

Identifying phylogeographic patterns and population history in Mediterranean rock ferns



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Research interests

- Spatial patterns of genetic variation in wild and cultivated plants
- Inferring population history/domestication history from phylogeographic data
- Evolution and distribution of phenotypic traits in domesticated cereals
- Reticulate evolutionary processes – hybridisation and polyploidisation

Asplenium (Aspleniaceae) – rock ferns

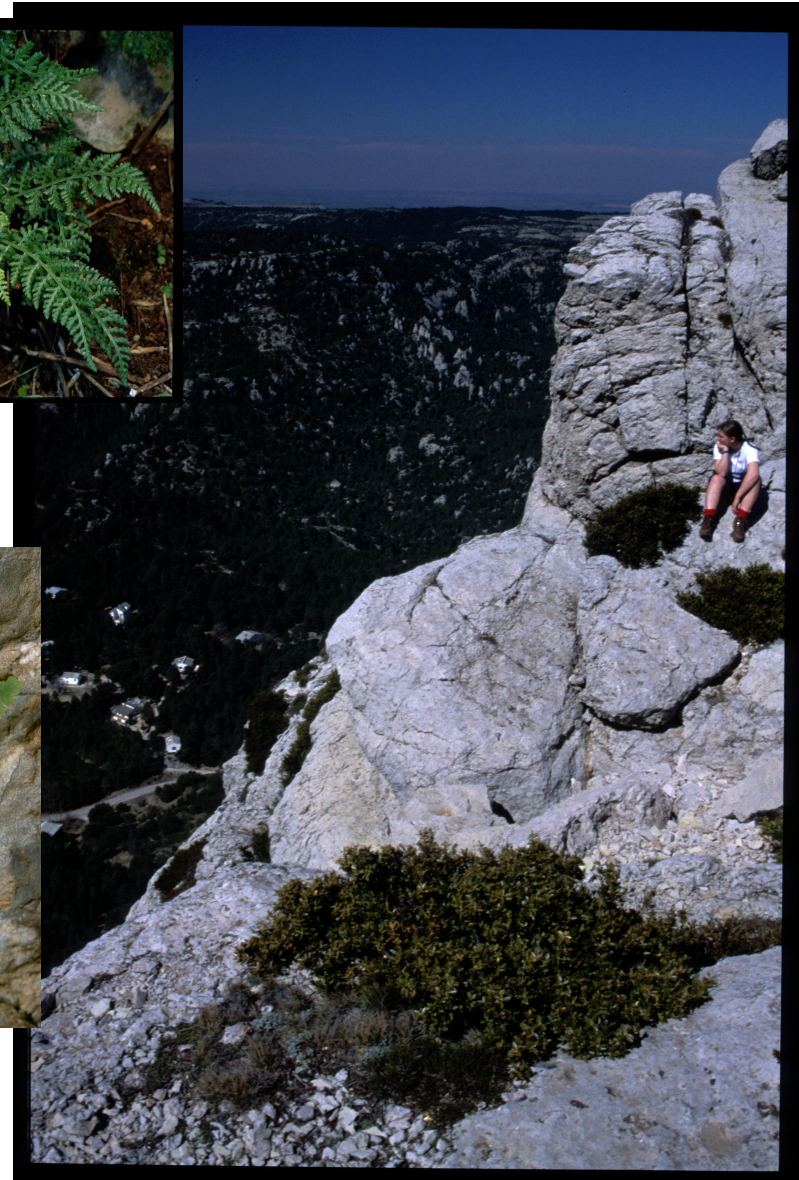
- Largest fern genus
- Over 700 species worldwide
- Over 50 species/subspecies in Europe
- Variation in ecological niche, breeding system, ploidal level
- Numerous well-analysed hybrids and neopolyploids



