Supplementary Table S2. Proteome characteristics, BUSCO completeness and orthogroup (OG) assignments for the nine resurrection plant species. For each species the table gives the total number of predicted proteins, the number of genes, the number of genes assigned to orthogroups by OrthoFinder and the number left unassigned, the mean protein length (amino acids), and the BUSCO completeness of the proteome (n = 1,614 BUSCO groups; C, complete; S, complete and single-copy; D, complete and duplicated; F, fragmented; M, missing). Species abbreviations: *Dorcoceras hygrometricum* (Bh); *Craterostigma plantagineum* (Cr); *Eragrostis nindensis* (En); *Haberlea rhodopensis* (Hrh); *Lindernia brevidens* (Lb); *Oropetium thomaeum* (Oth); *Sporobolus stapfianus* (Sst); *Xerophyta humilis* (Xh); *Xerophyta schlechteri* (Xs). BUSCO v6.0.0 was run in protein mode with the embryophyta_odb10 lineage dataset (2024-01-08). For *E. nindensis* (En), 278 duplicated sequence identifiers were removed before BUSCO (116,452 to 116,174 sequences); OrthoFinder was run on the full set.

Species	Total Proteins	Number of genes	Number of genes in orthogroups	Number of unassigned genes	Mean Length (AA)	BUSCO Completeness (%)
Bh	47778	47778	46552	1226	317	C:77.9%[S:75.7%,D:2.3%],F:5.5%,M:16.5%,n:1614
Cr	26635	26635	24870	1765	324.2	C:77.0%[S:74.2%,D:2.7%],F:5.0%,M:18.0%,n:1614
En	116452	116452	107742	8710	376.1	C:92.9%[S:26.1%,D:66.8%],F:2.2%,M:4.9%,n:1614
Hrh	44306	44306	39406	4900	327.7	C:91.1%[S:66.1%,D:25.0%],F:2.4%,M:6.5%,n:1614
Lb	21055	21055	19902	1153	413.6	C:77.0%[S:73.5%,D:3.5%],F:2.2%,M:20.8%,n:1614
Oth	28437	28437	24210	4227	318.1	C:71.4%[S:69.1%,D:2.3%],F:14.1%,M:14.5%,n:1614
Sst	48256	48256	47018	1238	373.1	C:80.8%[S:37.2%,D:43.6%],F:9.9%,M:9.4%,n:1614
Xh	61259	61259	37357	23902	174.4	C:53.3%[S:51.4%,D:1.9%],F:25.7%,M:20.9%,n:1614
Xs	25425	25425	24353	1072	410.2	C:85.1%[S:69.3%,D:15.8%],F:8.6%,M:6.4%,n:1614