Genetics of hybrid speciation in *Senecio* (Asteraceae)

S. aethnensis

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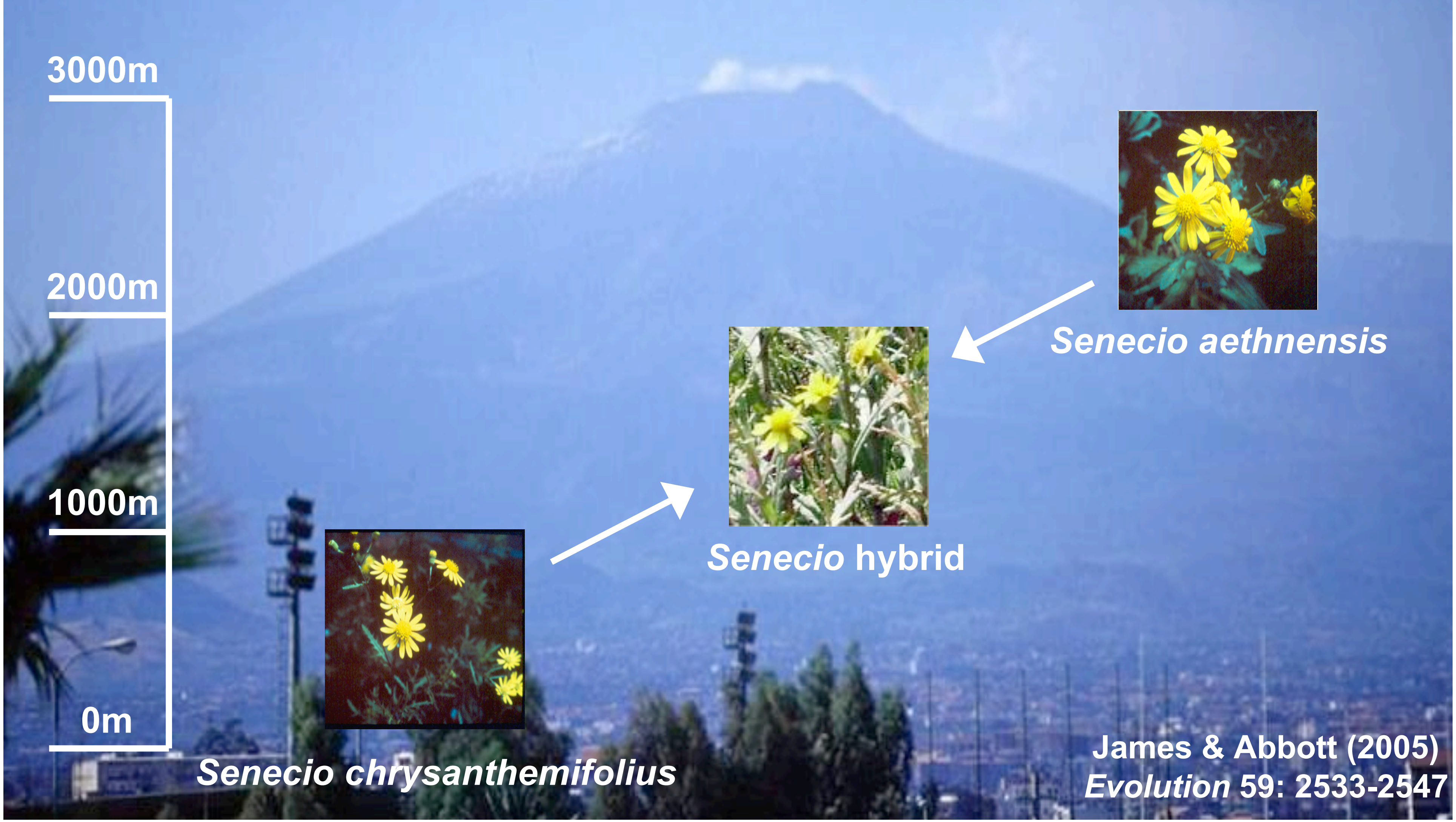
Postdoctoral research at
St Andrews University

S. chrysanthemifolius

S. squalidus

The *Senecio* hybrid zone on Mount Etna, Sicily.



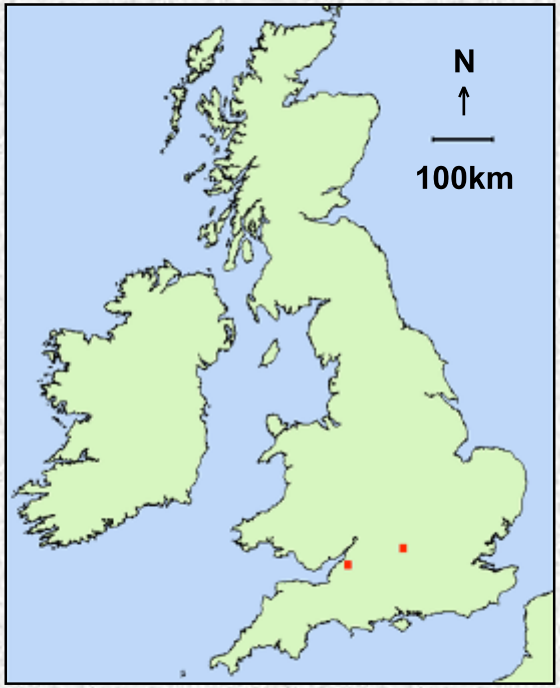
Senecio aethnensis

Senecio hybrid

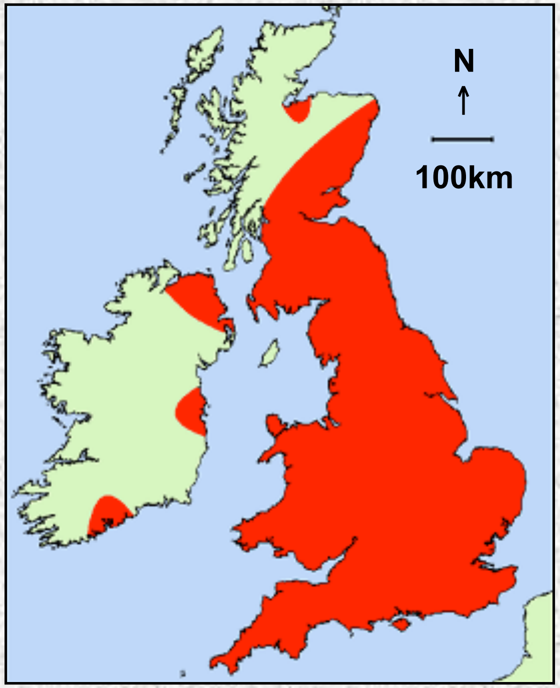
Senecio chrysanthemifolius

James & Abbott (2005)
Evolution 59: 2533-2547

Senecio squalidus: introduction and spread in the UK



1700 (Badminton/Oxford)



2000 (approximate range)

Cultivated in Oxford Botanic Gardens from 1700 for 150+ years.

Spread along railway lines during industrial revolution from 1800+.

Harris 2002. *Watsonia* 24: 31-43

Project objectives

Describe molecular and quantitative differentiation between species

Measure selection and identify its molecular and quantitative genetic targets

Investigate interactions between genetic architecture and species differentiation

Research strategies

Wild-sampled glasshouse-grown population samples and large interspecific F_2 families

Multiple quantitative trait measures

Molecular marker development and genotyping

Population genetic analyses of molecular and quantitative differentiation between species

Genetic and quantitative trait locus (QTL) mapping and analyses

Quantitative genetic traits

Twenty quantitative trait measures divided into six groups of related traits

(1) Seed **(2) Leaf** **(3) Floral**

aeth chrys squal

aeth chrys squal

aeth chrys squal

(4) Architecture **(5) Ecophysiology** **(6) Growth rates**

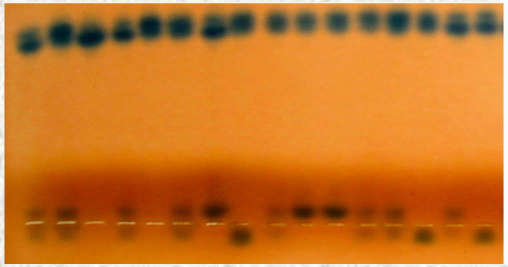
Molecular genetic markers

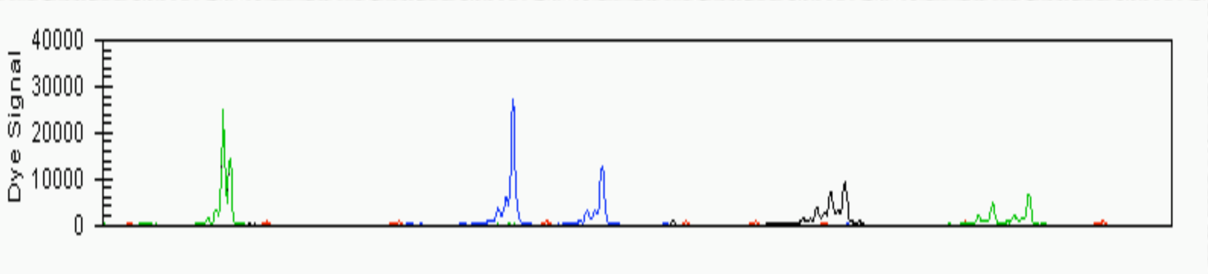
Allozymes (enzyme electrophoretic variants)

Simple sequence repeats (SSRs or microsatellites)

Random amplified polymorphic DNA (RAPDs) and amplified fragment length polymorphisms (AFLPs)

Expressed sequence tag (EST) markers: SSRs, insertion-deletions (indels)