Genetic diversity and phylogeography in diploid parent taxa

A. fontanum

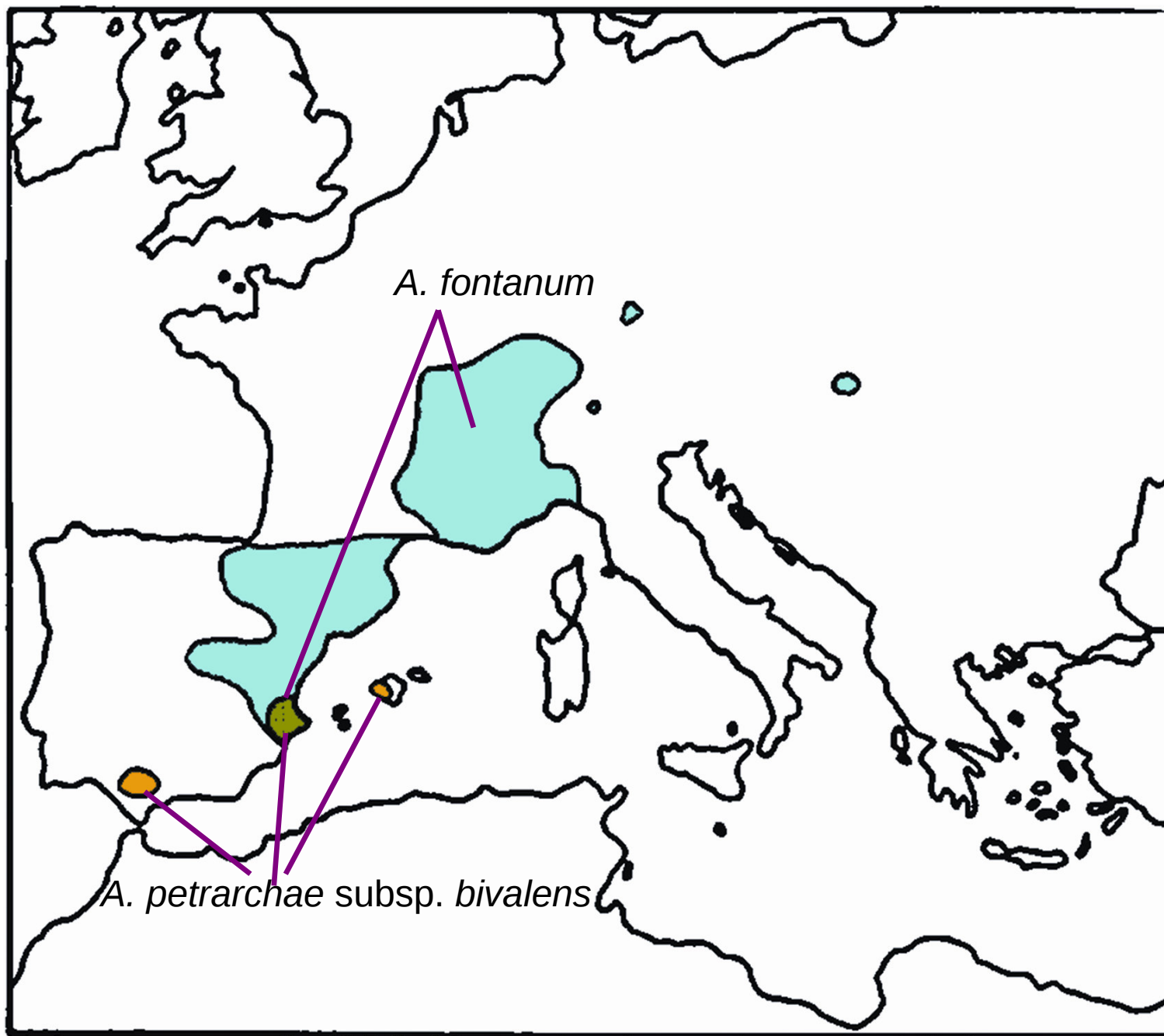
- widespread in SW Europe
- grows in limestone up to ~ 2100 m



A. petrarchae subsp. *bivalens*

- rare – Valencia, Majorca, ? Grazalema
- grows in limestone up to ~ 700 m





Questions

- How is genetic diversity partitioned in *A. fontanum* and *A. petrarchae* subsp. *bivalens*?
- What is the population history of these taxa?



Methods

A. fontanum – 75 populations, 2026 plants

A. petrarchae subsp. *bivalens* – 12 populations, 621 plants

- Allozyme electrophoresis (14 loci) – all plants

Data analysed using diversity statistics, F-statistics, STRUCTURE, genetic distance measures

