Flathead sole genetic summary (I. Spies)

A collection of flathead sole from the Aleutian Islands (n=24) was analyzed using low coverage whole genome sequencing along with collections of yellowfin sole (*Limanda aspera*) and Bering flounder (*Hippoglossoides robustus*) (Figure 1). Results confirmed that flathead sole is genetically distinct from Bering flounder, which is significant given that they are identical at cytochrome b (Kartavtsev et al. 2008). A principal components analysis (Figure 2) shows clear separation among flathead sole, Bering flounder, and yellowfin sole, and the differences are all relatively similar; no two species appear more similar than others. This is significant because previous analyses based on cytochrome b, morphometric, and protein data have suggested synonymization of *Hippoglossoides robustus* under *H. elassodon*. (Hardy et al. 2011). Further analysis is needed to examine whether there is genetic diversity among flathead sole from the Aleutian Islands vs. eastern Bering Sea. We recommend that a collection of flathead sole (n=25) from the eastern Bering Sea survey be sequenced in 2025.

References

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Kartavtsev YP, Park TJ, Lee JS, Vinnikov KA, Ivankov VN, Sharina SN, Ponomarev AS (2008) Phylogenetic inferences introduced on cytochrome b gene sequence data for six flatfish species (Teleostei, Pleuronectidae) and species synonymy between representatives of genera *Pseuopleuronectes* and *Hippoglossoides* from Far Eastern seas. Russ J Genet 44:451–458

