

Supplementary Table 1 Pair-wise inter-population diversity, gene differentiation and estimate of gene flow of six different populations of *Badis badis*

Population Pairs	$H_T$	$H_S$	$D_{ST}$	$F_{ST}$	Nm
TR-1and TR-2	0.2954 ±0.0386	0.1183 ±0.0178	0.1771	0.5996	0.3339
TR-1and TR-3	0.2966 ±0.0372	0.1379 ±0.0188	0.1587	0.5352	0.4343
TR-1and TR-4	0.2822 ±0.0385	0.1280 ±0.0178	0.1542	0.5466	0.4147
TR-1and TR-5	0.3124 ±0.0362	0.1276 ±0.0185	0.1848	0.5917	0.3450
TR-1and TR-6	0.3032 ±0.0390	0.1280 ±0.0198	0.1752	0.5778	0.3653
TR-2 and TR-4	0.1848 ±0.0367	0.1220 ±0.0195	0.0628	0.3402	0.9698
TR-2 and TR-5	0.1962 ±0.0404	0.1216 ±0.0220	0.0746	0.3803	0.8148
TR-2 and TR-3	0.2135 ±0.0395	0.1319 ±0.0219	0.0816	0.3822	0.8081
TR-2 and TR-6	0.2037 ±0.0413	0.1220 ±0.0225	0.0817	0.4012	0.7463
TR-3 and TR-4	0.1988 ±0.0406	0.1415 ±0.0276	0.0573	0.2881	1.2355
TR-3 and TR-5	0.2045 ±0.0367	0.1411 ±.0214	0.0634	0.3098	1.1138
TR-3 and TR-6	0.2030 ±0.0377	0.1416 ±0.0229	0.0614	0.3025	1.1529
TR-4 and TR-5	0.1764 ±0.0387	0.1312 ±0.0261	0.0452	0.2560	1.4534
TR-4 and TR-6	0.1955 ±0.0403	0.1317 ±0.0239	0.0638	0.3263	1.0321
TR-5 and TR-6	0.2003 ±0.0391	0.1313 ±0.0227	0.0690	0.3445	0.9514
All Population	0.2983 ±0.0203	0.1304 ±0.0096	0.1010	0.5629	0.3883

$H_T$  = Expected heterozygosity in random mating total population;  $H_S$  = Mean expected heterozygosity within random mating subpopulations;  $D_{ST}$  = diversity among populations;  $F_{ST}$  = Degree of gene differentiation among populations in terms of allele frequencies; Nm = Estimate of gene flow