Updates of genetic information for the white – clawed crayfish in Spain, with new insights into its population genetics and origin

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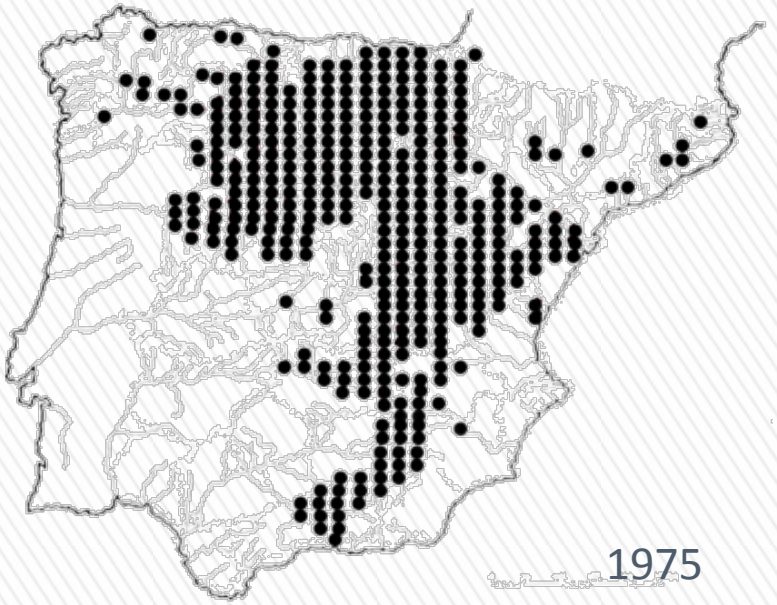
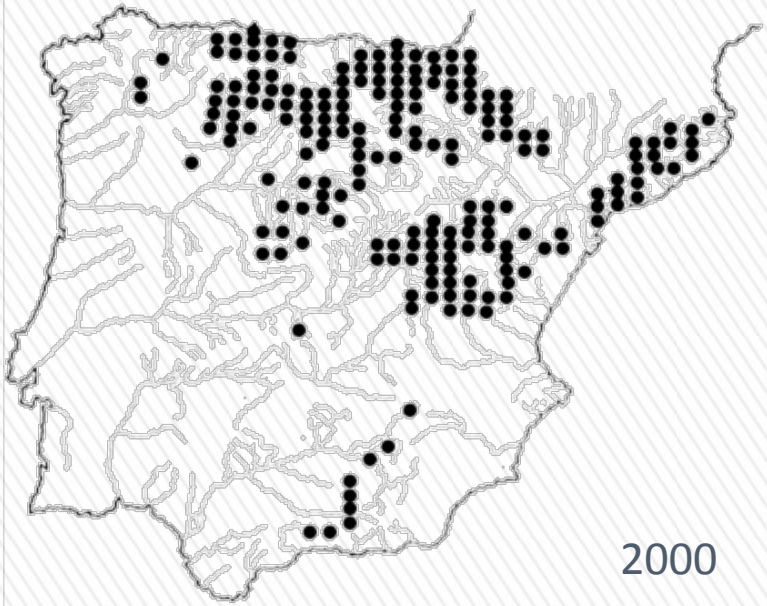


1975



2000

(Alonso et al. 2000)

