Supplemental Figures

Drozdova et al.

November 30, 2020

1 Diversity of opsin transcripts and their phylogenetic distribution

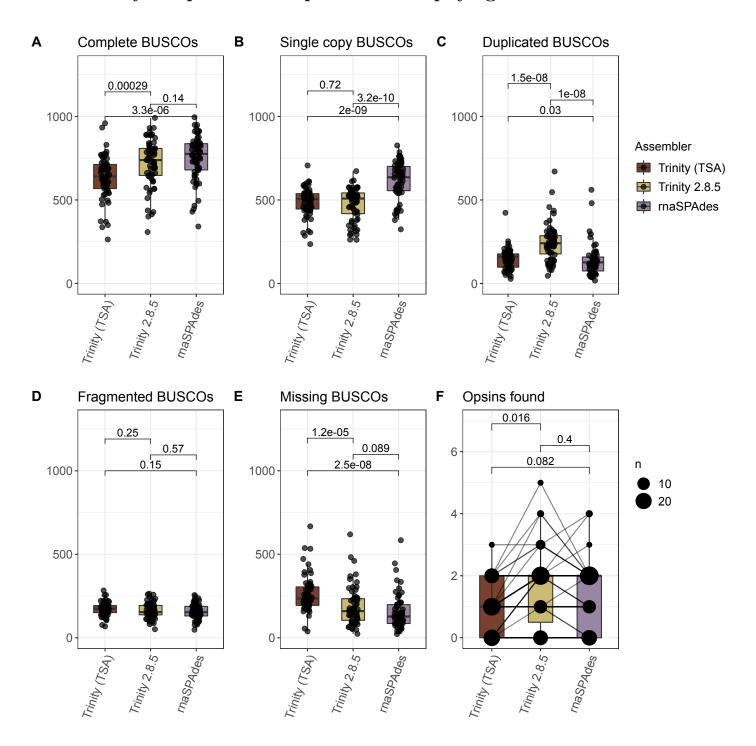


Figure S1: Quality of transcriptome assemblies according to BUSCO metrics (A-E) and the number of opsins found in each assembly (F).

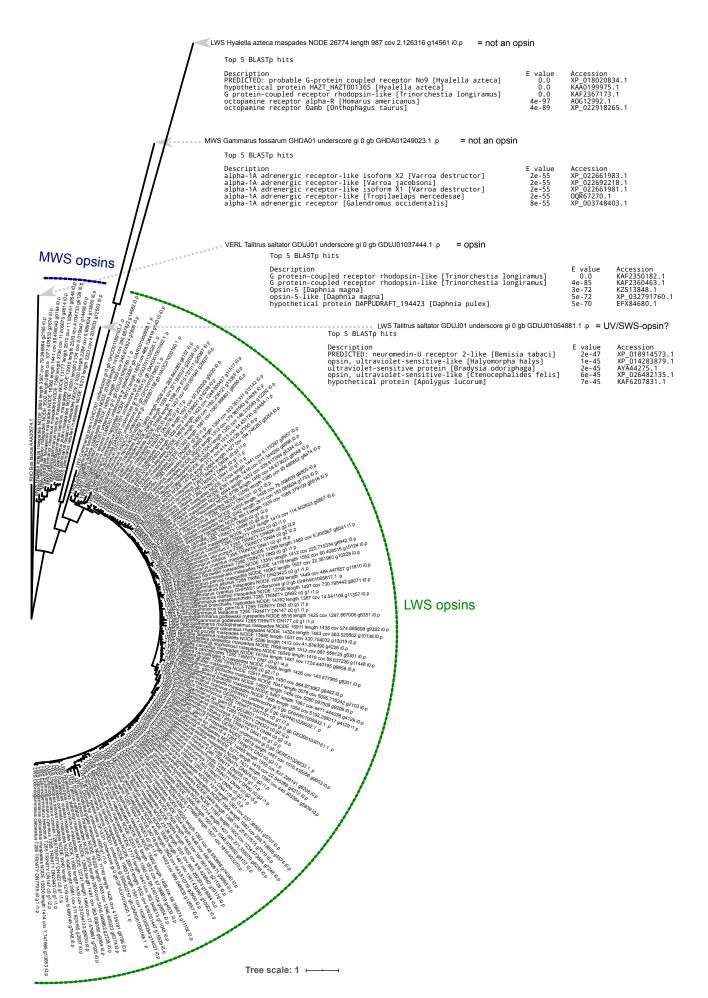


Figure S2: (A) An amino acid-based maximum likelihood tree of all found opsin sequences and reanalysis of long branches with NCBI BLAST.

