

Estimates of microsatellite genetic variability of *Anopheles atroparvus* in Europe

		Macul3	MacuQ72	MacuG66	MacuU182	MacuUF	MacuW161	MacuO177	MacuGQ	All Loci
Castro Marim	A	13	4	5	14	4	6	6	6	7
	H_e	0.826	0.676	0.627	0.827	0.734	0.576	0.751	0.658	0.709
	F_{is}	0.085	0.046	0.239	0.140	-0.239	-0.157	0.381	0.460	0.122
Barrancos	A	13	4	5	8	4	6	6	6	7
	H_e	0.854	0.661	0.577	0.730	0.610	0.646	0.769	0.644	0.686
	F_{is}	0.167	0.159	0.436	0.012	-0.229	0.085	0.274	0.400	0.163
Comporta	A	14	8	5	13	4	4	8	6	8
	H_e	0.897	0.713	0.623	0.829	0.641	0.698	0.845	0.625	0.734
	F_{is}	0.182	0.178	0.287	-0.019	0.029	0.140	0.327	0.238	0.170
Aveiro	A	16	3	6	12	4	6	7	7	8
	H_e	0.854	0.590	0.554	0.792	0.639	0.681	0.757	0.692	0.695
	F_{is}	0.201	0.247	0.426	-0.011	0.235	-0.110	0.501	0.174	0.202
Tarragona	A	14	6	4	11	2	6	6	4	7
	H_e	0.840	0.653	0.473	0.854	0.280	0.645	0.702	0.560	0.626
	F_{is}	-0.006	0.183	0.060	-0.035	-0.189	0.173	0.177	-0.088	0.049
Mèjanès	A	12	4	4	11	4	8	7	7	7
	H_e	0.825	0.555	0.590	0.846	0.646	0.690	0.810	0.674	0.705
	F_{is}	0.084	0.166	0.473	-0.103	-0.372	-0.021	0.411	0.164	0.096
Venice	A	8	5	5	9	3	4	5	5	6
	H_e	0.793	0.668	0.657	0.833	0.483	0.524	0.656	0.617	0.654
	F_{is}	0.019	0.501	0.066	-0.014	-0.474	0.000	0.377	0.531	0.139
Salcioara	A	10	5	5	9	3	3	8	6	6
	H_e	0.820	0.530	0.565	0.826	0.239	0.383	0.756	0.745	0.608
	F_{is}	-0.129	0.161	0.764	-0.046	0.070	0.304	0.148	0.429	0.193
All <i>An. atroparvus</i> samples	A	23	12	8	21	11	11	10	10	13
	H_e	0.876	0.655	0.617	0.820	0.588	0.649	0.800	0.682	0.711
	F_{is}	0.118	0.199	0.323	0.013	-0.108	0.019	0.242	0.213	0.129
Montalegre (<i>An. maculipennis</i> s.s.)	A	7	7	2	5	11	3	3	4	5
	H_e	0.529	0.752	0.164	0.709	0.842	0.458	0.390	0.191	0.504
	F_{is}	0.075	0.172	-0.086	0.123	0.190	0.563	-0.083	0.169	0.164
$P(R_{ST} > pR_{ST})$		0.319	0.414	0.718	0.227	0.015	0.624	0.007	0.028	0.029

A: number of alleles. H_e : unbiased estimate of expected heterozygosity. Significant departures from H-W proportions after Bonferroni corrections are indicated in bold. F_{is} : Inbreeding coefficient. All Loci: mean values over loci. $P(R_{ST} > pR_{ST})$: probability of a one-sided permutation test to evaluate the influence of stepwise mutations in the differentiation among samples (see Methods).