

Supplementary Information

Transcriptome sequencing of three *Ranunculus* species (Ranunculaceae) reveals candidate genes in adaptation from terrestrial to aquatic habitats

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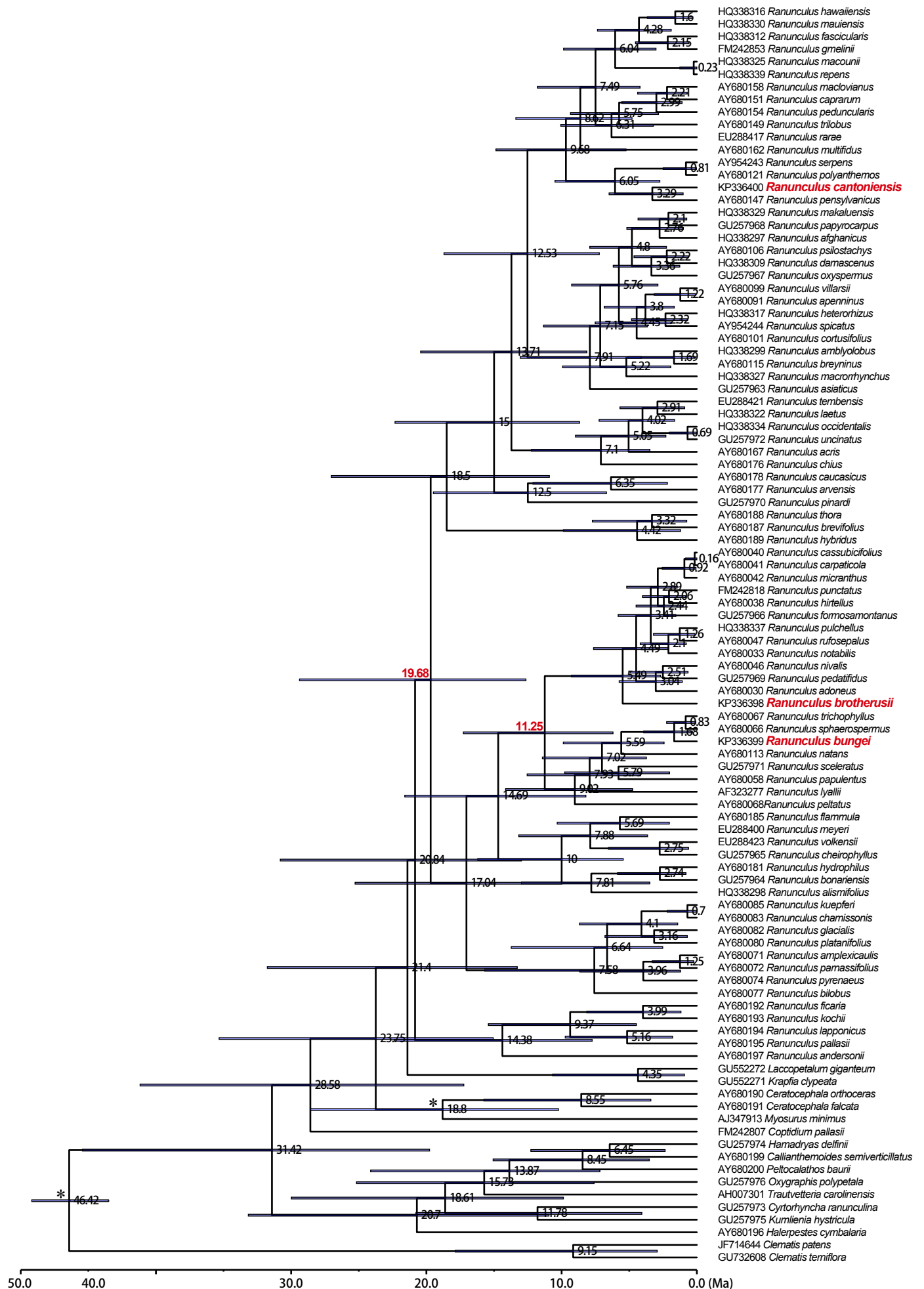


Fig. S1. Chronogram of *Ranunculus* using ITS. Blue bars indicate 95% highest posterior distributions, numbers along nodes indicate the mean ages, stars indicate the two fossil calibration points. The 3 species used for transcriptome analysis were highlighted in red colour and bold font. Genbank nos. were provided in front of species name.