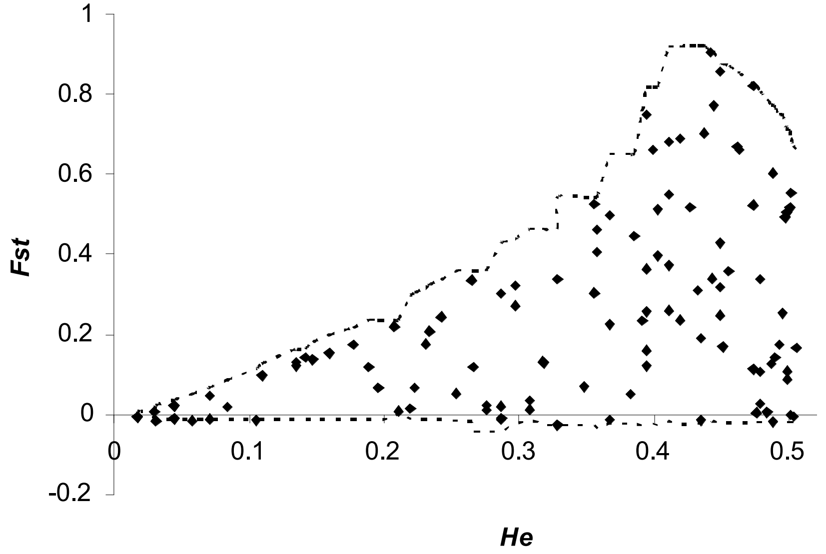


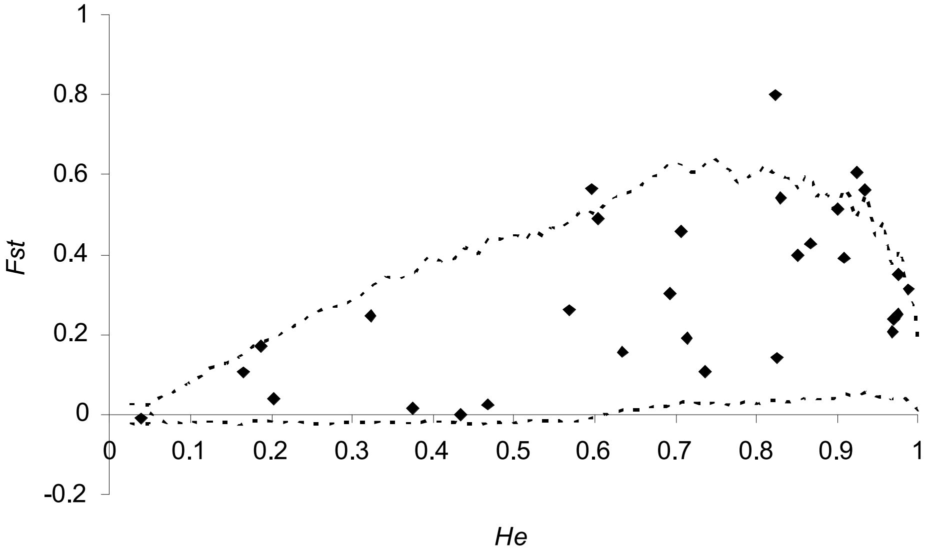


Differentiation tests for loci under selection

S. aeth. versus *S. chrys.*

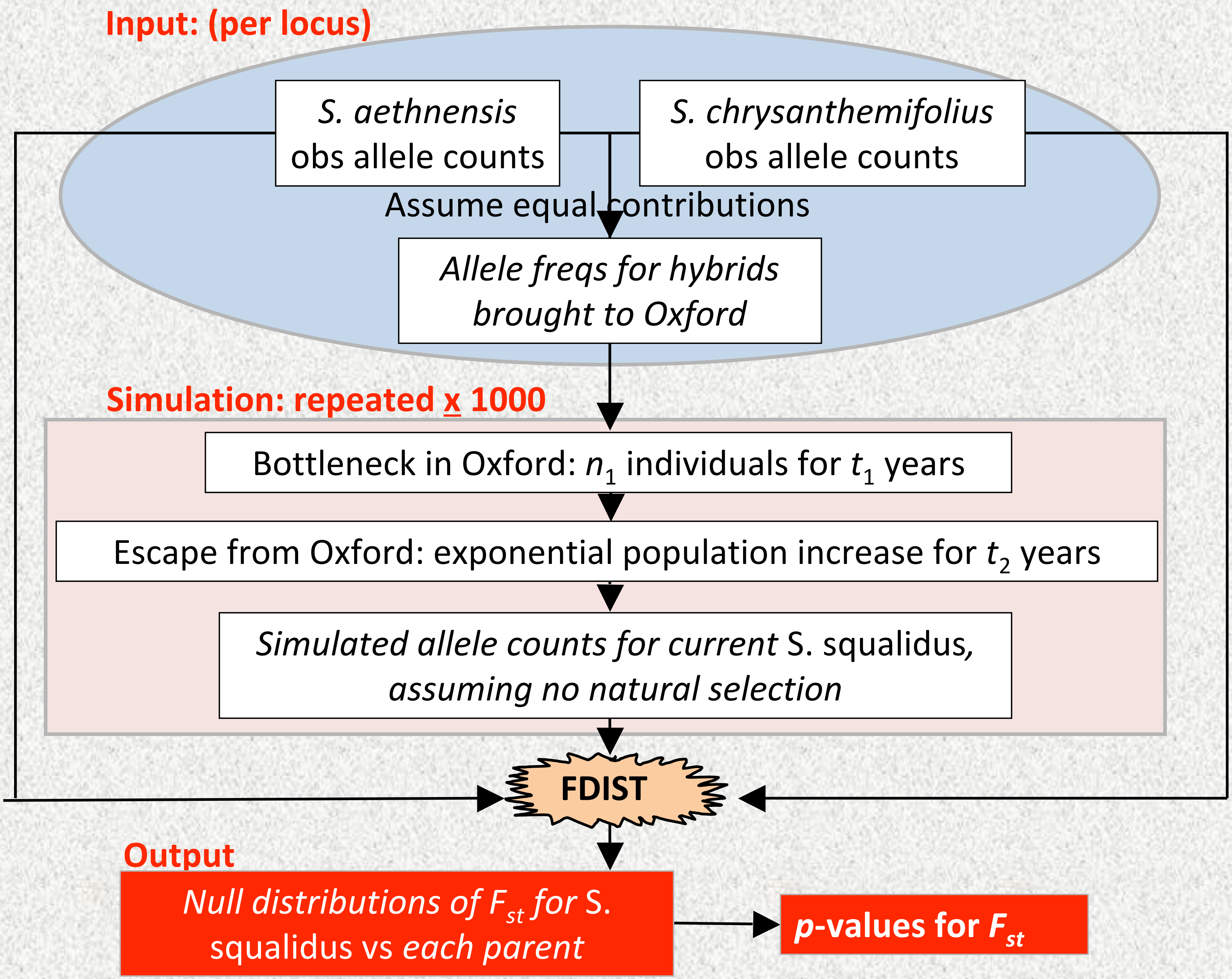
Dom. AFLPs; dFdist   Codom. markers; LOSITAN





0.31 dom. and 0.35 codom simulated mean F_{st} differentiation

2.7% dom. and 30.0% codom. markers >95% signif. divergent



Input: (per locus)

S. aethnensis obs allele counts

S. chrysanthemifolius obs allele counts

Assume equal contributions

Allele freqs for hybrids brought to Oxford

Simulation: repeated x 1000

Bottleneck in Oxford: n_1 individuals for t_1 years

Escape from Oxford: exponential population increase for t_2 years

Simulated allele counts for current S. squalidus, *assuming no natural selection*

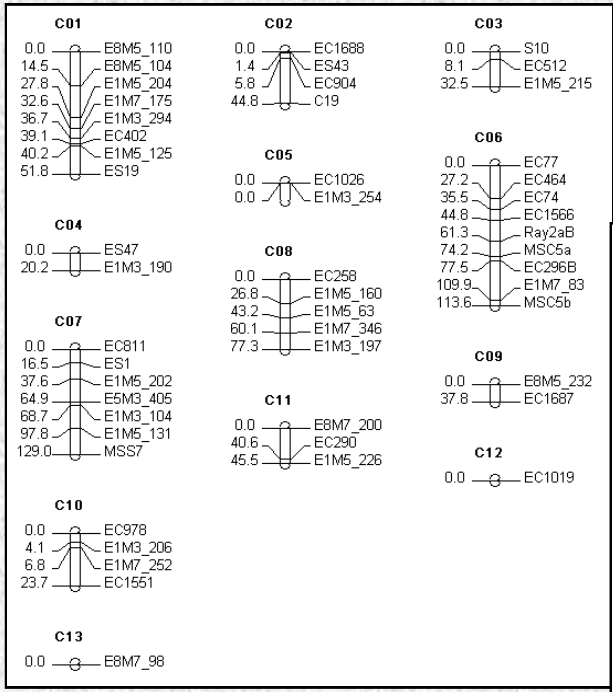
FDIST

Output

Null distributions of F_{st} *for* S. squalidus vs *each parent*

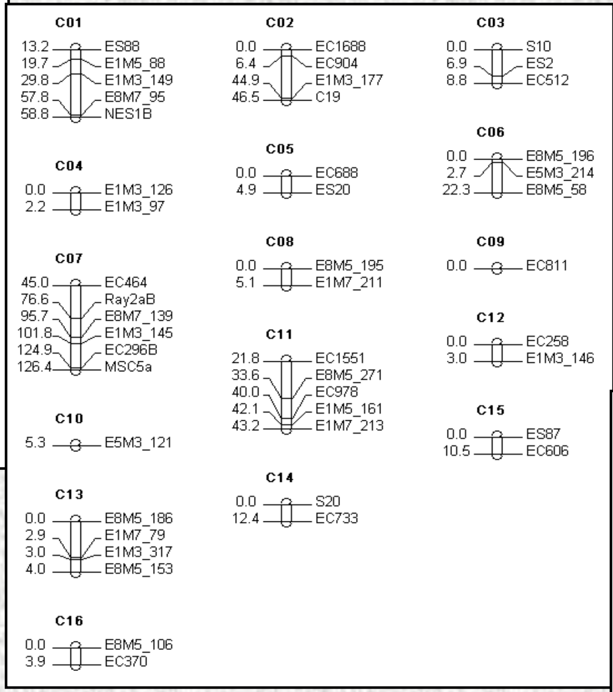
p-values for F_{st}

Genetic maps of F_2 interspecies crosses



S. aeth. map

(AxC F_2 cross)

