Supplementary material

Figures and Tables

Figures:

Map with provenances and occurrences (Fig. S1)

RAxML tree topology (Fig. S2)

Amino acids alignment from the selection analysis (Fig. S3)

Tables:

Table with samples used in this study (Table S1) – excel format

Table with genes for dating and selection analysis (Table S2)

Table with samples from Zhou et al.,2022 (Table S3) – excel format

Tables with Bayes Empirical Bayes (BEB) analysis for the *ccsA* and *rbcL* genes respectively (Table S4 and S5)

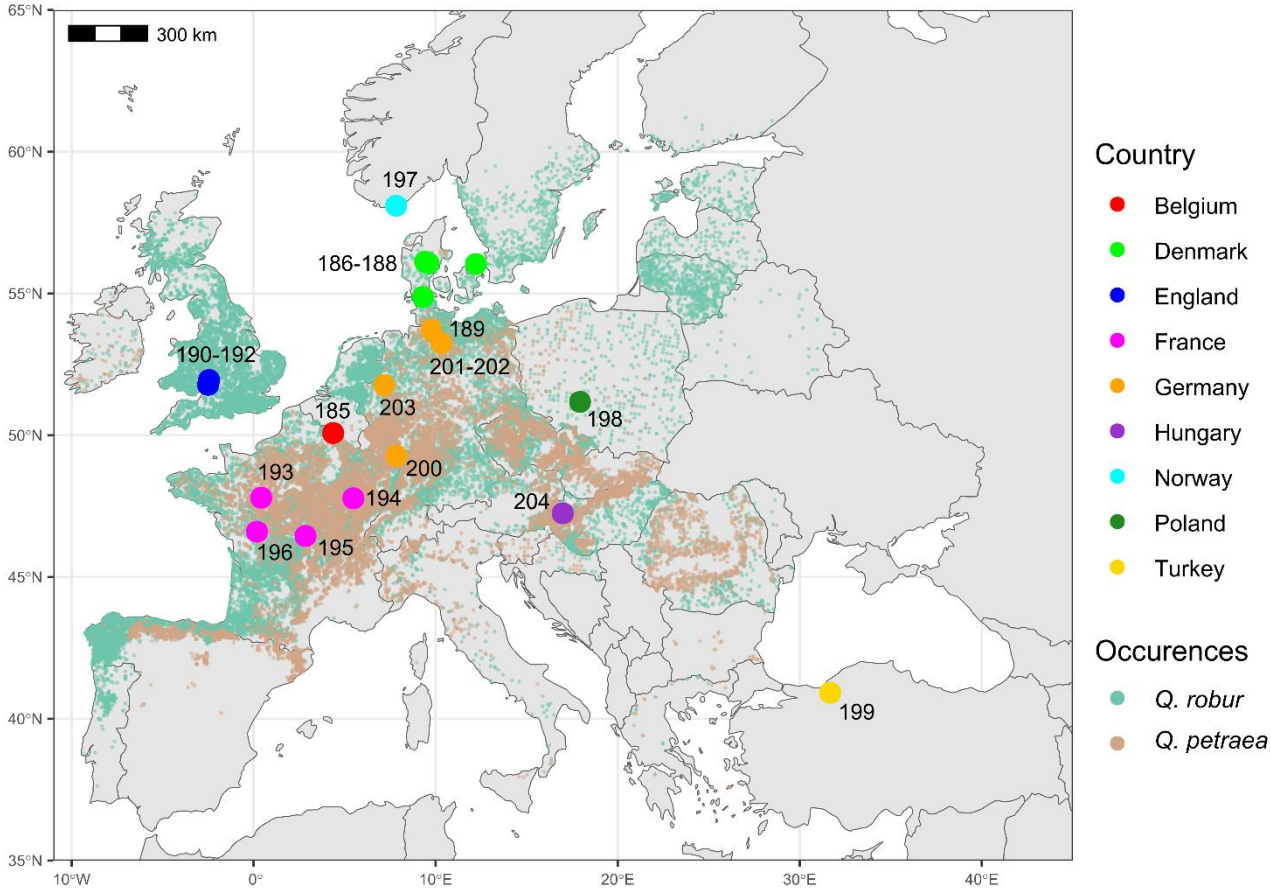


Figure S1. Geographic locations of the individuals used in this study. Each colour represents a different provenance, while numbers refer to provenance codes as shown in **Table S1**. *Q. robur* and *Q. petraea* occurrences in Europe are shown on the map with light green and light brown respectively, according to the legend. Further information on samples is shown in **Table S1**.