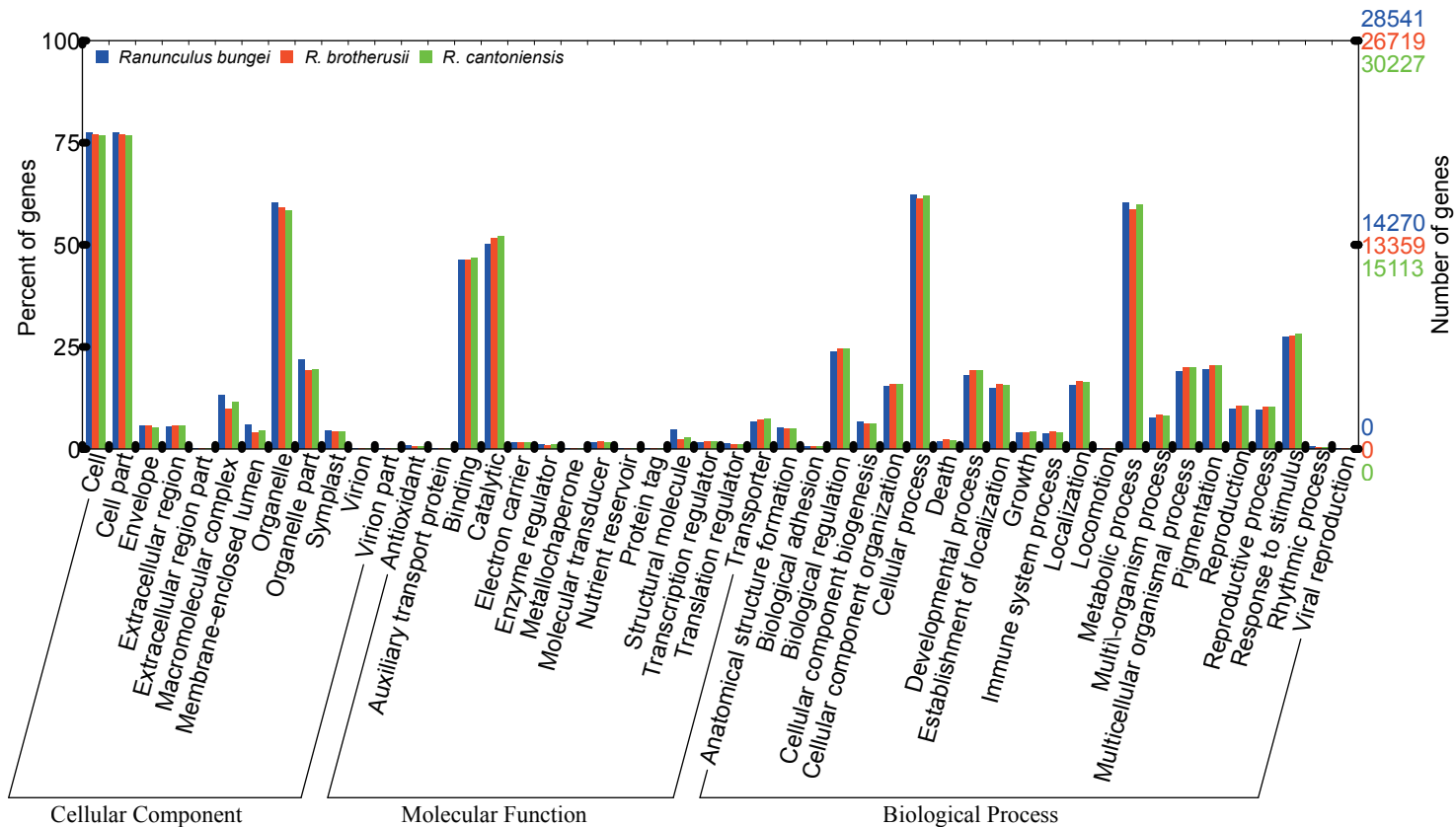


Fig. S2. GO categories of the unigenes of *Ranunculus bungei*, *R. brotherusii* and *R. cantoniensis* as plotted by WEGO.