Genetic studies

Nuclear genome

Mitochondrial genome

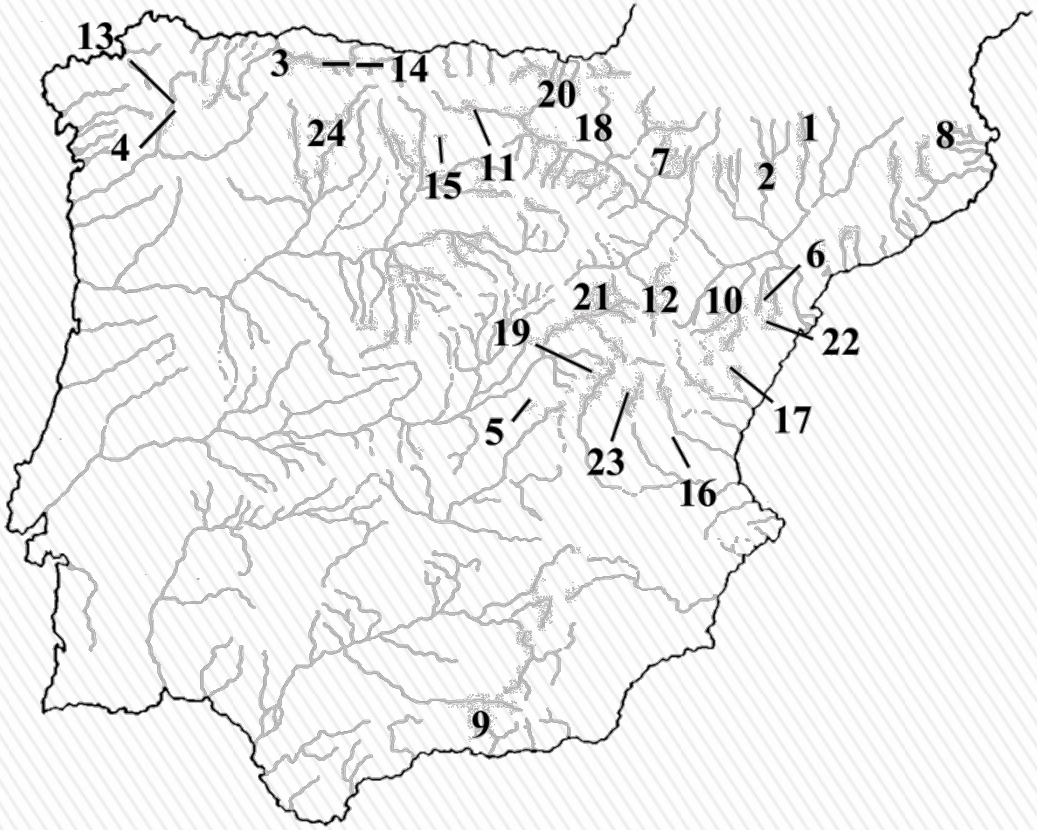
↓ Populations

↓ Individuals / Population

1 molecular marker

↑ Populations
↑ Specimens/ population

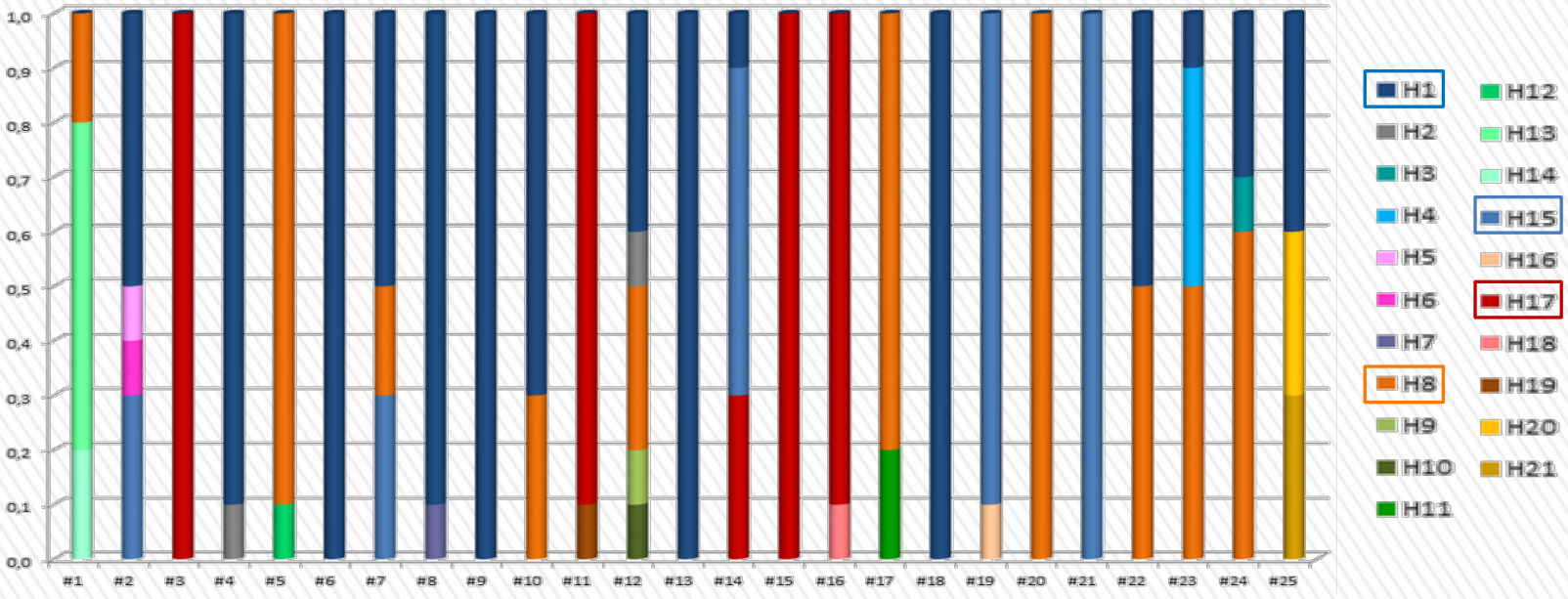
mtDNA: 250 crayfish
SSR: 394 crayfish



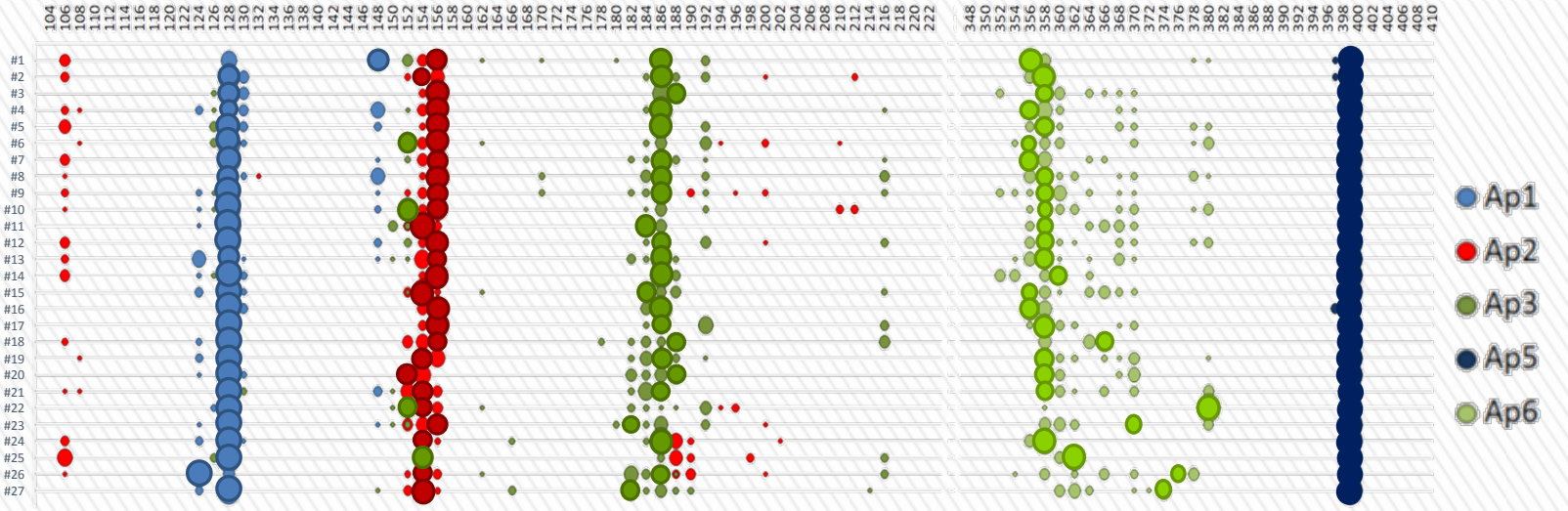