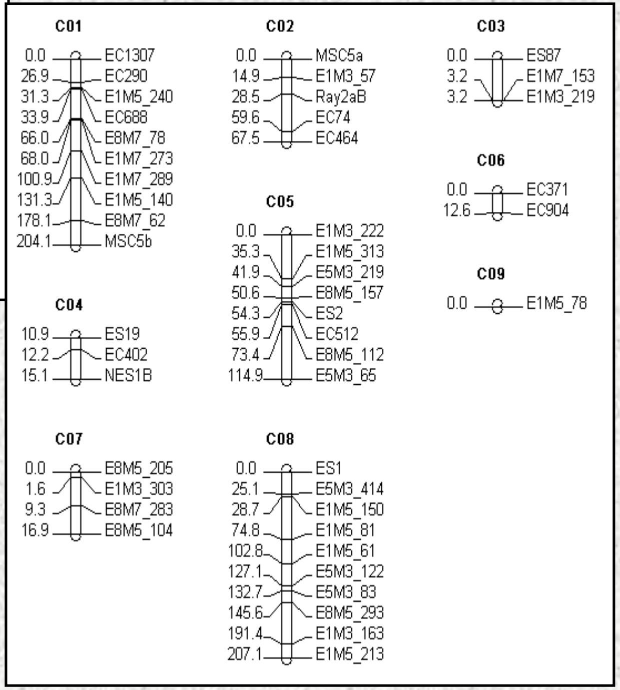


S. chrys. map

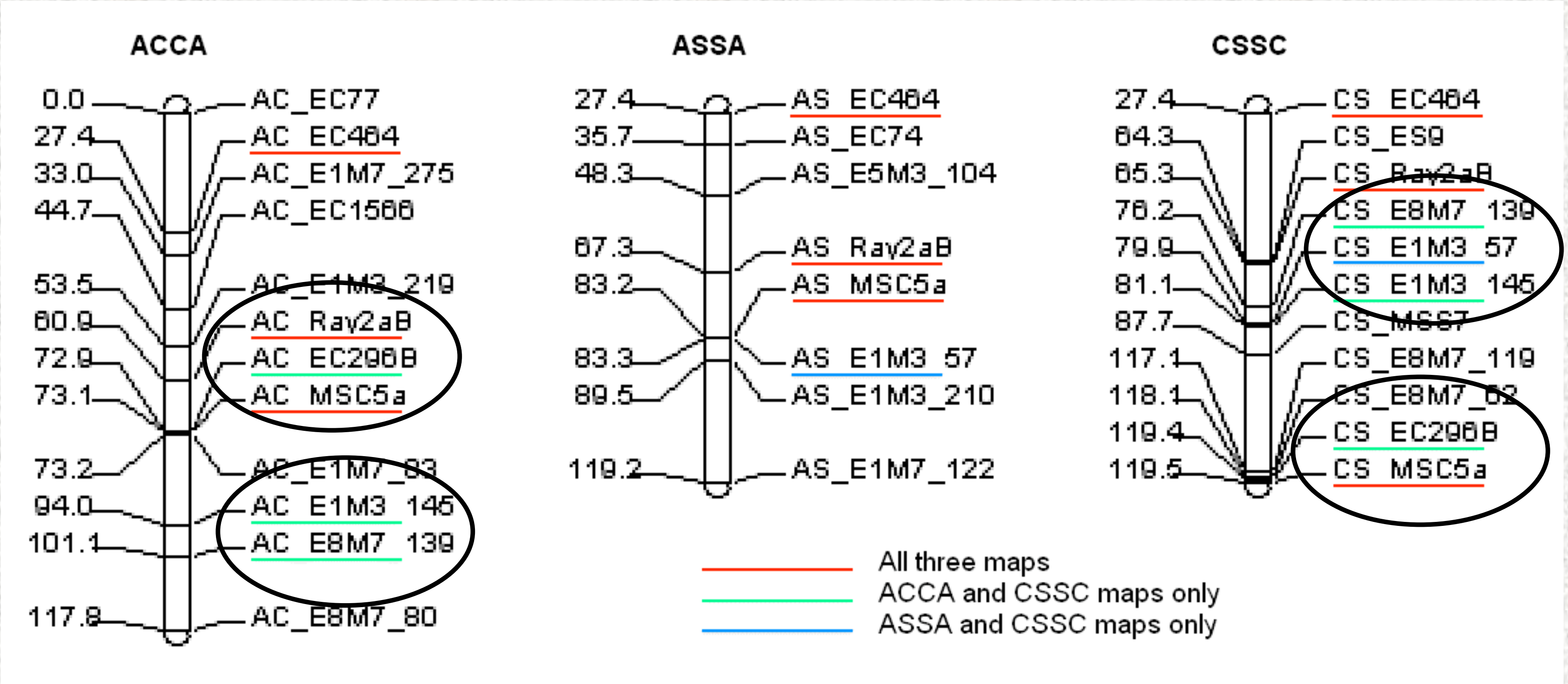
(CxS F_2 cross)

S. squal. map

(SxA F_2 cross)

