

Supporting Information

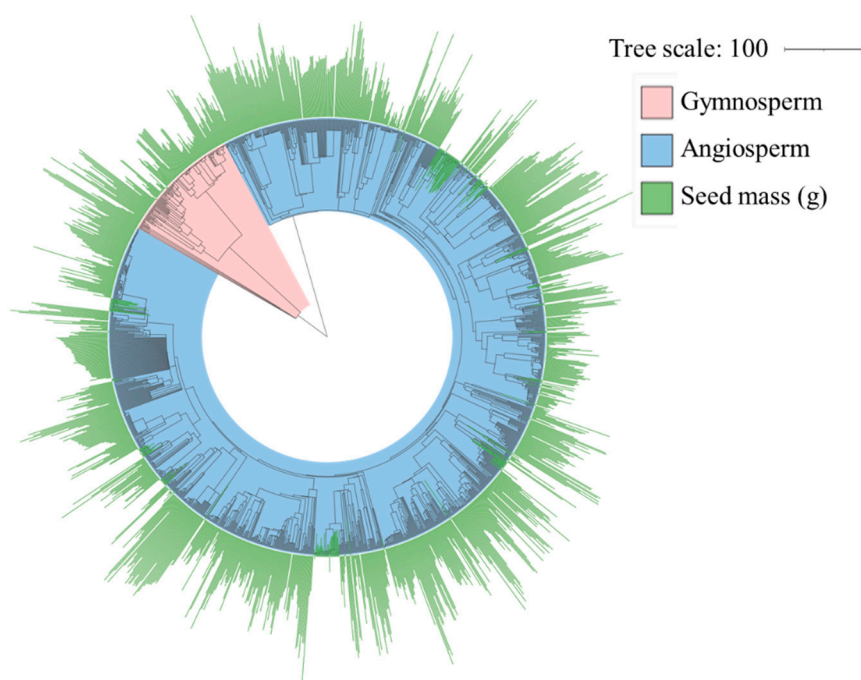


Figure S1 The phylogenetic tree generated using the ‘V.PhyloMaker’ package in R. The pink range represented gymnosperms and the blue range represented angiosperms. The height of the histogram showed the seed mass (logarithmically processed) of the different species.

Table S1 Relationship between average, minimum and maximum seed mass and environmental factors. G_{mean} represents the mean value of gymnosperm seed mass within the grid. G_{min} represents the minimum value of gymnosperm seed mass, and G_{max} represents the maximum value. A_{mean} represents the mean value of angiosperm seed mass within the grid. A_{min} represents the minimum value of angiosperm seed mass, and A_{max} represents the maximum value. Red indicates that the slope of the fit is negative, black indicates that the slope of the fit is positive, the bold value indicates that the fitting result is significant ($P < 0.05$), and the value without bold indicates that the fitting result is not significant ($P > 0.05$).

	MAT		SRAD		Wind		MPWQ		MAP		AI	
	Slope	R ²	Slope	R ²	Slope	R ²	Slope	R ²	Slope	R ²	Slope	R ²
G_{mean}	0.160	0.355	-2.843	0.042	-1.204	0.168	0.005	0.347	0.002	0.374	2.362	0.315
G_{min}	0.030	0.016	1.722	0.021	-0.133	0.003	0.001	0.016	0.000	0.004	-0.000	0.000
G_{max}	0.202	0.313	-5.909	0.099	-1.426	0.137	0.008	0.358	0.003	0.403	3.555	0.375
A_{mean}	0.096	0.200	-2.610	0.057	-0.789	0.128	0.003	0.208	0.001	0.188	1.348	0.165
A_{min}	-0.049	0.031	3.067	0.046	0.647	0.049	-0.003	0.071	-0.001	0.077	-1.264	0.083
A_{max}	0.182	0.258	-6.295	0.114	-1.491	0.162	0.007	0.254	0.002	0.260	2.867	0.243