

# Adaptation at ecological and genetic margins in *Senecio*

## Selection, gene flow and recombination

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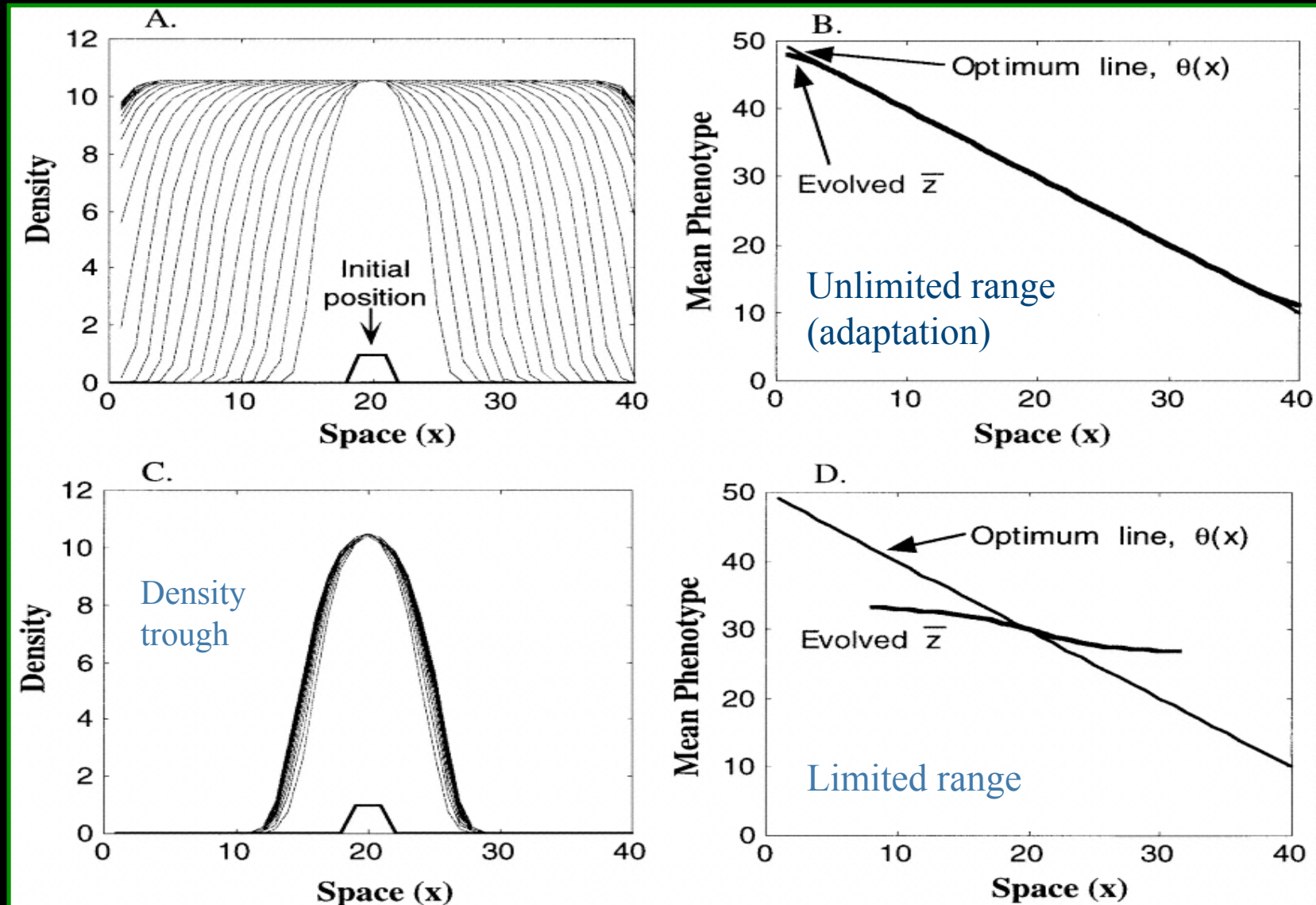
# Limits to adaptation are everywhere



When and why does evolution stop at range margins?