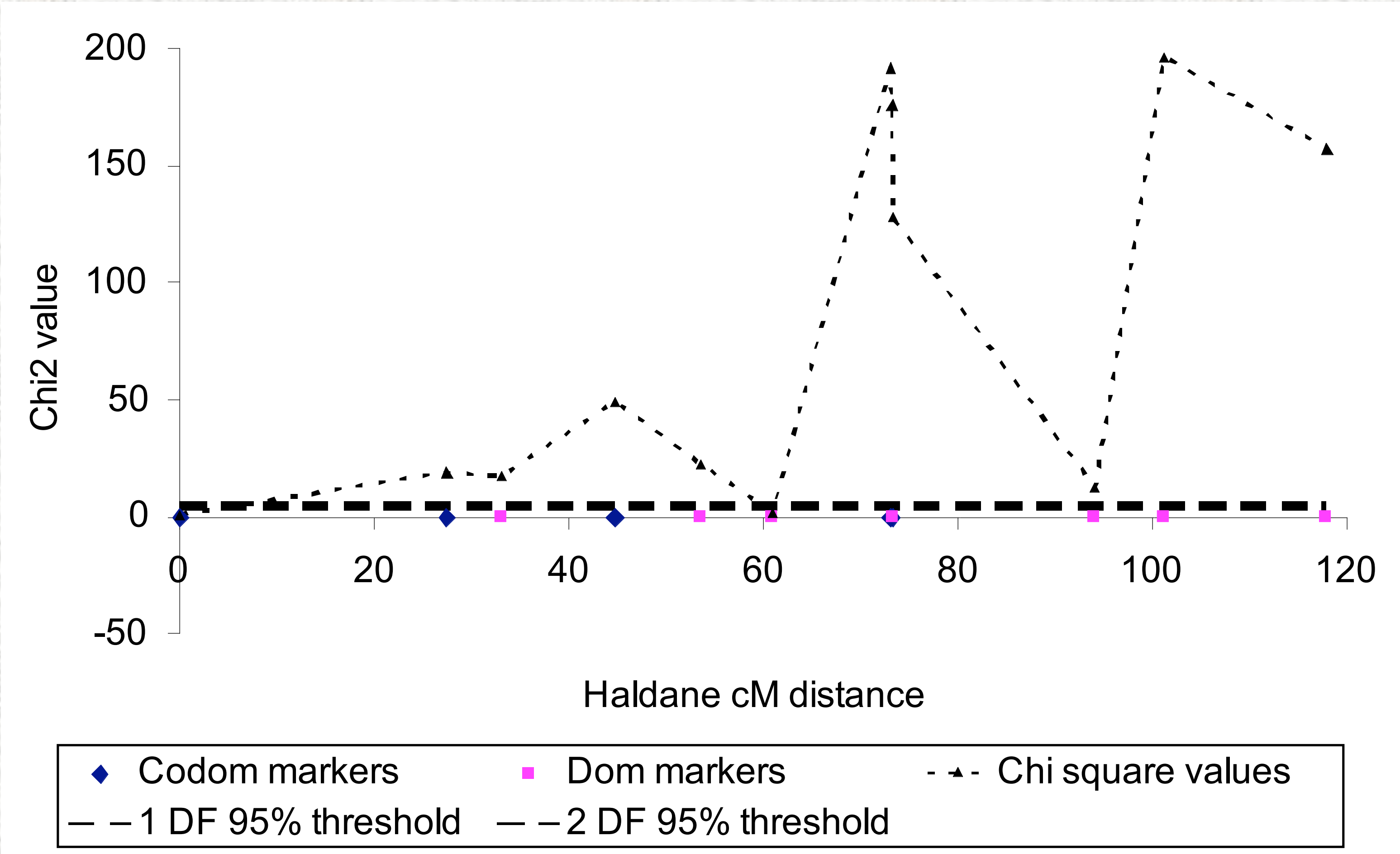


Case study: *Ray2* chromosome



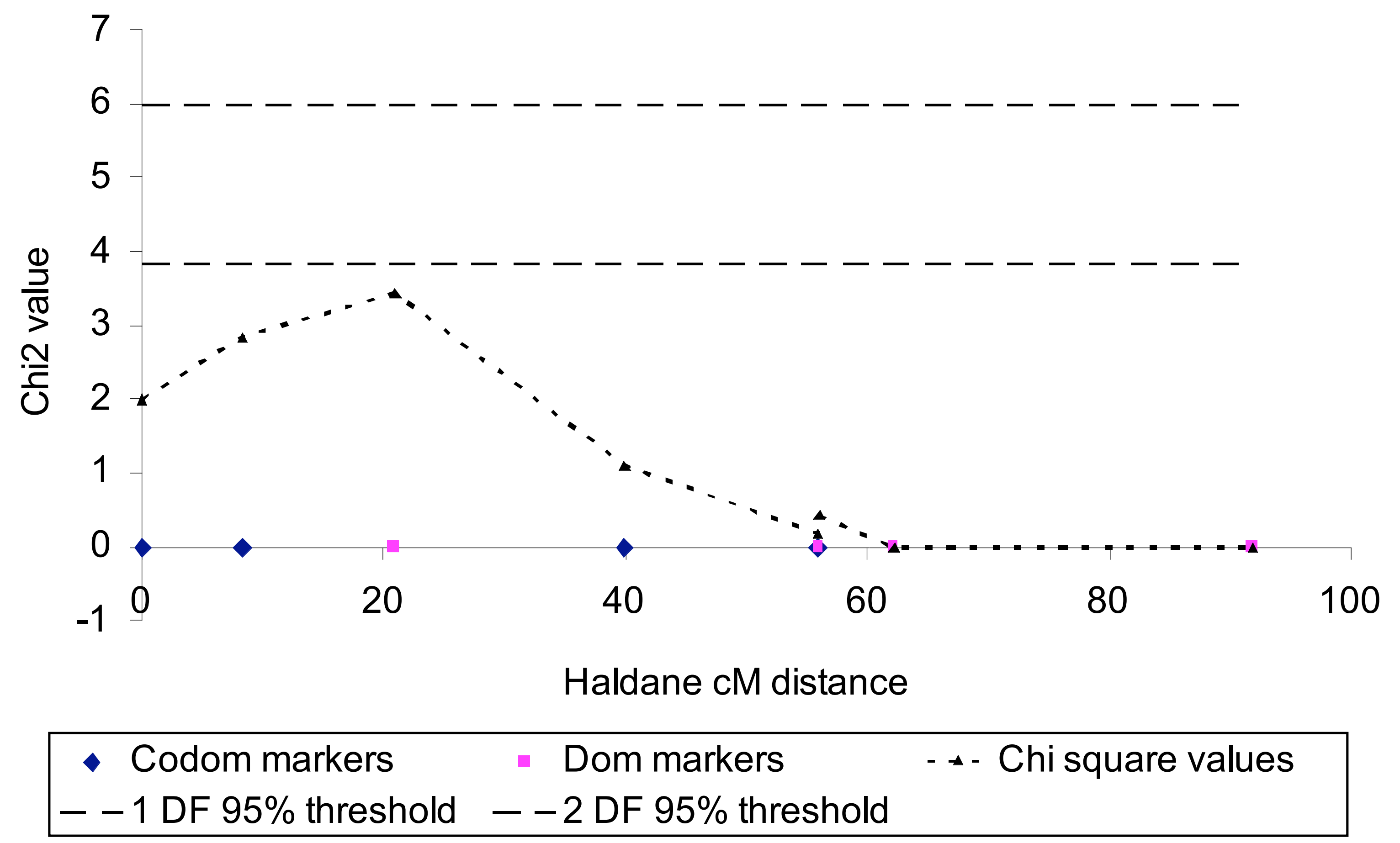
Case study: *Ray2* chromosome

S. aeth. x *S.chrys*. chromosome segregation distortion



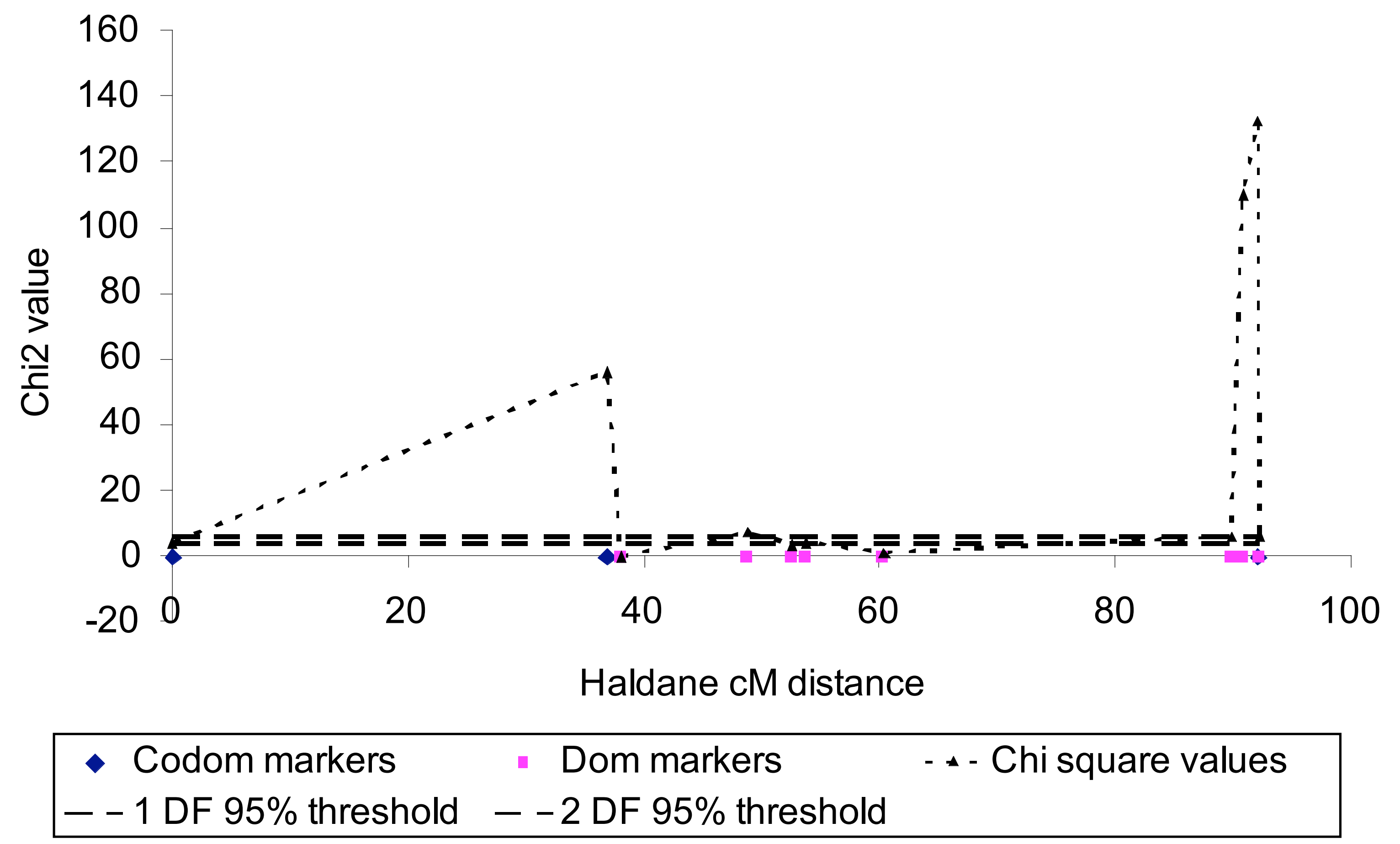
Case study: *Ray2* chromosome

S. aeth. x *S. squal*. chromosome segregation distortion



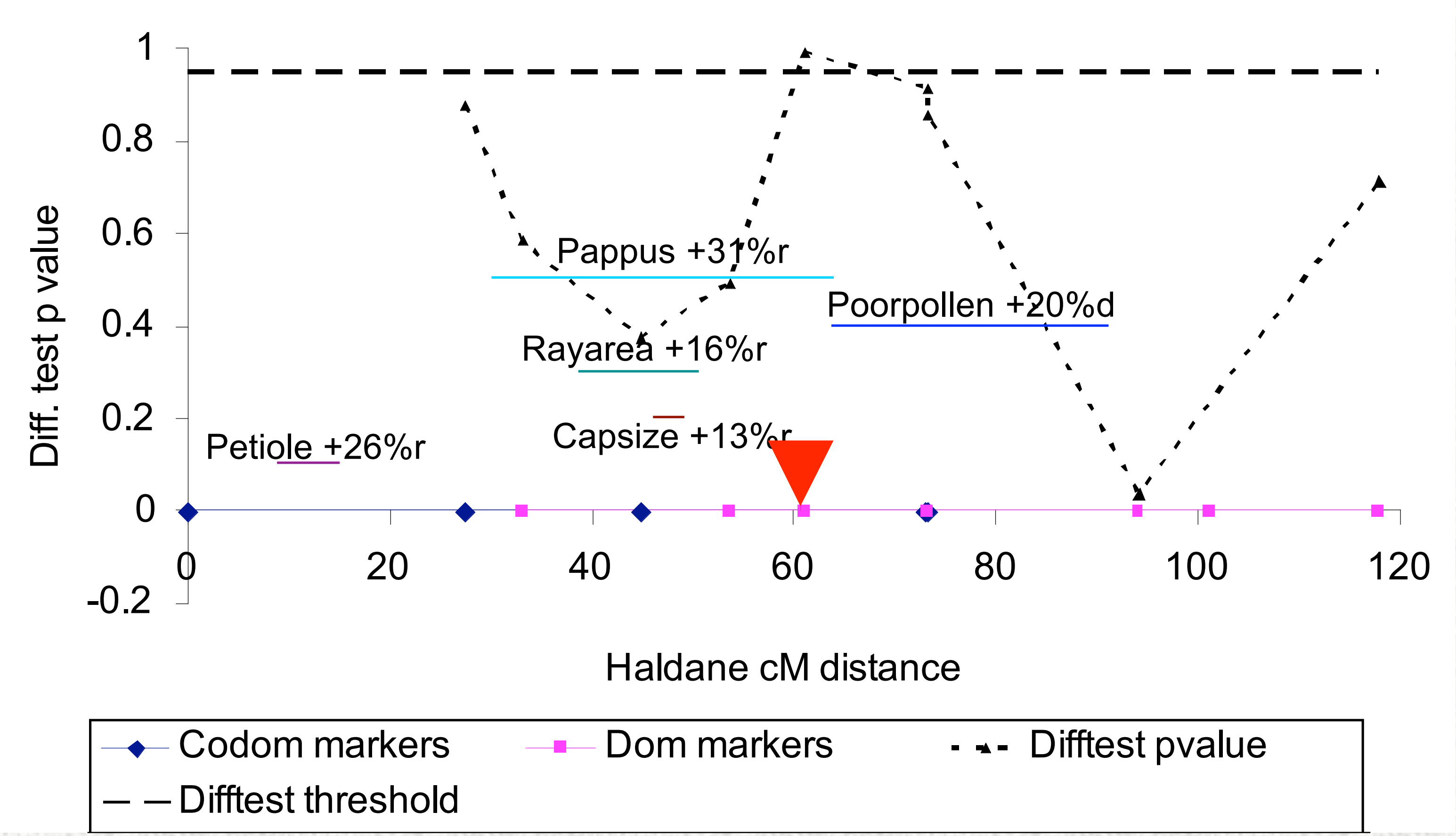
Case study: *Ray2* chromosome

