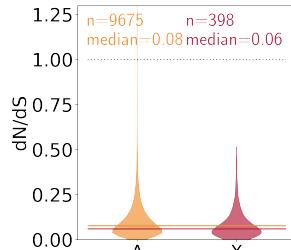
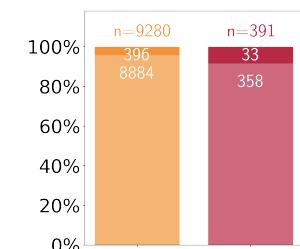
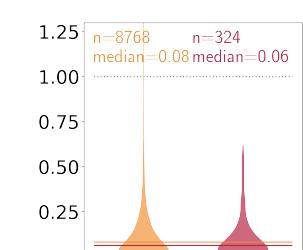
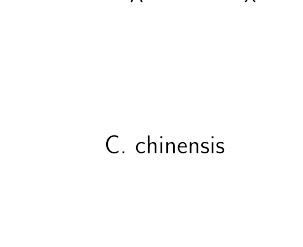
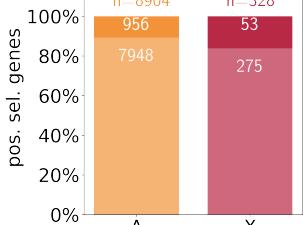
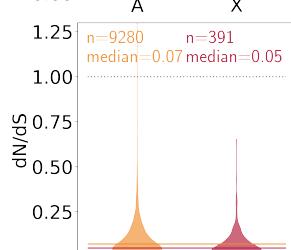
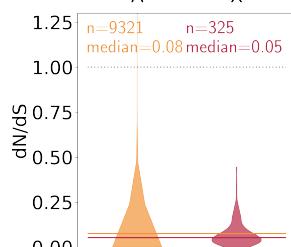
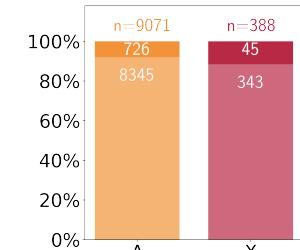
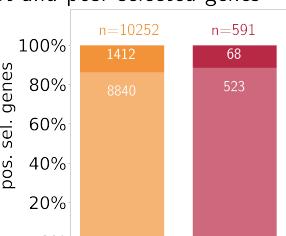
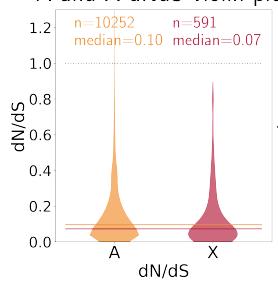
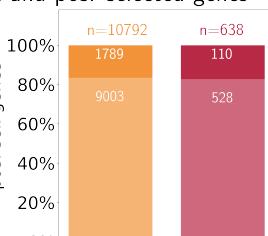
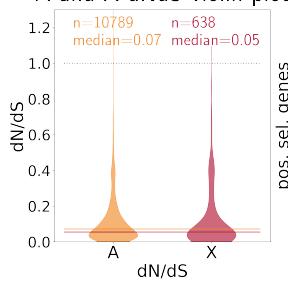
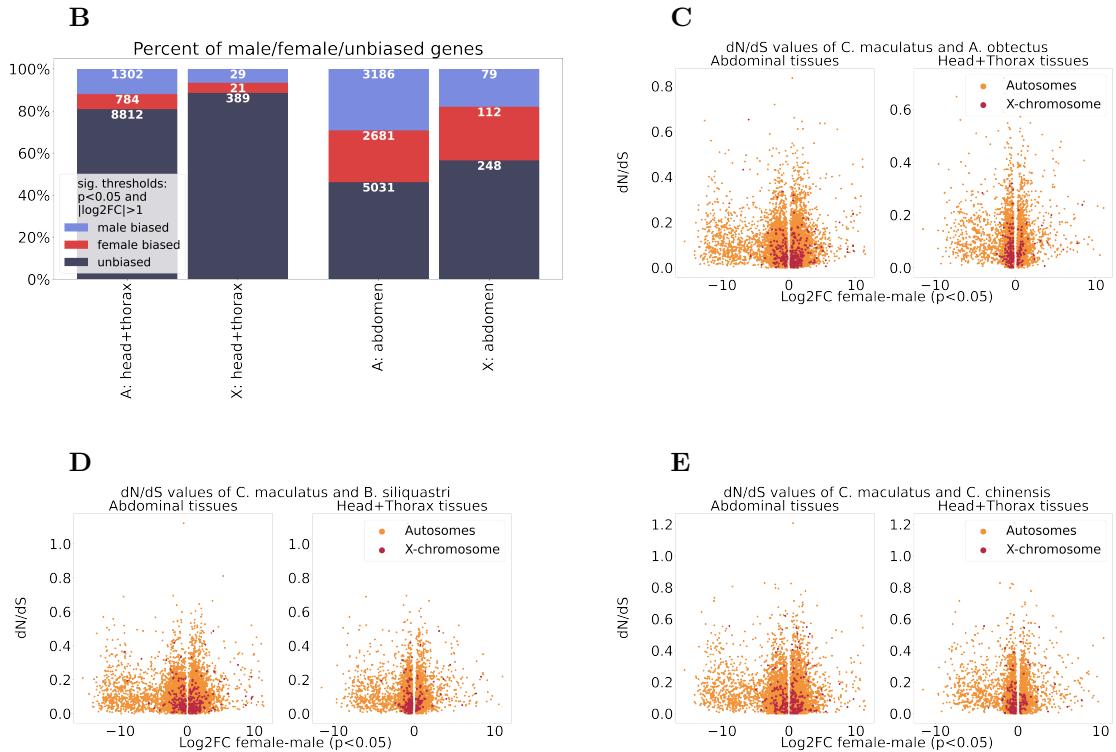