mtDNA: mitochondrial DNA
SSR: nuclear microsatellites

Proportion of the mitochondrial haplotypes into the populations studied

mtDNA

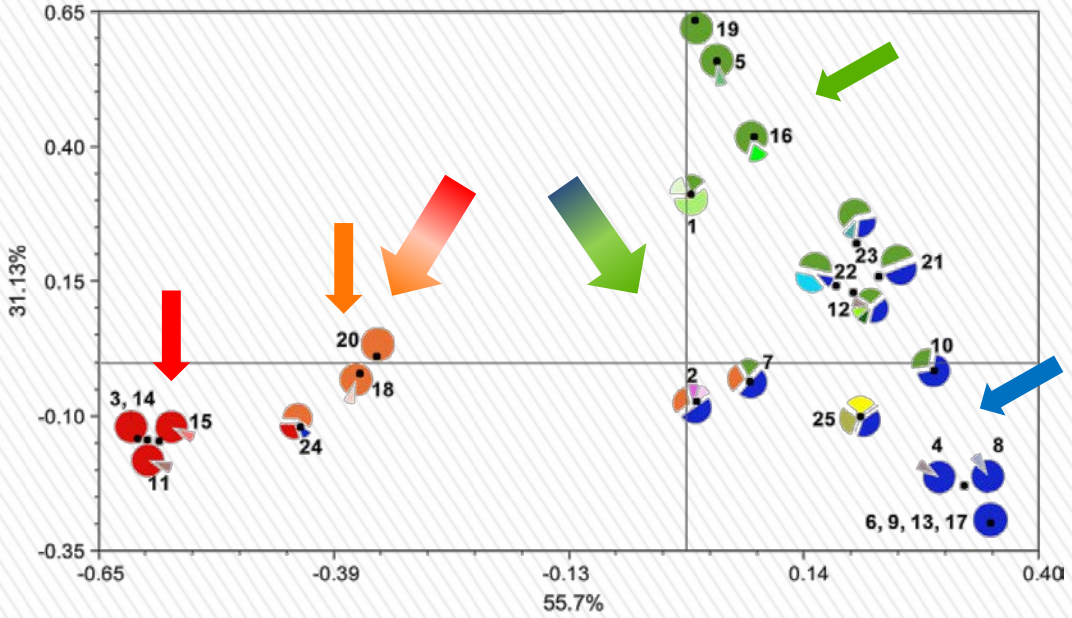


SSR



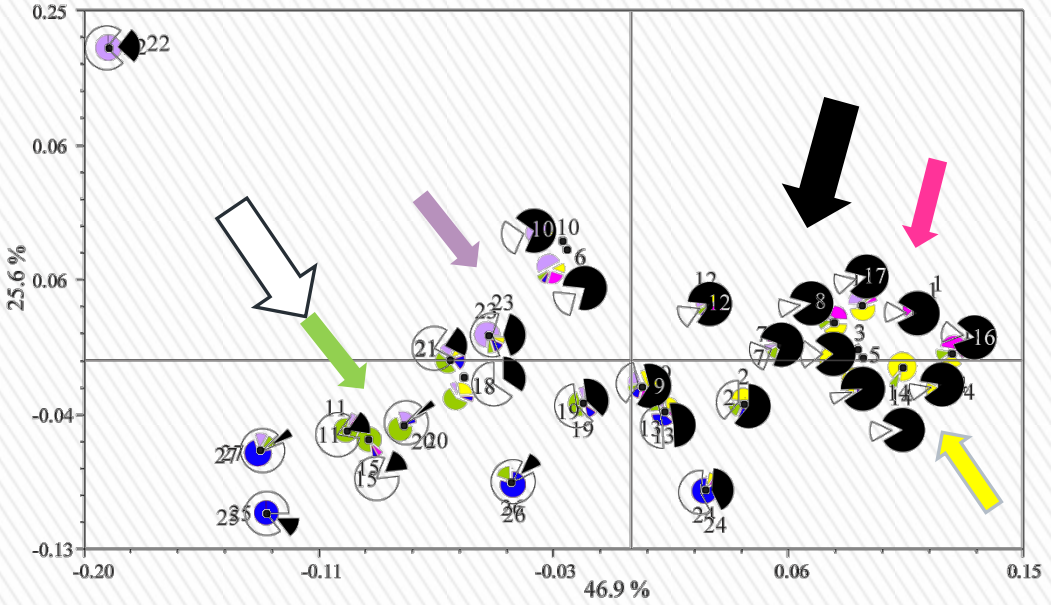
Allele frequency (bubble area) and size distributions (in base pairs) of the studied SSR loci

