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Presented by:

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I'm the
platypus!



THE INFLUENCE OF DAMS ON PLATYPUS POPULATIONS; INSIGHTS FROM GENOME-WIDE NEUTRAL AND ADAPTIVE LOCI

We recognise and pay respect to the Elders and communities – past, present, and emerging – of the lands that the University of Sydney's campuses stand on. For thousands of years they have shared and exchanged knowledges across innumerable generations for the benefit of all.



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Previous genetic work (Mijangos et al 2022) studied
**HOW FUNCTIONAL LANDSCAPE CONNECTIVITY IS
FOR PLATYPUSES?**



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The influence of dams in platypus populations; insights from genome-wide neutral and adaptive loci



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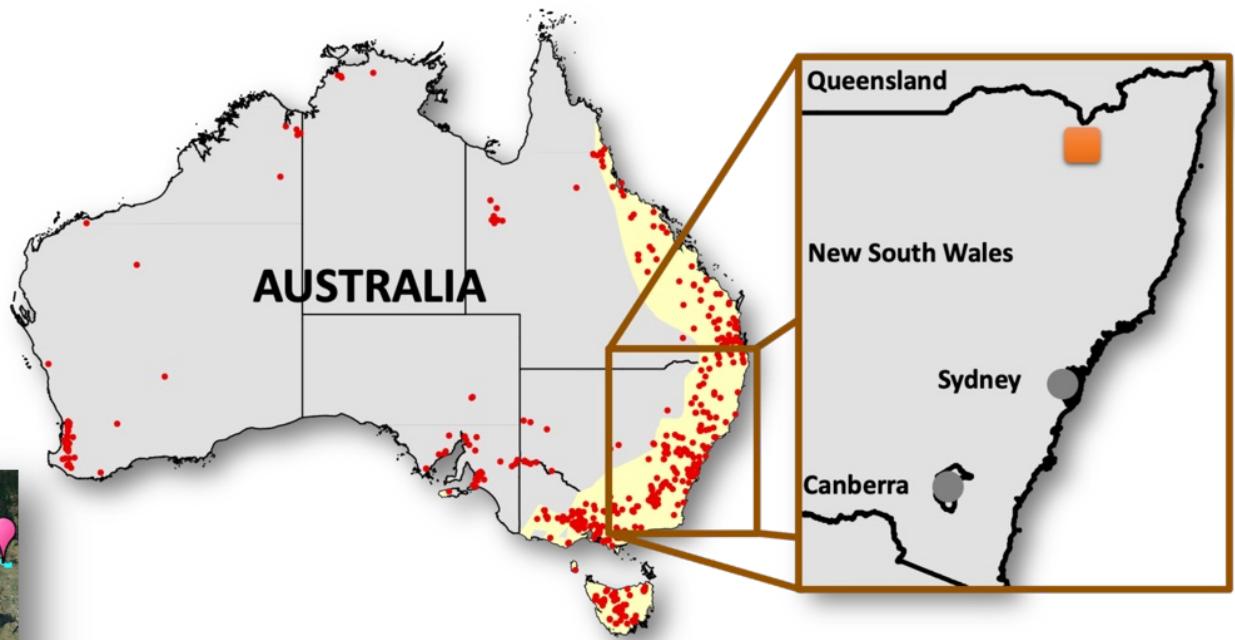
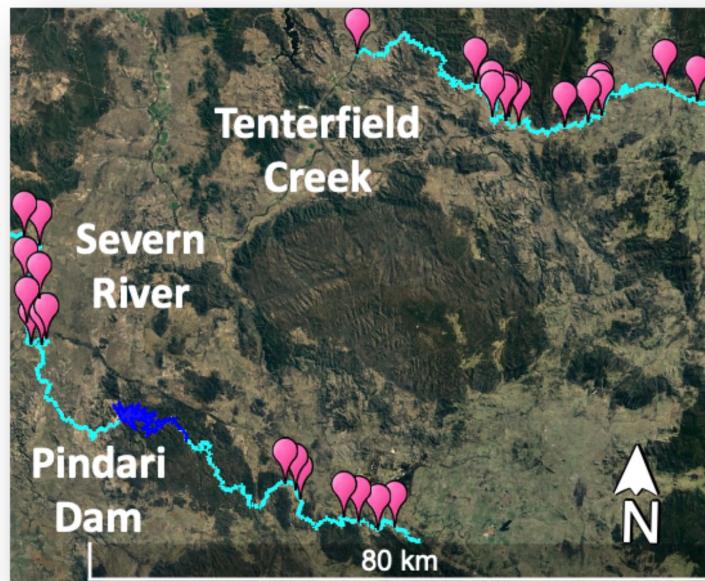
Introduction

