1. I chose the genomes of Mitochondrion Thylamys elegans and Mitochondrion Eudromia elegans for my work.

A screenshot of a computer program

Description automatically generated

1. Although they are both elegans, but they differ in their evolution; Eudromia is a bird class and Thylamys is a mammal, but I want to test if they have a common lineage and conserved genes during the evolutionary process.
2. Yes, both genomes are well assembled.
3. 1 contigs; Mitochondrion Thylamys elegans (NC\_005825.gbk) and Mitochondrion Eudromia elegans (NC\_002772.gbk).
4. Both of the species are diploid.
5. No such information found.
6. They share macrosynteny, as we can see in the regions in the above figure. Both organisms are diploid in nature and show no clear signs of polyploidy.

A screen shot of a graph

Description automatically generated

The diagonal lines with gaps in between show that there are some syntenic genes in between that are conserved in both species. The gaps in between the diagonal line suggest the missing or non-syntenic genes in both organisms.

Yes, the dotplot matches my expectation because they are from different classes: aves and mammals, and are supposed to have a different genetic makeup, although they would share some genetic composition and evolutionary history.

They have the following metrics:

|  |
| --- |
|  |
| HSP: | 1  (NC\_005825.gbk-NC\_002772.gbk) |
| Location: | 18-13,556 (++) |
| Match: | 9107 nt |
| Length: | 13,539 nt |
| Identity: | 69.51% |
| E\_val: | N/A |
| Score: | 452468 |

|  |
| --- |
|  |
| HSP: | 2  (NC\_005825.gbk-NC\_002772.gbk) |
| Location: | 14,227-15,450 (++) |
| Match: | 862 nt |
| Length: | 1,224 nt |
| Identity: | 71.20% |
| E\_val: | N/A |
| Score: | 52637 |

This shows they have a common identity of 69-71 % in their genetic makeup.

1. No clear inversions noted.
2. Yes, they are well-assembled and share a similar genetic makeup to some extent with a common identity of around 69-71%. Have good signs of evolutionary lineage.
3. In the species Mitochondrion Thylamys elegans, I have chosen the chromosomal regions of 1-15452, whereas in the species Mitochondrion Eudromia elegans, it is 1-18305.
4. Yes, there is a strong microsynteny in the organisms. The straight diagonal lines show a clear synteny, although the gaps in between suggest a breakage.

69-71 % of gene models are conserved.

1. Yes, there are noticeable gaps between the two species, as they belong to different classes of animalia. The diagonal line dotplot also shows a lineage; however, the gaps in between the diagonal line show the breakage or gaps.

This could be due to various reasons in the biological and evolutionary processes; it could be gene duplication, mutation, and other processes; hard to pinpoint the exact reason.

1. They have a common identity of 69-71 % in their genetic makeup. So, nearly 70% of sequence homology.