mtDNA

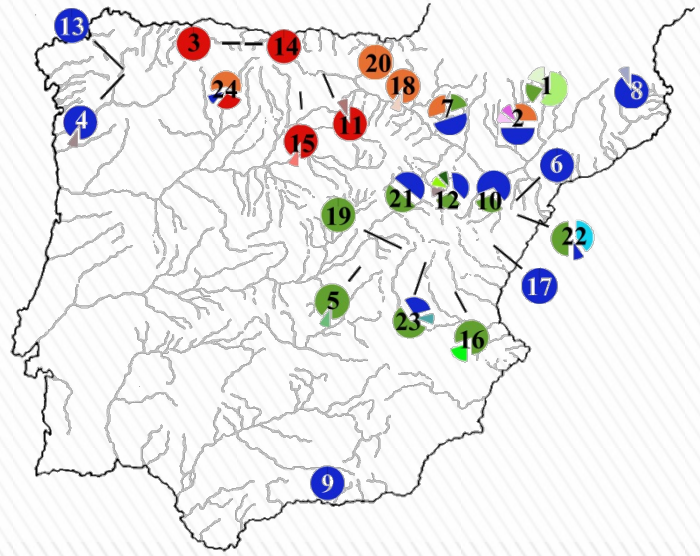


Principal Coordinate Analysis with F_{ST} values from with mtDNA markers (top) and nuclear microsatellites (bottom) in the populations studied

SSR



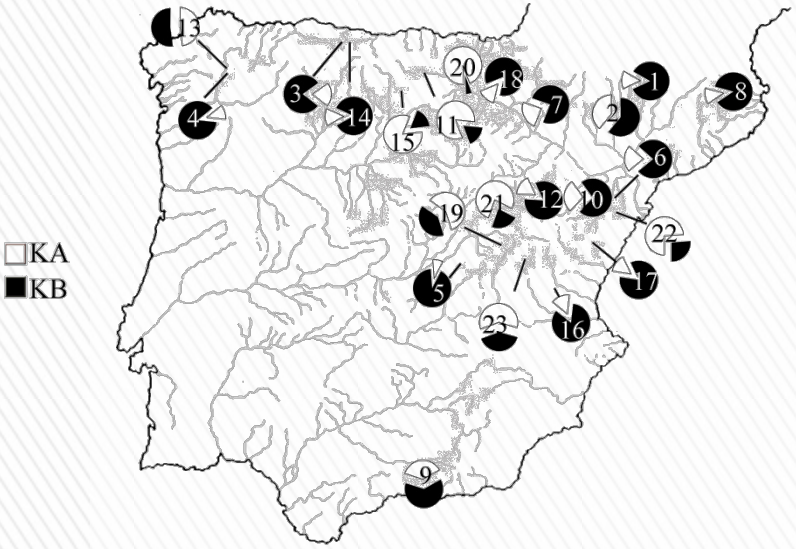
mtDNA



	% Variance	P value
Spanish populations: 2 groups		
Among groups	72,83	P < 0,001
Among populations within groups	12,90	P < 0,001
Within populations	14,27	P < 0,001

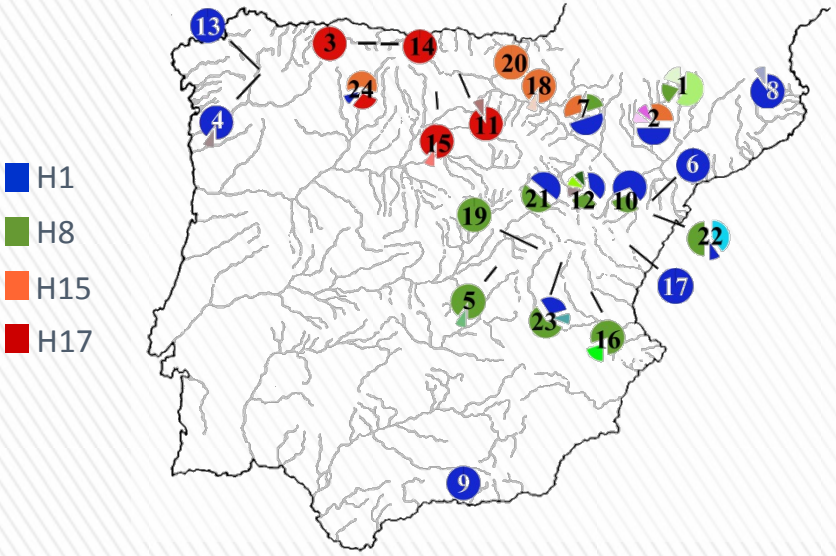
Molecular Variance Analysis of the sampled populations.
%Variance: percentage of the total variance contributed by each component
P-value: significance

