

## Supplementary Material

**Table S1** Characteristics of 35 preselected chloroplast microsatellites loci identified in a screening panel of 282 samples of *Q. robur* & *Q. petraea*

**Table S2** Genotypes of all haplotypes based on 14 chloroplast microsatellites (*cmcs12*, *cmcs5*, *cmcs6*, *cmcs7*, *cmcs8*, *μdt1*, *μdt3*, *μdt4*, *ccmp4*, *cmcs9*, *μcd1*, *μcd4*, *μcd5*, *μkk4*)

**Figure S1** Map of oak individuals from which samples were collected in Poland (green dots - *Quercus robur*, red dots - *Quercus petraea*).

**Figure S2** A possible maximum parsimony haplotype tree for all 85 haplotypes established based on 14 cpSSR loci. Grey circles indicate haplotypes H18-H85 detected in 7 or fewer individuals. Haplotypes H01-H17 indicated with the same colours as in Fig. 1.

**Table S1.** Characteristics of 35 preselected chloroplast microsatellites loci studied in 282 individuals of *Q. robur* & *Q. petraea*.

Locus	Primer sequences forward & reverse	Motif	Number of alleles ( <i>Q. robur</i> + <i>Q. petraea</i> )	Dye	Size (bp)	Temp of annealing	Diversity ( <i>Q. robur</i> + <i>Q. petraea</i> )	Reference
<i>μcd4</i>	5'-TTATTTGTTTTTGGTTTCACC-3' 5'-TTTCCCATAGAGAGTCTGTAT-3'	(T)12	4	PET	97	45	0.503	Dequilloux <i>et al.</i> 2003
<i>ccmp10</i>	5'-TTTTTTTTTAGTGAACGTGTCA-3' 5'-TTCGTCGDCGTAGTAAATAG-3'	(T)14	2	PET	103	56/58	0.143	Weising & Gardner 1999
<i>μdt3</i>	5'-TGTTAGTAATCCTTCGTTT-3' 5'-AGGTATAAAGTCTAAGGTAA-3'	(A)11	4	PET	126	46	0.454	Dequilloux <i>et al.</i> 2003
<i>cmcs8</i>	5'-GGTCTATTTTCCACTCACAA-3' 5'-AGAAATAAACACCCCCATTA-3'	(A)10	3	PET	101	55	0.058	Sebastiani <i>et al.</i> 2004
<i>cmcs9</i>	5'-AAAAATACTTCTTTTTCGTTTTC-3' 5'-CCTGAATAAAATTCAAATCAA-3'	(T)9	4	VIC	101	55	0.398	Sebastiani <i>et al.</i> 2004
<i>cmcs7</i>	5'-AAGCGAGATGAATGAGTTTT-3' 5'-AAAATTGGATTGATTATTGACT-3'	(T)12	2	VIC	205	54	0.057	Sebastiani <i>et al.</i> 2004
<i>ccmp4</i>	5'-AATGCTGAATCGAYGACCTA-3' 5'-CCAAAATATTBGGAGGACTCT-3'	(T)13	3	VIC	126	60/58	0.365	Weising & Gardner 1999
<i>ccmp2</i>	5'-GATCCCGGACGTAATCCTG-3' 5'-ATCGTACCGAGGGTTCGAAT-3'	(A)11	2	VIC	189	60	0.085	Weising & Gardner 1999
<i>μcd5</i>	5'-CCCCGGATCTCTGTCAACTG-3' 5'-TAATAAACGAGAATCACATAA-3'	(A)8	2	FAM	77	45	0.098	Dequilloux <i>et al.</i> 2003
<i>μcd1</i>	5'-ATAACTTAACAACTTTTCCA-3' 5'-GGATTTACATCATTTTAGAGA-3'	(G)7	2	FAM	110	50	0.064	Dequilloux <i>et al.</i> 2003
<i>cmcs5</i>	5'TTTATCTTAAAGGGTAGTTTTAGAC3' 5'-CGGTTTCTTTCGTTTATTTT-3'	(T)9	3	FAM	151	55	0.343	Sebastiani <i>et al.</i> 2004
<i>cmcs12</i>	5'-ATATTGGTAAACGGCAACT-3' 5'-TTTATGGCATGAAACAACCTC-3'	(A)9	3	FAM	226	55	0.015	Sebastiani <i>et al.</i> 2004
<i>μdt1</i>	5'-ATCTTACACTAAGCTCGGAA-3' 5'-TTCAATAACTTGTTGATCCC-3'	(A)11	4	NED	86	48	0.267	Dequilloux <i>et al.</i> 2003
<i>μkk4</i>	5'-TTGTTTACCTATAATTGGAGC-3' 5'-TAGCGGATCGGTTCAAACCTT-3'	(T)9	2	NED	114	50	0.306	Dequilloux <i>et al.</i> 2003

