	MAL	MAD	NAV	SAL1	TAR	BAD	BAL	CAC	COR	GER	GRA	JAE	SAL2	TER	VAL	POR1	POR2	ITA	TUN1	TUN2	TUN3	GRE1	GRE2	GRE3	ISR1	ISR2
MAD	0,000																									
NAV	0,006	0,000																								
SAL1	0,004	0,026	0,072																							
TAR	0,000	0,000	0,028	0,030																						
BAD	0,010	0,027	0,063	0,006	0,005																					
BAL	0,021	0,000	0,000	0,101	0,037	0,096																				
CAC	0,000	0,000	0,000	0,012	0,000	0,004	0,000																			
COR	0,000	0,002	0,004	0,019	0,000	0,036	0,034	0,000																		
GER	0,019	0,028	0,000	0,063	0,050	0,039	0,061	0,000	0,005																	
GRA	0,018	0,000	0,046	0,074	0,000	0,045	0,000	0,000	0,060	0,091																
JAE	0,000	0,000	0,023	0,035	0,000	0,015	0,042	0,000	0,000	0,051	0,000															
SAL2	0,016	0,000	0,000	0,071	0,010	0,066	0,000	0,000	0,000	0,006	0,032	0,001														
TER	0,009	0,019	0,000	0,048	0,046	0,060	0,042	0,000	0,000	0,000	0,100	0,048	0,000													
VAL	0,000	0,000	0,000	0,018	0,000	0,015	0,051	0,000	0,000	0,000	0,063	0,006	0,006	0,000												
POR1	0,000	0,000	0,000	0,031	0,000	0,031	0,000	0,000	0,000	0,010	0,000	0,000	0,000	0,017	0,000											
POR2	0,013	0,022	0,000	0,047	0,050	0,041	0,079	0,011	0,000	0,000	0,116	0,051	0,018	0,000	0,000	0,044										
ITA	**0,345**	**0,339**	0,220	**0,338**	**0,386**	0,258	**0,381**	**0,268**	**0,290**	0,107	**0,366**	**0,329**	0,245	0,215	0,186	**0,322**	0,146									
TUN1	**0,337**	**0,320**	**0,232**	**0,337**	**0,366**	**0,276**	**0,350**	**0,261**	**0,297**	0,158	**0,345**	**0,325**	**0,250**	**0,243**	0,199	**0,312**	0,178	0,039								
TUN2	**0,257**	0,241	0,185	**0,260**	0,280	**0,222**	**0,284**	0,199	0,227	0,136	**0,284**	**0,253**	**0,202**	0,190	0,133	0,249	0,126	0,121	0,000							
TUN3	0,135	0,116	0,000	**0,181**	0,176	0,144	0,122	0,059	0,088	0,000	0,178	**0,145**	0,029	0,016	0,015	0,092	0,014	0,127	**0,158**	0,148						
GRE1	**0,390**	**0,375**	**0,307**	**0,383**	**0,417**	**0,328**	**0,412**	**0,321**	**0,352**	**0,237**	**0,398**	**0,377**	**0,315**	**0,313**	0,256	**0,372**	0,243	0,126	0,000	0,000	**0,250**					
GRE2	**0,282**	**0,274**	0,185	**0,282**	**0,318**	**0,230**	**0,319**	**0,209**	0,236	0,107	**0,315**	**0,280**	**0,212**	0,190	0,136	**0,274**	0,115	0,036	0,000	0,000	0,114	0,000				
GRE3	**0,717**	**0,700**	**0,696**	**0,697**	**0,745**	**0,646**	**0,729**	**0,663**	**0,675**	**0,643**	**0,695**	**0,692**	**0,650**	**0,671**	**0,625**	**0,689**	**0,603**	**0,650**	**0,424**	0,278	**0,711**	0,338	**0,435**			
ISR1	**0,735**	**0,719**	**0,718**	**0,716**	**0,754**	**0,672**	**0,743**	**0,689**	**0,696**	**0,675**	**0,712**	**0,709**	**0,676**	**0,695**	**0,659**	**0,710**	**0,640**	0,684	**0,477**	0,318	**0,732**	0,407	**0,504**	0,093		
ISR2	**0,783**	**0,766**	**0,768**	**0,760**	**0,807**	**0,713**	**0,791**	**0,735**	**0,741**	**0,720**	**0,756**	**0,756**	**0,719**	**0,741**	**0,704**	**0,754**	**0,681**	**0,736**	**0,525**	**0,359**	**0,789**	**0,455**	**0,556**	0,075	0,000	
ISR3	**0,732**	**0,716**	**0,716**	**0,714**	**0,752**	**0,671**	**0,740**	**0,687**	**0,696**	**0,673**	**0,711**	**0,709**	**0,675**	**0,694**	**0,658**	**0,708**	**0,641**	**0,682**	**0,473**	0,307	**0,729**	**0,410**	**0,509**	**0,169**	0,000	0,002

Table S1. F_{ST} fixation indices among the *olf* populations analysed. Statistically significant values ($p < 0.05$) after applying Bonferroni corrections are shown in bold.



Figure S1. SAMOVA analysis with the most probable genetic groups for the *B. oleae* populations sampled.