SSR



	% Variance	P value
Spanish populations: 2 groups		
Among groups	9,53	P < 0,001
Among populations within groups	12,39	P < 0,001
Within populations	78,07	P < 0,001

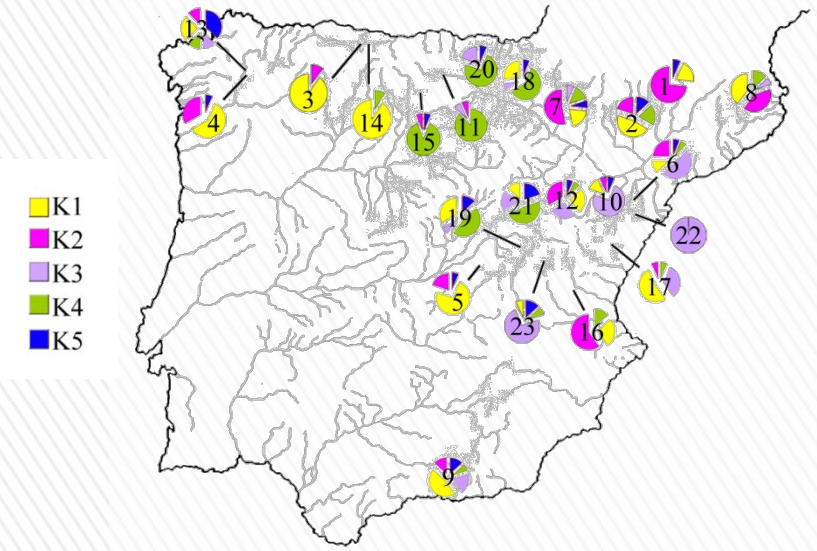
mtDNA



	% Variance	P value
Spanish populations: 4 groups		
Among groups	73,51	P < 0,001
Among populations within groups	7,66	P < 0,001
Within populations	18,83	P < 0,001

Molecular Variance Analysis of the sampled populations.
%Variance: percentage of the total variance contributed by each component
P-value: significance

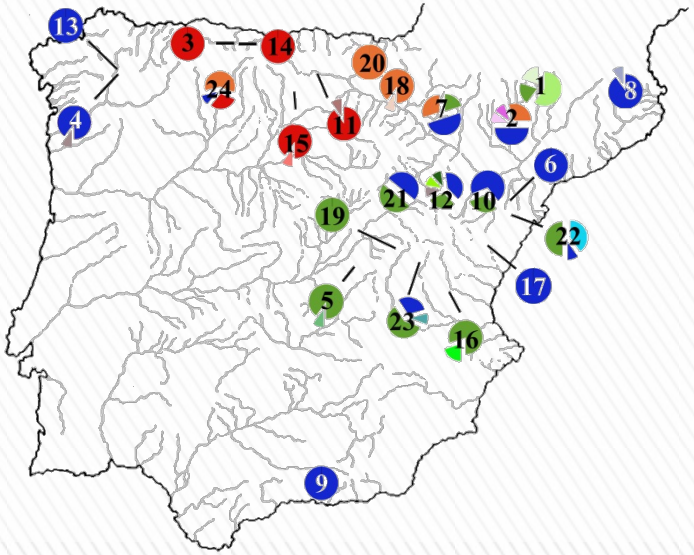
SSR

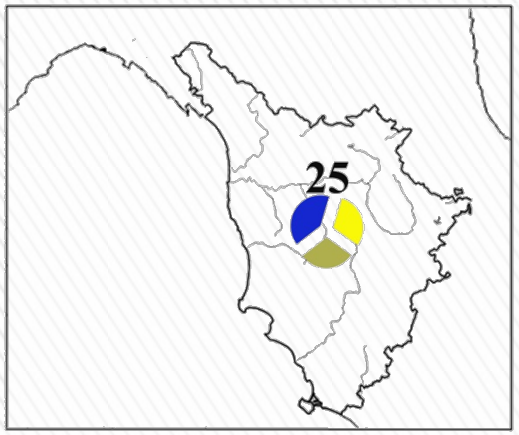


	% Variance	P value
Spanish populations: 4 groups		
Among groups	10,01	P < 0,001
Among populations within groups	9,30	P < 0,001
Within populations	80,69	P < 0,001

