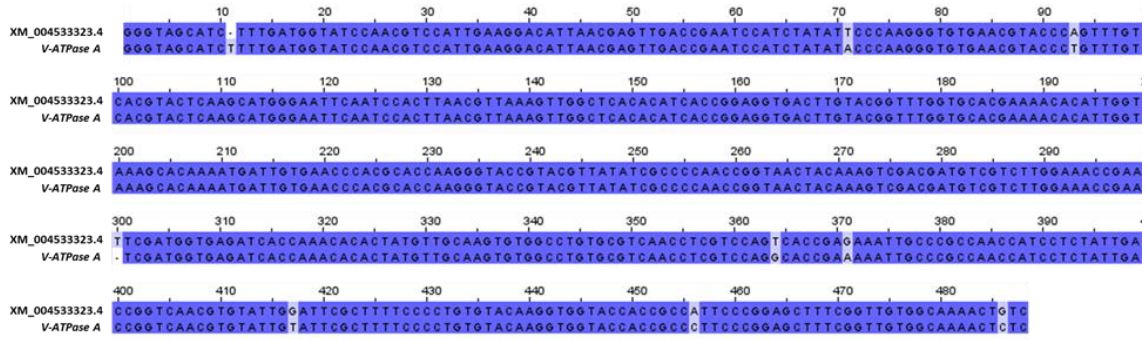


Figure S1. Alignment between dsRNA sequence of *v-ATPase A (CcVha68-1)* gene and XM_004533323.4 (NCBI).

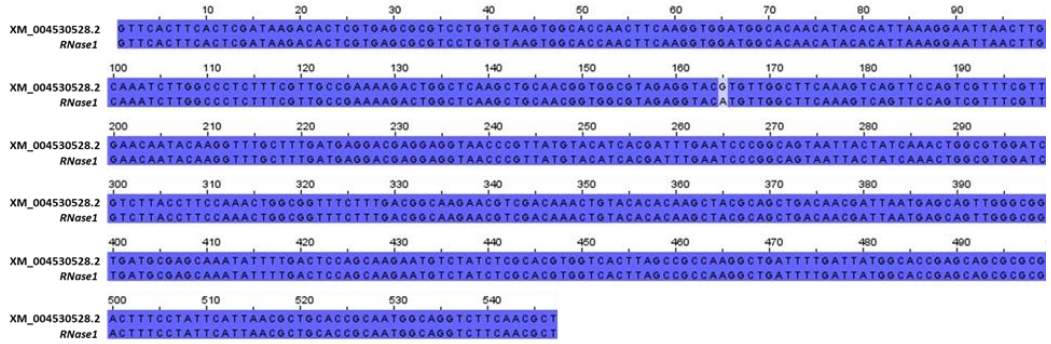


Figure S2. Alignment between dsRNA sequence of *RNase1 (CcdsRNase1)* gene and XM_004530528.2 (NCBI).

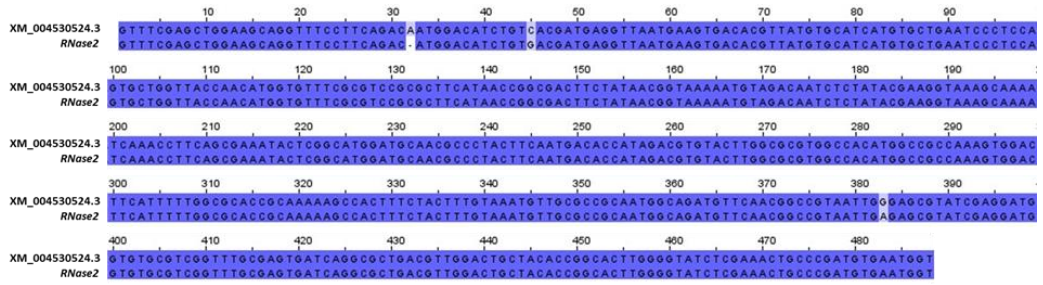


Figure S3. Alignment between dsRNA sequence of *RNase2 (CcdsRNase2)* gene and XM_004530524.3 (NCBI).

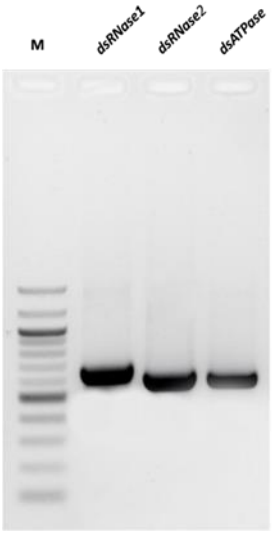


Figure S4. Agarose gel of the synthesized dsRNAs. Lane 1: marker 100 bp; lane 2: dsRNase1(613 bp); lane 3: dsRNase2 (557 bp); lane 4: dsATPase (553 bp).

