



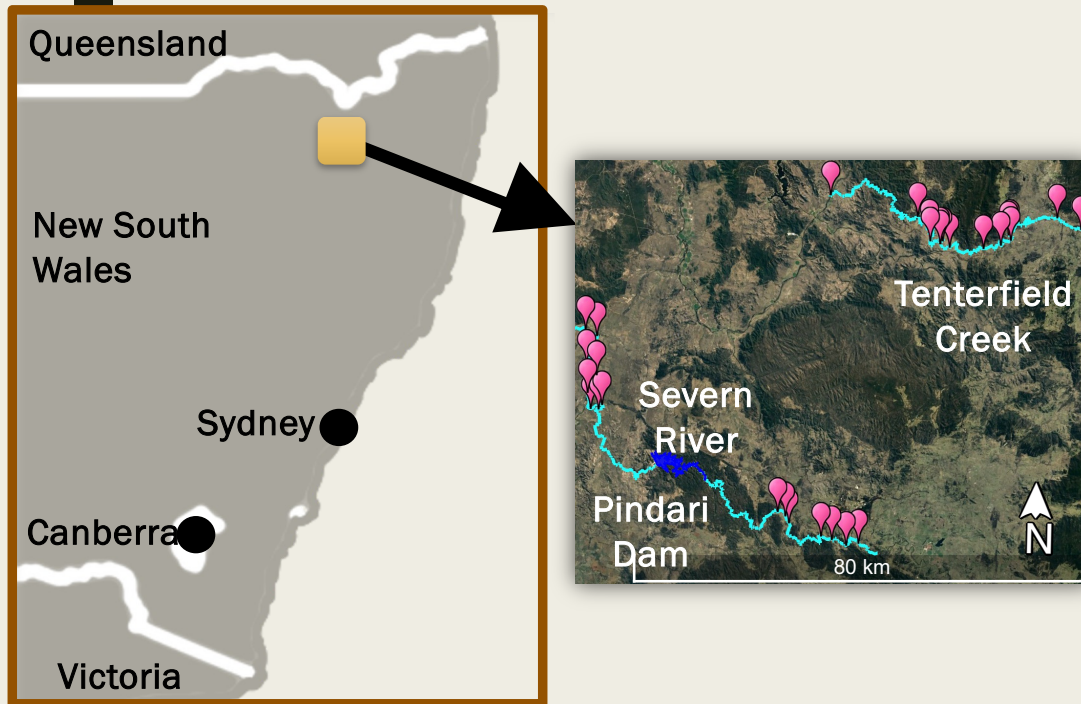
THE INFLUENCE OF DAMS IN PLATYPUS
POPULATIONS; INSIGHTS FROM GENOME-
WIDE NEUTRAL AND ADAPTIVE LOCI

Introduction

- The platypus is one of Australia's most iconic species.
- Populations have declined dramatically.
- Major dams constitute obstacles to gene flow as well as challenging environmental circumstances.
- Recent research on 214 platypuses (Mijangos, Bino, *et al.*, 2022) using reduced-representation sequencing (2.6K SNPs) on putatively neutral loci (i.e. non-coding genomic regions) found that genetic differentiation between populations (F_{ST}) across dams was 4- to 20-fold higher than along similar stretches of adjacent undammed rivers, indicating that major dams act as major barriers to platypus movement.

Mijangos, J. L., Bino, G., *et al.* (2022). Fragmentation by major dams and implications for the future viability of platypus populations. *Communications Biology*, 5(1), 1127.

Study area



Dataset

Whole genome sequencing data consisting of 26 platypus samples that were collected in the unregulated Tenterfield Creek ($n=11$) and below the dam ($n=8$), and above the dam ($n=7$) in the regulated Severn River.

Three potential effects of dam construction were evaluated in this study:

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

Dividing the dataset

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.

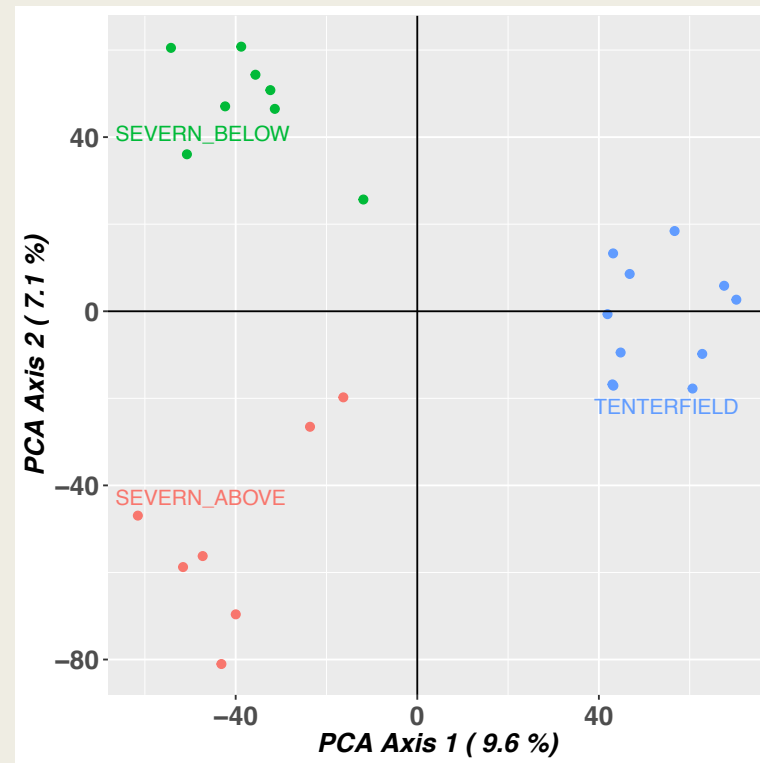
Identifying loci under selection

- The program Outflank (Whitlock & Lotterhos 2015) was used to identify loci with unusually large values of F_{ST} .
- Loci with some alleles favored in some places and other alleles favored elsewhere should be more genetically differentiated among populations than otherwise.