mtDNA

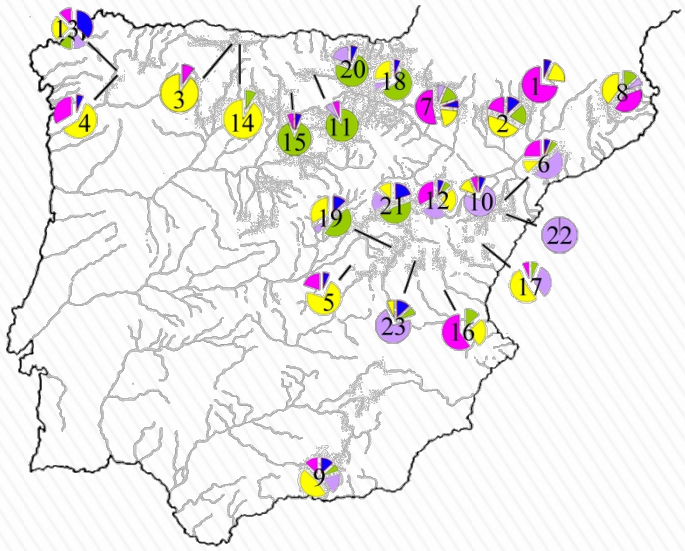
H1
H8
H15
H17

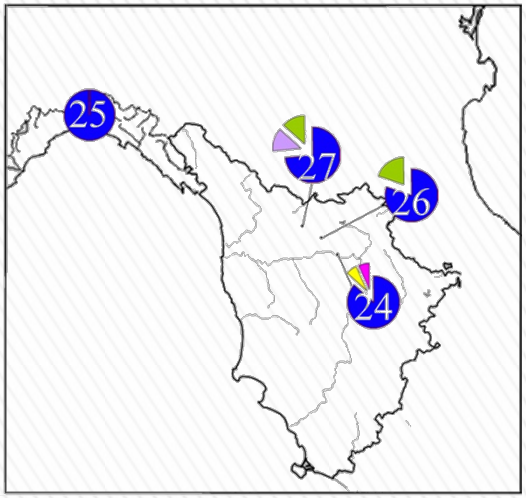


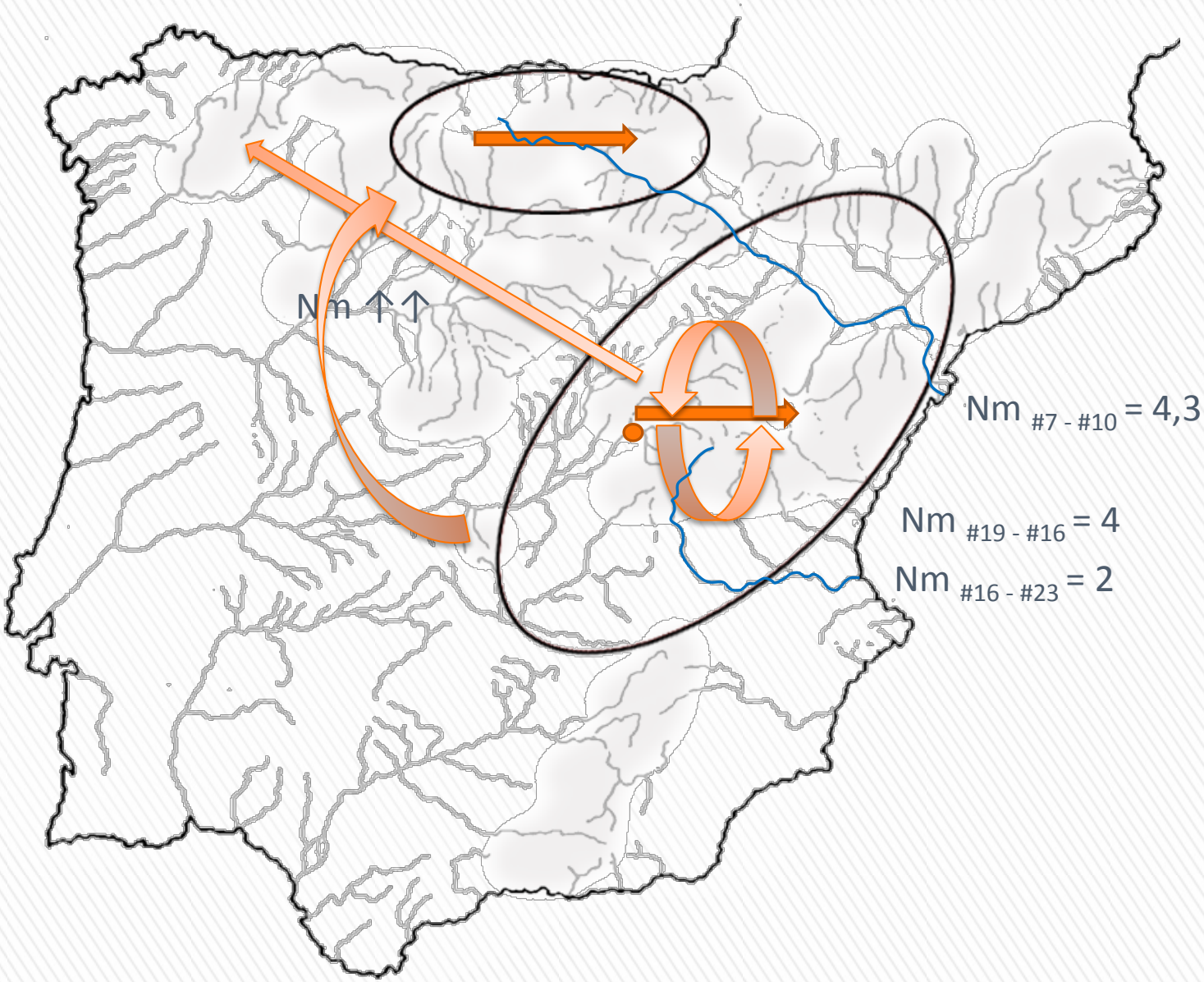


SSR

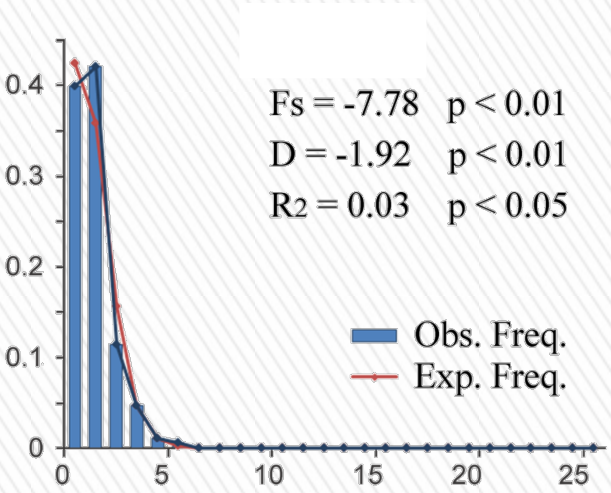
K1
K2
K3
K4
K5



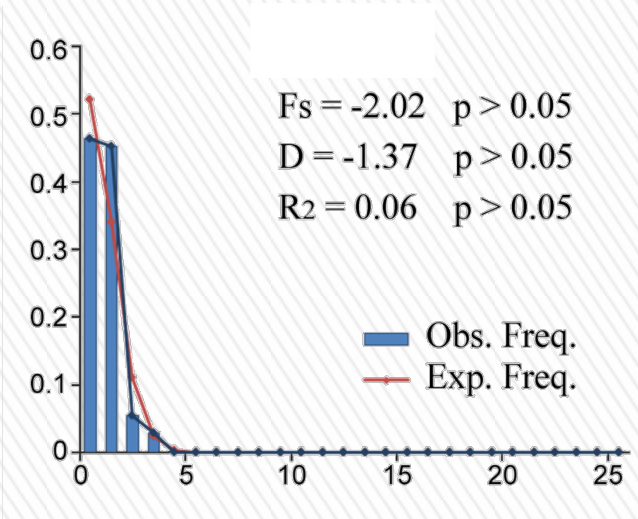



Nm ↑↑
Nm #7 - #10 = 4,3
Nm #19 - #16 = 4
Nm #16 - #23 = 2

‘Central’ group



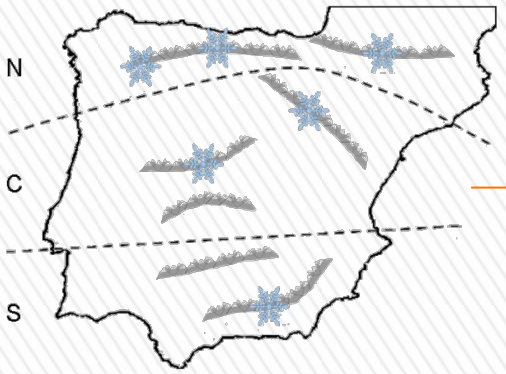
