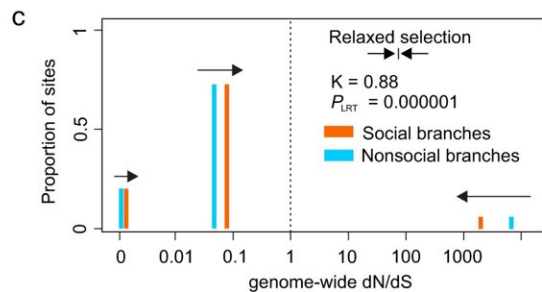
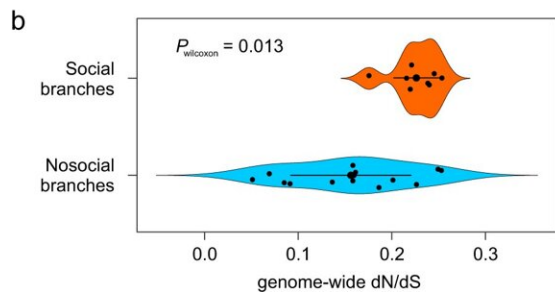
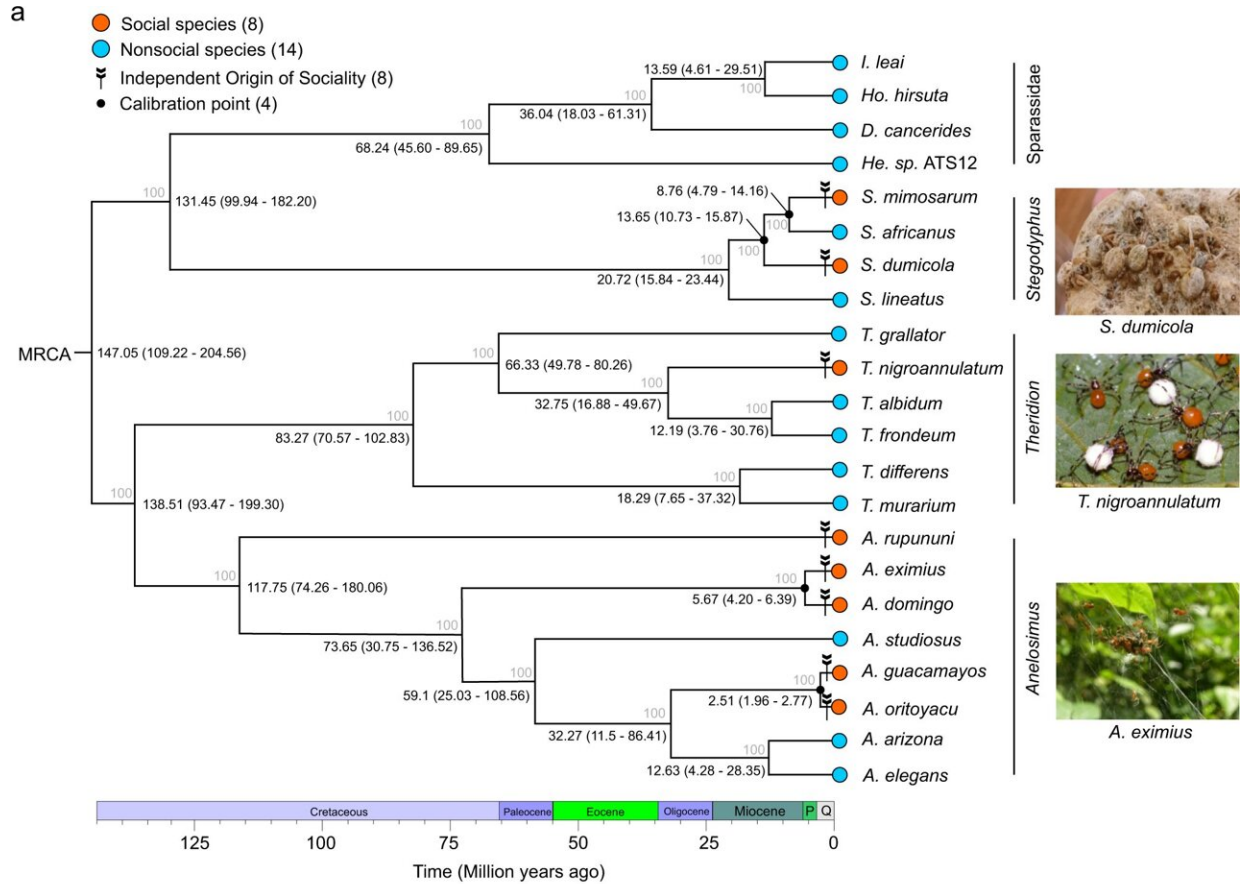


# Sociability genes found in some spiders

November 28 2022, by Bob Yirka



Phylogeny of study species and genome-wide pattern of molecular evolution in social and nonsocial branches. a The maximum likelihood (ML) phylogenetic

tree with estimated divergence time of the 22 spider species included in the study. The ML tree was inferred from 3832 core-shared single-copy orthologs. Bootstrap values are indicated along the branches. The divergence times at the nodes were estimated using four calibrations indicated with solid black dots. Median age estimates and 95% highest posterior densities (Mya) are shown for each node. Q and P represent the Quaternary Period and the Pliocene Epoch, respectively. Four lineages of spiders are distinguished by dark columns: genera *Anelosimus*, *Theridion*, *Stegodyphus* and the family Sparassidae. Orange dots represent social spider species, light blue dots represent nonsocial species including prolonged subsocial, subsocial, and solitary spider species, the arrow tails represent the independent origins of sociality in spiders. Pictures of social spiders (from top to bottom) from *Stegodyphus dumicola* (photo credit: Noa Pinter-Wollman), *Theridion nigroannulatum* and *Anelosimus eximius* (photo credit: Leticia Avilés). b Violin plot depicting the genome-wide pattern of molecular evolution (dN/dS) between social (n = 8) and nonsocial spider (n = 14) branches across the phylogeny (horizontal bars indicate 95% CI of the means). P value was calculated by using Wilcoxon rank-sum test. Social spiders experienced convergent elevated genome-wide molecular evolution during the transition to social life. c Multi-bar plot depicting the patterns of selection experienced across sites in the genomes of social and nonsocial spiders, estimated with the Partitioned Descriptive model in RELAX. P value as calculated by using Likelihood-ratio test (LRT). The distribution of dN/dS across sites in the genomes are illustrated by three categories of dN/dS for social (orange) and nonsocial (light blue) branches. The vertical dashed line at dN/dS = 1 represents neutral evolution, bars at dN/dS > 1 represent sites experiencing positive selection, and bars at dN/dS

Citation: Sociability genes found in some spiders (2022, November 28) retrieved 27 April 2024 from <https://phys.org/news/2022-11-sociability-genes-spiders.html>

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