Whitlock, M.C. and Lotterhos K.J. (2015) Reliable detection of loci responsible for local adaptation: inference of a neutral model through trimming the distribution of F_{ST} . *The American Naturalist* 186: 24 - 36.

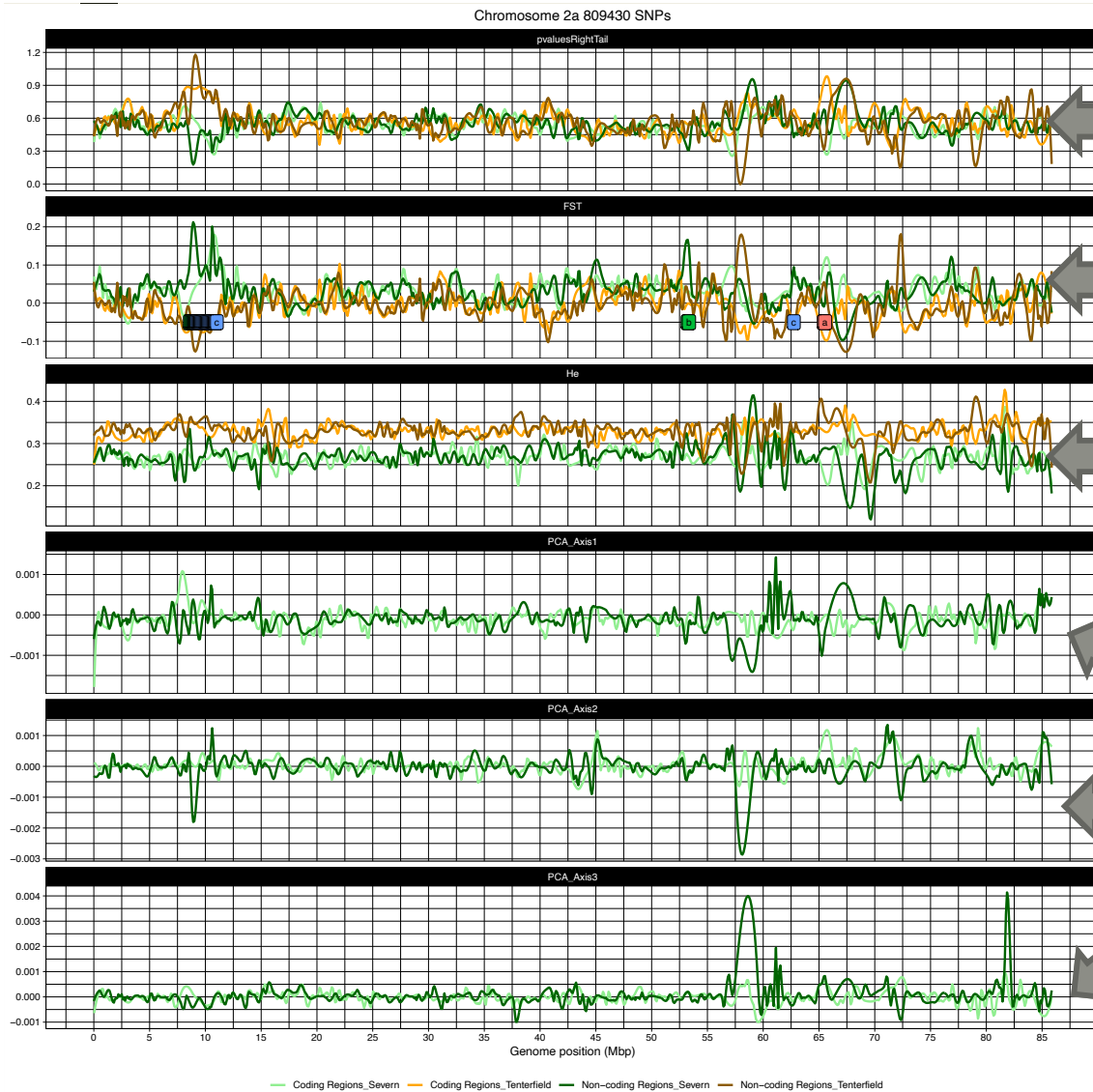
Principal Component Analysis (PCA)

PCA were performed to determine which loci contributed the most to genetic structure between the groups below and above the dam, as well as the group in the undammed river



Extracting PCA loadings

- PCA loadings describe how much each variable contributes to a particular principal component.
- Large loadings (positive or negative) indicate that a particular variable has a strong relationship to a particular principal component.
- The sign of a loading indicates whether a variable and a principal component are positively or negatively correlated.



p-value of the probability that a locus is under directional selection (Outflank)

FST and labels are shown to indicate the scenario (a, b or c) identified in that region.

Heterozygosity

PCA loadings of the loci of axis 1, 2 and 3 respectively of the principal component analyses using the 3 populations (below and above the dam and undammed river [Tenterfield]).

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