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Characterization of a New mtDNA Minicircle in a Chewing Louse, Geomydoecus aurei

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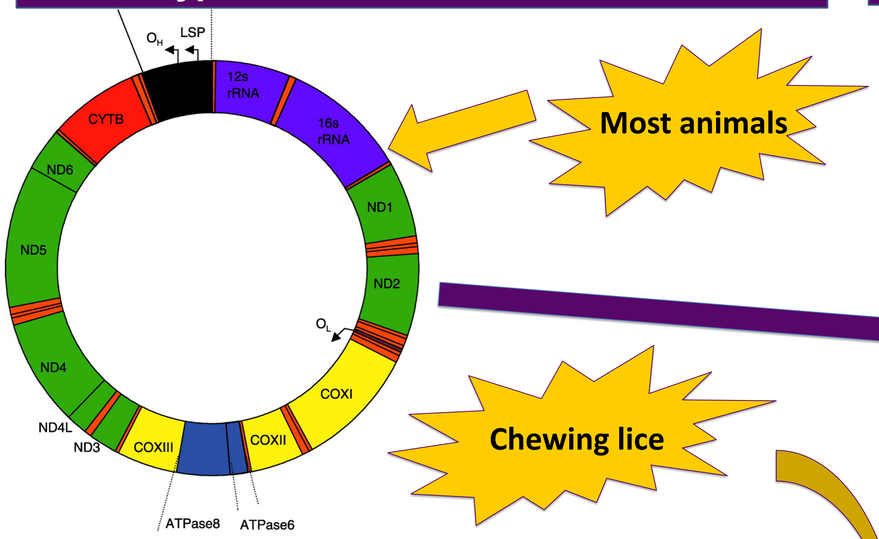
Background