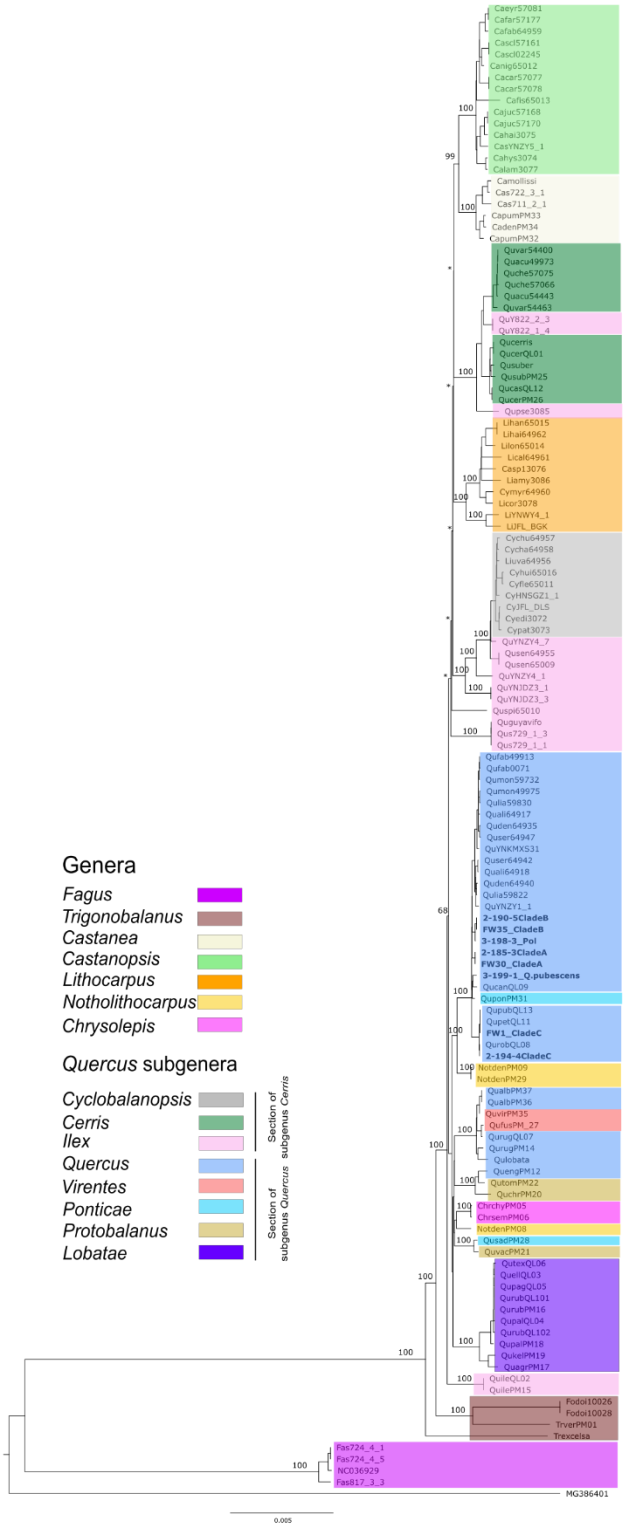


Figure S2. Maximum Likelihood Phylogeny of Fagaceae based on 69 plastid genes using RAxML with 100 bootstrap replicates for inspection of the topology and decision on the fossil calibrations. Colors represent different genera according to the legend. Bootstrap values are shown on the main nodes; asterisks (*) indicate bootstrap values <50. *Betula pentula* (MG386401) was used as an outgroup; *Q. robur* and *Q. petraea* samples from this study are shown in **bold**; *Q. robur* samples have the initials FW.