**A**

Bruchini: A and X dNdS violin plot and pos. selected genes

*A. obtectus**B. siliquastri**C. chinensis**C. maculatus***B**C. magnifica vs. C. septempunctata:  
A and X dNdS violin plot and pos. selected genes**C**T. castaneum vs. T. freemani:  
A and X dNdS violin plot and pos. selected genes

**Figure 1:  $d_N/d_S$  and abundance of positively selected genes.** Bottom left: Pairwise comparisons between members of three species groups with violin plots of  $d_N/d_S$  values for X-linked and autosomal 1-to-1 orthologs, and scatterplots of  $d_S$  vs.  $d_N$ . Permutation tests ( $n=10000$ ) show that  $d_N/d_S$  is significantly lower for X-linked orthologs in all comparisons within *Bruchini* (A) and *Coccinella* (B), but not *Tribolium* (C). Top right: The bar plot show the percentage of genes that contain codons under positive selection according to paml site-model analysis (likelihood ratio test comparison between paml site models M1a and M2a). *Bruchini* (A), show an enrichment of positively selected X-linked orthologs in all pairwise comparisons, while *Coccinella* (B) and *Tribolium* (C) show no significant difference.



**Figure 2: Differential expression analysis.** We are utilizing the log2 fold change (og2LFC) information from genes in *C. maculatus* and combining it with  $d_N/d_S$  between these genes and their 1-to-1 orthologs in other bruchids. The log2FC contrast is always female-male, therefore positive values indicate female-bias and negative values indicate male-bias. **A:** log2FC of all genes on X-linked contigs in somatic (head+thorax) and reproductive (abdominal) tissues. Positive log2FC indicates female bias. Vertical lines are the median log2FC for each tissue, and the shaded area is the standard error of that mean. **B:** number of sex biased genes in abdominal (reproductive) tissues and head and thorax (somatic) tissues. **C-E:** Scatterplot of significantly differentially expressed genes showing  $d_N/d_S$  of *A. obtectus* (**C**), *B. siliquastri* (**D**) and *C. chinensis* (**E**) respectively.