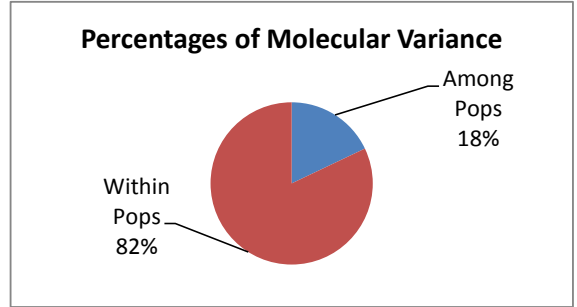


**Results of Analysis of Molecular Variance**

<b>Data Sheet</b>	File S4
<b>Data Title</b>	Gen Pop separation
<b>No. Samples</b>	1230
<b>No. Pops</b>	8
<b>No. Permutations</b>	999
<b>NO</b>	146.213
<b>SSTOT</b>	4830.342



Pop	Pop1	Pop2	Pop3	Pop4	Pop5	Pop6	Pop7	Pop8
<b>n</b>	8	230	95	165	206	90	120	316
<b>SSWP</b>	14.375	906.652	273.526	507.527	699.500	303.944	334.200	1023.630

**Summary AMOVA Table**

Source	df	SS	MS	Est. Var.	%
<b>Among Pops</b>	7	766.987	109.570	0.727	18%
<b>Within Pops</b>	1222	4063.355	3.325	3.325	82%
<b>Total</b>	1229	4830.342		4.052	100%

**Stat Value** P(rand >= data) Probability, P(rand >= data), for PhiPT is based on standard permutation across the full data set.

**PhiPT** 0.179 0.001 **PhiPT = AP / (WP + AP) = AP / TOT**

**PhiPT max** 0.263

**Phi'PT** 0.683

**Nm (Haploid)** 2.288 **Nm (Haploid) = [(1 / PhiPT) - 1] / 2**

Key: AP = Est. Var. Among Pops, WP = Est. Var. Within Pops

**Pairwise Population PhiPT Values**

Pop1	Pop2	Pop3	Pop4	Pop5	Pop6	Pop7	Pop8	
	0.001	0.001	0.001	0.001	0.001	0.001	0.001	<b>Pop1</b>
0.216		0.001	0.001	0.001	0.001	0.001	0.001	<b>Pop2</b>
0.373	0.135		0.001	0.001	0.001	0.001	0.001	<b>Pop3</b>
0.344	0.099	0.194		0.001	0.001	0.001	0.001	<b>Pop4</b>
0.247	0.104	0.220	0.180		0.001	0.001	0.001	<b>Pop5</b>
0.300	0.083	0.195	0.157	0.162		0.001	0.001	<b>Pop6</b>
0.365	0.152	0.257	0.244	0.144	0.202		0.001	<b>Pop7</b>
0.336	0.145	0.242	0.249	0.184	0.188	0.243		<b>Pop8</b>

PhiPT Values below diagonal. Probability, P(rand >= data) based on 999 permutations is shown above diagonal.