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Investigating contaminant-related health effects in killer whales in British Columbia using omics

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Investigating contaminant-related health effects in killer whales in British Columbia using molecular "omics" approach

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Introduction

Killer whales (*Orcinus orca*) are an iconic species in the Salish Sea with three populations inhabiting the area: the Northern Resident (NRKW), Southern Resident (SRKW), and Bigg's (BKW) populations. Complementing contaminant profiles presented elsewhere (refer to snapshot presentation by Marie Noel), we present differences in gene expression measured using RNAseq. Building upon decades of research, these findings will provide a clearer understanding of health effects associated with contaminants in killer whales that can be used to inform risk-based prioritization of conservation efforts.

Methods

Blubber biopsies were collected using pneumatic darts from NRKW (n=12) and BKW (n=9) populations in British Columbia in collaboration with Bay Cetology/DFO. SRKW samples (SRKW, n=10) included in this study came from Ocean Wise's archive (collected by NOAA, 2016). RNA was extracted using QIAzol-chloroform protocols. RNA was sequenced at UBC's Sequencing and Bioinformatics Core using ribodepletion prepared libraries. Samples with abundant read percentage >10% were excluded from analysis. Gene expression was quantified using Salmon, and DESeq2 was used to test for statistically different gene expression ($p<0.05$) between populations. Gene Ontology (GO) term enrichment was analyzed via www.webgestalt.org, mapped to the *Bos taurus* genome.

Results & Conclusions

Differential gene expression was observed when comparing the SRKW to the NRKW (1509 genes) and BKW (2351 genes: Figure 1.) Fewer genes were found to differ between the NRKW and the BKW (34 genes; Figure 1). Principal components analysis shows greater variance within the NRKW and BKW populations, than within the SRKW population (Figure 2). GO term enrichment analysis shows over-represented pathways involved in biological processes, molecular function, and cellular components (Figure 3). These findings illustrate differences in gene expression in the SRKW compared to the NRKW and BKW, suggesting that specialized management strategies may help optimize conservation efforts of killer whale populations.

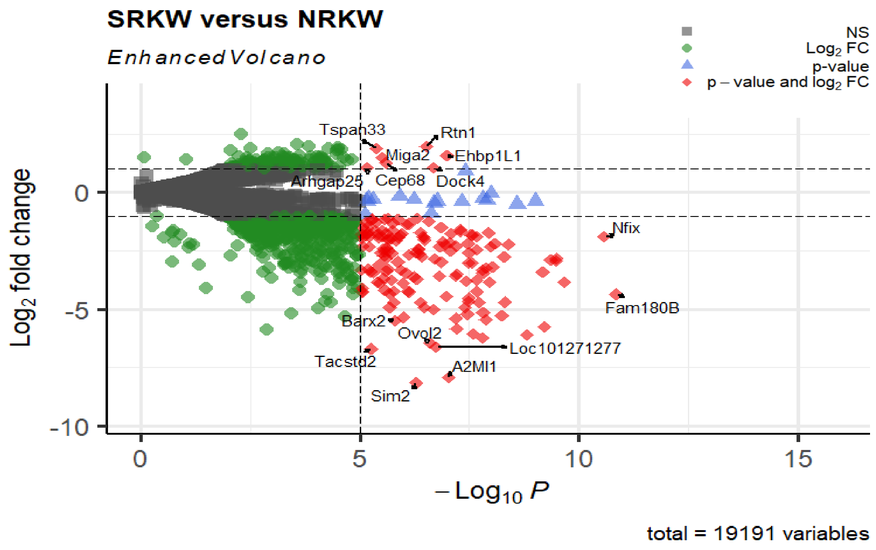

Figure 1. Enhanced volcano plots comparing $\log_2$ shrunken (apeglm) fold change (FC) and p-values between 3 populations of killer whales (pairwise). Log_2FC cutoff was set to 1.0 and p-value cutoff was set to $10e^{-6}$. Grey square markers indicate non-significance, green circle markers indicate values that fall above the FC cutoff, blue triangle markers indicate points that fall above the p-value cutoff, red diamond markers represent points that fall above both the p-value and fold change cutoffs.

