One hundred mitochondrial genomes of cicadas

Piotr Łukasik, Rebecca A. Chong, Katherine Nazario, Yu Matsuura, DeAnna Bublitz, Matthew A. Campbell, Mariah Meyer, James T. Van Leuven, Pablo Pessacq, Claudio Veloso, Chris Simon, John P. McCutcheon

Supplementary figures

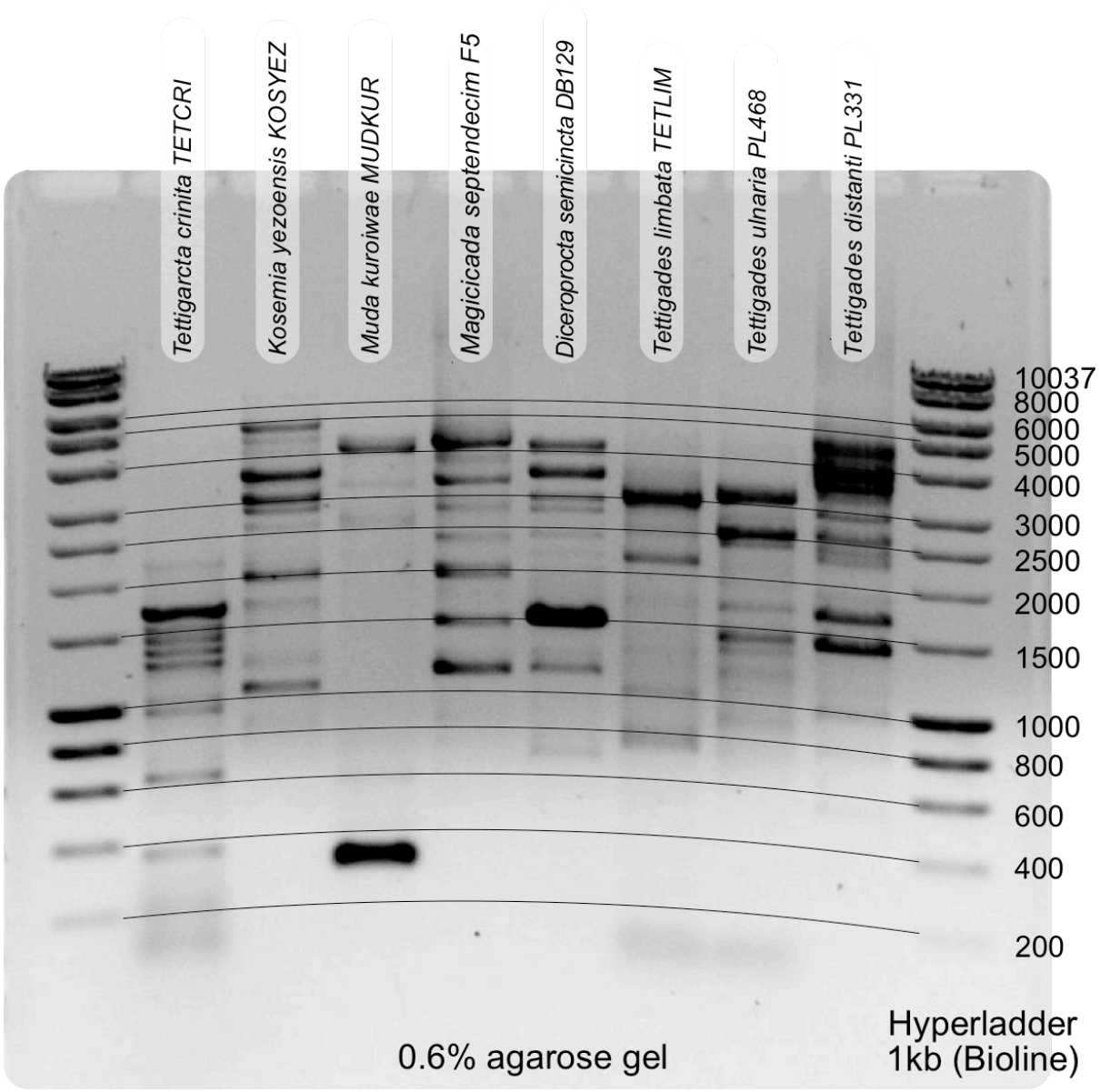

Fig. S1. PCR products obtained using outwards-facing primers for the outer portions of the gene-encoding mitogenome region in eight cicada species. For most cicada species, the strongest bands are in the 1.5-5 kb range. Despite trying a wide range of samples, primers, polymerases and reaction conditions, we have been unable to consistently obtain a single dominant product, such as in *T. limbata*. Sanger-sequencing has confirmed the specificity of the dominant product in four cicada species, but the read quality dropped rapidly after the ends of the gene-encoding region. Our interpretation is that the genomes are circular, but the extreme AT bias, the repetitive nature of the control region, and perhaps heteroplasmy, result in noisy patterns even when high-fidelity, high-processivity polymerases are used.

