Table S4. Results of the analysis of molecular variance (AMOVA) based on ITS sequences of 489 *T. ganbajun* specimens from 30 location populations in nine municipalities from Yunnan, southwestern China.

	Source	df	SS	MS	Est. Var.	%	Stat	Value	*p*(rand >= data)
ITS SNPs	Among Regions	9	656.338	72.926	0	0%	PhiRT	-0.017	0.904
	Among Pops	20	1077.678	53.884	3.356	27%	PhiPR	0.272	0.001
	Within Pops	459	4115.090	8.965	8.965	73%	PhiPT	0.260	0.001
	Total	488	5849.106		12.322	100%			