Locus	Primer sequences forward & reverse	Motif	Number of alleles ( <i>Q. robur</i> + <i>Q. petraea</i> )	Dye	Size (bp)	Temp of annealing	Diversity ( <i>Q. robur</i> + <i>Q. petraea</i> )	Reference
<i>μdt4</i>	5'-GATAATATAAAGAGTCAAAT-3' 5'-CCGAAAGGTCCTATACCTCG-3'	(A)9	4	NED	147	44	0.391	Dequilloux <i>et al.</i> 2003
<i>cmcs6</i>	5'-GAAAAAGGACCCTTCCTAAT-3' 5'-CTTATGATCGTCACGAATTG-3'	(T)10	5	NED	199	55	0.427	Sebastiani <i>et al.</i> 2004
<i>μcd2</i>	5'-AATAGACTATCGTCCCATTAT-3' 5'-TGACCTTCATTTTCATTATCAT-3'	(T)7	1	FAM	152	50	0.000	Dequilloux <i>et al.</i> 2003
<i>μcd6</i>	5'-AAAAATTATGTGATTCTCGTT-3' 5'-TATGAGAATCCTGGTATCCAC-3'	(T)7	1	PET	91	50	0.000	Dequilloux <i>et al.</i> 2003
<i>μkk2</i>	5'-TTAACACAAGAAAGCCGAAGT-3' 5'-TTTATCGGATTTTGAGATTAT-3'	(T)9	1	VIC	129	50	0.000	Dequilloux <i>et al.</i> 2003
<i>μdt5</i>	5'-TAAATCTGGAAATCTGGGAA-3' 5'-TTGATACATAGACTTGCCAA-3'	(A)8	1	PET	159	46	0.000	Dequilloux <i>et al.</i> 2003
<i>μcd7</i>	5'-AATTCTGCTATTTGTTCTCCC-3' 5'-CAGTCCGACGGATCCAAATAC-3'	(T)9	1	FAM	86	50	0.000	Dequilloux <i>et al.</i> 2003
<i>μkk3</i>	5'-TTAGATCGGGTAATCGTTCAA-3' 5'-AAGTGAATAAATGGATAGAGC-3'	(T)10	1	VIC	99	50	0.000	Dequilloux <i>et al.</i> 2003
<i>ccmp8</i>	5'-TTGGCTACTCTAACCTTCCC-3' 5'-TTCCTTCTTATTTTCGCAGDGAA-3'	(T)6C(T)14	1	PET	77	60/58	0.000	Weising & Gardner 1999
<i>cmcs13</i>	5'-CACATCTTCTTAACCCGAAA-3' 5'-CCACGTGCTCTAATCCTCT-3'	(T)14	1	PET	126	55	0.000	Sebastiani <i>et al.</i> 2004
<i>μkk1</i>	5'-CGATCAACCTCTACTCTTACT-3' 5'-GTTATGAGACCTTGGAATGG-3'	(T)7	1	NED	110	50	0.000	Dequilloux <i>et al.</i> 2003
<i>cmcs2</i>	5'-GAGCCATTCCCTTTTAGAAT-3' 5'-TTGAAAACCGGTATAGTTTCG-3'	(AT)9	1	FAM	151	55	0.000	Sebastiani <i>et al.</i> 2004
<i>μcd8</i>	5'-TCTAGGAATTAGAACCGTAAG-3' 5'-CTATTTAATTTGTGTTGATTG-3'	(T)7	1	VIC	81	50	0.000	Dequilloux <i>et al.</i> 2003
<i>ccmp3</i>	5'-CAGACCAAAAGCTGACATAG-3' 5'-GTTTCATTCGGCTCCTTTAT-3'	(T)11	1	VIC	112	58/56	0.000	Weising & Gardner 1999
<i>μdt6</i>	5'-CTAGATGGATCATTAGCAAA-3' 5'-TCTGATATATTTTTACCGCT-3'	(A)7	1	NED	83	46	0.000	Dequilloux <i>et al.</i> 2003