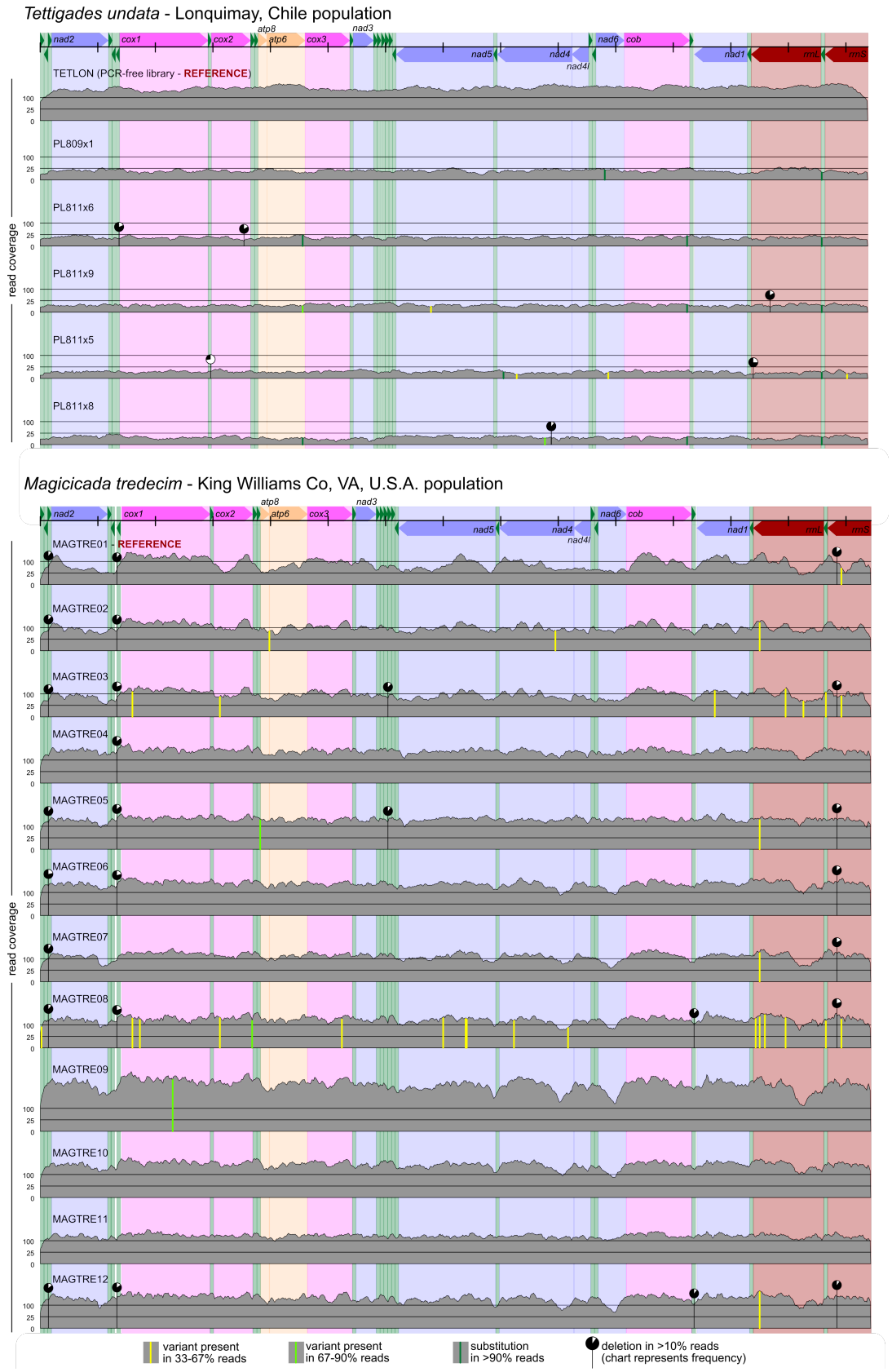

Fig. S2. The read coverage along the length of the mitochondrial genome in replicate specimens from two cicada populations, calculated in 10-basepair windows. The vertical scale has been square root transformed. Colored bars indicate nucleotide positions where at least 33% of mapped bases disagree with the reference sequence. Black bars with pie chart on top indicate nucleotide positions where at least 10% of mapped reads contain a deletion; the white area in the chart correspond to the proportion of reads with the deletion. The annotation and background colors correspond to those in Fig. 1A.