S. chrys. x *S. squal*. chromosome segregation distortion



Case study: *Ray2* chromosome

S. aeth. x *S. chrys*. quantitative trait loci



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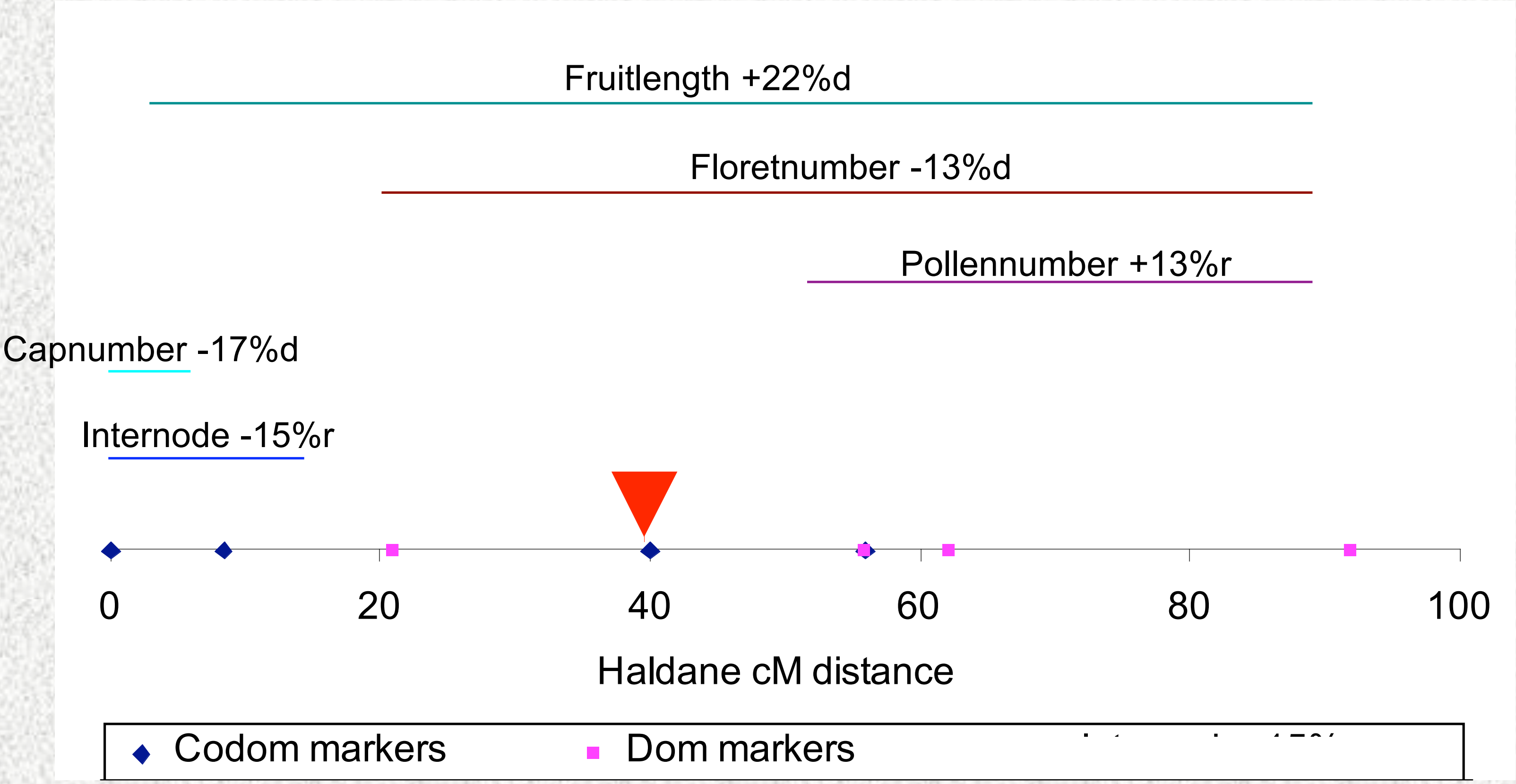
S. aeth. x *S. squal*. quantitative trait loci



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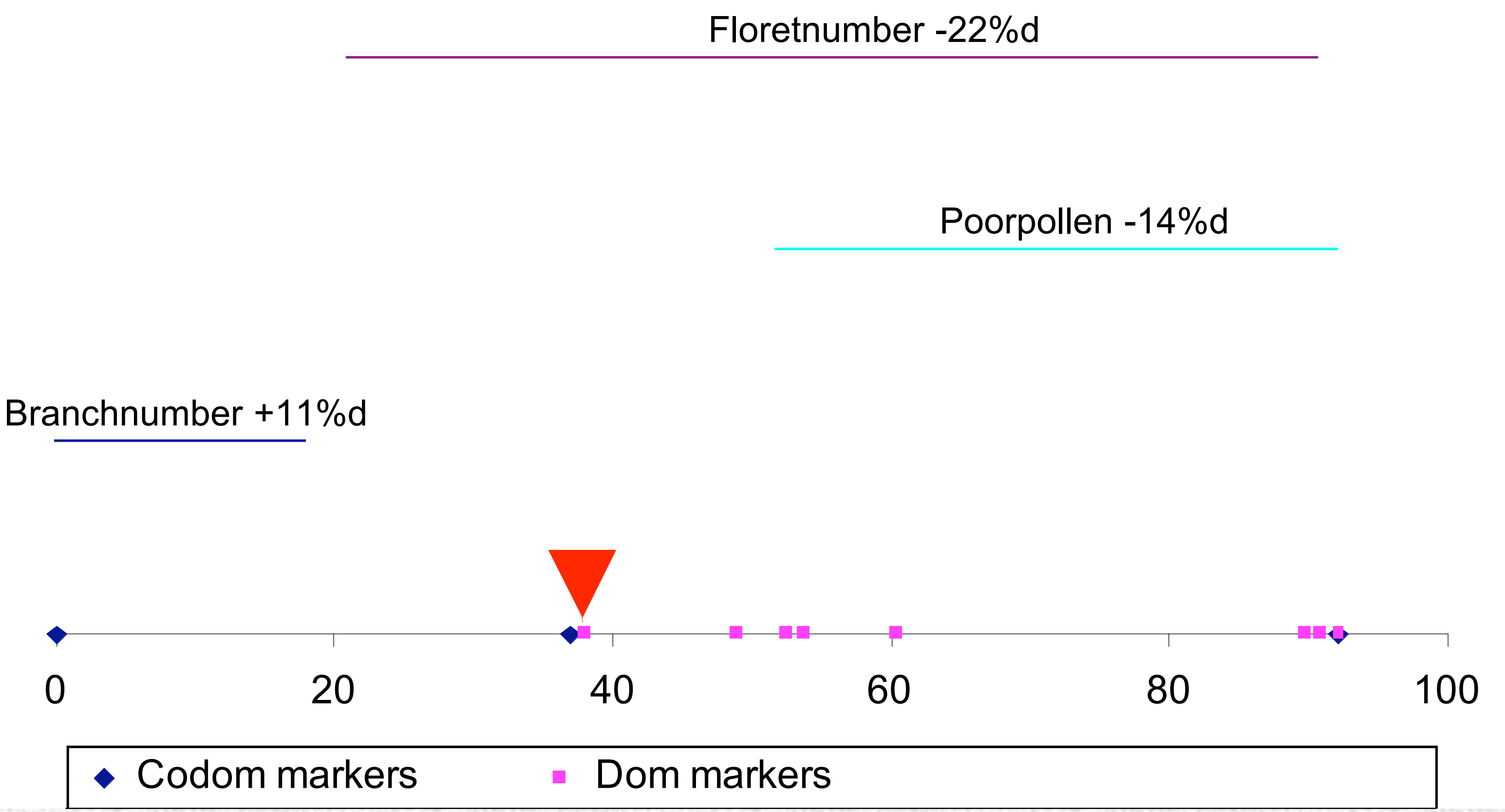

