

Table S3 – F_{ST} values of pair-wise comparisons between populations of *Acromyrmex striatus*, estimated from the mitochondrial COI gene.

Values shown in bold are significant ($p < 0.05$).

	FLOR	CONT	CABO	LAGU	SOUT	EXTR	NORT	MOTD	RIOG	INTE	SAMA	WEST	ARGE
FLOR	0.0000												
CONT	0.2871	0.0000											
CABO	0.1140	0.0903	0.0000										
LAGU	0.0000	0.0222	0.0134	0.0000									
SOUT	0.0318	0.0418	-0.0112	-0.0251	0.0000								
EXTR	0.0811	0.0387	0.1030	0.0165	0.0192	0.0000							
NORT	0.5808	0.5145	0.5160	0.5369	0.5370	0.5652	0.0000						
MOTD	0.9023	0.8758	0.8460	0.8513	0.8473	0.8712	0.3625	0.0000					
RIOG	0.8703	0.8442	0.8244	0.8306	0.8284	0.8451	0.6427	0.8475	0.0000				
INTE	0.7765	0.7349	0.7189	0.7270	0.7264	0.7458	0.3622	0.5283	0.7930	0.0000			
SAMA	0.8790	0.8429	0.8133	0.8221	0.8177	0.8400	0.3989	0.6719	0.8301	0.1276	0.0000		
WEST	0.9376	0.9163	0.8815	0.8833	0.8769	0.8977	0.4999	0.7271	0.8702	0.0405	0.2810	0.0000	
ARGE	0.9494	0.9297	0.9128	0.9195	0.9179	0.9296	0.7090	0.9103	0.8805	0.8585	0.8872	0.9289	0.000