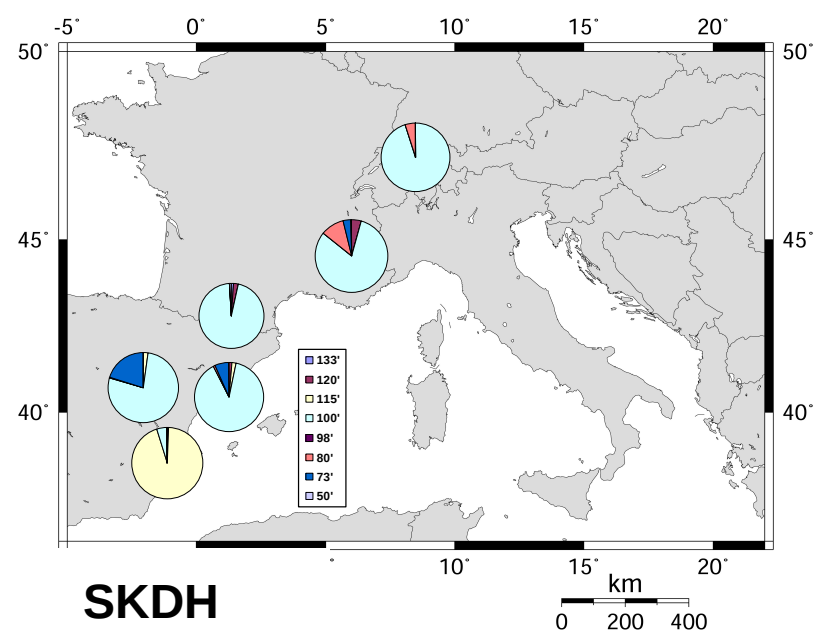
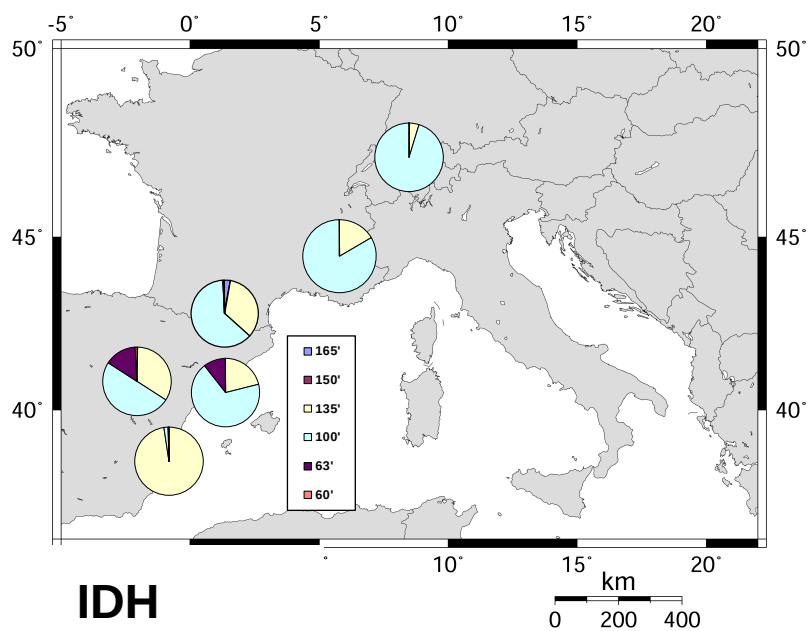
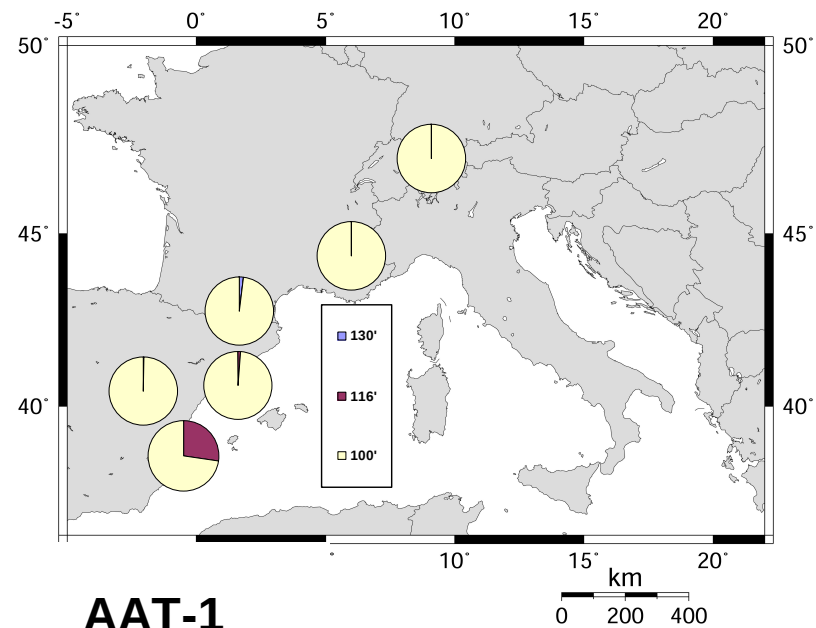
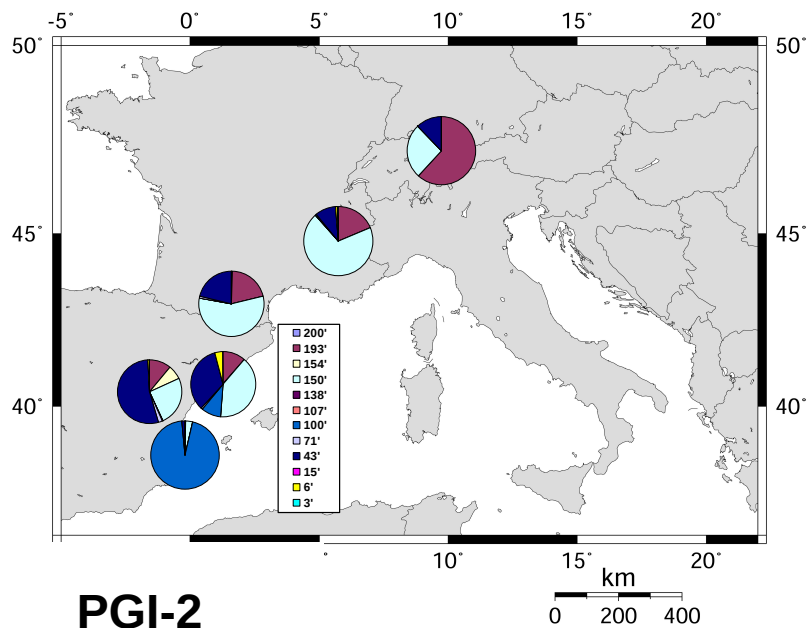
- Chloroplast DNA sequencing

(*rps4* – *trnS* intergenic spacer – *A. fontanum* – c. 900 bp)

(*trnL* – *trnF* intergenic spacer – *A. petrarchae* subsp. *bivalens* - c. 900bp)

Sequenced in c. 10% of plants

Data analysis: networks, AMOVA



F-statistics

Valencia versus all other regions: interregional differentiation (F_{CT}) = 0.552

