



THE UNIVERSITY OF  
SYDNEY



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?

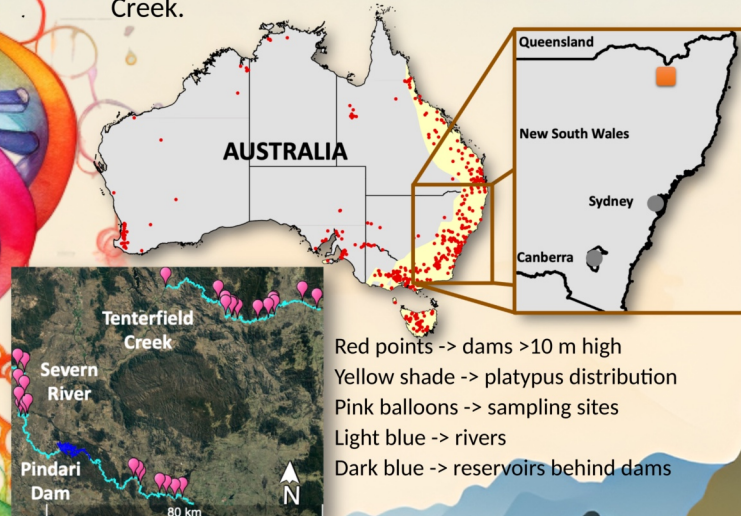
9.2 million SNPs in  
25,862 genomic regions:

- Coding sequences (possibly adaptive)
- Non-coding regions (usually presumed neutral)

# THE INFLUENCE OF DAMS IN PLATYPUS POPULATIONS: INSIGHTS FROM GENOME-WIDE NEUTRAL AND ADAPTIVE LOCI

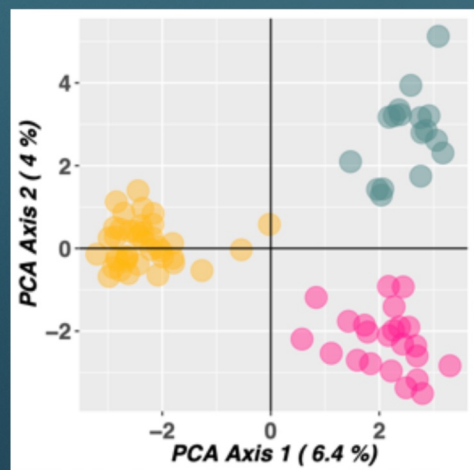
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The platypus (*Ornithorhynchus anatinus*) is one of Australia's most iconic native animals but has declined dramatically due to a variety of factors. Previous research of platypuses on putatively neutral loci (i.e. non-coding genomic regions) found that genetic differentiation ( $F_{ST}$ ) between below and above Pindari Dam populations on the Severn River was 4- to 20-fold higher than along similar stretches of adjacent undammed Tenterfield Creek.



I'm the platypus!

We searched for cases where  $F_{ST}$  differed by more than three standard deviations between any combination of the dammed (Severn) versus undammed (Tenterfield) streams and coding versus non-coding.

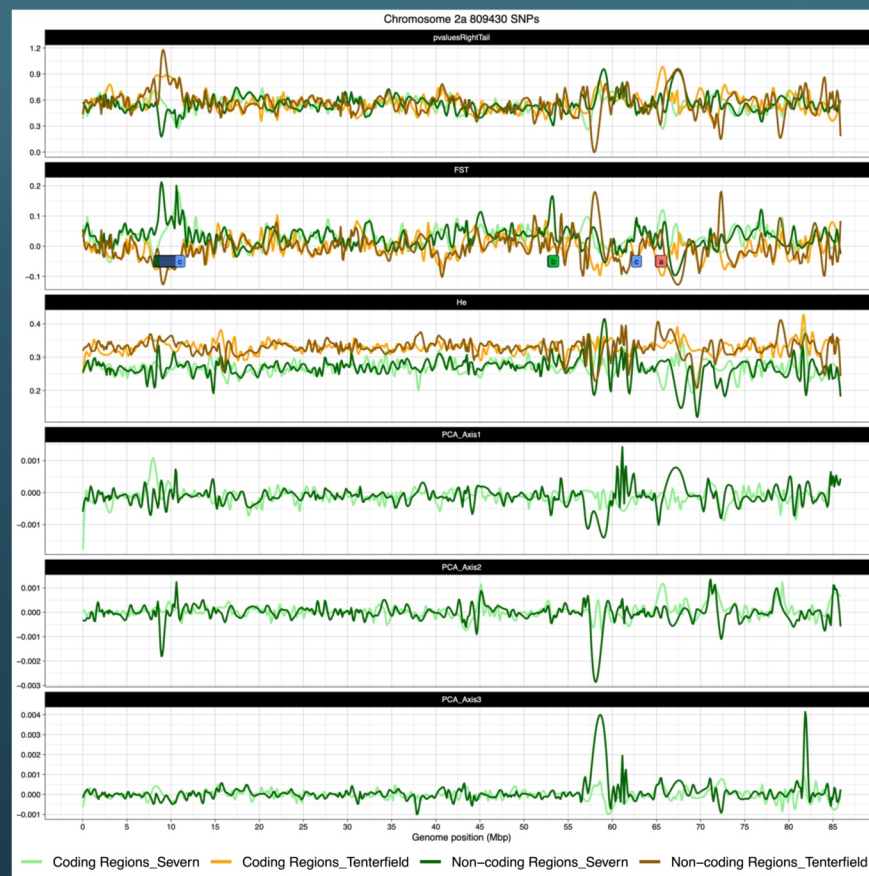


● Severn River above the dam ● Severn River below the dam ● Tenterfield Creek

We found 115, 46, and 185 genomic regions explained by scenarios a), b) and c), respectively. Our preliminary analyses identified potential genomic regions under natural selection in genes with metabolic and development functions, including *KCNIP4*, *ADAM10* and *OXR1*.

Three potential effects of the dam:

- only adaptive regions diverged
- only neutral regions diverged
- adaptive regions diverged and influenced adjacent neutral loci



Next steps

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

**Thank you!**

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