Neutral markers have shown that large dams restrict connectivity and disturb platypus habitat
(Mijangos et al 2022).

However, it is unclear as to whether this impact on neutral markers have also extended onto adaptive changes.



Study area



Red points -> dams >10 m high

Yellow shade -> platypus distribution

Pink balloons -> sampling sites

Light blue -> rivers

Dark blue -> reservoirs behind dams

Could river regulation differentially impact on the fate of adaptive and neutral loci of platypuses from below and above Pindari Dam populations on the Severn River?

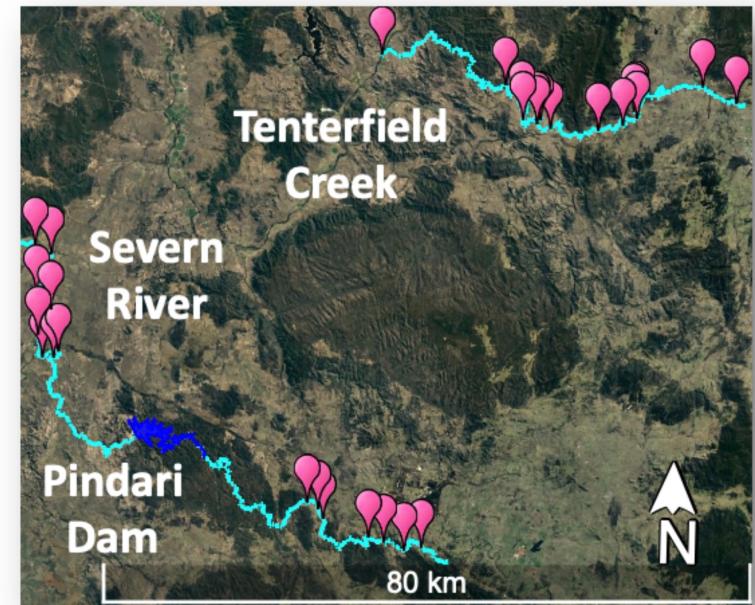
Whole genome sequencing of 26 platypuses

(9.2-million SNPs/genome)

- Unregulated Tenterfield Creek (n=11)
- Severn River Below the dam (n=8)
- Severn River Above the dam (n=7)



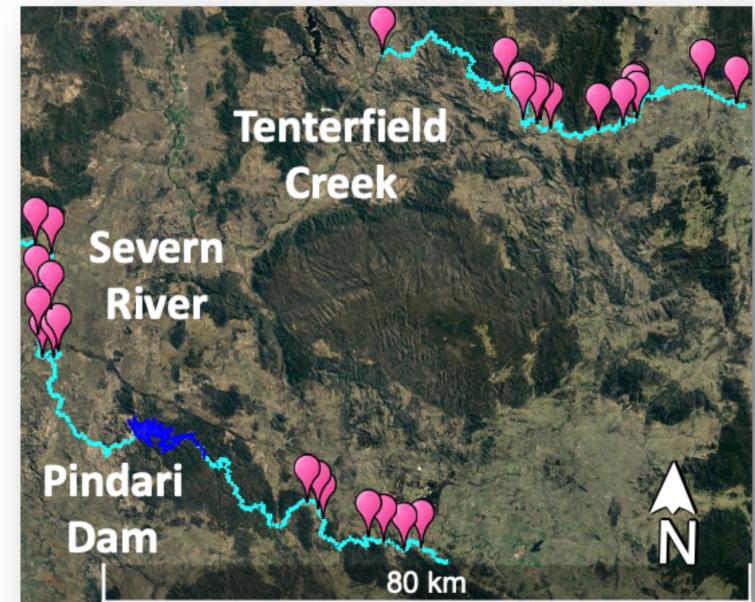
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Dividing the genome dataset for analyses

