

TWO MAIN GENETIC CLUSTERS WITH HIGH ADMIXTURE BETWEEN FOREST AND CULTIVATED CHESTNUT (*CASTANEA SATIVA* MILL.) IN FRANCE

ESM_6 HIERARCHICAL AMOVA AND F-STATISTICS

ESM_6A HIERARCHICAL AMOVA AND F-STATISTICS FOR 17 FRENCH SAMPLING REGIONS GENOTYPED AT 10 SSRs WITHOUT MLGS (10UNIK DATA SET)

df: degrees of freedom, Alter: alternative hypothesis, 95% confidence intervals, *** p value \leq 0.001.

Source of variation	df	Variance component	% of variation	p value	Alter	F statistic
Among chestnut type	1	-0.078	-1.23	0.831	greater	Fct -0.007 [-0.011 ; -0.002]
Among sampling regions within chestnut types	15	0.799	12.58	0.001***	greater	Fst 0.083 [0.07 ; 0.095]
Within sampling regions	1033	5.629	88.64	0.001***	less	Fis 0.015 [-0.009 ; 0.046]
Total	1049	6.351	100.00			Fit 0.09 [-0.06 ; 0.125]

ESM_6B HIERARCHICAL AMOVA AND F-STATISTICS FOR SIX GENETIC CLUSTERS GENOTYPED AT 10 SSRs WITHOUT MLGS (10UNIK DATA SET)

df: degrees of freedom, Alter: alternative hypothesis, 95% confidence intervals, *** p value \leq 0.001

Source of variation	df	Variance component	% of variation	p value	Alter	F statistic
Among Clusters	5	0.729	11.3	0.001***	greater	Fst 0.078 [0.064 ; 0.091]
Within Clusters	1044	5.709	88.7			Fis 0.022 [-0.005 ; 0.055]
Total	1049	6.438	100.00			Fit 0.098 [0.063 ; 0.136]

ESM_6C HIERARCHICAL AMOVA AND F-STATISTICS FOR SIX GENETIC CLUSTERS GENOTYPED OF STRONGLY ASSIGNED INDIVIDUALS ($QL \geq 80\%$) AT 10 SSRs WITHOUT MLGS (10UNIK DATA SET)

df: degrees of freedom, Alter: alternative hypothesis, 95% confidence intervals, *** p value \leq 0.001

Source of variation	df	Variance component	% of variation	p value	Alter	F statistic
Among Clusters	5	1.21	18.1	0.001***	greater	Fst 0.125 [0.104 ; 0.144]
Within Clusters	558	5.46	81.9			Fis 0.002 [-0.03 ; 0.042]
Total	563	6.67	100.00			Fit 0.126 [0.085 ; 0.173]