Interregional differentiation excluding Valencia: $F_{CT} = 0.059$

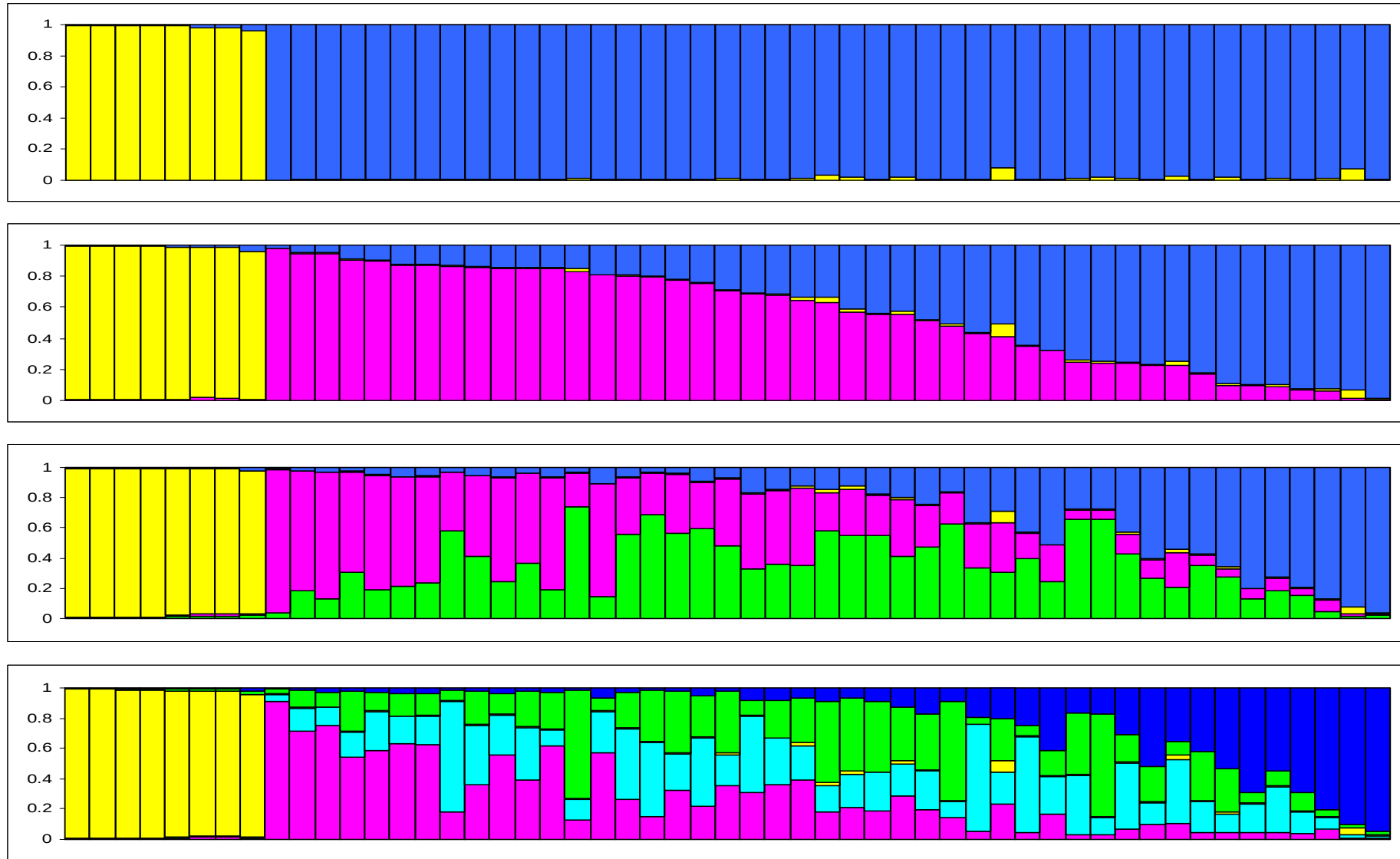
Limitation of F-statistic analysis: requires *a priori* determination of clusters

STRUCTURE (Pritchard et al., *Genetics* **155**: 945 (2000))