Preliminary mapping conclusions

Genomic rearrangements exist between these closely related *Senecio* species (marker order, segregation distortion, fertility)

Genetics of species differences relatively simple (few QTLs of intermediate effect per trait and overlapping QTLs for different traits)

No good candidate loci for species differences yet (population differentiation or QTLs but not both)

Acknowledgements

- Colleagues (St Andrews): Richard Abbott, Daniel Barker and Paris Veltsos
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- Technicians: David Forbes and Harry Hodge
- Project students: Ail-Lan Wang, Amy Millar, Cameron Hunt

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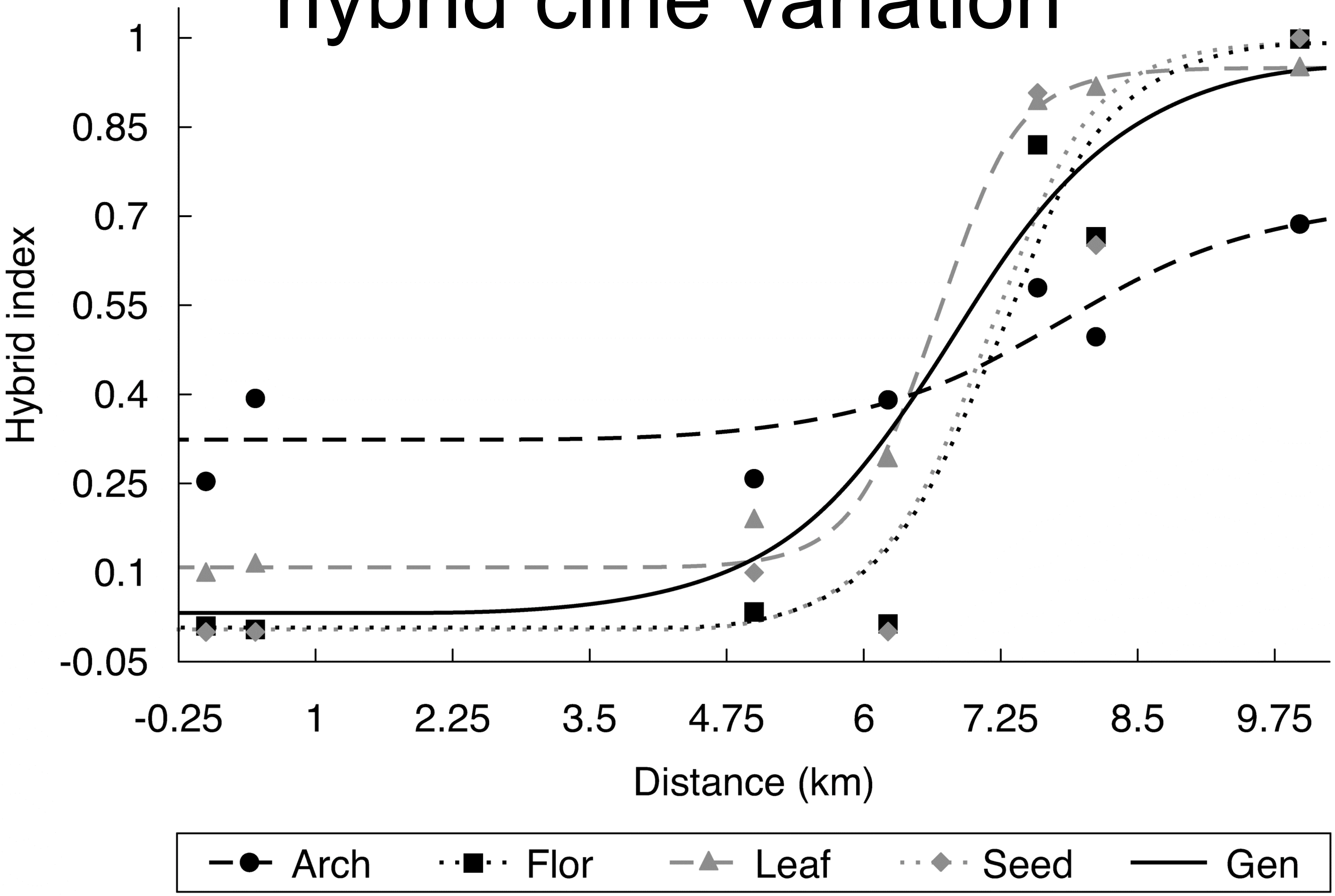
Quantitative genetic hybrid cline variation



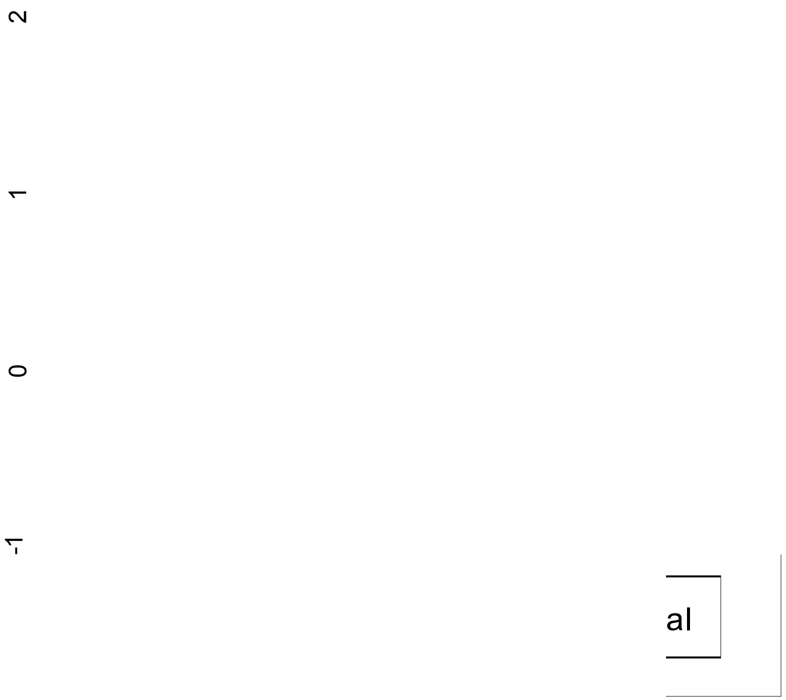
Indirect estimates of selection and dispersal

Marker type\ Parameter estimate	Molecular genetic	Quantitative genetic
Cline width (km)	3.24	2.38
Elevation in disequilibrium\ covariance	0.03	0.03
Recombination rate	0.1 – 0.5	0.1 – 0.5
Dispersal rate generation^{-1} (km)	0.17 – 0.38	0.24 – 0.54
Selection against hybrids (%)	2.2 – 11.2	8.1 – 40.6
Generations of contact	11 – 57	3 – 16

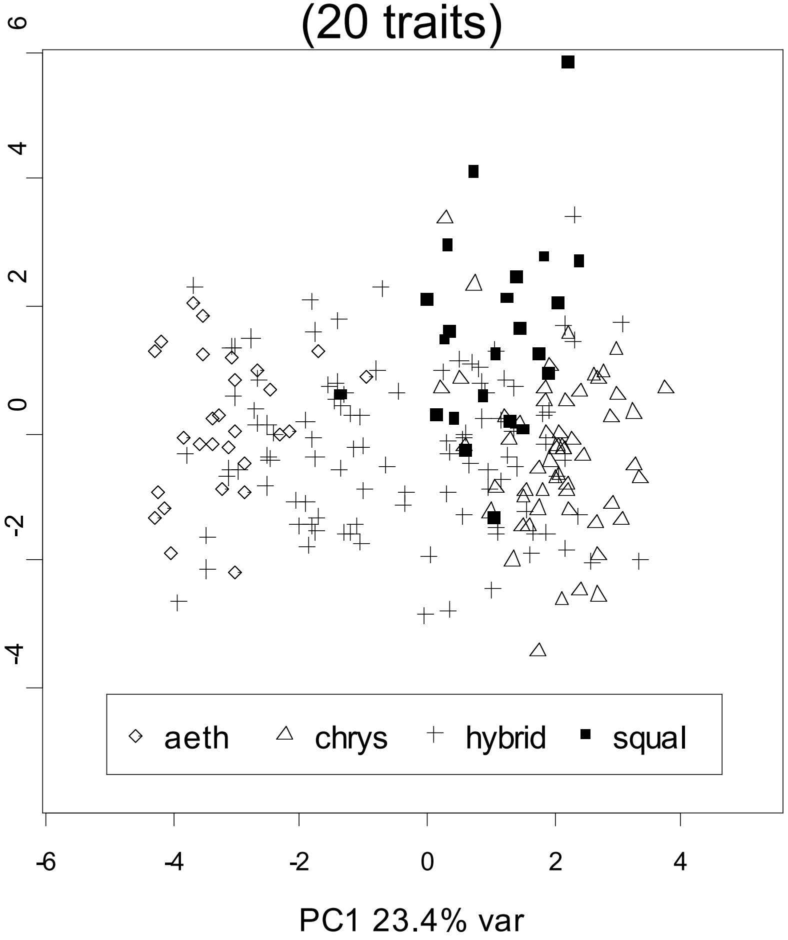
Brennan et al. 2009. Adaptation and selection in the *Senecio* (Asteraceae) hybrid zone on Mount Etna, Sicily. *New Phytol*. 183: 702 – 717