<b>Locus</b>	<b>Primer sequences forward &amp; reverse</b>	<b>Motif</b>	<b>Number of alleles (<i>Q. robur</i> + <i>Q. petraea</i>)</b>	<b>Dye</b>	<b>Size (bp)</b>	<b>Temp of annealing</b>	<b>Diversity (<i>Q. robur</i> + <i>Q. petraea</i>)</b>	<b>Reference</b>
<i>ccmp5</i>	5'-TGTTCCAATATCTTCTTGTCATTT3' 5'-AGGTTCCATCGGAACAATTAT-3'	(C)7(T)10 (T)5C(A)11	1	PET	121	62/58	0.000	Weising & Gardner 1999
<i>ccmp6</i>	5'-CGATGCATATGTAGAAAGCC-3' 5'-CATTACGTGCGACTATCTCC-3'	(T)5C(T)17	1	NED	103	58/60	0.000	Weising & Gardner 1999
<i>cmcs4</i>	5'-ATTCATTCCCCTTCTATATC-3' 5'-CCTAGTATCCCACCAATTA-3'	(TC)5	1	VIC	110	55	0.000	Sebastiani <i>et al.</i> 2004
<i>cmcs10</i>	5'-TCTTGCTCTTTGATTTTGAA-3' 5'-GACCGCGAGAGTTATTTATT-3'	(A)9	1	PET	170	56/58	0.000	Sebastiani <i>et al.</i> 2004
<i>cmcs8</i>	5'-GGTCTATTTTTCCACTCACAA-3' 5'-AGAAATAAACACCCCATTA-3'	(A)10	1	NED	101	55	0.000	Sebastiani <i>et al.</i> 2004
<i>ccmp7</i>	5'-CAACATATACCACTGTCAAG-3' 5'-ACATCATTATTGTATACTCTTTC-3'	(A)13	1	PET	133	56/58	0.000	Weising & Gardner 1999

**Table S2**

Details of 85 haplotypes detected based on fourteen chloroplast microsatellites (*cmcs12*, *cmcs5*, *cmcs6*, *cmcs7*, *cmcs8*, *μdt1*, *μdt3*, *μdt4*, *ccmp4*, *cmcs9*, *μcd1*, *μcd4*, *μcd5*, *μkk4*), which were polymorphic based on a subset of 282 individuals. Allele name is given by allele size (bp).