‘Northern’ group

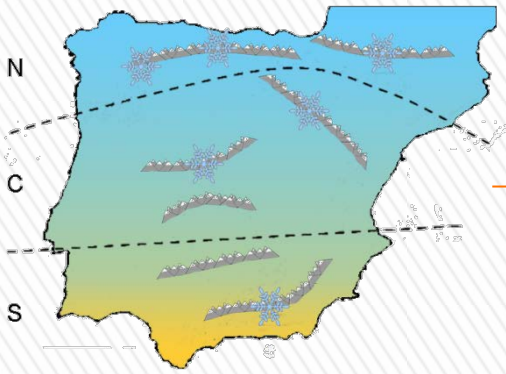


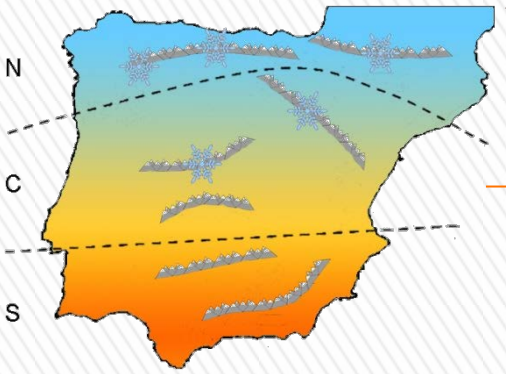
Unimodal left – handed pick in the mismatch distributions support an expansion event.
Fu’s Fs, Tajima’s D and R2 tests reveal departure from neutrality

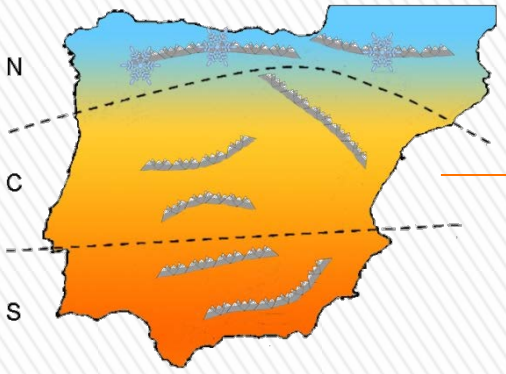
Time elapsed from last expansion in the ‘Central’ group: 14,000 years