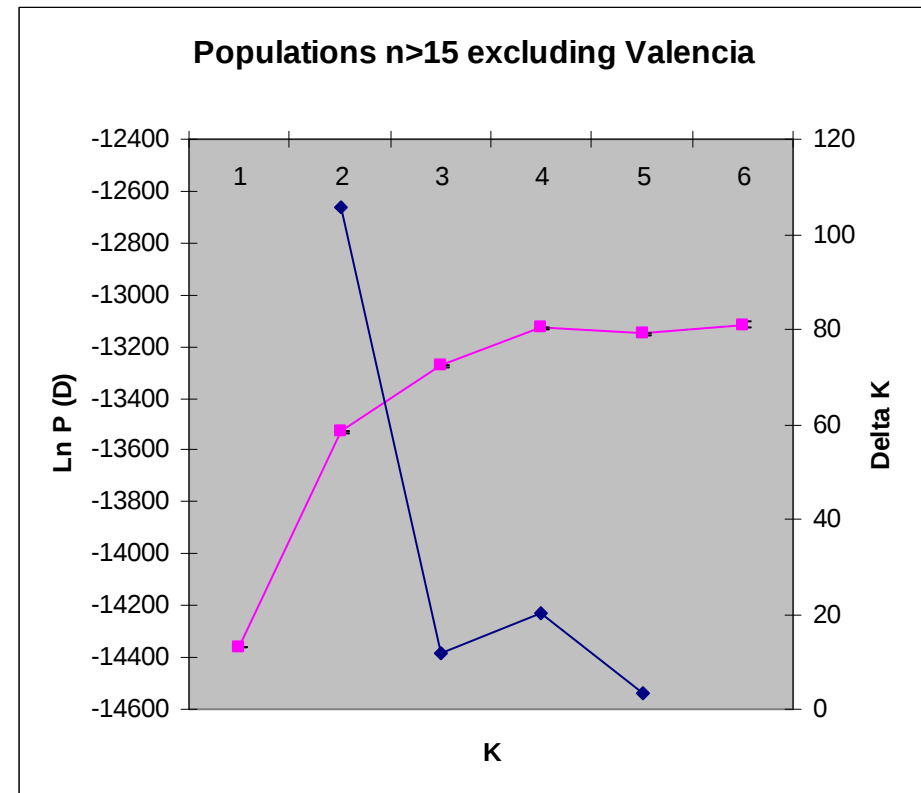
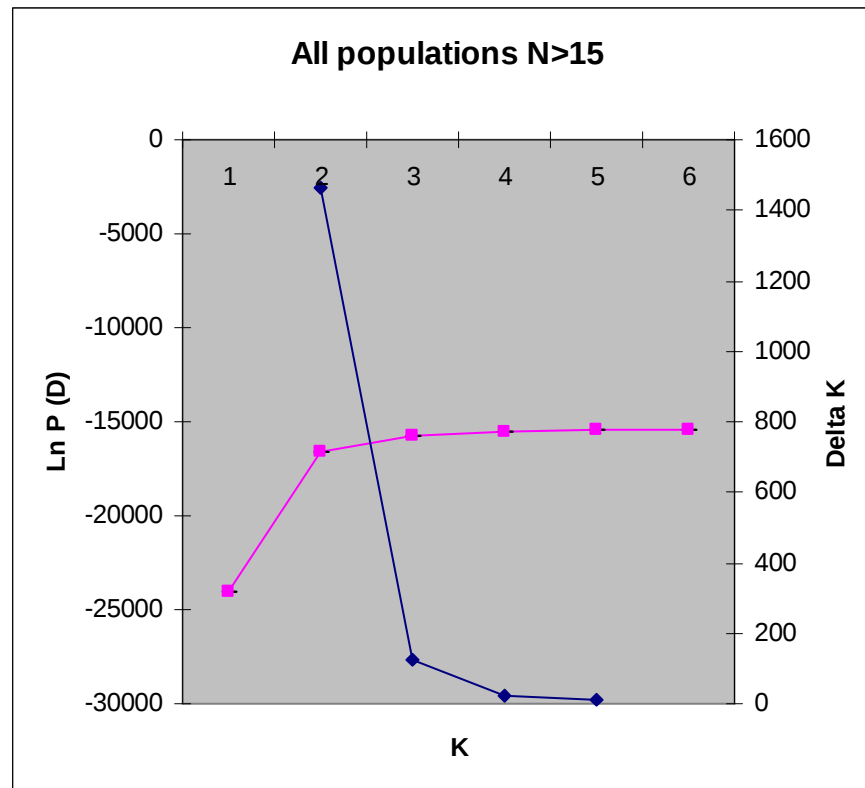
- Models number of ancestral populations/genepools (K), each with specific allele frequencies
- Multilocus genotype data (e.g. allozymes, microsatellites, SNPs)
- Bayesian modelling algorithm: posterior probability of the data ($\ln P(D)$)
- for each K , overall $\ln P(D)$ of the model and matrix of Q – proportion of genotype of each sample derived from each of the K genepools
- samples can be individuals and/or sampled populations
- meaningful values of K are those that capture the major structure present in the data

