

Table E3: Parameter estimates under models of variable ω ratios among lineages and LRTs of their fit to the *Ldh-A* and *Ldh-C* gene family.

Models	ω_{A0}	ω_{A1}	ω_{C1}	ω_{C0}	ℓ	LRT
H ₀ : $\omega_{A0} = \omega_{A1} = \omega_{C1} = \omega_{C0}$?	= $\omega_{A.0}$	= $\omega_{A.0}$	= $\omega_{A.0}$?	?
H ₁ : $\omega_{A0} = \omega_{A1} = \omega_{C1} \neq \omega_{C0}$?	= $\omega_{A.0}$	= $\omega_{A.0}$?	?	?
H ₂ : $\omega_{A0} = \omega_{A1} \neq \omega_{C1} = \omega_{C0}$?	= $\omega_{A.0}$?	= $\omega_{C.1}$?	?
H ₃ : $\omega_{A0} \neq \omega_{A1} \neq \omega_{C1} = \omega_{C0}$?	?	?	= $\omega_{C.1}$?	?

The topology and branch specific ω ratios are presented in Figure 5.

H₀ v H₁: df = 1

H₀ v H₂: df = 1

H₂ v H₃: df = 1

$\chi^2_{df=1, \alpha=0.05} = 3.841$