Phylogenetic tree of avian *Haemoproteus* lineages from birds of the Turdidae

Maximum Likelihood tree calculated based on an alignment of *CytB* sequences (474 bp) from avian haemosporidian parasites.

Maximum Likelihood boostrap values and Bayesian posterior probabilities are indicated at most nodes.

Lineages in bold type were isolated from Turdidae birds, lineages in regular type from other bird families.

Labelled clades comprise lineages contained in the DNA hyplotype networks.

The scale bar indicates the expected mean number of substitutions per site according to the model of sequence evolution applied.