<http://pritch.bsd.uchicago.edu/structure.html> or on elephant/CamGrid

A. fontanum, Q -matrix plots of $K=2$ through $K=5$ for 53 sampled populations

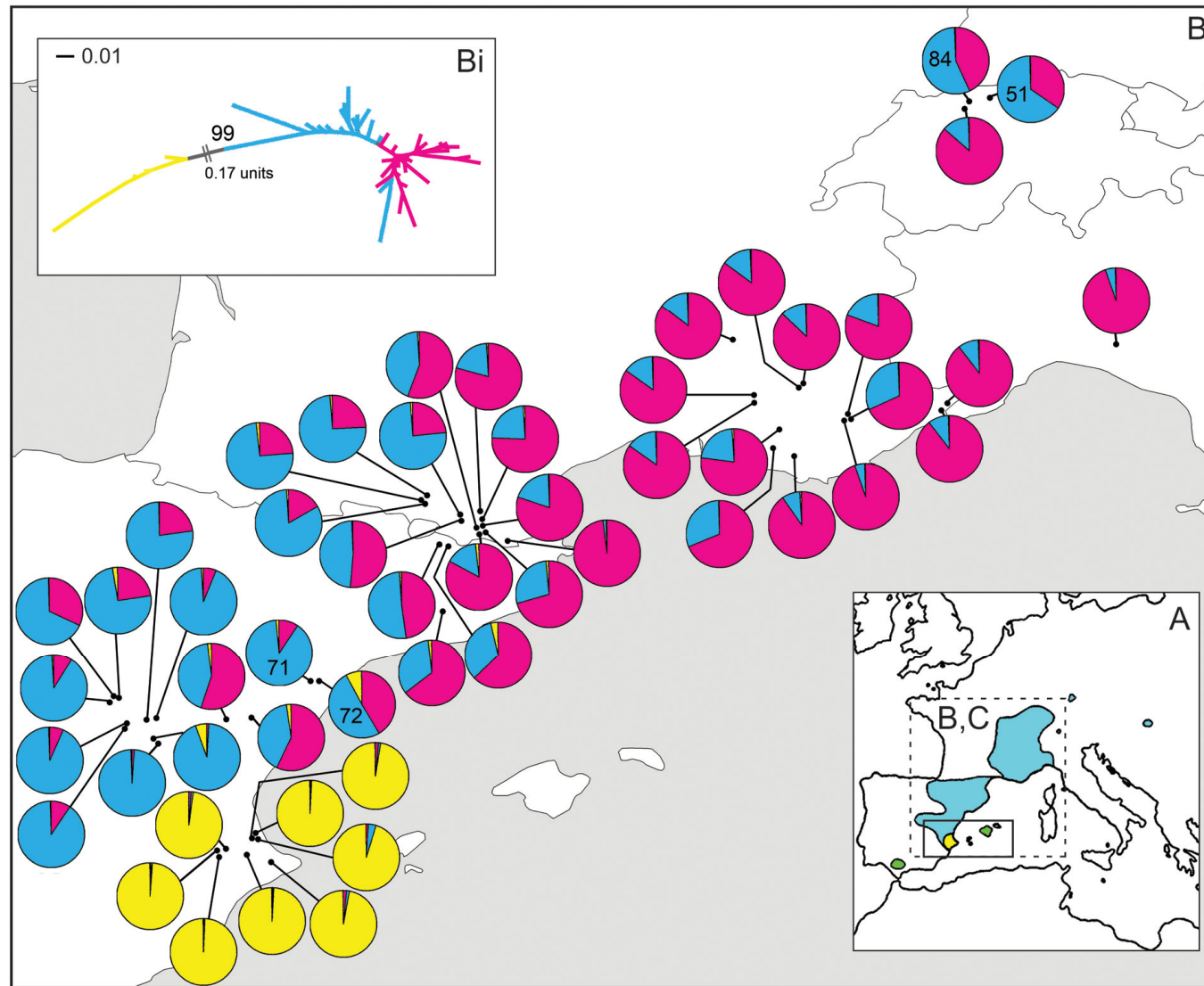


Evaluating meaningful values of K



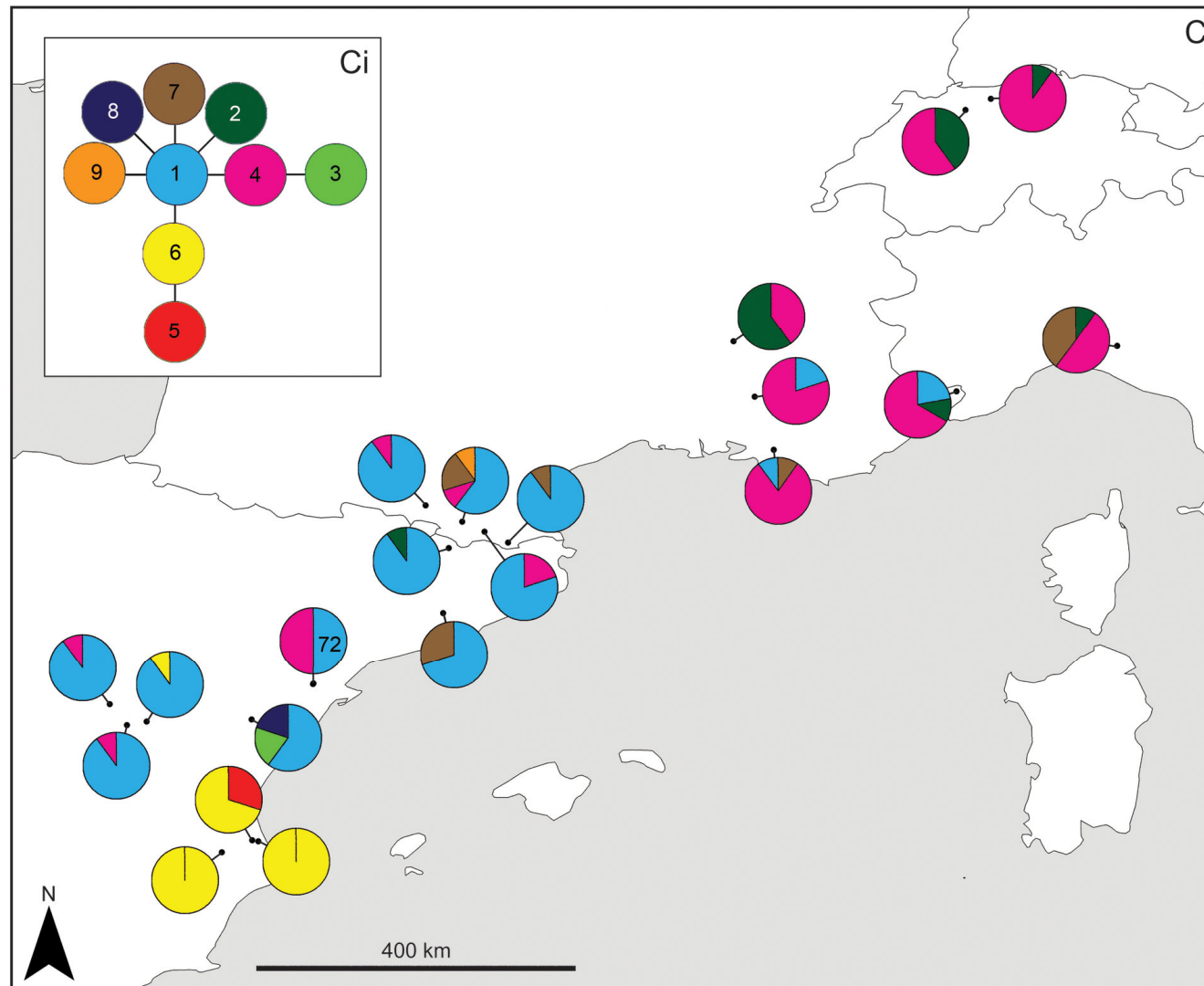
Delta K *sensu* Evanno et al., *Mol. Ecol.* **14**: 2611 (2005)

