

A

Taxonomic group	Tubulin subunit		
	Alpha	Beta	Gamma
Cryptosporidia	1	1	1
Intestinal coccidia	1	1-2	1
Cystic coccidia	3	2	1
Plasmodia	2	1	1
Piroplasmids	2	1	1
Gregarina	2	2	1

B

Posterior probability = 1.0

Alpha

Beta

Gamma

A) Number of isoforms of individual tubulin subunits identified from the genomes of major taxonomic groups of apicomplexans. **B)** Consensus tree inferred from α -, β - and γ -tubulin proteins from representative apicomplexan species by Bayesian inference using a mixed model for amino acid substitution rates with the consideration of invariable sites and four rates of gamma-distribution across the sites (arithmetic mean of log likelihood = -15257.76). Tree was rooted using γ -Tubulin sequences as the outgroup. Posterior analysis showed that Jones amino acid substitution model was the most fit model with 100% posterior probability. Numbers at the major nodes indicate proportion support by posterior probability, in which nodes with 100% support were indicated by black round dots. Some species names are colored for better visualization and comparison. Bar indicates amino acid substitution rate.