

Table S4. Microsatellite diversity values for *D. turbinatus* using GenAlEx¹, Micro-checker², FSTAT³, Genepop⁴ and Cervus⁵

N_A : number of alleles, A_E : effective alleles, A_R : number of allelic richness, PIC: polymorphism information content, H_O and H_E : observed and expected heterozygosity, F_{IS} : fixation index, Null allele the average null allele frequency, F_{IT} : coefficient of total inbreeding, F_{ST} : genetic differentiation index of Weir and Cockerham (1984), G'_{ST} : genetic differentiation index of Hedrick (2005), N_m : number of migrants, SE: standard error, nd: no determined, ns: no significance, * $p < 0.05$, ** $p < 0.01$ *** $p < 0.0001$.

Locus	N_A	A_E	A_R	PIC	H_O (SE)	H_E (SE)	F_{IS} (SE)	Null allele	F_{IT} (SE)	F_{ST} (SE)	G'_{ST} (SE)	HW	N_m (SE)
DT07	2	1.7	2	0.375	0.331	0.411	0.193***	0.154	0.337	0.179	0.292	***	1.149
DT09	3	1.7	2.9	0.382	0.34	0.383	0.112***	0.085	0.206	0.105	0.151	ns	2.127
Sh01	4	1.4	2.9	0.24	0.201	0.239	0.161*	0.089	0.249	0.105	0.118	**	2.141
Shc11	4	1.6	3.8	0.371	0.296	0.356	0.167**	0.097	0.025	0.1	0.135	*	2.241
DT38	5	1.7	4.3	0.435	0.312	0.41	0.241***	0.147	0.338	0.128	0.198	**	1.704
DT20	4	1.4	3.7	0.411	0.241	0.237	-0.015	no	0.492	0.499	0.664	***	0.251
Shc07	3	1.3	2.6	0.401	0.196	0.225	0.128***	no	0.613	0.556	0.728	***	0.2
DT18	2	1.6	2	0.309	0.321	0.337	0.049	0.071	0.148	0.104	0.14	ns	2.144
DT10	2	1.6	2	0.304	0.326	0.357	0.085*	no	0.126	0.045	0.044	ns	5.343
Mean	3.2	1.5	2.9	0.359	0.285 (0.012)	0.328 (0.014)	0.125*** (0.026)		0.306 (0.053)	0.202 (0.063)	0.320 (0.103)		1.922 (0.505)

¹ Peakall R, Smouse PE (2012) GenAlEx 6.5: genetic analysis in excel. Population genetic software for teaching and research an update. Bioinformatics 28: 2537-2539. <http://dx.doi.org/10.1111/j.1471-8286.2005.01155.x>

² van Oosterhout C., Hutchinson W.F., Wills D.P.M., Shipley P. (2004) Micro-Checker: software for identifying and correcting genotyping errors in microsatellite data. Molecular Ecology Notes 4: 435-538. <http://dx.doi.org/10.1111/j.1471-8286.2004.00684.x>

³ Goudet J (2001) FSTAT, a program to estimate and test gene diversities and fixation indices (version 2.9.3). Available from <http://www.unil.ch/izea/software/fstat.html>.

⁴ Rousset F (2008) GENEPOP'007: a complete re-implementation of the GENEPOP software for Windows and Linux. Molecular Ecology Research 8: 103–106. <https://doi.org/10.1111/j.1471-8286.2007.01931.x>

⁵ Kalinowski ST, Taper ML, Marshall TC (2007) Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular Ecology 16: 1099-1106. doi:10.1111/j.1365-294X.2007.03089.x