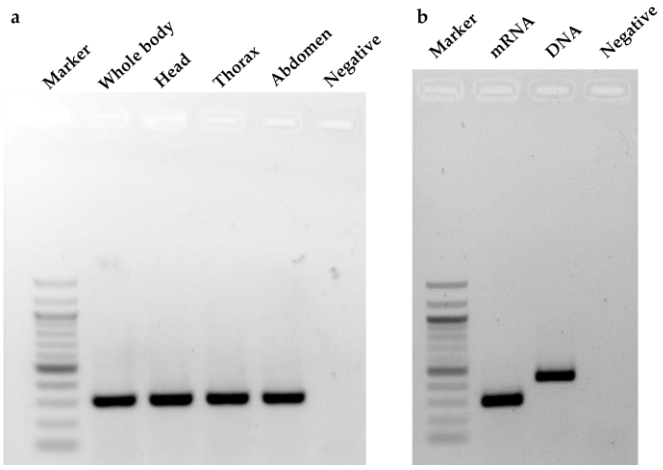


Figure S5. Agarose gel of *CcSOD* gene (housekeeping) expression in different adult tissues. (A) shows a 300 bp band in all samples; lane 1: marker 100 bp; lane 2: whole body; lane 3: head; lane 4: thorax; lane 5: abdomen; lane 6: negative control; (B) shows the difference between the presence/absence of an intron-sequence; lane 1: marker 100 bp; lane 2: mRNA (cDNA); lane 3: DNA (genomic); lane 4: negative control.

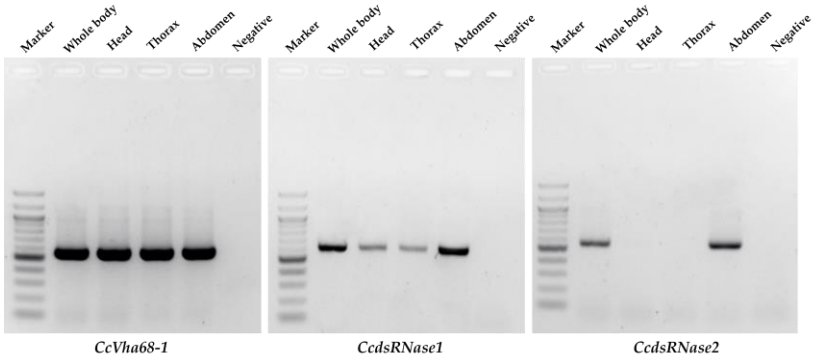


Figure S6. Agarose gel of *CcVha68-1*, *CcdsRNase1*, and *CcdsRNase2* gene expression in different adult tissues. For each gel: lane 1: marker 100 bp; lane 2: whole body; lane 3: head; lane 4: thorax; lane 5: abdomen; lane 6: negative control.

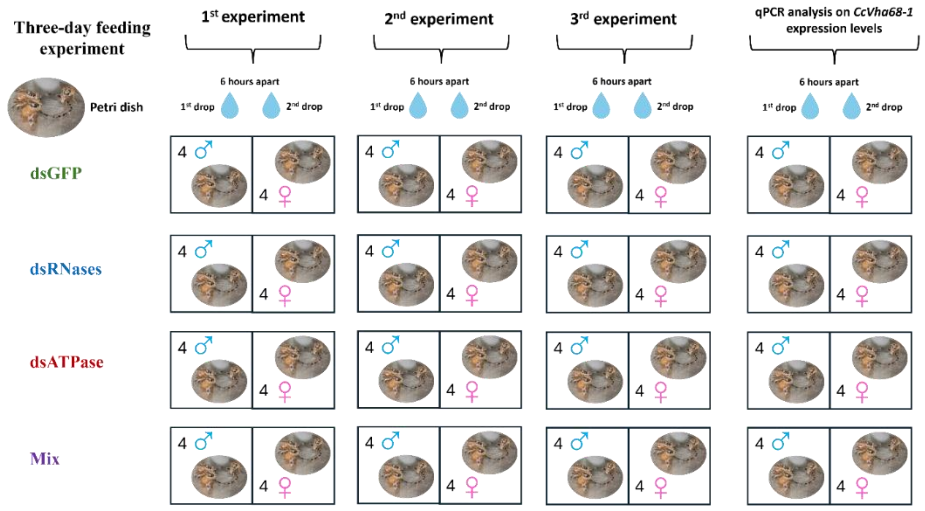


Figure S7. Schematic illustration of the mortality assay experiment.

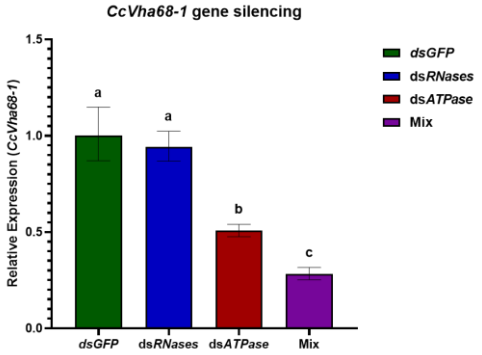


Figure S8. Transcript levels of *CcVha68-1* gene after three-day feeding experiment (one-way ANOVA: $F(3,24) = 34.84$, $P < 0.0001$). Different letters denote a significant difference between mean values recorded for each group (the obtained values passed normality tests). The values reported are the mean ± standard error.