Typical Animal mtDNA Genome

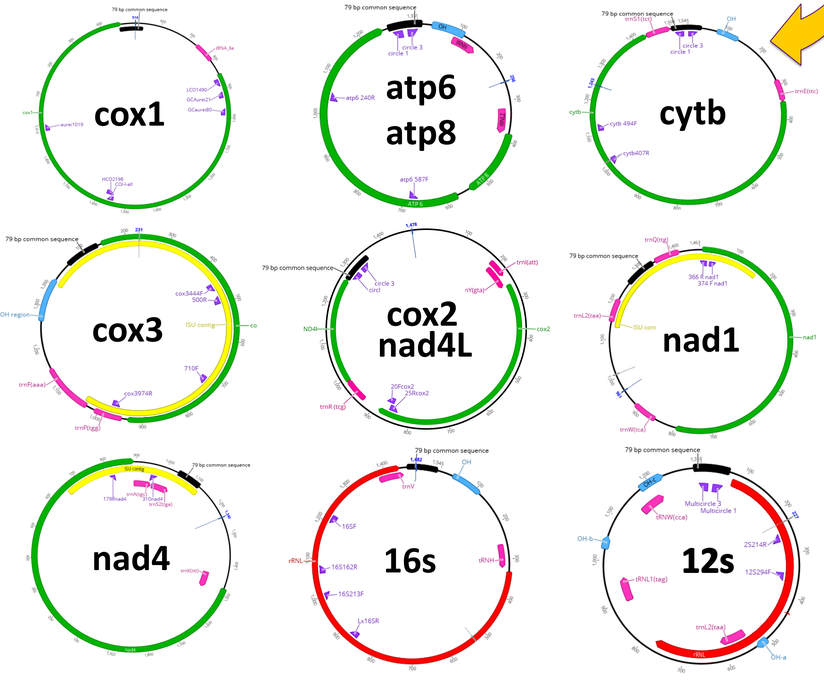


Most animals

Chewing lice

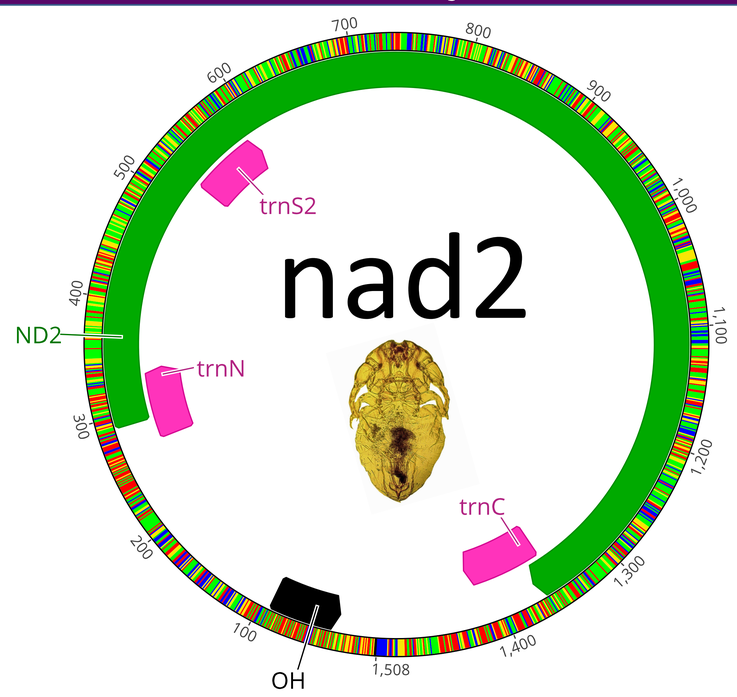
- In most animals, the mitochondrial genome is very conserved with 13 protein coding genes, 22 tRNAs, and two rRNAs in a single circular chromosome (Cameron et al., 2011).
- Many species of lice are unique in the sense that they contain multiple minicircles of fragmented mtDNA instead of a single circular chromosome.

Characterized Minicircles in *G. aurei*



Results

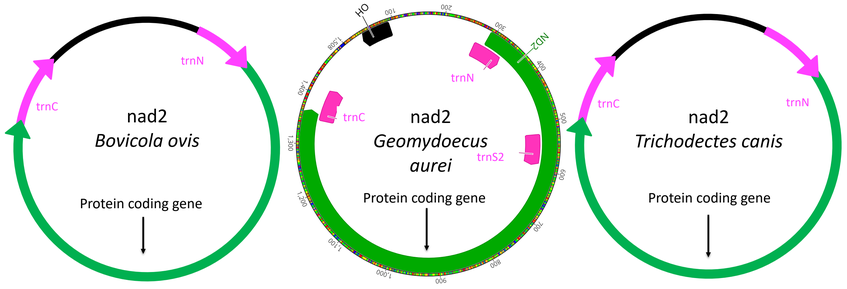
Nad2 Minicircle of *Geomydoecus aurei*



- The newly characterized *nad2* minicircle contains the nad2 gene and three putative tRNAs: *trnN*, *trnS2*, and *trnC*.
- The *nad2* gene is 1077 bp in length.
- The *nad2* minicircle contains the conserved 79-bp region, shown above in black, that has been identified in all *G. aurei* minicircles characterized to date.
- The *nad2* minicircle was identified and characterized using PCR, cloning reactions, and Sanger sequencing.

Conclusions

- The 79-bp DNA sequence found on this circle is identical to sequence found on nine other *G. aurei* minichromosomes, suggesting functional importance.
- The majority of the tRNAs identified in minicircles containing protein coding genes have been found nearly adjacent to the coding region or to very minimally overlap with the coding sequence.
- The gene order of the *G. aurei nad*2 minichromosome (*trnN-nad2-trnC*) is seen in other mammalian louse species (Song et al, 2018), including *B. ovis,* and *T. canis* (shown below).
- The position of *trnS2* within the interior of the *nad2* gene is unusual and requires further investigation. Another DNA sequence that is a likely *tRNS2* gene is found on the *G. aurei* nad4 minichromosome in a position also seen in other louse species. *tRNS2* has not been associated with *nad2* in other lice.



Literature

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Next Steps

- Two protein coding genes, *nad3* and *nad5* have been identified and are in the process of being characterized and mapped.
- There are four tRNAs (*trnD*, *trnG*, *trnM*, and *trnT*) expected to be found upon the mapping of the remaining minicircles.
- Discovery of the remaining gene, nad6, has been problematic in this and other studies of many insects.
- Additional PCR, cloning reactions, and Sanger sequencing will be performed in an effort to identify *nad6* and map the mitochondrial genome of *G. aurei* to completion.

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