Haplotype	<i>cmcs12</i>	<i>cmcs5</i>	<i>cmcs6</i>	<i>cmcs7</i>	<i>cmcs8</i>	<i>μdt1</i>	<i>μdt3</i>	<i>μdt4</i>	<i>ccmp4</i>	<i>cmcs9</i>	<i>μcd1</i>	<i>μcd4</i>	<i>μcd5</i>	<i>μkk4</i>	Frequency
H01	217	147	200	207	177	79	125	142	114	99	106	96	73	109	0.3281
H02	217	146	198	207	177	79	124	143	114	100	106	97	73	110	0.1749
H03	217	147	200	207	177	78	125	142	114	99	106	97	73	109	0.1731
H04	217	147	200	207	177	79	125	142	115	99	106	96	73	109	0.1135
H05	217	147	200	207	177	81	124	141	114	101	106	97	74	109	0.0442
H06	217	147	197	207	177	79	124	142	114	99	106	96	73	109	0.0366
H07	217	146	198	207	177	79	124	143	115	100	107	95	73	110	0.0261
H08	217	147	200	207	177	80	124	141	114	101	106	97	74	109	0.0245
H09	217	147	201	207	177	79	126	142	114	99	106	96	73	109	0.0178
H10	217	147	200	207	177	79	125	142	114	99	106	97	73	109	0.0154
H11	217	147	199	207	176	80	124	141	114	101	106	97	74	109	0.0088
H12	217	148	200	207	178	79	123	141	114	100	106	96	74	109	0.0037
H13	217	147	200	207	177	78	125	142	114	99	106	96	73	109	0.0027
H14	217	146	200	207	177	79	125	142	114	99	106	96	73	109	0.0025
H15	217	146	197	207	177	79	124	143	115	100	107	97	73	110	0.0024
H16	217	146	198	207	177	79	124	143	114	100	106	96	73	110	0.0024
H17	217	146	200	207	177	78	125	142	114	99	106	97	73	109	0.0019
H18	217	147	200	207	177	78	125	142	114	100	106	97	73	110	0.0010
H19	217	146	198	207	177	79	124	143	114	99	106	96	73	109	0.0009
H20	217	146	200	207	177	79	125	142	115	99	106	96	73	109	0.0009
H21	217	146	200	207	177	81	124	141	114	101	106	97	74	109	0.0009
H22	217	147	200	207	177	79	125	142	114	98	106	96	73	109	0.0009

