

**Comparative transcriptome analysis of venom glands from
Cotesia vestalis and *Diadromus collaris*, two endoparasitoids
of the host *Plutella xylostella***

Wei Zhao ^{a,b}, Min Shi ^{a,b}, Xi-qian Ye ^{a,b}, Fei Li ^{a,b}, Xiao-wei Wang ^{a,b}, Xue-xin Chen ^{a,b,c,*}

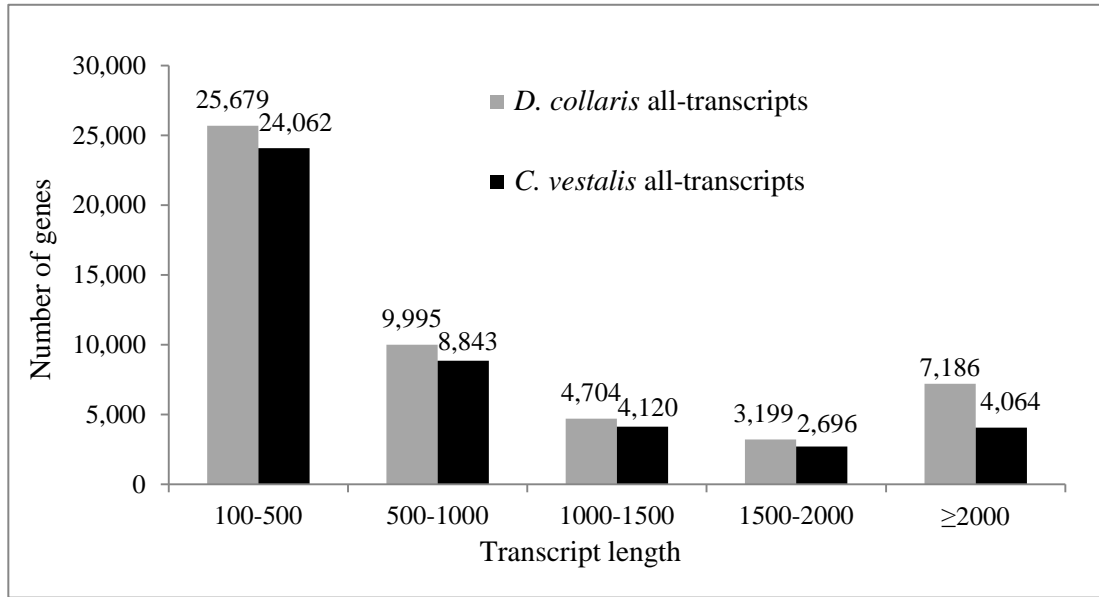
^a Institute of Insect Sciences, Zhejiang University, 866 Yuhangtang Road, Hangzhou 310058, China

^b Ministry of Agriculture Key Lab of Agricultural Entomology, Zhejiang University, 866 Yuhangtang Road, Hangzhou 310058, China

^c State Key Lab of Rice Biology, Zhejiang University, 866 Yuhangtang Road, Hangzhou 310058, China

***Corresponding author:** xxchen@zju.edu.cn, phone number: +86 571 88982868

A



B

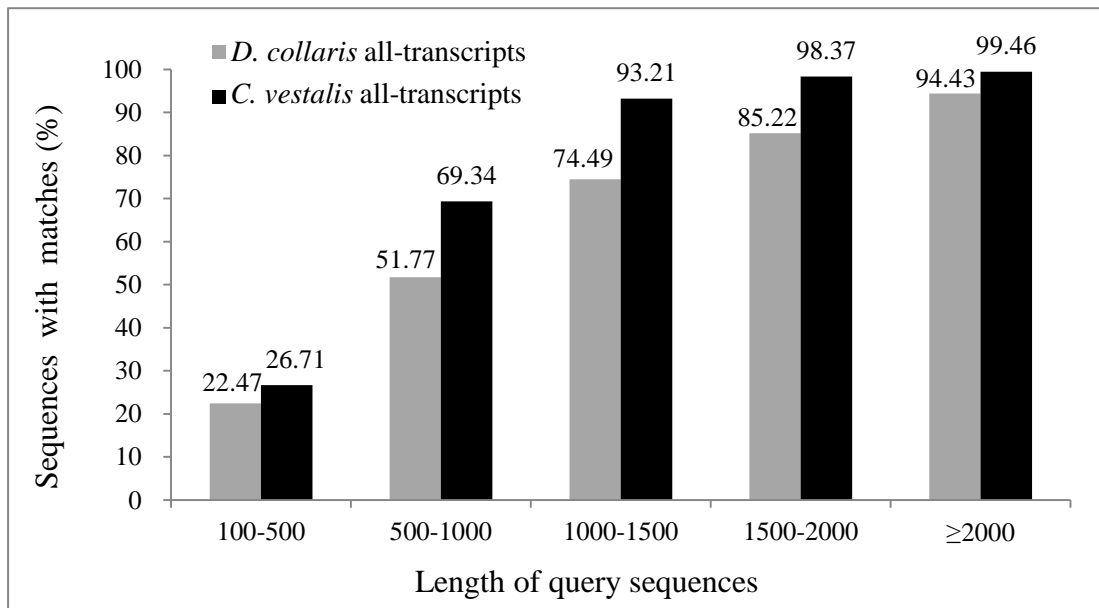


Figure S1. Size distribution for all-transcripts (A) and effect of query sequence length on the percentage of sequences for which significant matches were found (B).