Table S5: Pairwise genetic differentiation among the ten *D. turbinatus* populations using GenAlEx[1]; ns: no significant, +: significant level (p) < 0.05

Pairwise genetic differentiation (F_{ST})[2]:

Population	BNNC	BHMA	CHUH	CHPR	CMRA	YORD	BGMA	LGXM	MADA	THPU
BNNC		+	+	+	+	+	+	+	+	+
BHMA	0.055		+	+	+	+	+	+	+	+
CHUH	0.163	0.227		+	+	ns	+	+	+	+
CHPR	0.198	0.247	0.032		ns	+	+	+	+	+
CMRA	0.196	0.25	0.038	0.022		+	+	+	+	+
YORD	0.199	0,275	0.018	0.041	0.031		+	+	+	+
BGMA	0.137	0.159	0.146	0.137	0.158	0.162		+	+	+
LGXM	0.163	0.194	0.152	0.149	0.146	0.157	0.062		+	+
MADA	0.143	0.163	0.115	0.127	0.14	0.132	0.043	0.088		+
THPU	0.186	0.201	0.123	0.126	0.156	0.143	0.054	0.089	0.03	

Pairwise genetic differentiation (G'_{ST})[3]:

Population	BNNC	BHMA	CHUH	CHPR	CMRA	YORD	BGMA	LGXM	MADA	TPHU
BNNC		+	+	+	+	+	+	+	+	+
BHMA	0.079		+	+	+	+	+	+	+	+
CHUH	0.343	0.42			+	+	+	+	+	+
CHPR	0.383	0.42	0.049		+	+	+	+	+	+
CMRA	0.412	0.461	0.066	0.025		+	+	+	+	+
YORD	0.416	0.505	0.02	0.066	0.049		+	+	+	+
BGMA	0.242	0.249	0.274	0.235	0.295	0.303		+	+	+
LGXM	0.334	0.35	0.329	0.292	0.313	0.335	0.101		+	+
MADA	0.27	0.271	0.227	0.23	0.278	0.26	0.062	0.164		+
THPU	0.33	0.313	0.224	0.211	0.287	0.26	0.075	0.151	0.036	

[1] Peakall R., Smouse P.E. (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] Weir B., Cookerham C. (1984) Estimating F-statistics for the analysis of population structure. *Evolution* 38:1358–1370.

[3] Hedrick P.W. (2005) A standardized genetic differentiation measure. *Evolution* 59:1633-1638. https://doi.org/10.1111/j.0014-3820.2005.tb01814.x