To determine the scenarios regarding the fate of neutral and potential adaptive loci following dam construction, the dataset was divided in four groups:

1. Coding regions in Severn.
2. Non-coding regions in Severn.
3. Coding regions in Tenterfield.
4. Non-coding regions in Tenterfield.



Three potential scenarios of dam construction

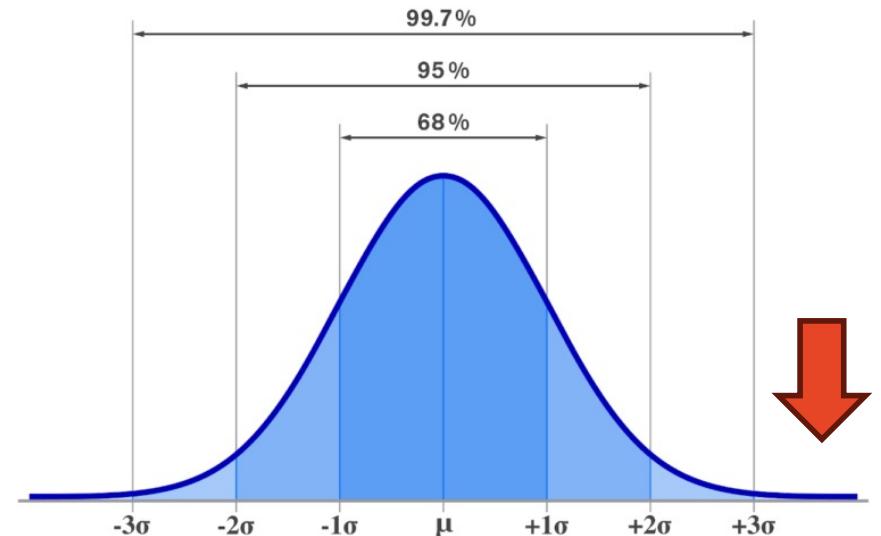
Dataset (adaptive and neutral loci) was used to assess three potential scenarios of dam construction in the Severn River:

- A. Only adaptive regions diverged;
- B. Only neutral regions diverged;
- C. Adaptive regions diverged and influenced adjacent neutral loci.

