



Family relations in African beetles

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Who are those beetles?



Ambrosiodmus obliquus

This research project is about the phylogeny for Ambrosia beetles, a type of weevil in the superfamily Curculionidae. These beetles form eusocial groups and live in tunnels and chambers that they excavate in trees. These small communities don't feed on the trees themselves but live in symbiotic relationships with the ambrosia fungus that grow into the xylem tissue to extract nutrition that they convert to food for the beetles(1). In return the beetles store fungus spores in special cavities in their bodies and spread those wherever they venture, and due to their permanent inbreeding nature, they are excellent



Pattern of tunnels from weevils colonizers of new territories.

New methods

Traditional taxonomy based on morphology have many limitations, specially when it comes to insects that often look almost identical. Molecular methods with barcoding was used, giving genetic information that can be compared to an increasing amount of information stored in databases.

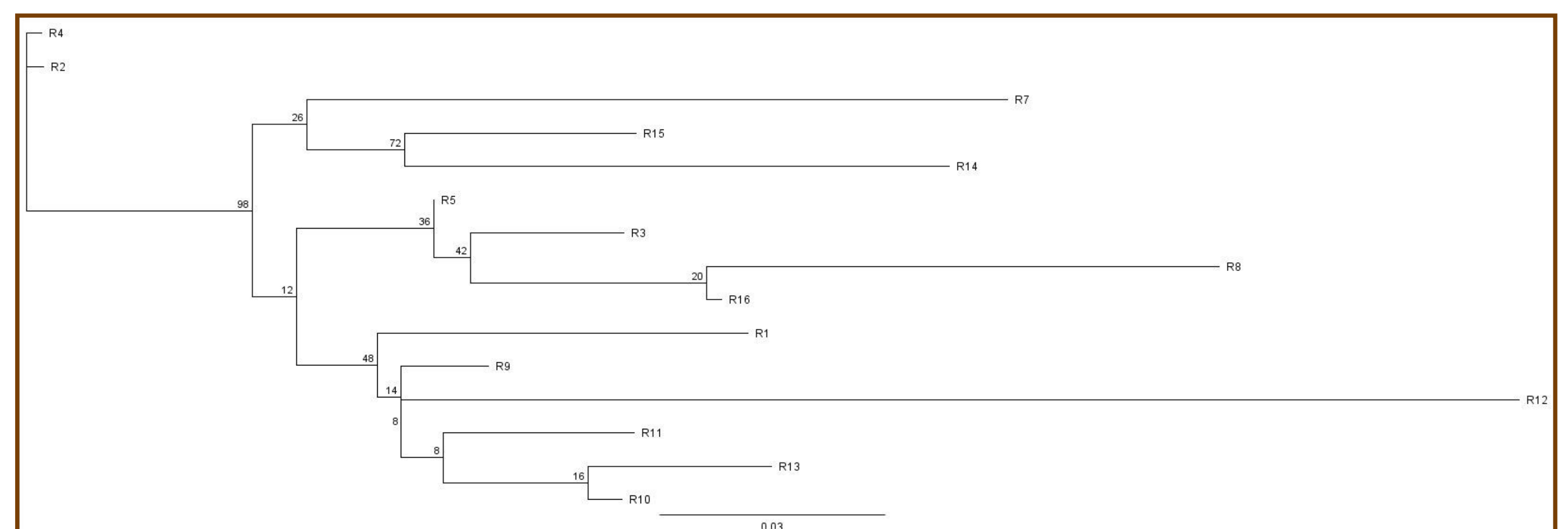
How was the sequencing done?

Three genes were sequenced, COI, a mitochondrial gene with good accuracy on species level and close relations. To get higher accuracy on more distant relatives 28S, a ribosomal RNA, was used and CAD was added for redundancy giving greater precision in the analysis.

The samples collected from different sites in Africa was partially dissolved to extract tissue and DNA which was then purified. Specific Primers was applied to amplify the concentrations of the respective genes, using polymerase chain reaction (PCR). The DNA was further run through a sequencing reaction that attaches fluorescent dye to the nucleotides. To read the DNA sanger sequencing was used, and the resulting chromatograms was interpreted and refined using Geneious software.

What did we find ?

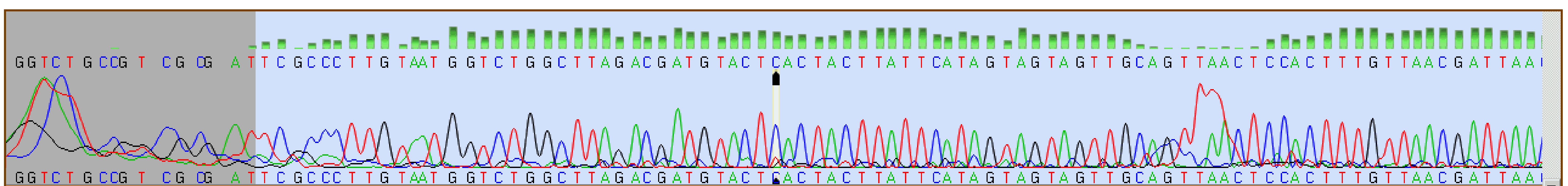
The sequences will be compared with others from the genebank and an outgroup will be added to the tree.



Phylogenetic tree made from the data extracted from the samples

Why is this interesting?

These beetles along with their cousins have despite their small size, an unprecedented impact on forest rendering millions of acres of trees rotting. Understanding their phylogeny and distribution through history can lead to better predictions in how they will behave and spread.



A chromatogram from the sequencing, used to determine the different nucleotides

References:

1. Peer, K. and Taborsky, M. (2005) *OUTBREEDING DEPRESSION, BUT NO INBREEDING DEPRESSION IN HAPLODIPLOID AMBROSIA BEETLES WITH REGULAR SIBLING MATING*, *Evolution*.