# Limits to adaptation at ecological margins

Kirkpatrick and Barton (1997): *Am. Nat.*

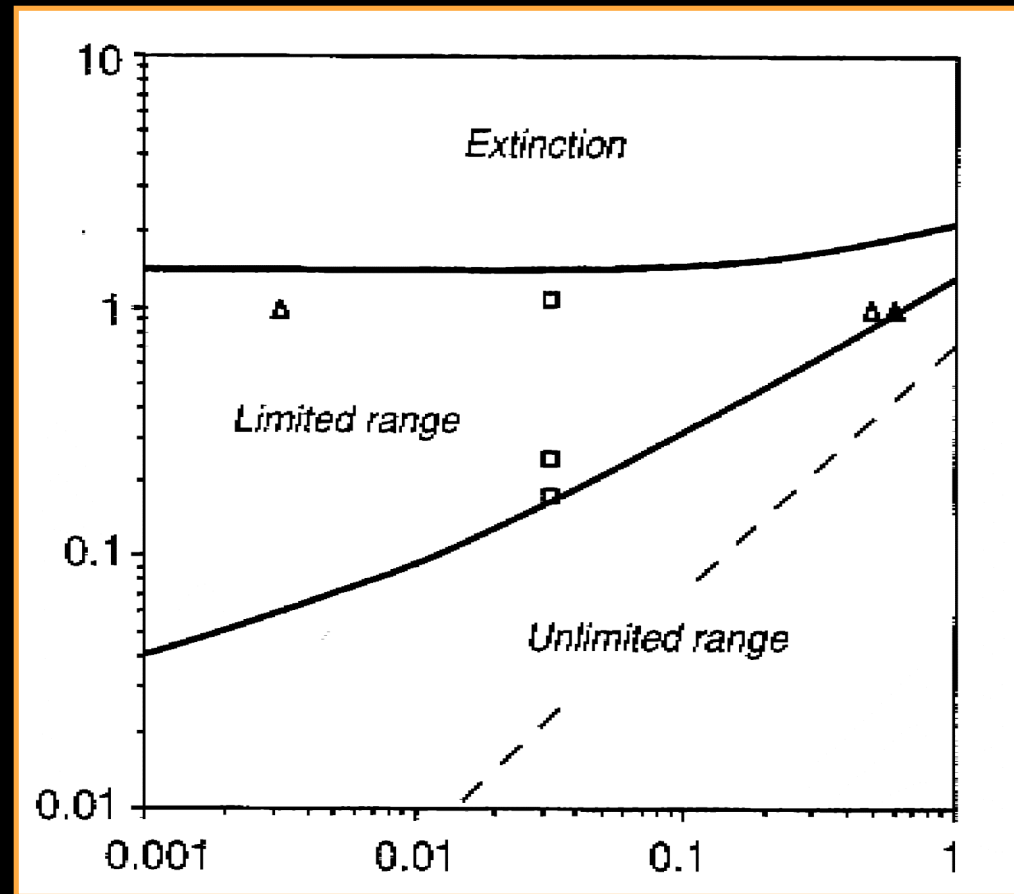


# An explanation for limited species' ranges?

(Kirkpatrick and Barton, *Am. Nat.* 1997)

“Rate of  
change in  
selection”

(*dispersal* +  
*steepness*)



“Additive genetic variance in fitness”



## BUT...more realistic models (Barton, 2001)

- Gene flow between divergent populations also increases additive genetic variation, so increasing the response to selection
- For a range of models of quantitative traits, this “spreading” effect outweighs the “swamping” effect
- Adaptation is possible to virtually any steepness of gradient, until a critical limit is reached



# Theoretical predictions:

Bridle, Polechova & Vines, 2009: In:  
*Speciation and patterns of diversity*

Bridle et al. (2010) *Ecology Letters*

## (1) *Swamping effect of gene flow*

Adaptation should stop when the required trait gradient ( $b$ ) exceeds...

$$b > \frac{1}{\sigma} \left( \frac{V_G}{\sqrt{V_S}} + 2\bar{r}_{\max} \sqrt{V_S} \right)$$



## (2) *Spreading effect of gene flow*

Increase in  $V_G$  should follow

$$V_G = b\sigma\sqrt{V_S}$$

Until critical limit

$$b > \frac{2r_m\sqrt{V_S}}{\sigma}$$

*where the cost of  
variance = pop  
growth rate*

## How relevant to natural populations?

- At what temporal or spatial scale do population genetic effects become important?
- How do they trait divergence and variance interact with the pattern of ecological change?
- How much genetic variance (in fitness) is there in natural populations? How is it distributed? Does fitness variance increase freely as a result of gene flow?