Identifying loci under selection

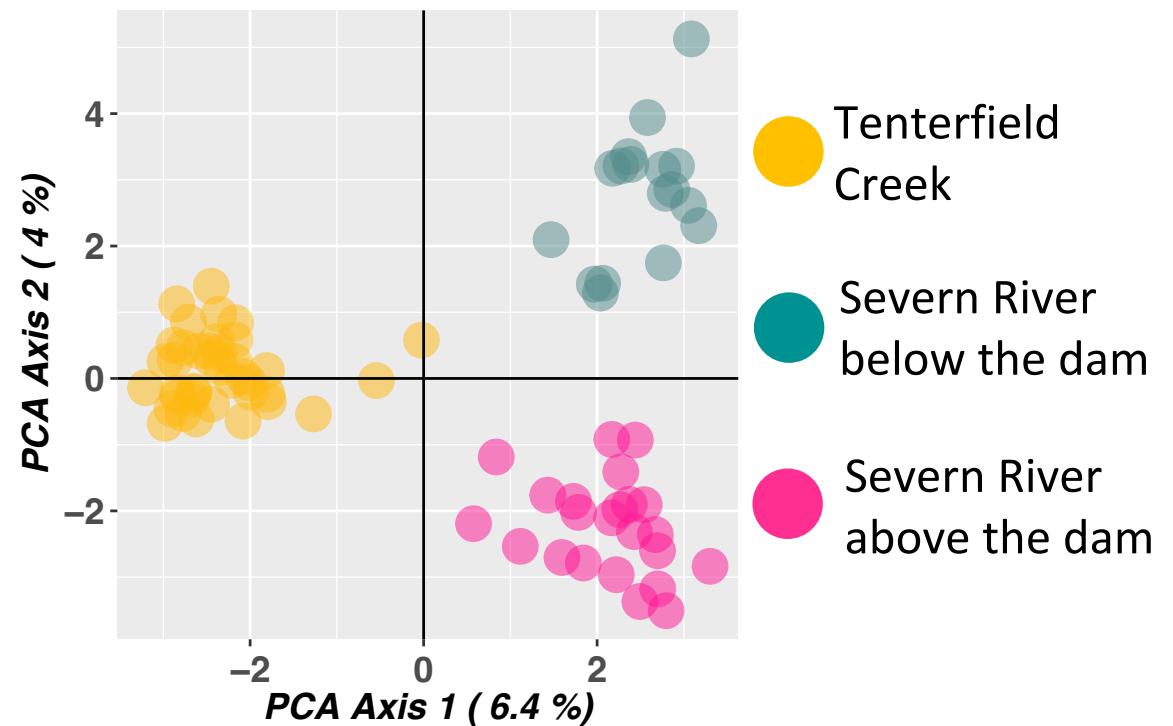
Loci with some *alleles favored* in some places and other alleles favored elsewhere should be more genetically differentiated among populations than otherwise.

Candidate SNPs under selection in the groups below and above the dam were those with unusually large values of F_{ST} (>3 standard deviations ($+3\sigma$) of F_{ST} between below and above Tenterfield Creek).