Molecular and quantitative genetic differentiation

Molecular markers (22 SSR, allozyme and indel loci)



Quantitative markers (20 traits)

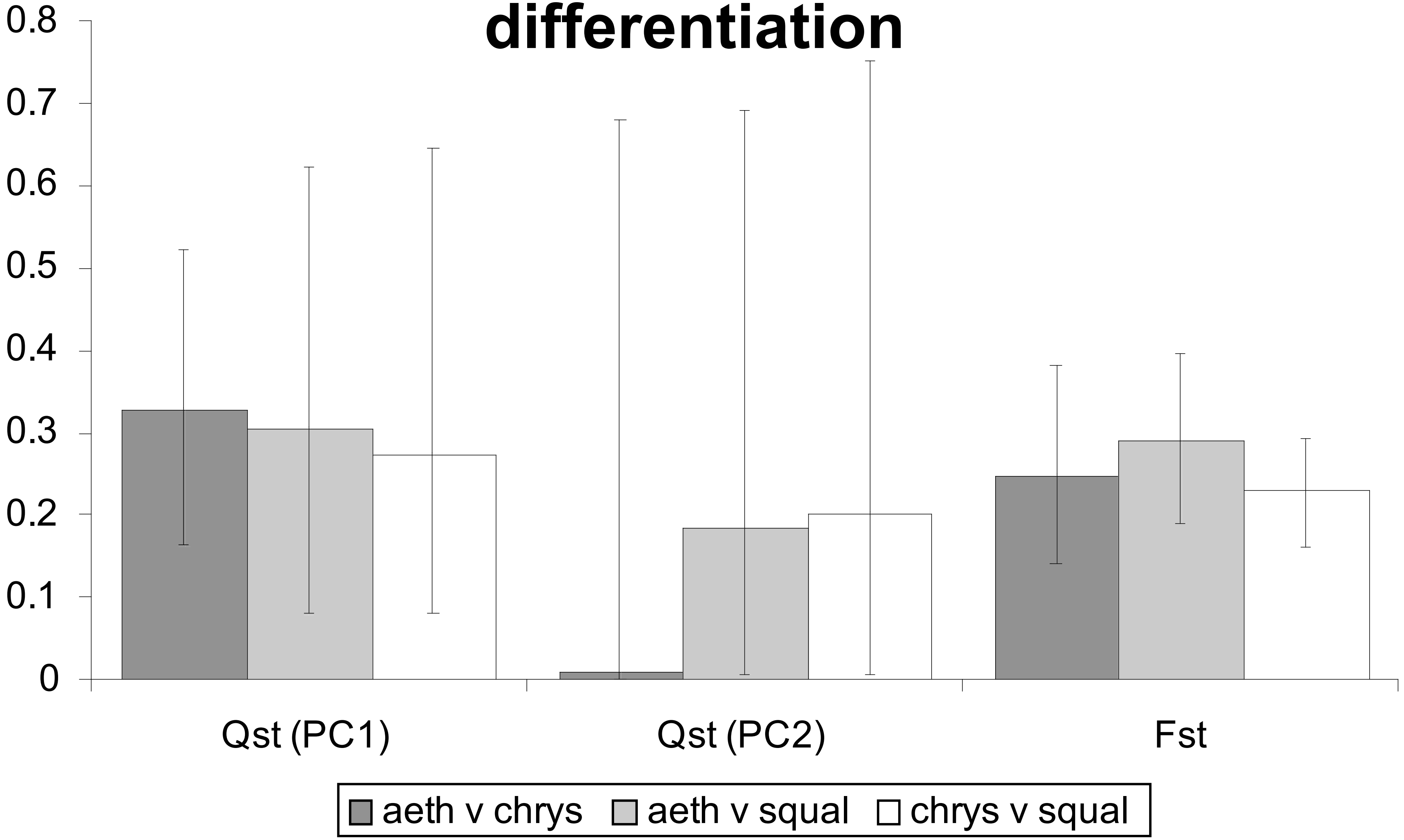


***Senecio squalidus* is distinct from Sicilian hybrid *Senecio*, particularly for molecular genetic markers**

Quantitative genetic differentiation

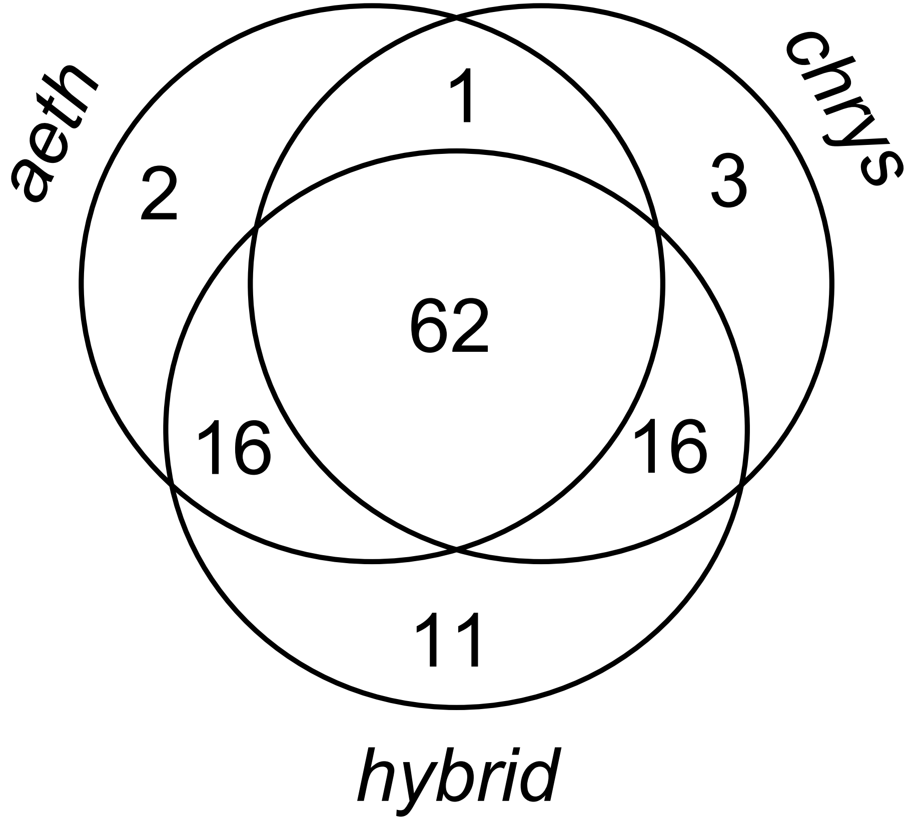
Ranked contribution	1st principal coordinate (*S. aeth* v. *S. chrys*)	2nd principal coordinate (*S. squal* v. Sicilian *Senecio*)
First	Fruit length	Plant height
Second	Leaf dissection	Days true leaf to flowering
Third	Floral display area	Days germination to true leaf
Fourth	Leaf base width	Photosynthesis at 7 C
Fifth	Pappus (parachute) length	Branch number
Sixth	Floret number	Photosynthesis at 20 C

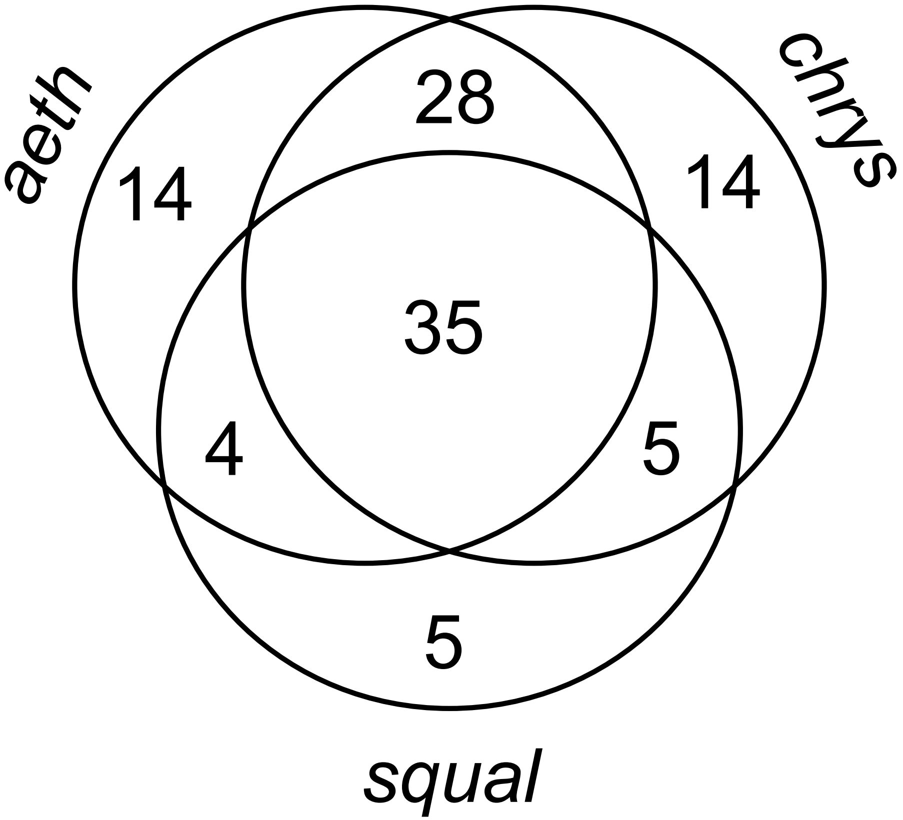
Molecular and quantitative genetic differentiation



