Table A1.1. A comparison of the taxon and gene sampling in a selection of previous estimates of the angiosperm evolutionary timescale, based on data sets including ≥50 angiosperm taxa and/or ≥4 genes. Abbreviations: "PL" = penalised likelihood.

Study	Mean Age Estimate	Lower Age Estimate	Upper Age Estimate	Angiosperm Taxa	Genes	Method	Notes
Magallón *et al*. (2015)	139.4	139.01	139.5	792	5	Bayesian	Constraints set as lognormal priors.
Bell *et al*. (2010)	183	167	199	560	3	Bayesian	Constraints set as lognormal priors.
Magallón and Castillo (2009)	241.7	241.46	241.95	265	5	PL	–
Chapter 2 of this thesis	221	192	251	193	76	Bayesian	Analysis with optimal values.
Smith *et al*. (2010)	217	182	257	113	3	Bayesian	Analysis with a calibration applied to eudicots.
Schneider *et al*. (2004)	246.4	231.5	261.3	84	4	PL	–
Magallón *et al*. (2013)	193.8	162.2	209.7	44	5	Bayesian	Analysis implementing uncorrelated lognormal relaxed clock and all genes.
Moore *et al*. (2007)	169.6	165.8	173.4	43	61	PL	Results for their "unconstrained" analysis.
Magallón and Sanderson (2005)	185	176.9	317.65	32	4	PL	The "mean" age chosen here is the median value from a range of analyses.
Laroche *et al*. (1995)	204	170	238	21	12	Other	Analysis implementing maize-wheat divergence secondary calibration.
Clarke *et al*. (2011)	198	170	231	8	7	Bayesian	Embryophyta crown age constrained at 509 Ma.
Goremykin *et al*. (1997)	160	144	176	3	58	Other	Age estimate corresponds to monocot/eudicot divergence.
Soltis *et al*. (2002)	332.6	–	–	2	4	PL	Analysis implementing a calibration for *Angiopteris/Marattia.*