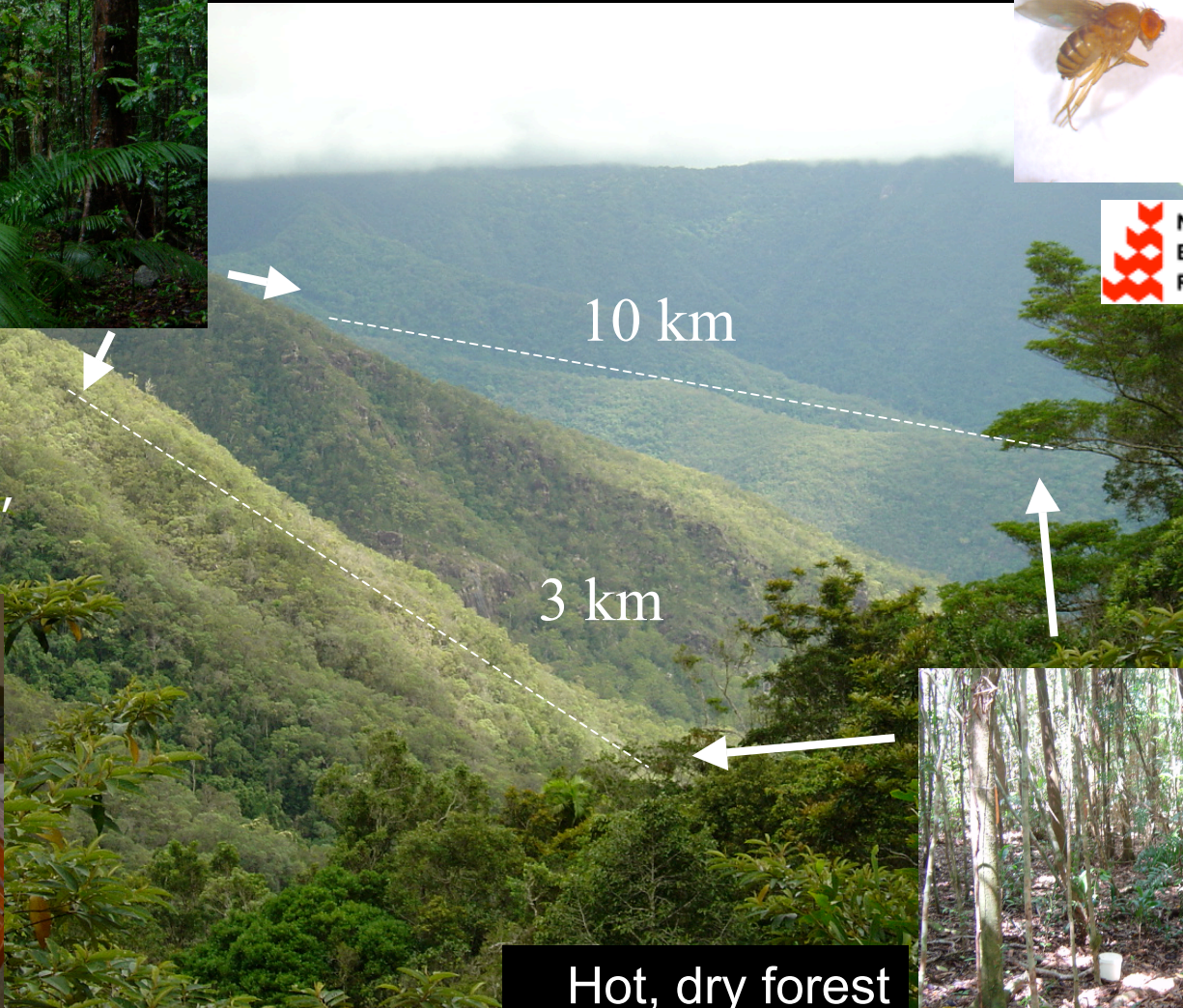
# NERC grant (2010-3): Testing limits to adaptation along multiple altitudinal gradients in *Drosophila birchii*