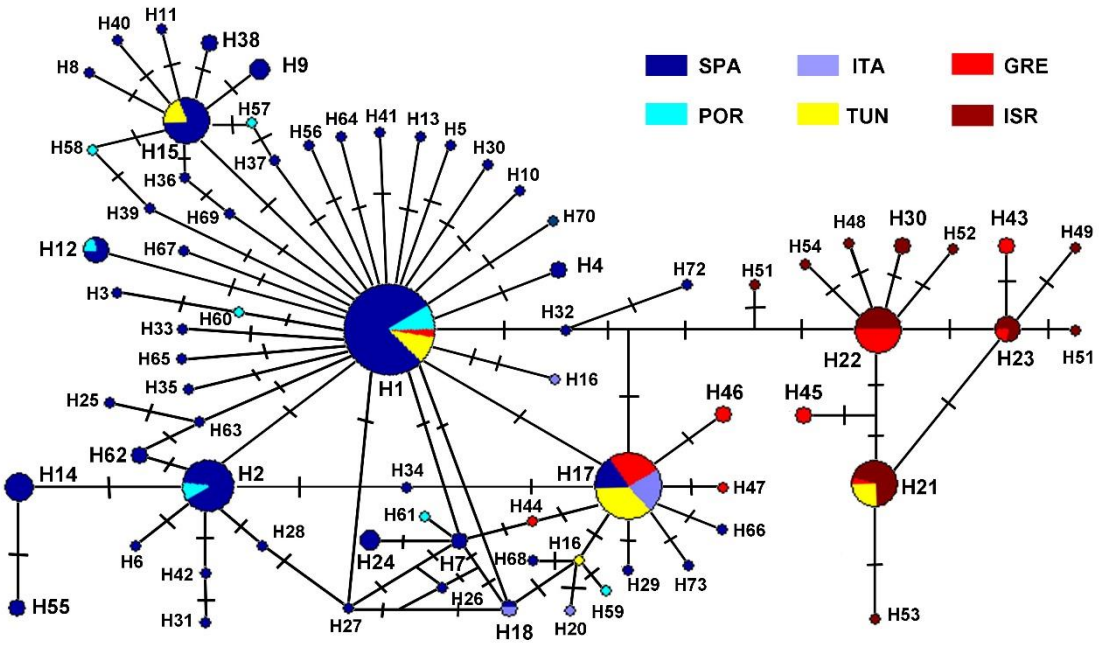


Figure S2. Network of the 73 haplotypes detected in the *B. oleae* populations analysed. Countries are identified by colour. Bars indicate the mutational steps separating the different haplotypes. Intersections represent unsampled haplotypes. H17 is the designated ancestral haplotype.

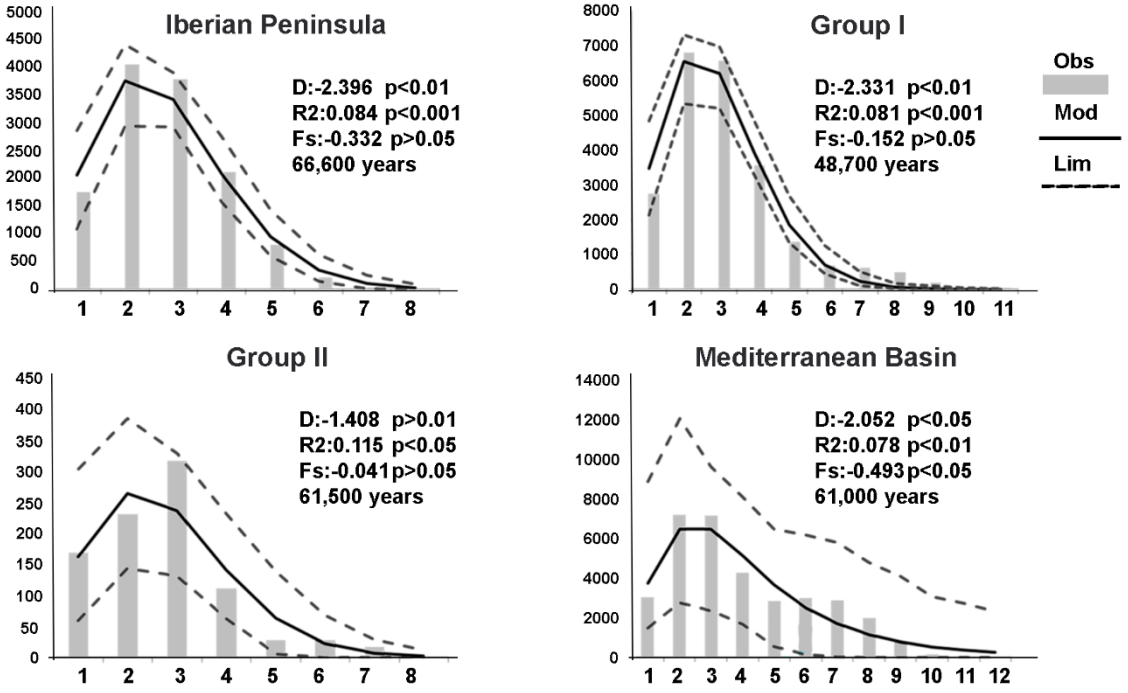


Figure S3. Mismatch distributions, observed and expected, in the Spanish populations as a whole and in the 'Western and 'Eastern genetic clusters detected. The neutrality test Fs, D R2 values and time elapsed since last expansion are also shown