

# Phylogenetic tree of avian *Haemoproteus* lineages from birds of the Turridae

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

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

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

Labelled clades comprise lineages contained in the DNA haplotype networks.

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

## Region

- Eastern Europe (Russia)
- Western Europe
- Western Asia
- Northern America
- Central America
- Caribbean
- South America
- Eastern Asia
- South-Eastern Asia
- Melanesia (P.N.G.)
- Southern Asia (India)
- Northern Africa
- Central Africa
- Eastern Africa
- Western Africa
- Southern Africa
- Pacific
- Australia

0.04

// 98 0.77