Wet, cool forest



NE Queensland,  
Australia



Hot, dry forest

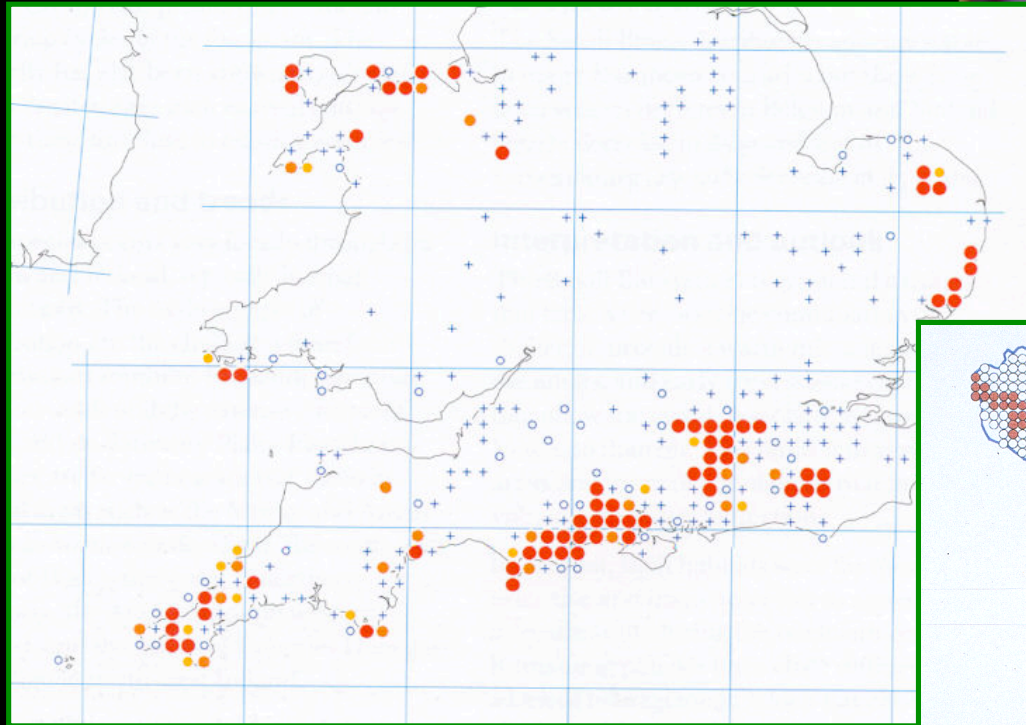




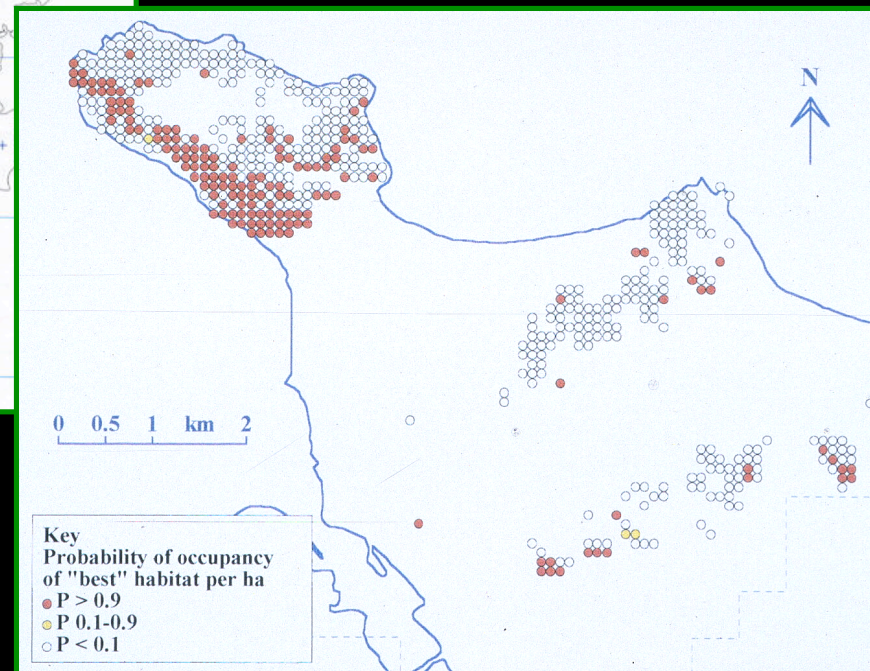
# Ecological gradients are rarely smooth from the organisms' perspective