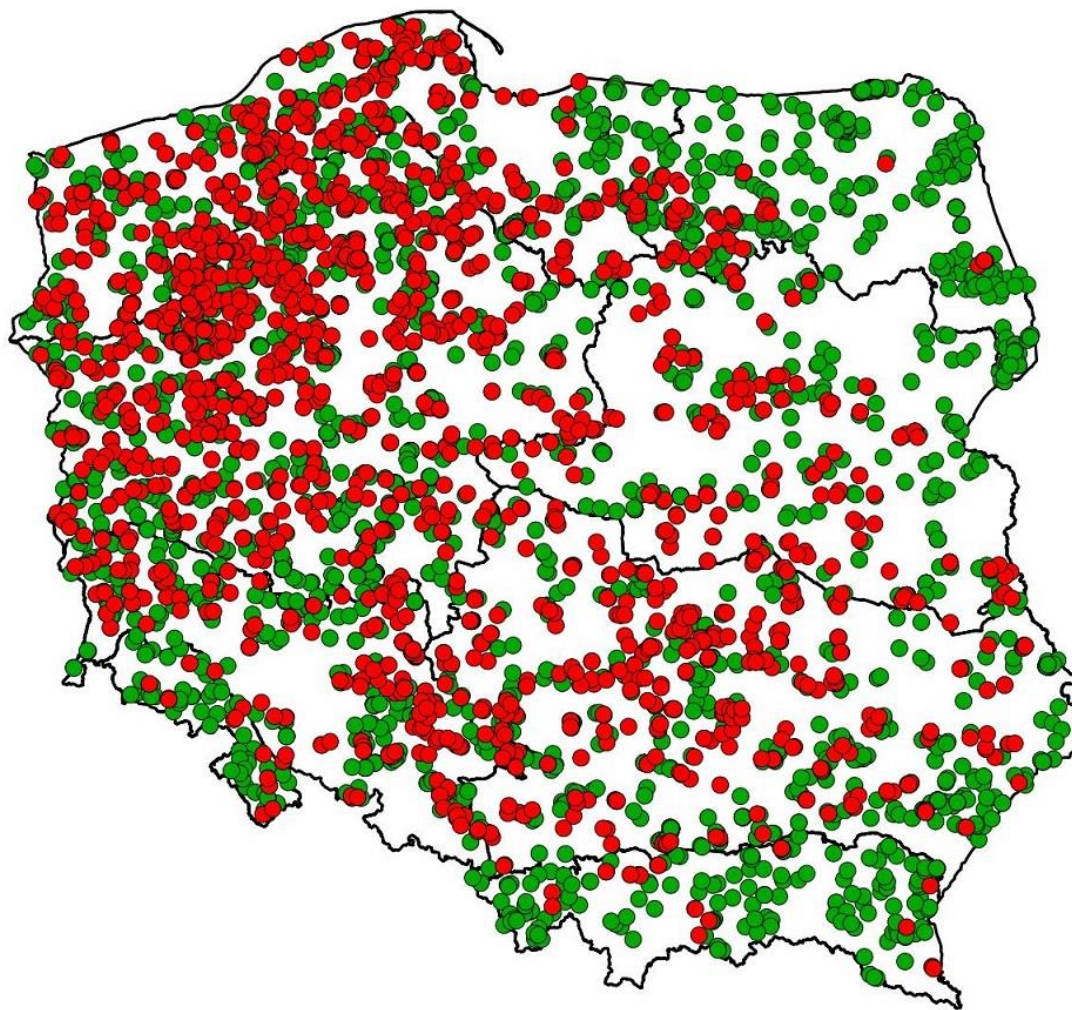
H23	217	147	200	207	177	80	124	141	114	101	106	96	74	109	0.0009
H24	217	147	200	206	177	79	125	142	114	99	106	96	73	109	0.0007
H25	217	147	200	207	176	80	124	161	113	101	106	98	74	109	0.0007
H26	217	147	200	207	177	79	125	142	115	99	106	97	73	109	0.0007
H27	217	146	200	207	177	80	124	141	114	101	106	97	74	109	0.0006
H28	217	147	200	207	177	79	125	142	114	100	106	97	73	110	0.0006
H29	217	148	200	207	177	78	125	142	114	99	106	97	73	109	0.0006
H30	217	147	199	207	177	79	125	142	114	99	106	96	73	109	0.0004
H31	217	147	199	207	177	79	125	142	115	99	106	96	73	109	0.0004
H32	217	147	200	207	178	79	125	142	114	99	106	96	73	109	0.0004
H33	217	147	201	207	177	79	125	142	114	99	106	96	73	109	0.0004
H34	216	147	200	207	177	79	125	142	114	99	106	96	73	109	0.0003
H35	217	146	198	207	177	79	124	143	114	100	106	97	73	109	0.0003
H36	217	146	198	207	177	79	124	143	114	101	106	97	73	110	0.0003
H37	217	146	198	207	177	79	124	143	114	101	106	97	74	109	0.0003
H38	217	147	200	207	177	79	124	141	114	99	106	96	73	109	0.0003
H39	217	147	200	207	177	79	124	141	115	99	106	96	73	109	0.0003
H40	217	147	200	207	177	79	125	142	114	101	106	97	74	109	0.0003
H41	217	147	200	207	177	79	125	142	115	100	107	95	73	110	0.0003
H42	217	147	200	207	177	79	126	142	115	99	106	96	73	109	0.0003
H43	217	147	200	207	177	80	125	142	114	99	106	97	73	109	0.0003
H44	217	147	200	207	177	80	125	142	115	99	106	96	73	109	0.0003
H45	217	147	200	207	177	81	124	141	114	101	106	97	73	109	0.0003
H46	217	147	200	207	177	81	124	141	114	99	106	96	73	109	0.0003
H47	217	147	201	207	177	79	126	142	114	98	106	96	73	109	0.0003
H48	217	148	200	207	177	79	125	142	114	99	106	96	73	109	0.0003
H49	217	146	198	207	177	79	124	143	114	99	106	97	73	109	0.0001
H50	217	146	198	207	177	79	124	143	114	99	106	97	73	110	0.0001