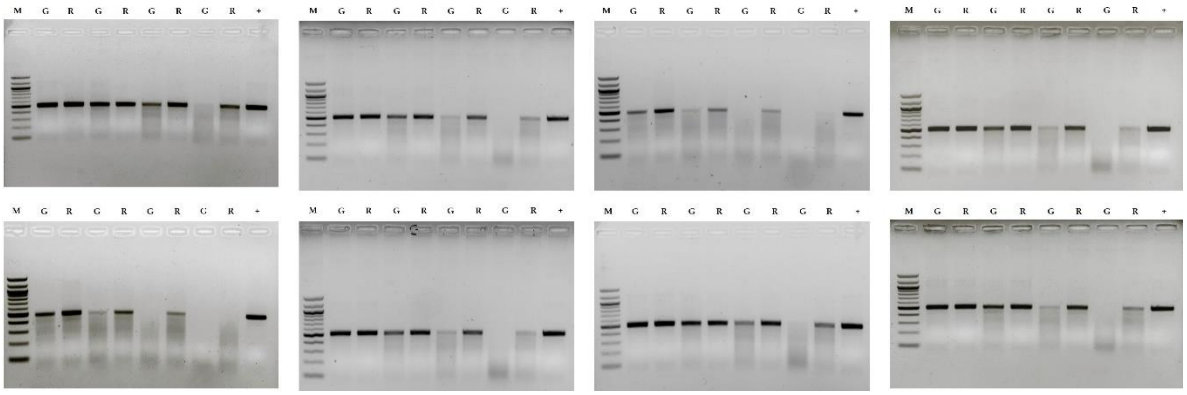


Figure S9. Agarose gels of *ex vivo* experiment. M: marker; G: dsGFP; R: dsRNases; +: positive control (dsATPase, 100 ng).

Primers	Sequences	Amplicon size (bp)	Tm (°C)
T7_dsRNase1_Fwd	TAATACGACTCACTATAGGGAGA GGATTTGTGGTGTCCCGGTA	613 bp	60
T7_dsRNase1_Rev	TAATACGACTCACTATAGGGAGA GCGTTGAAGACCTGCCATTG		
T7_dsRNase2_Fwd	TAATACGACTCACTATAGGGAGA CGGCACTGATCTTCTGGAGG	557 bp	60
T7_dsRNase2_Rev	TAATACGACTCACTATAGGGAGA ACCATTCACATCGGGCAGTT		
T7_dsATPase_Fwd	TAATACGACTCACTATAGGGAGA TGTTGAATTGGGTCCCGGTA	553 bp	60
T7_dsATPase_Rev	TAATACGACTCACTATAGGGAGA GTTTTGCCACAACCGAAAGC		
CcSOD_Fwd	TGCTCCGAGAACGTTCACG	300 bp	60
CcSOD_Rev	TCATCGGTCAATTCGTGCAC		

Table S1. Primers for *CcSOD* gene amplification and the synthesis of dsRNAs target.

Primers	Sequences	Amplicon size (bp)	Tm (°C)
RT_RNase1_Fwd	ATTCATTAACGCTGCACCGC	118 bp	60
RT_RNase1_Rev	ACCCGTCCAGCAGTCTACAT		
RT_RNase2_Fwd	GGTCAAATATTCCGTGCCGC	113 bp	60
RT_RNase2_Rev	TAGCTGGTGTACTCGGTCCA		
RT_ATPase_Fwd	TCCCCGAACTTACTTGCGAA	83 bp	60
RT_ATPase_Rev	CATGTTGGAGGTGTTGGCAA		
Rpl19_FWD	AACAAACGTTGTACTGATGG	103 bp	60
Rpl19_REV	CACGTACTTTATGTCGTCTG		

Table S2. Primers for qPCR analysis.

dsGFP	dsRNases	dsATPase	Mix
ddH_2O	ddH_2O	ddH_2O	ddH_2O
Sucrose 10%	Sucrose 10%	Sucrose 10%	Sucrose 10%
dsGFP (200 ng/µL)	dsRNase1 (100 ng/µL)	dsATPase (200 ng/µL)	dsRNase1 (100 ng/µL)
/	dsRNase2 (100 ng/µL)	/	dsRNase2 (100 ng/µL)
/	/	/	dsATPase (200 ng/µL)

Table S3. dsRNAs feeding experimental groups.

Additional information: aminoacidic sequences for phylogenetic analyses

Vha68-1 aa sequences

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