Time elapsed from last expansion in the ‘Northern’ group: 10,000 years



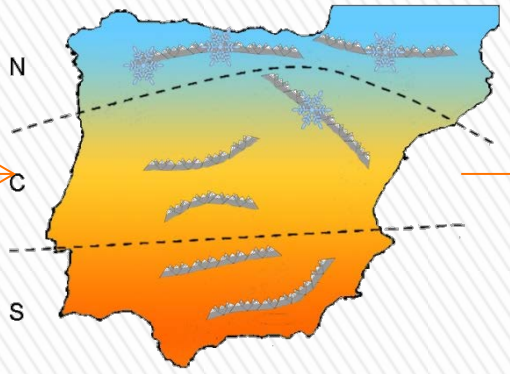


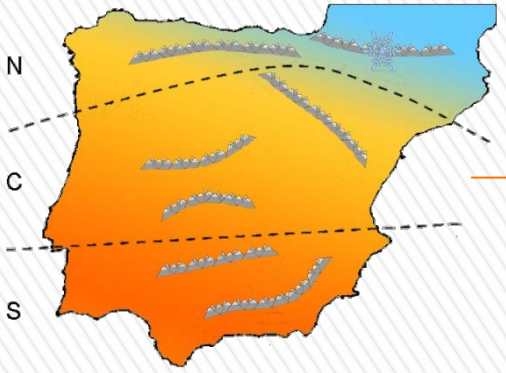


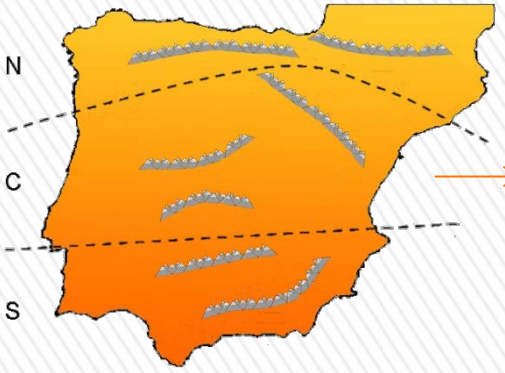


Population expansion in the 'Central' group:

14,000 years

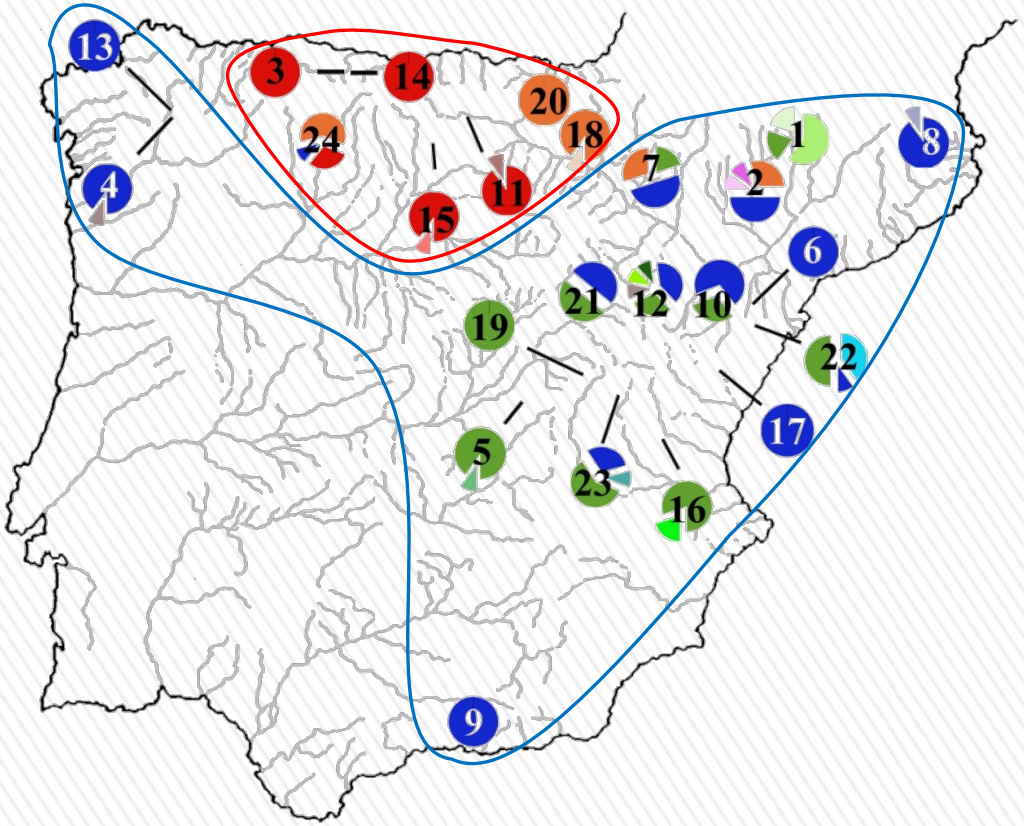






Population expansion in the 'Northern' group:

10,000 years



1 ESU (*Evolutionary Significant Unit*)

2 MU (*Management Unit*)