H51	217	146	198	207	177	79	124	143	115	100	106	97	73	110	0.0001
H52	217	146	198	207	177	79	124	143	115	99	106	96	73	109	0.0001
H53	217	146	198	207	177	79	124	143	115	99	107	95	73	110	0.0001
H54	217	146	199	207	177	79	124	143	115	100	107	95	73	110	0.0001
H55	217	146	200	207	177	79	125	143	114	100	106	96	73	109	0.0001
H56	217	146	201	207	177	79	126	142	114	99	106	96	73	109	0.0001
H57	217	147	197	207	177	79	124	142	114	99	106	95	73	109	0.0001
H58	217	147	197	207	177	79	124	142	114	99	106	97	73	109	0.0001
H59	217	147	197	207	177	80	123	141	114	100	106	97	73	109	0.0001
H60	217	147	197	207	177	80	124	142	114	99	106	96	73	109	0.0001
H61	217	147	198	207	177	79	124	143	114	100	106	97	73	110	0.0001
H62	217	147	198	207	177	79	124	143	115	100	107	95	73	110	0.0001
H63	217	147	199	207	176	78	124	141	114	101	106	97	74	109	0.0001
H64	217	147	200	207	176	80	124	141	114	99	106	96	73	109	0.0001
H65	217	147	200	207	176	80	124	142	114	99	106	97	73	109	0.0001
H66	217	147	200	207	176	81	124	141	114	101	106	97	74	109	0.0001
H67	217	147	200	207	177	78	124	142	114	99	106	97	73	109	0.0001
H68	217	147	200	207	177	78	125	141	114	99	106	97	73	109	0.0001
H69	217	147	200	207	177	78	125	142	114	98	106	97	73	109	0.0001
H70	217	147	200	207	177	79	124	142	114	99	106	96	73	109	0.0001
H71	217	147	200	207	177	79	124	142	115	99	106	96	73	109	0.0001
H72	217	147	200	207	177	79	125	142	114	99	106	95	73	109	0.0001
H73	217	147	200	207	177	79	125	142	114	99	106	96	73	110	0.0001
H74	217	147	200	207	177	79	125	142	115	98	106	96	73	109	0.0001
H75	217	147	200	207	177	80	124	141	114	100	106	97	73	110	0.0001
H76	217	147	200	207	177	80	125	142	114	99	106	96	73	109	0.0001
H77	217	147	200	207	177	81	124	141	114	100	106	97	73	110	0.0001
H78	217	147	200	207	177	81	124	141	114	100	106	97	74	109	0.0001

H79	217	147	200	207	178	79	123	141	114	100	106	96	74	109	0.0001
H80	217	147	200	207	178	79	125	142	115	99	106	96	73	109	0.0001
H81	217	147	200	207	178	81	124	141	114	101	106	97	74	109	0.0001
H82	217	147	201	207	177	79	126	142	114	100	106	97	73	110	0.0001
H83	217	148	200	207	177	79	125	142	115	99	106	96	73	109	0.0001
H84	217	148	200	207	178	79	123	141	114	100	106	96	73	109	0.0001
H85	218	147	200	207	177	79	125	142	114	99	106	96	73	109	0.0001



**Figure S1** Map of individual oak trees sampled in Poland (green dots - *Quercus robur*, red dots - *Quercus petraea*).



**Figure S2** A possible maximum parsimony haplotype tree for all 85 haplotypes established based on 14 cpSSR loci. Grey circles indicate haplotypes H18-H85 detected in 7 or fewer individuals. Haplotypes H01-H17 indicated with the same colours as in Fig. 1.

