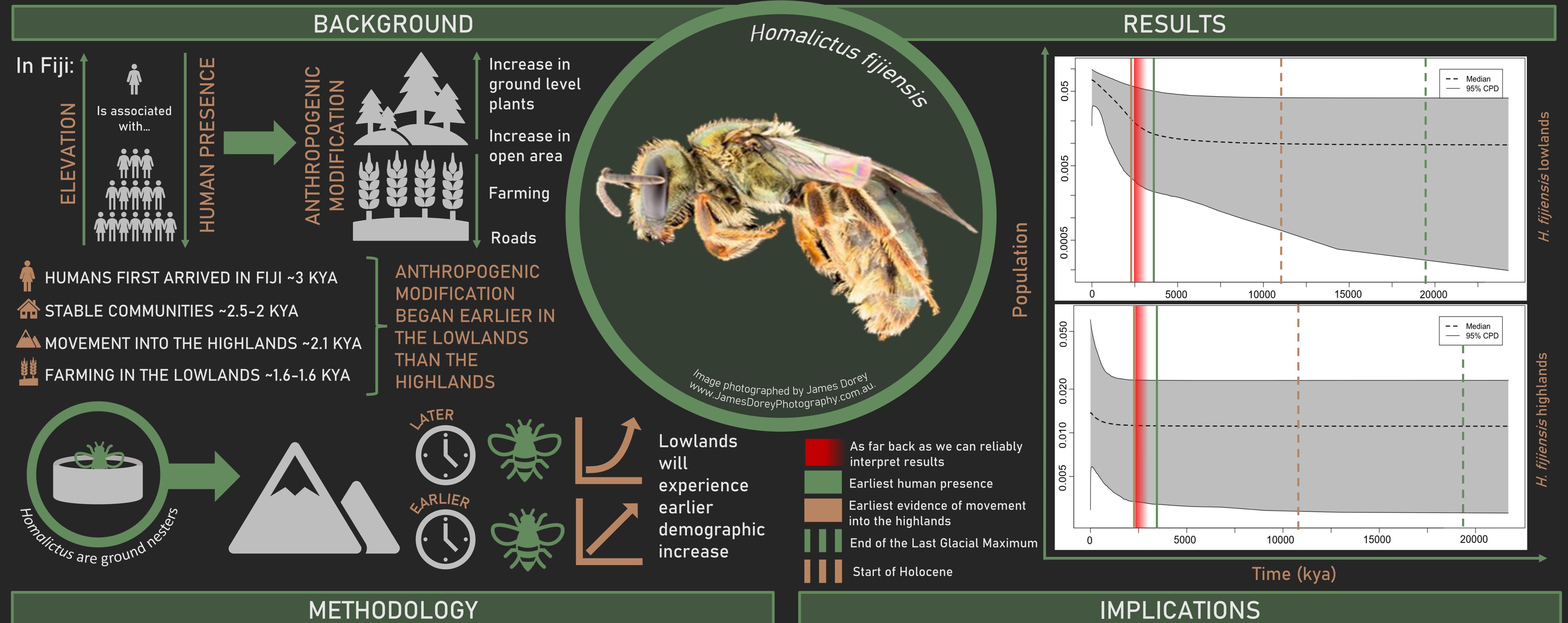
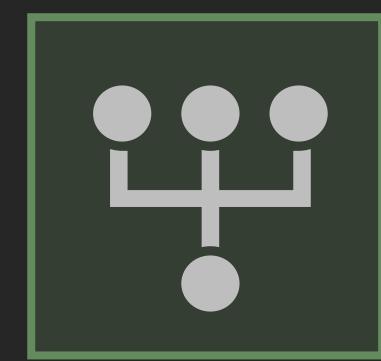


Disentangling climate and human-mediated environmental change as drivers of historical demography in endemic Fijian bees

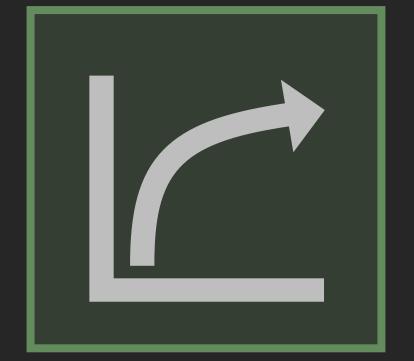


Patricia Slattery, Associate Professor Michael Schwarz, Dr. Mark Stevens and James Dorey

