Table S1. Meta-table of spectral sensitivity data and ecological assignments of adult ray-finned fishes. Bolded λ_{max} values have appeared at least twice across different cone morphological types for a given species. † designations indicate λ_{max} values for which cone morphological type had not been identified. § indicate λ_{max} values that are associated with a rare morphological 'triple' cone type. ‡ indicate species whose synonymized names are listed in the published phylogeny (Rabosky, 2013). Species listed without ecological assignments had adult spectral sensitivity data available, but were not present in the phylogeny. See supplemental .xls file.

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Table S2. Cone λ_{max} (nm) averages across morphological types of cones and levels of chromacy for the 213 species included in analysis. In cases where λ_{max} values were associated with two or more morphological types in a given retina, cone λ_{max} were assigned as "mixed."

Cone Morphological Type	Mean Cone λ_{max} (nm) ± s.d.
Single	455 ± 50
Double	532 ± 34
Twin	529 ± 27
Mixed	532 ± 39
Chromacy Level	
Monochromacy	496 ± 37
Dichromacy	494 ± 49
Trichromacy	505 ± 54
Tetrachromacy	496 ± 59
Pentachromacy	496 ± 70

Table S3. Summary of the MCMC chains from the multivariate phylogenetic latent liability models produced in BEAST.

Chain	Phylogeny	Steps (x10^6)	Samples	Samples (Post burn-in)	MPSRF	Log Marginal Likelihood
1	normal	200	20000	18000		-2981.03
2	normal	200	20000	18000	1.010798	-3224.91
3	normal	200	20000	18000		-3125.70
4	normal	200	20000	18000		-3100.92
merged	normal	800	80000	72000	N/A	-2957.76
5	star	200	20000	18000		-3546.85
6	star	200	20000	18000	1.001739	-3563.12
7	star	200	20000	18000		-3588.41
8	star	200	20000	18000		-3294.80
merged	star	800	80000	72000	N/A	-3303.40

Table S4. Pairwise Bayes factors analysis of model likelihood.

	Chain 1	Chain 2	Chain 3	Chain 4	Merged (normal)
Chain 5	565.8	321.9	421.2	445.9	-
Chain 6	582.1	338.2	437.4	462.2	-
Chain 7	607.4	363.5	462.7	487.5	-
Chain 8	313.8	69.9	169.1	193.9	-
Merged (star)	-	-	-	-	345.6