A. fontanum: STRUCTURE proportions under $K=3$ (allozymes)

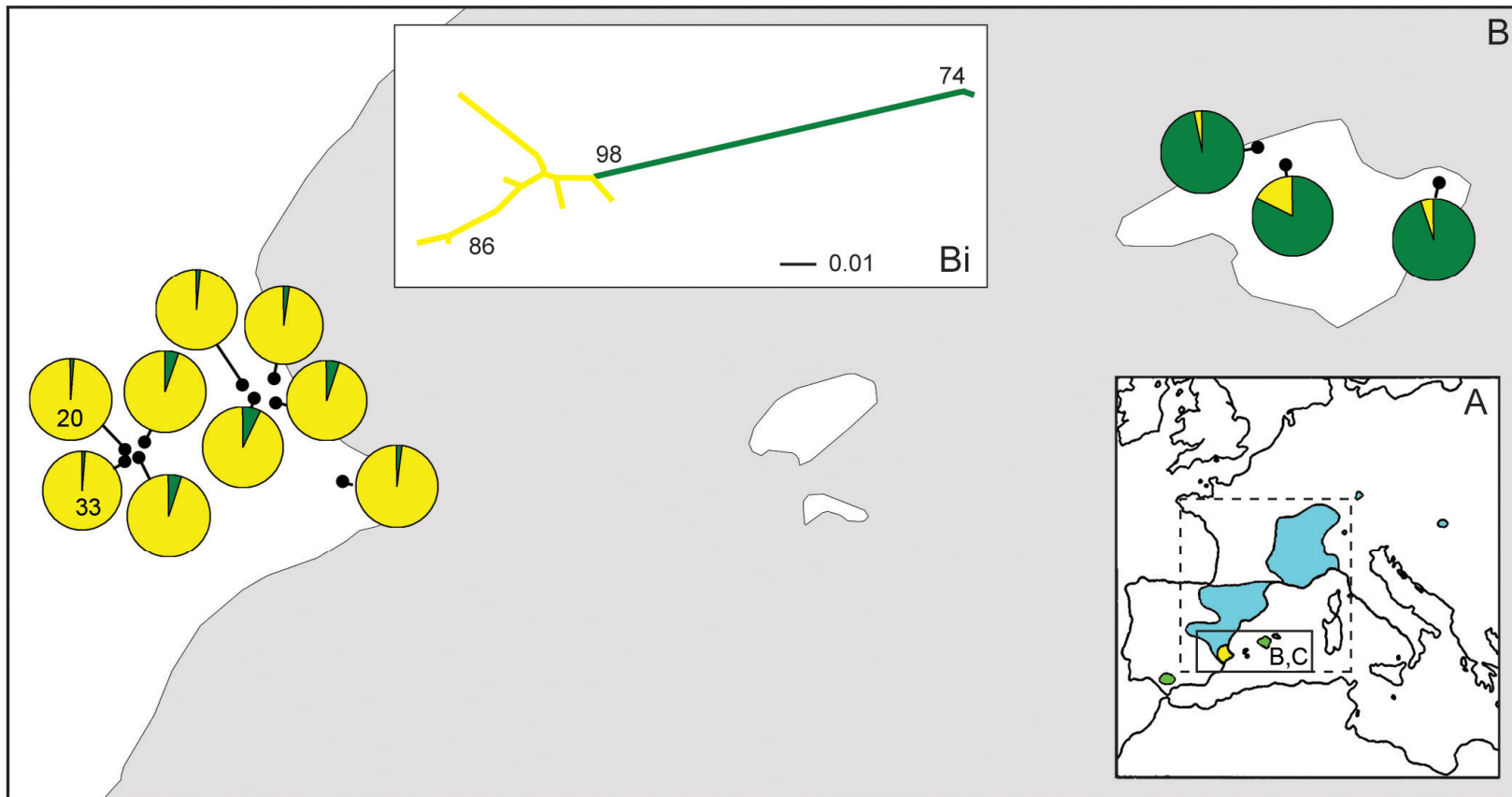


Hunt et al., *Mol. Ecol.* **18**: 4940 (2009)