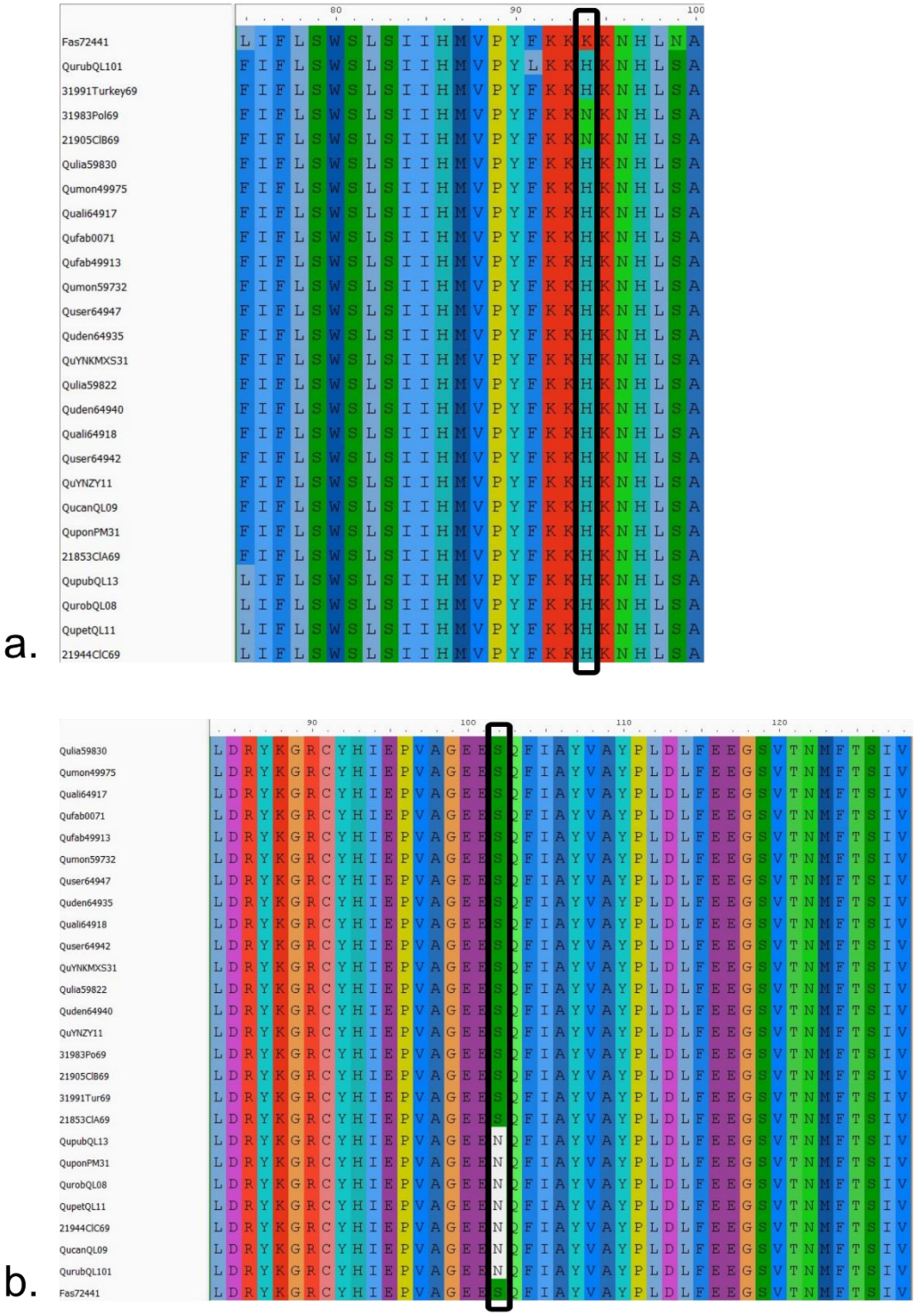


Figure S3. Part of the amino acids' alignments of the (a) *ccsA* gene and (b) *rbcL* gene. The position of the one site significantly detected as under selection in each gene is showing with a black border. The names of the 26 sequences included in the selection analyses are shown on the left. Further information on the samples used in the selection analysis are shown in Fig. 2b and Table S3.

Table S2. Names and alignment length of 69 plastid genes that were used in the study.

Gene name	Alignment length	Gene name	Alignment length
psbA	1068	petL	96
matK	1515	petG	114
rps16	258	**psaJ**	135
psbK	186	rpl33	210
psbI	111	rps18	360
atpA	1524	**rpl20**	354
atpF	558	rps12	375
atpH	246	**clpP**	591
atpI	744	psbB	1527
rps2	711	psbT	108
rpoC1	2058	**psbN**	132
rpoB	3222	psbH	222
petN	90	petB	648
psbM	105	**rpoA**	996
psbD	1062	rps11	417
psbC	1464	rpl36	114
psbZ	189	**rps8**	405
rps14	303	rpl14	369
psaB	2205	rpl16	408
psaA	2253	**rps3**	666
ycf3	507	**rps19**	285
rps4	609	**rpl2**	861
ndhJ	477	rpl23	282
ndhC	363	**ycf2**	6822
atpE	402	**rps7**	468
atpB	1497	**ccsA**	957
rbcl	1449	psaC	246
psal	105	ndhE	306
ycf4	555	**ndhG**	531
cemA	690	**ndhI**	498
petA	966	**ndhA**	1092
psbJ	123	**ndhH**	1182
psbL	117	rps15	273
psbF	120	**ycf1**	5658
psbE	252		

Note: All 69 genes were included in the dating analysis; genes shown in **bold** were used in the selection analysis.

Table S4. Bayes Empirical Bayes (BEB) analysis for the *ccsA* gene (Yang, Wong & Nielsen 2005. Mol. Biol. Evol. 22:1107-1118)

Position-aminoacid	Pr(w>1)	post mean +- SE for w
75 L	0.824	6.818 +- 3.333
91 F	0.546	4.653 +- 4.001
94 K	0.983*	7.968 +- 2.253
125 V	0.801	6.635 +- 3.428
173 E	0.823	6.807 +- 3.338
275 K	0.88	7.240 +- 3.048
288 T	0.875	7.206 +- 3.077

Note: Positively selected sites (*: P>95%; **: P>99%)

(amino acids refer to 1st sequence: Fas72441)

Table S5. Bayes Empirical Bayes (BEB) analysis for the *rbcL* gene (Yang, Wong & Nielsen 2005. Mol. Biol. Evol. 22:1107-1118)

Position-aminoacid	Pr(w>1)	post mean +- SE for w
102 S	0.954*	5.354 +- 2.560
226 L	0.558	3.395 +- 3.221
258 M	0.906	5.177 +- 2.688
456 A	0.876	5.026 +- 2.747

Note: Positively selected sites (*: P>95%; **: P>99%)

(amino acids refer to 1st sequence: Qulia59830)