Senecio squalidus is differentiated from Sicilian *Senecio* for both molecular markers and quantitative traits (Fst and Qst)

Molecular genetic differentiation





- *Senecio squalidus* has fewer alleles in common with parental species than Sicilian hybrids
- Allele frequency differences are greater for paired comparisons involving *S. squalidus* than Sicilian *Senecio*

Conclusions: Divergence across a natural hybrid zone

- The *Senecio* hybrid zone is maintained by moderate to strong selection against hybrids despite considerable dispersal
- Quantitative traits for floral, leaf and fruit structures show the strongest signals of divergent selection

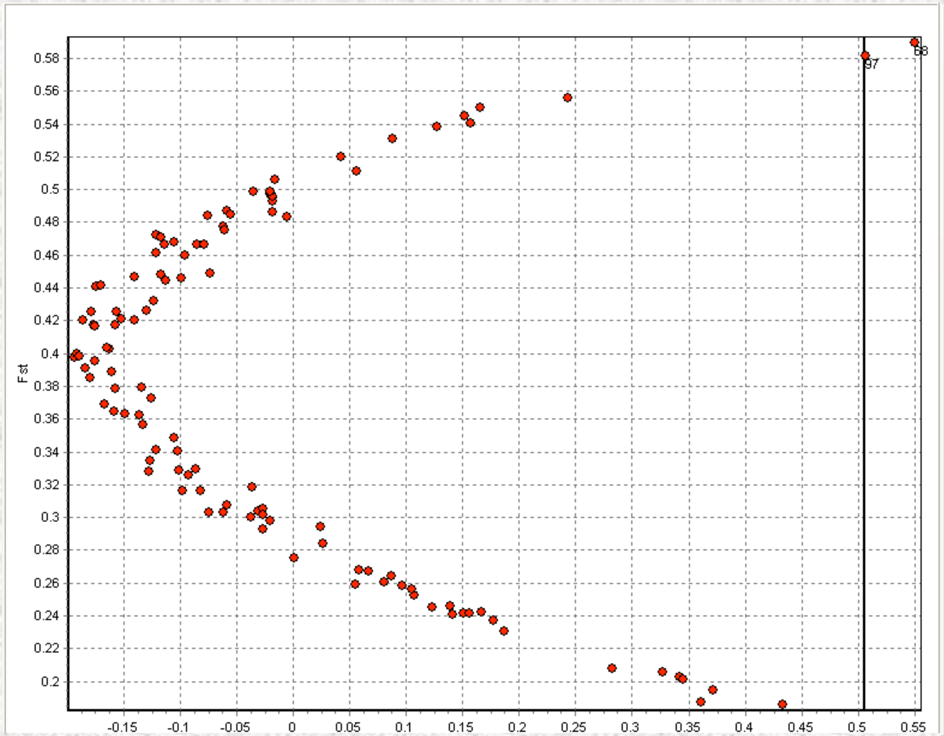
Conclusions: Divergence associated with invasiveness

- The population bottleneck associated with the introduction of *S. squalidus* has resulted in considerable molecular genetic divergence from its parental species
- A different set of quantitative traits differentiate *S. squalidus* and its parents than differentiate the species on Mt Etna.

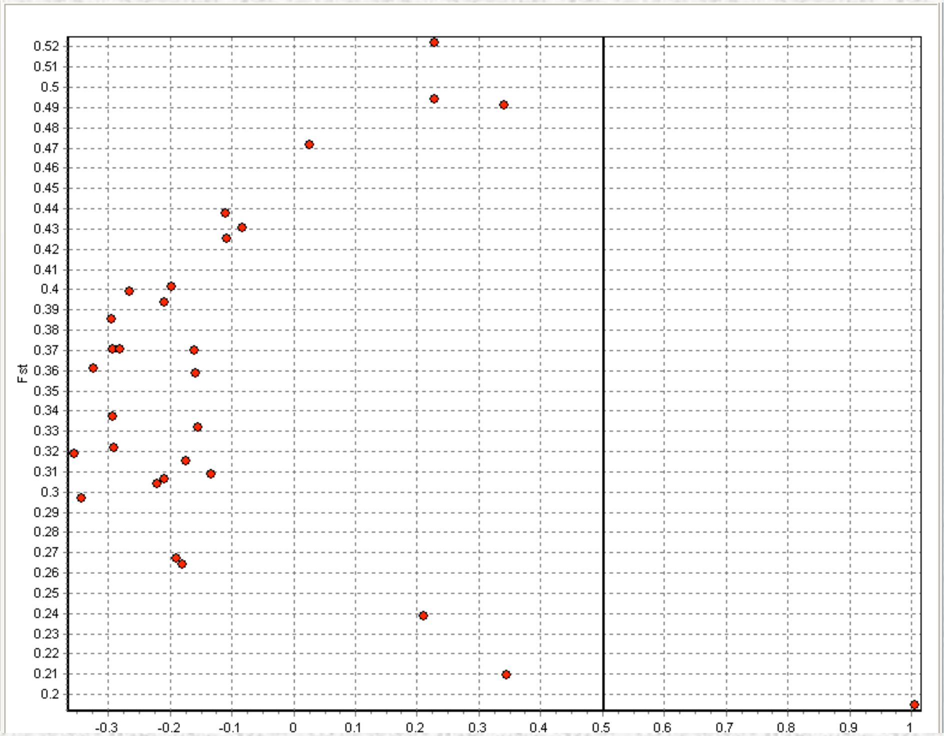
In progress: Differentiation tests of more loci; Bayescan

S. aeth. versus *S. chrys.*

AFLPs

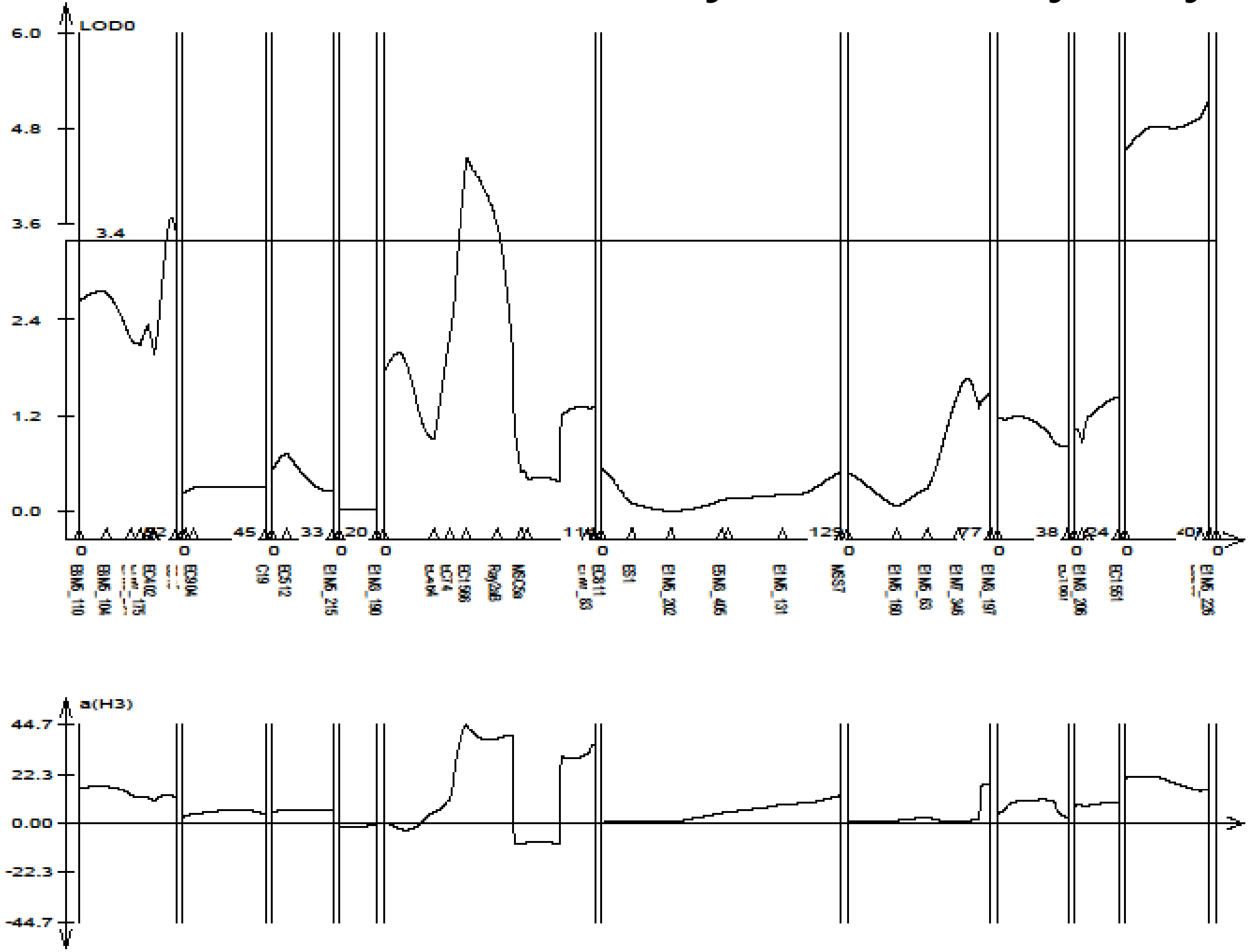


Codominant markers



In progress: Genetic and QTL mapping of these markers

S. aeth. markers; *aeth* x *chrys* F2 family; ray area



In progress: Genetic and QTL mapping of these markers

S. aeth. markers; *aeth* x ***squal*** F2 family; ray area