Thomas *et al.*  
Silver studded blue butterflies



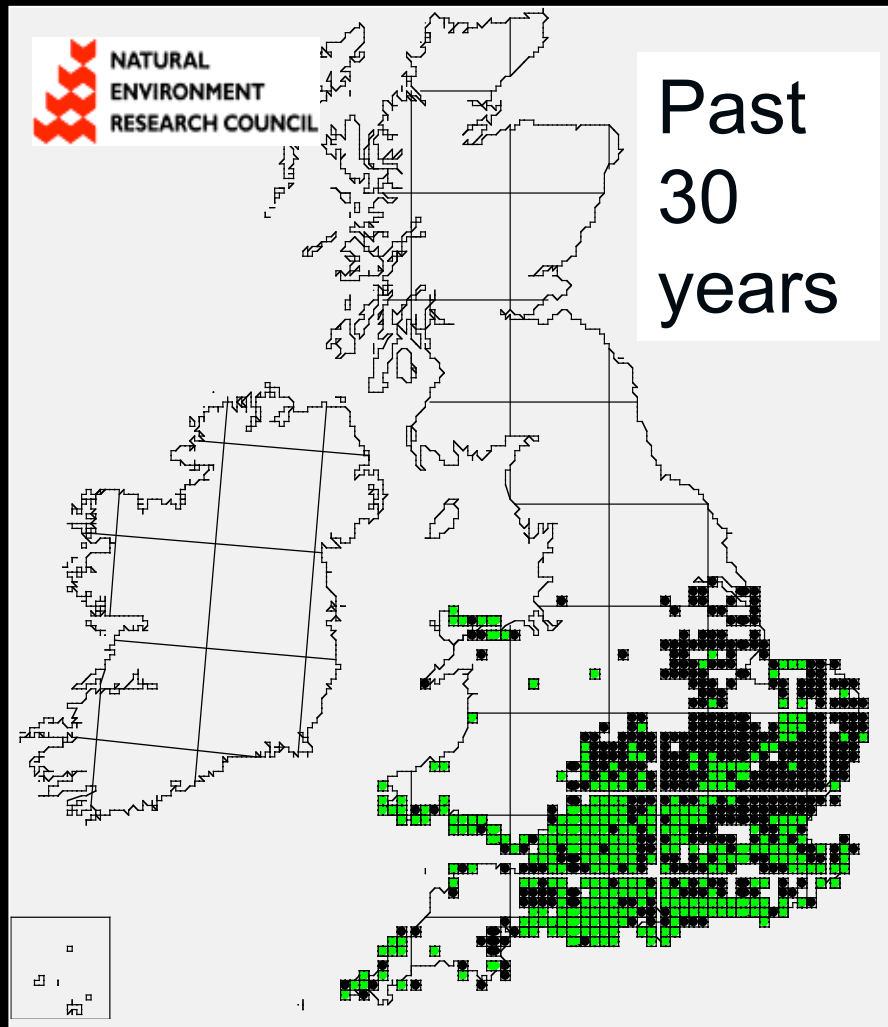
Patchiness at many length scales;  
smooth gradients only within patches  
Depends on biotic interactions