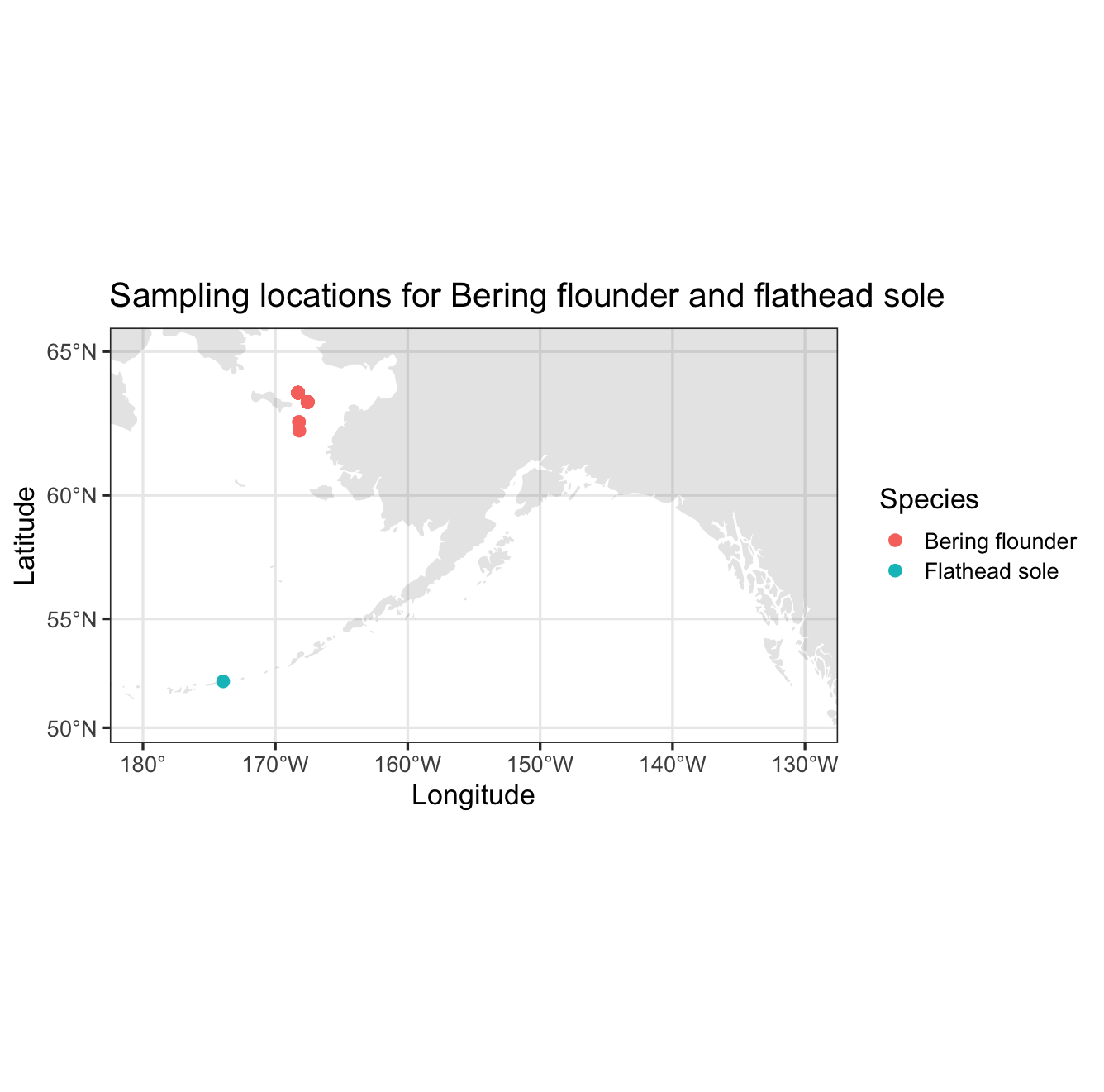


Figure 2. Collection locations of Bering flounder (n=23) and flathead sole (n=24) sequenced using low coverage whole genome sequencing.

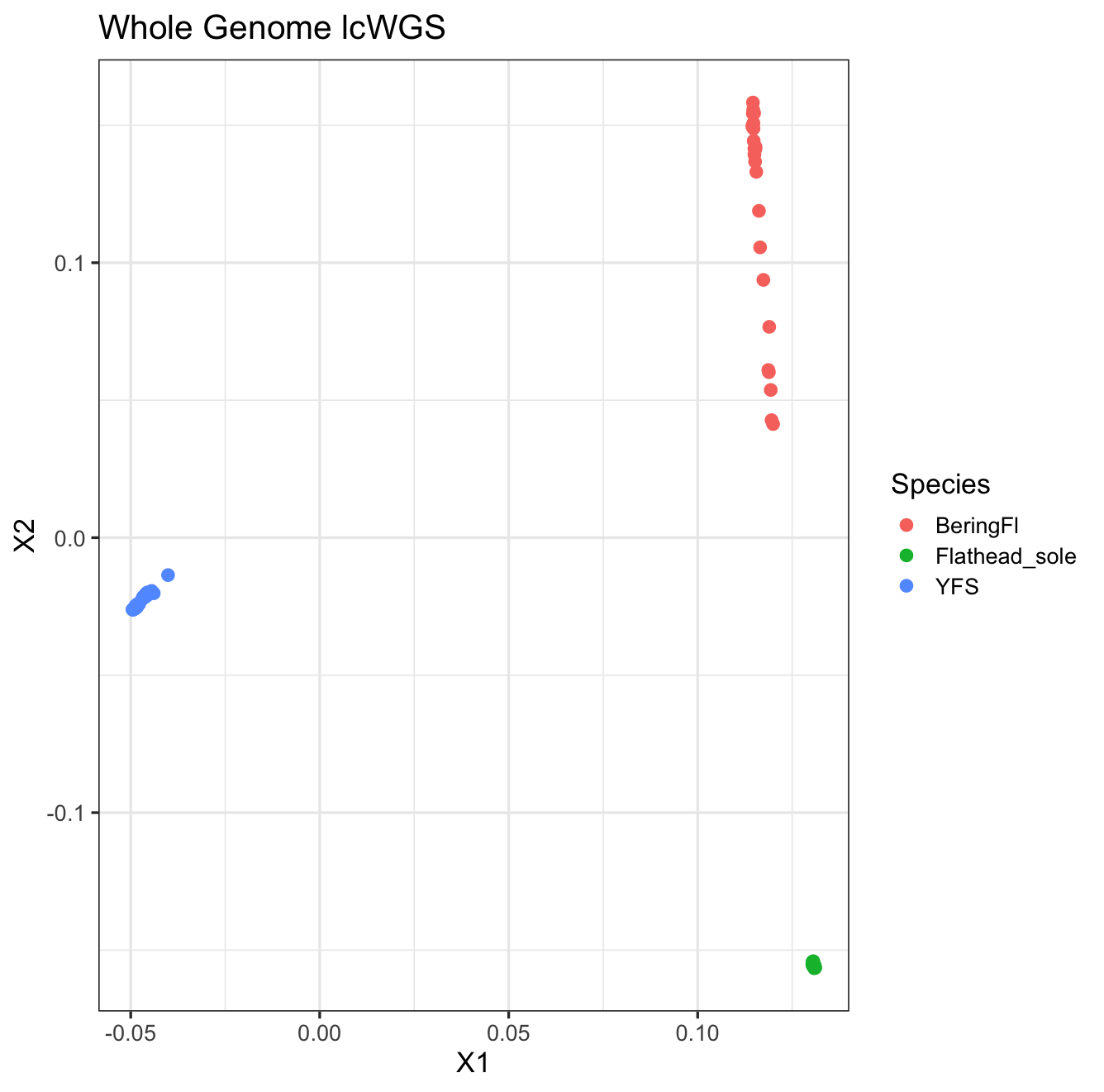


Figure 2. Principal components analysis of yellowfin sole (YFS), Bering flounder, and flathead sole, first and second principal components axes.