A. fontanum: *rps4-trnS* haplotype distribution

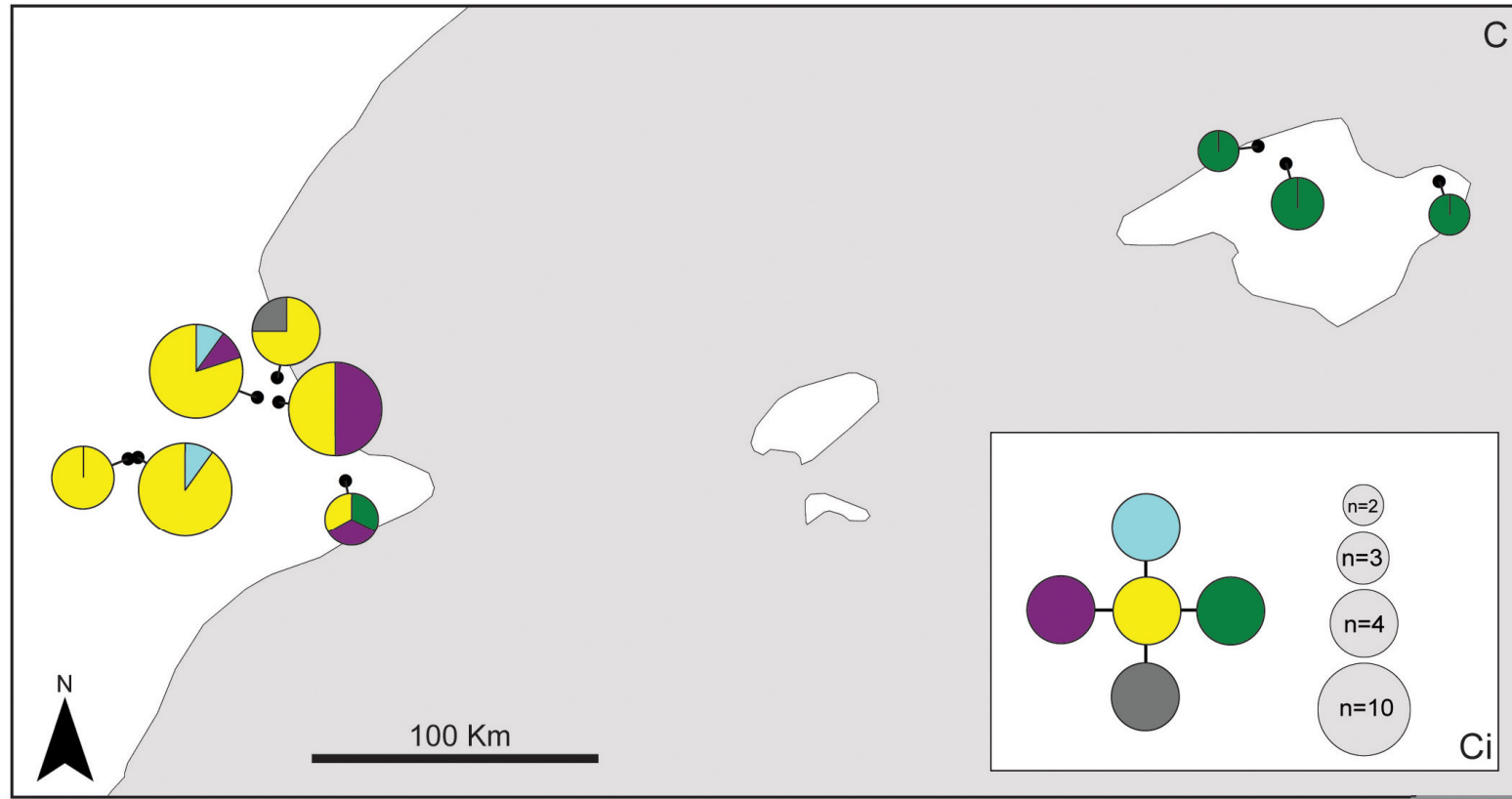


A. petrarchae subsp. *bivalens*: STRUCTURE proportions under $K=2$ (allozymes)



Hunt et al., *Mol. Ecol.* **18**: 4940 (2009)

A. petrarchae subsp. *bivalens*: *trnL-F* haplotype distribution



Conclusions: genetic diversity in *A. fontanum* and *A. petrarchae* subsp. *bivalens*

- Genetic differentiation between regions in both taxa
- *A. fontanum* – ancient split between Valencia and the rest of the range
- Pyrenees – a refugium or suture zone?
- *A. petrarchae* subsp. *bivalens* – Majorca less genetically diverse than Valencia
- *In situ* survival on Majorca or colonization from the mainland?

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