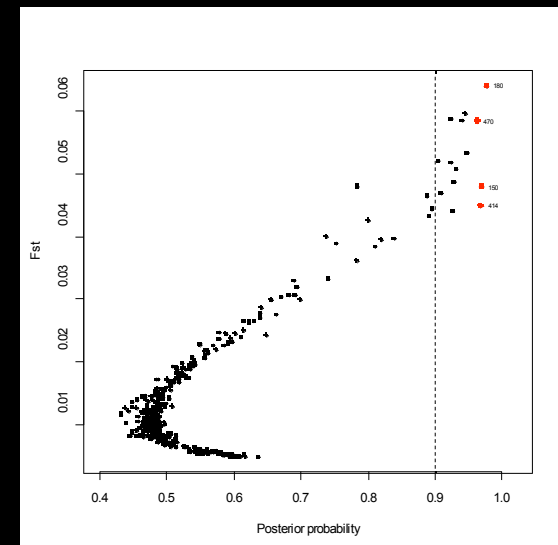


# Testing for evolutionary responses to climate change in the UK butterfly *Aricia agestis*

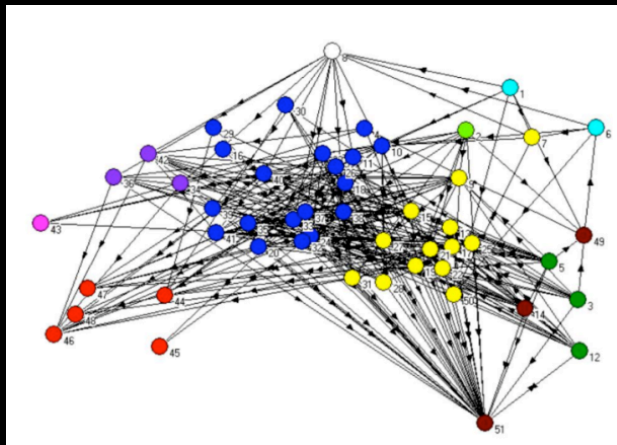
Field transplants



Genetic analysis



# Estimating evolutionary potential in plants and pollinators in response to climate change



- How much genetic variation is there in traits that determine the structure of pollination networks?

