# THE GENOME HISTORY OF MANATEES

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## MOTIVATION

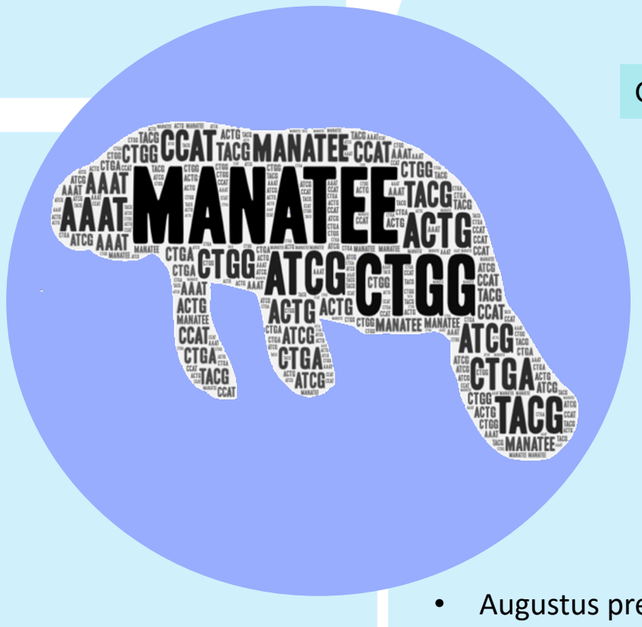
- ✓ **Manatees (Trichechidae: Sirenia) are herbivorous aquatic mammals, and all the three species are vulnerable to extinction according International Union for Conservation of Nature (IUCN)**
- ✓ **This study will help us to understand how evolution shaped their genomes and help the development of conservation strategies to guide better decisions on the management of wild manatees populations**

## METHODS

**1st step: Genome of two species**

*Trichechus inunguis* (freshwater)

*T. manatus* (marine water)




**2nd step: Genome Amount, Assembly, and Quality**

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**3rd step: Annotation, Predicition, and Quality**

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**4th step: Genome Evolution**

OrthoDB

## CONCLUSION and NEXT STEPS

- First time that *T. inunguis* genome was described;
- Resequencing for *T. manatus;*
- Higher proportion of LINE in the manatee's genome;
- Freshwater manatee have more exclusive genes than *T. manatus*;

## REFERENCES

SUPPORT
LABORATORY OF EVOLUTIONARY GENOMICS
UNICAMP
FAPESP

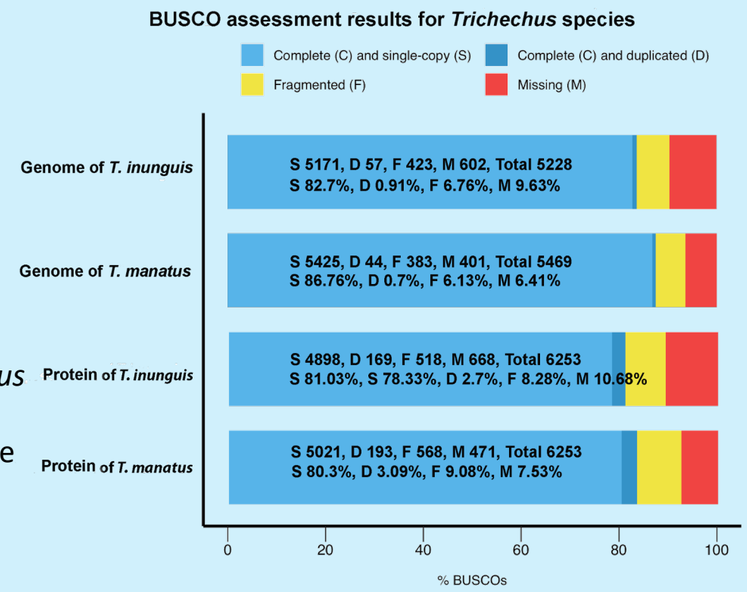
## RESULTS

Genome description

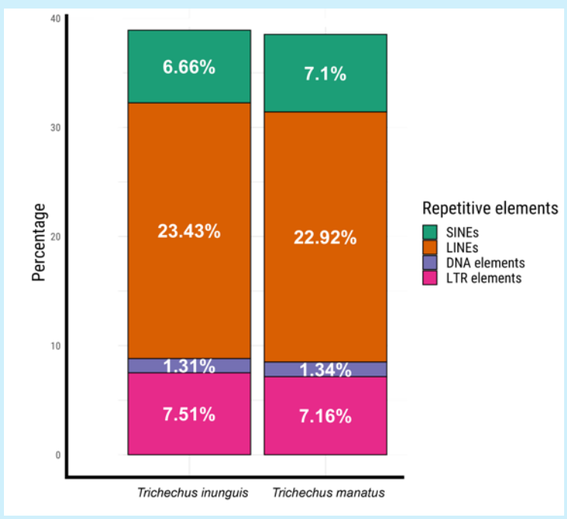
| Parameters | | |
|---|---|---|
| Total Length (bp) | 3,154,207,031 | 3,183,204,259 |
| Coverage | 111.47 X | 37.21 X |
| GC% | 40.67 | 40.65 |
| AT% | 59.33 | 59.70 |
| Q20 | 97.38 | 97.29 |
| Q30 | 93.91 | 93.68 |

- Augustus predicted 48,028 protein-coding sequences for T. *manatus* and 53,239 protein-coding sequences for *T. inunguis*.
- Comparing the two genomes, *T. manatus* had a greater number of single copies than *T. inunguis* probably due to the size of their scaffolds, 2.45X higher than *T. inunguis*.

Quality comparasion: genome amount, annotation, and prediction

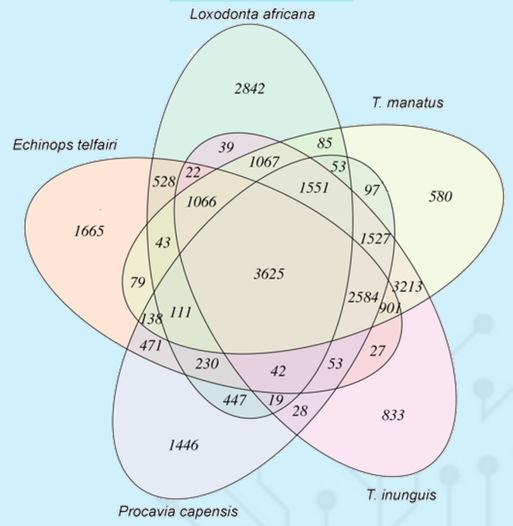



Types of repeat elements




Similar number of types of repeat elements, and a great portion of LINEs in the manatees

Orthology




Venn diagram between Afrotheria species, a mammalian superorder that manatee belongs, which shows the number of single copy gene that these species share.

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