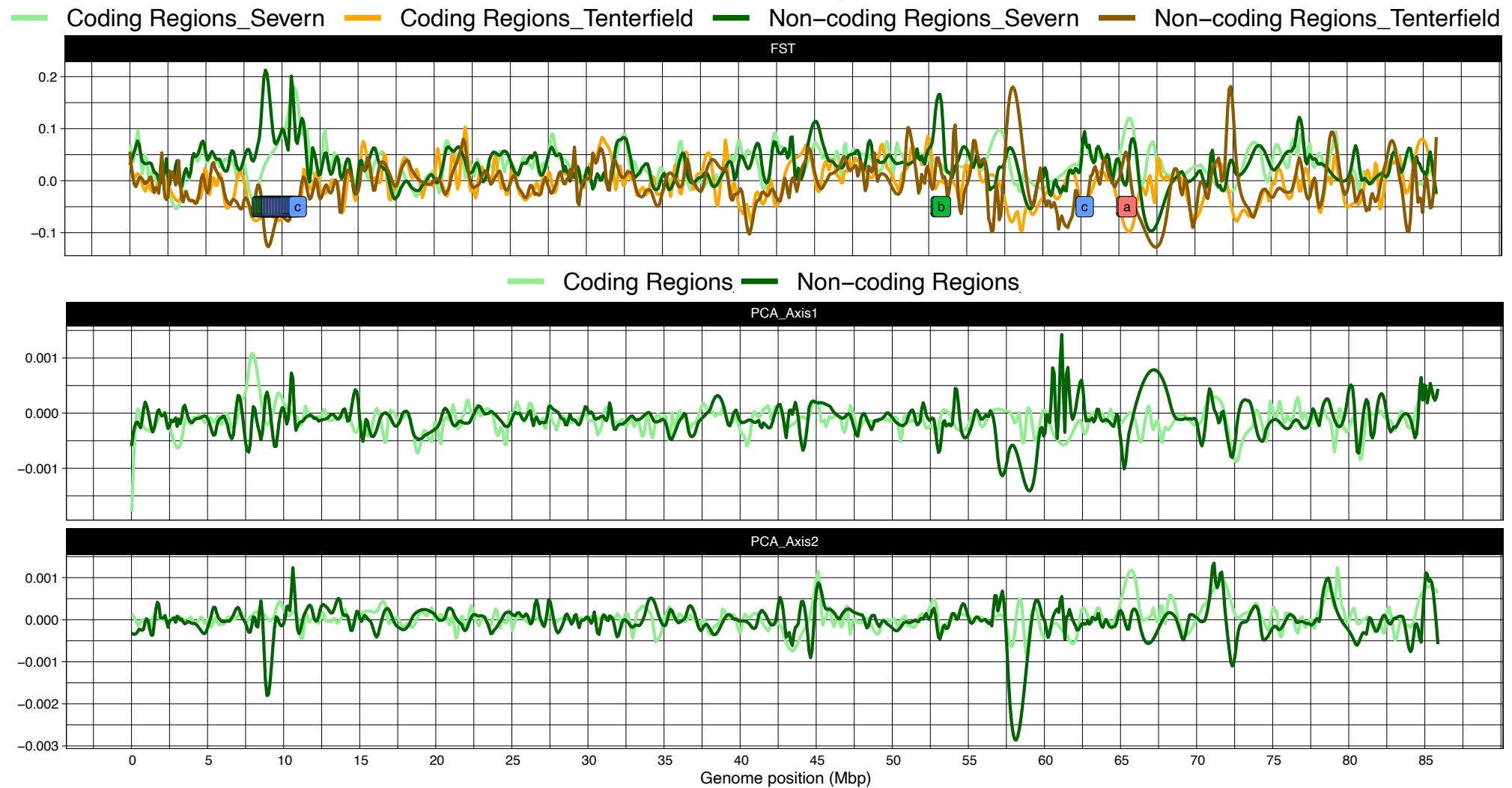


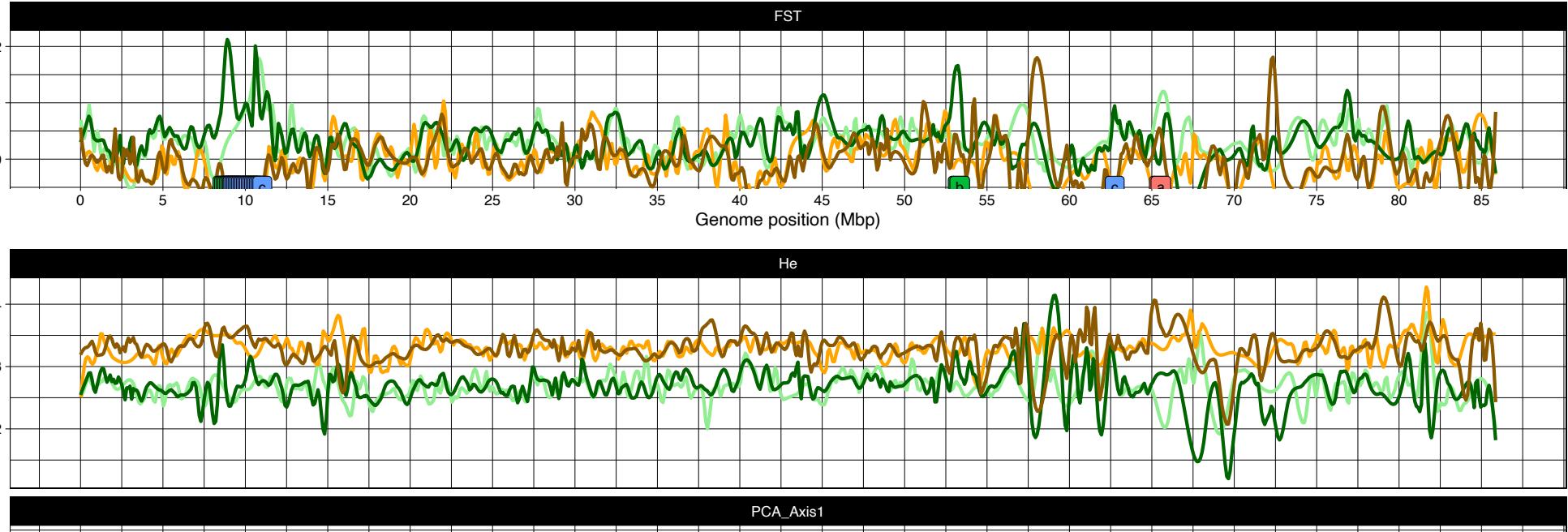
Principal Component Analysis (PCA)