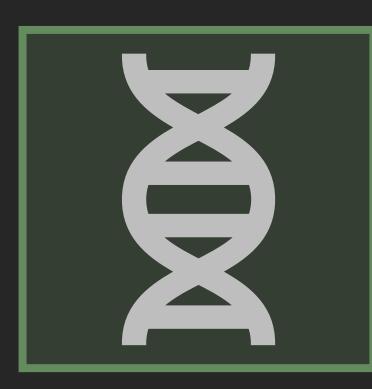




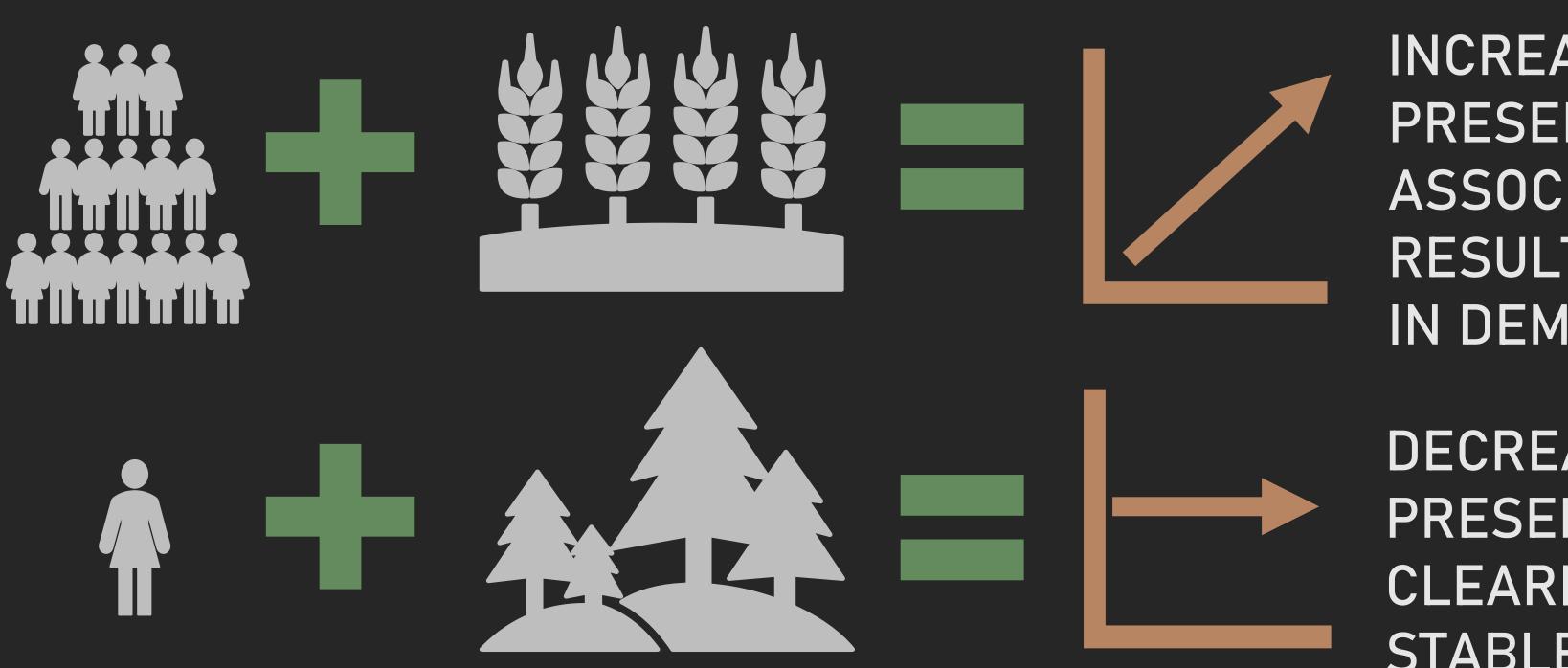
Compare mtDNA (COI), nDNA (SNPs) and UCE phylogenies to assess concordance between the genetic data. Calculate pairwise F_{ST} for *Homalictus fijiensis* populations: a significant difference in highland and lowland populations resulted in separattion for all COI analyses.



COI Extended Bayesian Skyline Plots (EBSP) were created using a HKY + Γ model, run in a single chain for 500 million iterations, sampled every 10,000 iterations and repeated 4 times. Combining the files was logged at a lower rate of every 100,000 iterations with a burnin of 10%.



SNP EBSPs were filtered for linkage (R^2 of 0.9), monomorphs, missing data, repeatability and to remove secondaries. SNP EBSPs used the same specifications as the COI EBSPs, except the model: the combined *H. fijiensis* used a GTR + Γ model.



INCREASED HUMAN
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DECREASED HUMAN
PRESENCE AND LACK OF
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These results highlighted the effect of human presence as a major driver of demography in Fijian *Homalictus* concurrent with the other species that were analysed. We cannot completely rule out climate as a driver as the refugia theory could explain much of the diversity in the highlands, but at least in the last 2,500 human presence is likely to be the primary driver of these bees demography.