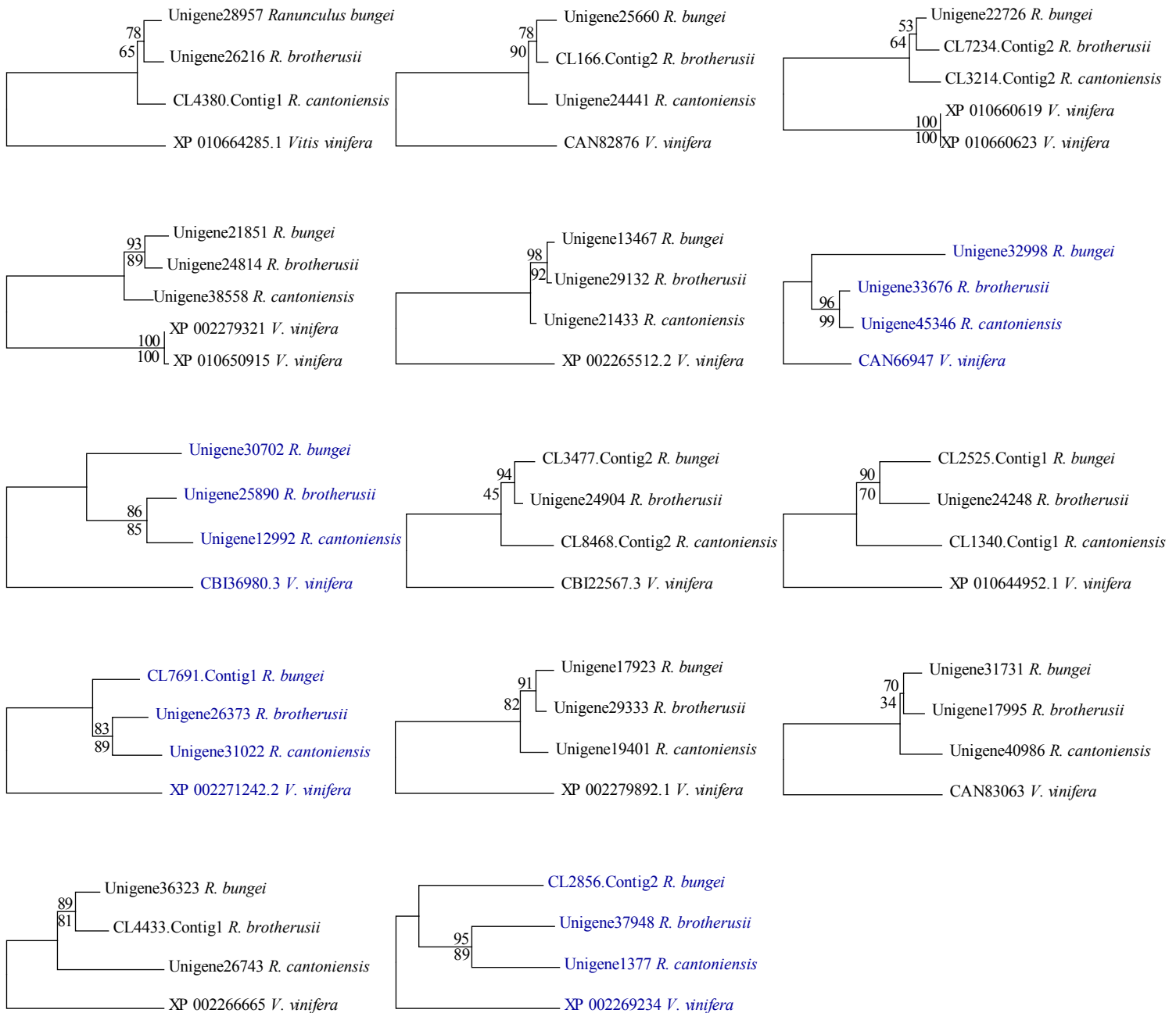


Fig. S3. Phylogenetic relationships of the PSGs in *R. bungei* and the orthologs in *R. brotherusii* and *R. cantoniensis*. Bootstrap values inferred from maximum likelihood and maximum parsimony are shown above and below the branches respectively. Orthologs with topologies inconsistent with that of ITS (Fig. 1) are in blue colour.

Table S1. *De novo* assembly from transcriptomes of *R. bungei*, *R. brotherusii* and *R. cantoniensis*, and annotations.

Sequences	<i>R. bungei</i>	<i>R. brotherusii</i>	<i>R. cantoniensis</i>
Clean reads			
No. of reads	106,256,806	106,580,162	102,823,982
No. of nucleotides (nt)	9,563,112,540	9,592,214,580	9,254,158,380
Q20 percentage	98.92%	98.97%	98.40%
N percentage	0.01%	0.01%	0.01%
GC percentage	45.22%	44.70%	44.08%
Contigs			
No. of contigs	126,037	114,753	140,218
Total length (nt)	45,026,691	39,928,897	47,992,342
Mean length (nt)	357	348	342
N50	692	727	649
Unigenes			
No. of unigenes	76,362	62,210	80,957
Total length (nt)	48,616,604	42,780,409	55,387,611
Mean length (nt)	637	688	684
N50	1132	1187	1170
Annotated unigenes^a number and percentage			
NR	39,669 (52%)	36,419 (64%)	41,926 (49%)
Swiss-prot	25,448 (33%)	23,465 (41%)	27,663 (31%)
KEGG	23,305 (31%)	20,767 (37%)	24,531 (29%)
COG	14,894 (20%)	12,839 (24%)	15,098 (18%)
GO	28,541 (37%)	26,718 (46%)	30,226 (35%)
NT	25,575 (33%)	24,392 (41%)	27,542 (32%)
Total	41,111 (54%)	37,427 (66%)	43,565 (51%)
Unannotated unigenes number and percentage			
Total	35,251 (46%)	24,783 (57%)	37392 (44%)

^a E-value <10⁻⁵