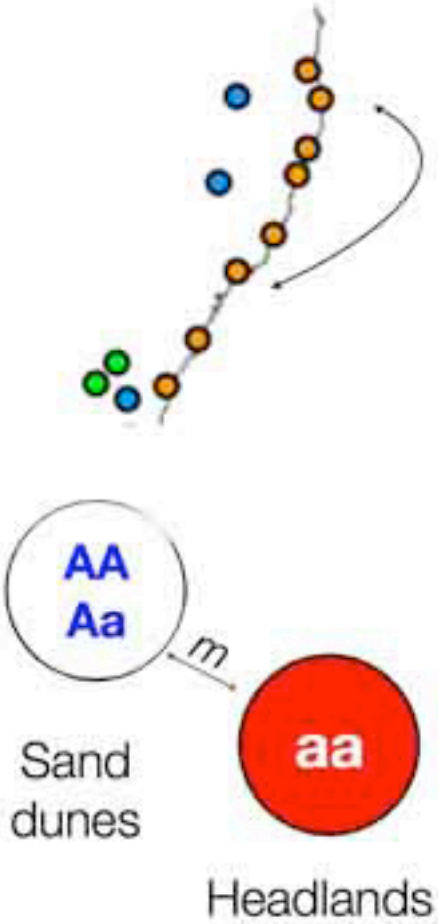
Nuclear genetic differentiation between parapatric ecotypes



Nucleotide diversity across the nuclear genome



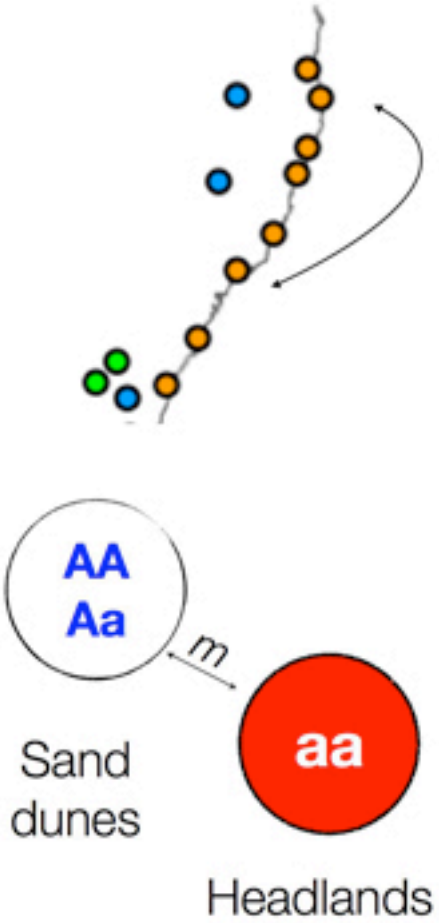
The genetic and ecological basis of the origin of ecotypes



1) Independent and repeated origins
2) Local adaptation
3) Dominant trait, with mendelian segregation
4) Selection for morphology
5) Extensive gene flow between parapatric populations
6) Strong extrinsic reproductive isolation
7) Partial intrinsic reproductive isolation

8) Development of population genomic approaches to study adaptation and speciation
9) Need of a reference gene space or genome

Acknowledgements



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