  
Avon Wildlife Trust

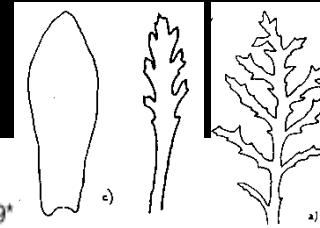


## More complex population margins...

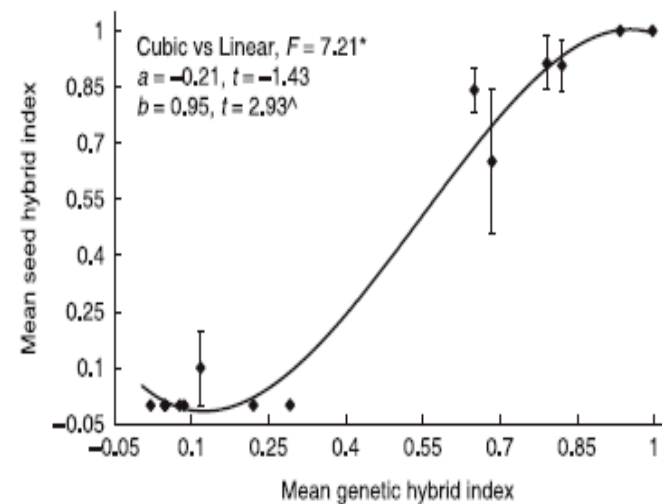
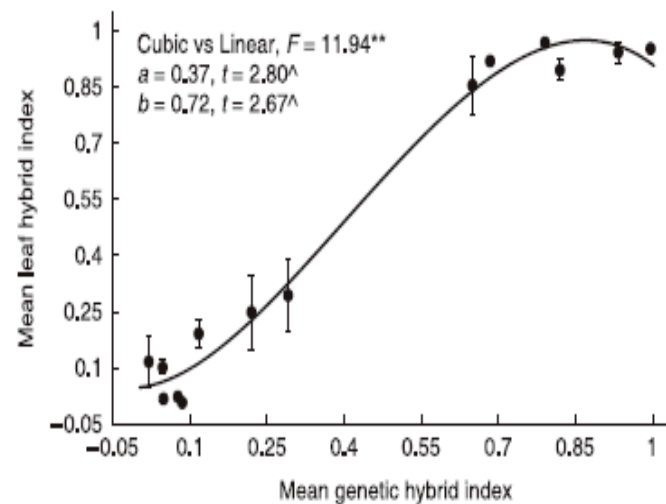
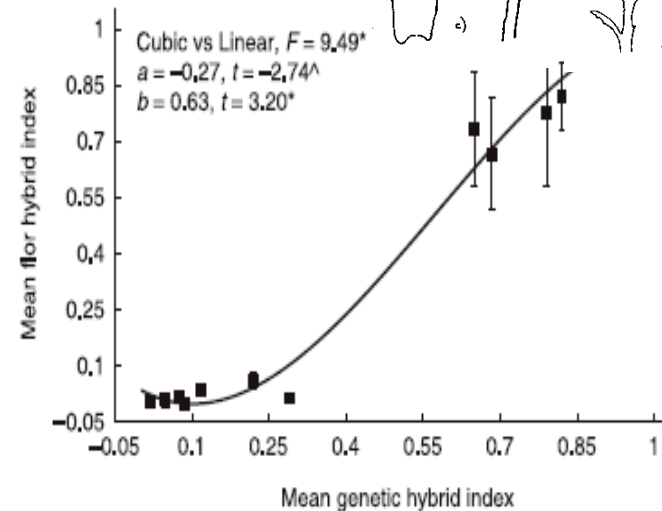
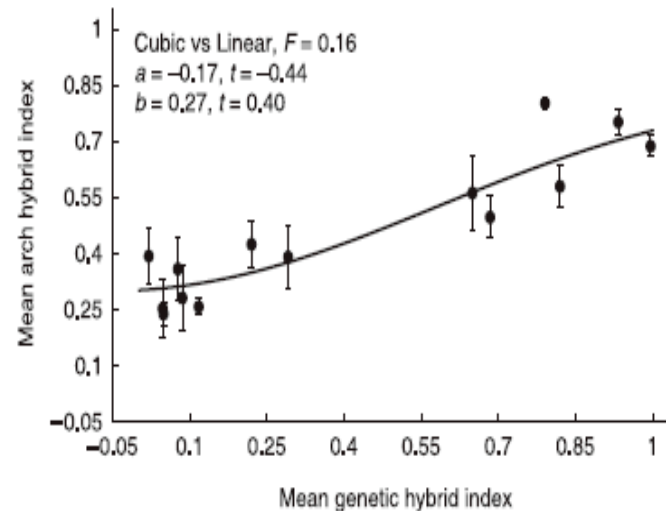
- Abiotic - biotic gradients; more patchy environments
- Real traits with complex genetic architecture (and species' interactions)
- Parapatric margins (hybrid zones): big changes in genetic as well as ecological background)
- Potential for the evolution of assortative mating; complex pattern of gene flow and recombination (SI vs SC, flowering time and morphology)

(Bridle and Vines, 2007, *Trends Ecol Evol*)

# Senecio hybrid zone on Mt Etna



Estimates of  
selection,  
recombination  
and gene flow  
for different  
traits



Brennan, Bridle *et al.* *New Phytol.* (2009)



## Plans for future research at Mt Etna

Quantitative genetic analysis along transects to estimate breeding values and explore genetic correlations among traits

Map ecological and genetic gradients: relate to local population density; Measure fitness cost of outbreeding along transects using reciprocal transplants of lab and field families

Compare these data to patterns of positive selection and LD from genomic data (and # loci, mode of gene action); spread of epistatic alleles at cline centre?

Explore evolution of mixed mating strategies (selfing vs outcrossing) depending on cost of gene flow vs recombination?



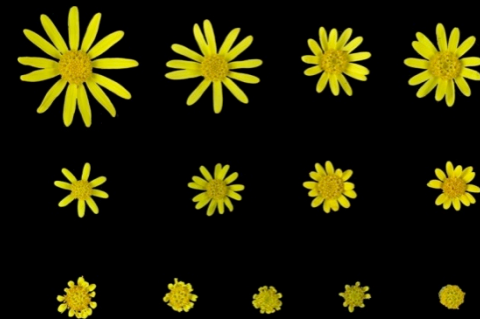
## Summary:

- Limits to evolution (and speciation) depend on the complex effects of recombination and gene flow on genetic variance
- Huge value in combining next generation sequencing with assays of phenotypic, ecological and fitness variation
- Need empirical data to test theoretical models

$$b > \frac{1}{\sigma} \left( \frac{V_G}{\sqrt{V_S}} + 2\bar{r}_{\max} \sqrt{V_S} \right)$$



(A) The actual rate and pattern of ecological change



(B) The amount of genetic variation in traits/fitness