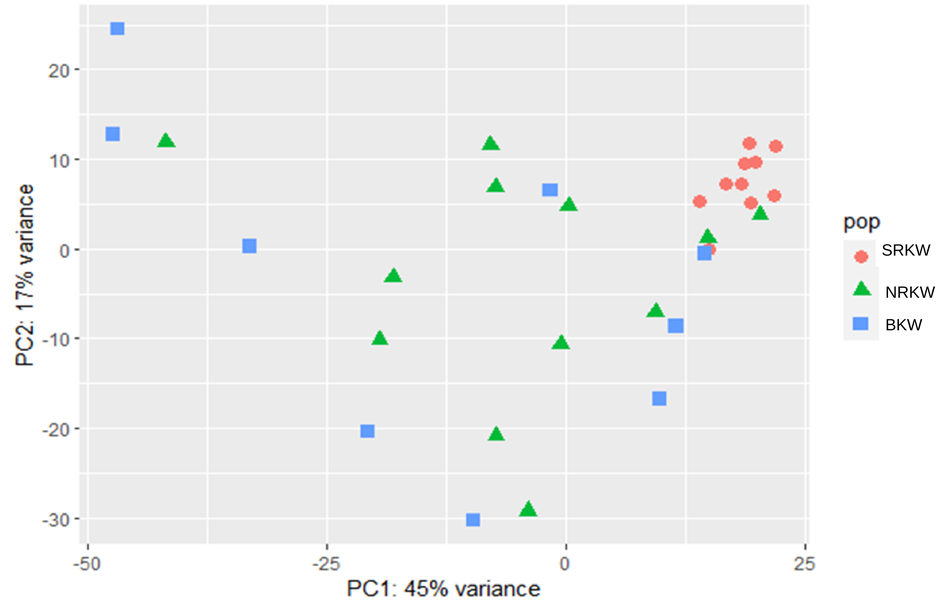

Figure 2. Principal components analysis displaying variance-stabilizing transformed values. Markers represent samples in the SRKW (red circles), NRKW (green triangles) and BKW (blue squares).

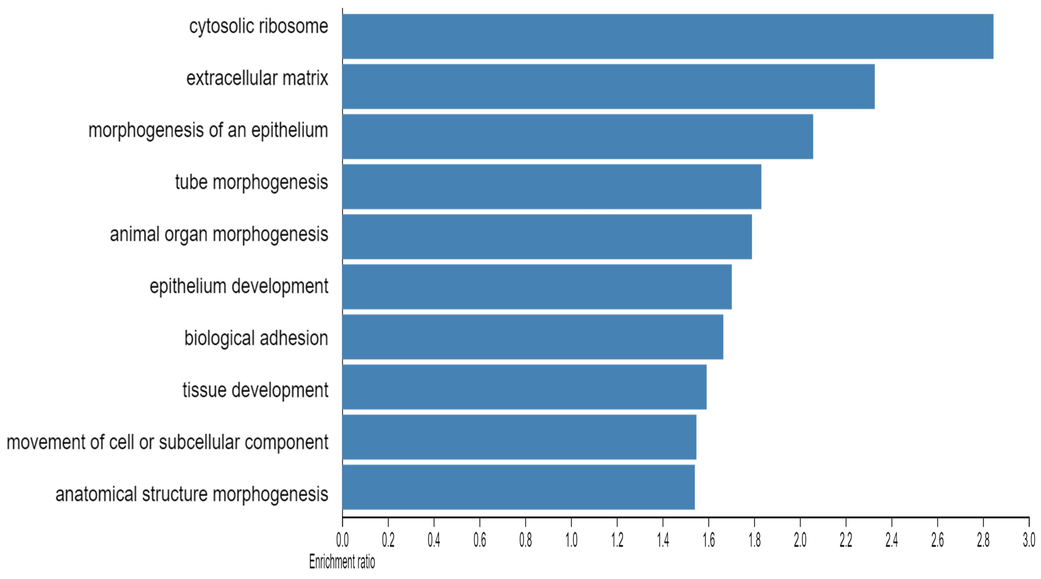

Figure 3. Enriched gene sets analyzed with WebGestalt (FDR p-value <0.05). Analysis included GO terms from the *Bos taurus* genome in the biological processes, molecular function, and cellular components categories.

Next steps

- **Further analyses will incorporate measured contaminant levels**
- **Key genes responsive to contaminant levels will be identified**
- **Metabolic profiles will be analyzed to provide a more complete estimate of organismal health**

Acknowledgments

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