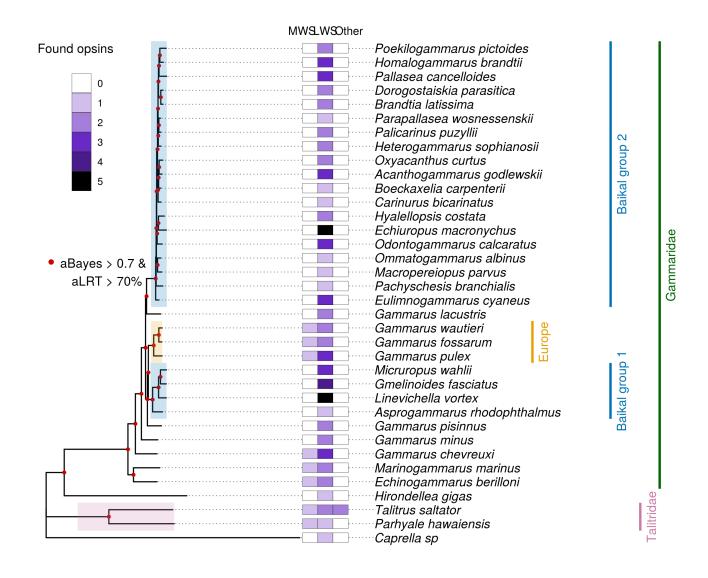
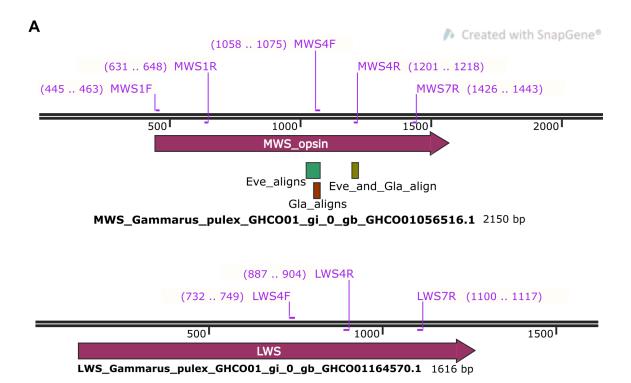
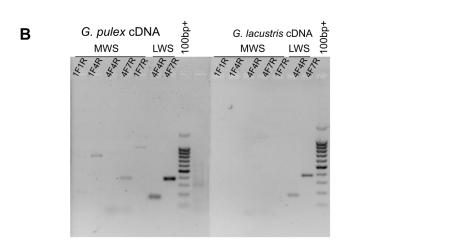


Figure S2: (B) Amino acid-based species tree based on one-copy orthologous proteins.





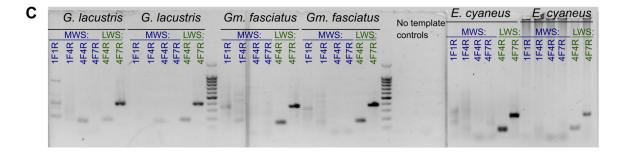
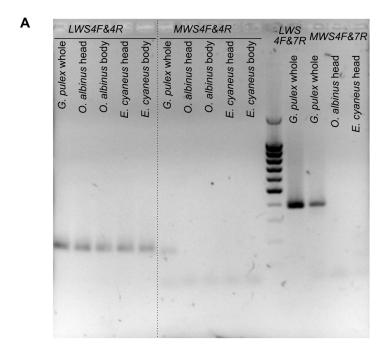


Figure S3: Amplification of MWS and LWS opsins from extracted genomic DNA of several species. (A) Schematic of primer binding sites. (B) Opsin amplification from G. pulex and G. lacustris cDNA. (C) Opsin amplification from genomic DNA of several species.



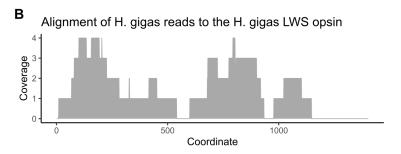


Figure S4: Evidence for extraocular expression of opsins in amphipods. (A) Opsin amplification from cDNA of several species. (B) Expression of the *H. gigas* LWS opsin in the sample from pereon and pleon.

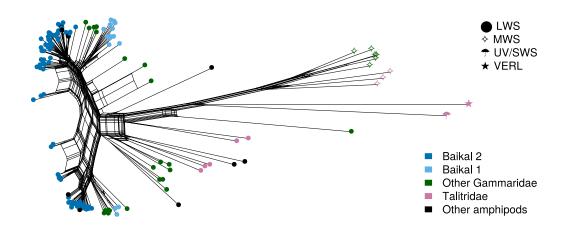


Figure S5: Phylogenetic network of all found amphipod opsins based on nucleotide sequences.

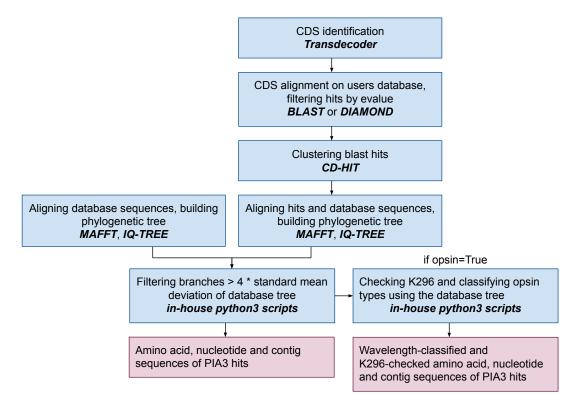


Figure S6: PIA principle.

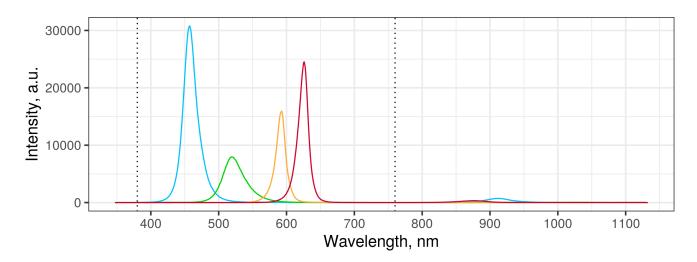


Figure S7: Emission spectra of the LED light sources.