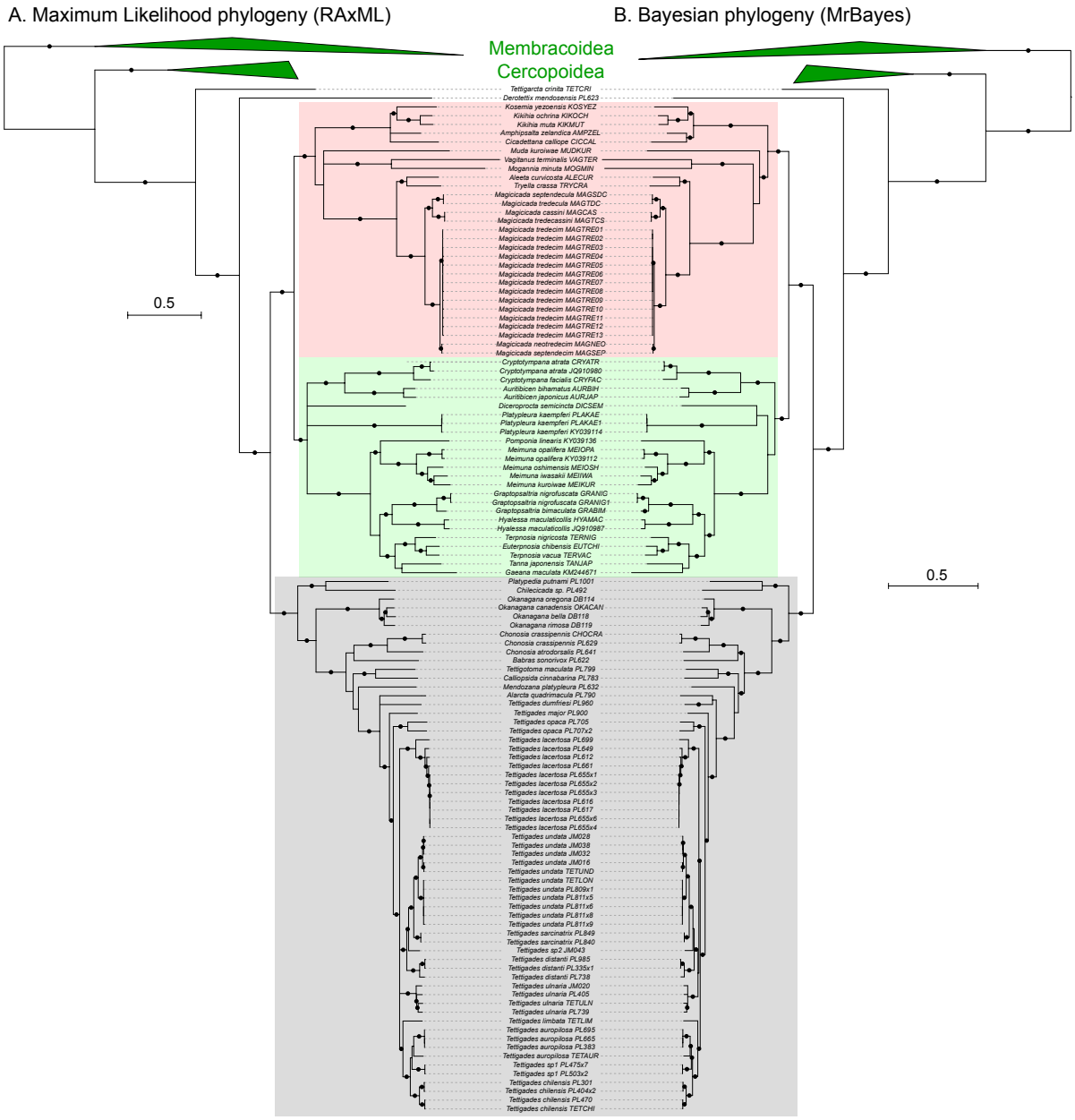

Fig. S3. The comparison of Maximum Likelihood (A) and Bayesian (B) phylogenies for 117 cicada specimens. The ML phylogeny was reconstructed based on 37 concatenated mitochondrial genes; the Bayesian phylogeny is based on 13 protein-coding genes. Nodes with bootstrap support values of <70% (A), or with posterior probabilities <0.7 (B), were collapsed. Nodes with bootstrap support of 100% (A), or with posterior probabilities of 1.0 (B), are represented by black dots. The colored rectangles correspond to the currently recognized Cicadidae subfamilies, as in Fig. 2.