

Table 2. Clade recovery results from ML analyses with varied taxon and character inclusion used to counter long-branch attraction.

Experiment								
Maximum Likelihood	Coleoptera		Basal	Mecopterida	Neuropteroidea			
	Strepsiptera	Halteria			(including Strepsiptera)	Amphiesmenoptera	Antliophora	Neuropterida
3rd pos included	+	-	+	+	+	+	+	+
Amino acids	+	-	+	+	+	+	+	+
Strepsiptera removed	N/A	N/A	+	+	+	+	+	+
Outgroups removed	+	-	N/A	+	+	+	+	+
3rds RY coded	+	-	+	+	+	+	+	+
1sts & 3rds RY coded	-	-	+	+	+	+	+	+
Conservative alignment	+	-	+	+	+	+	+	+
Taxa with base composition bias excluded	-	-	+	+	+	+	+	+

These variations on taxon and character inclusion (with the exception of the inclusion of 3rd positions) are cited as a means to rectify the effects of long-branch attraction. Clade recovery from these various methods are substantially in agreement with each other and with our final results. This finding signifies that LBA does not play a clearly detectable role in our analyses.