PCA were performed to determine which loci contributed the most to genetic structure between the groups below and above the dam (Severn River), as well as the group in the undammed (Tenterfield Creek).

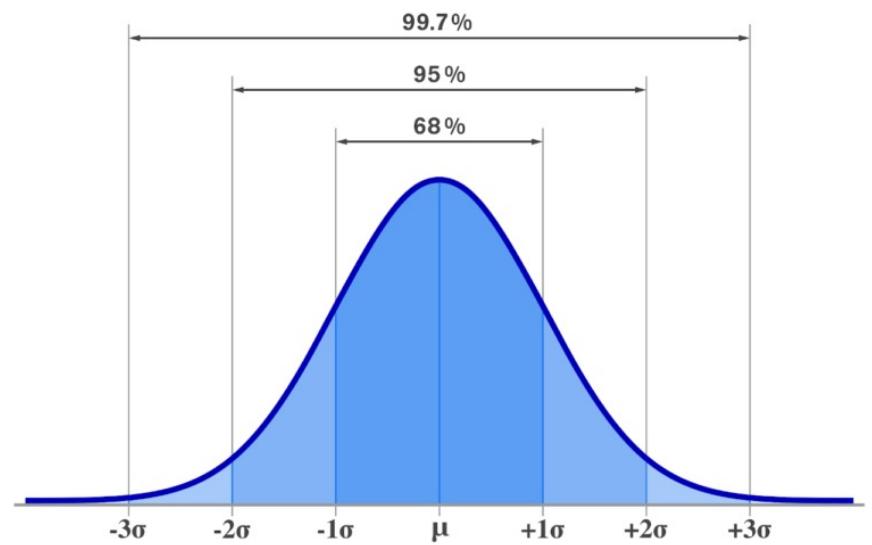


Chromosome 2a 809,430 SNPs





-
- Three standard deviations (σ)



Results

- We found 115, 46, and 185 genomic regions explained by scenarios a), b) and c) respectively.
- We found probable sites under selection selection in genes with metabolic and development functions including KCNIP4, ADAM10 and OXR1.



Discussion

- Impact on adaptive loci could be explained by differential environmental challenges above and below dams, resulting in natural selection.
- This could indicate that adaption to new environments may have occurred in as short as seven generations.
- Our results provide insight into the effect of large dams on adaptive loci in the platypus.

Next steps

- Further analyses using a two-criteria approach (i.e. confirmation with at least two measures of genetic differentiation such as GST, Jost's D, mutual information and Adjusted AFD) are underway to validate whether those loci are putatively under natural selection.

Next steps

- Further explore the genome adaptive (and neutral) loci diversity amongst platypus populations
- Inferring relatedness and pedigree of platypuses using whole genome sequence data
- Developing genome resources for reintroduction and captive breeding

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