

IOTC-2023-WPTT25-23



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BASQUE RESEARCH  
& TECHNOLOGY ALLIANCE

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# Bigeye tuna (*Thunnus obesus*) connectivity in the Indian Ocean based on genome wide genetic markers

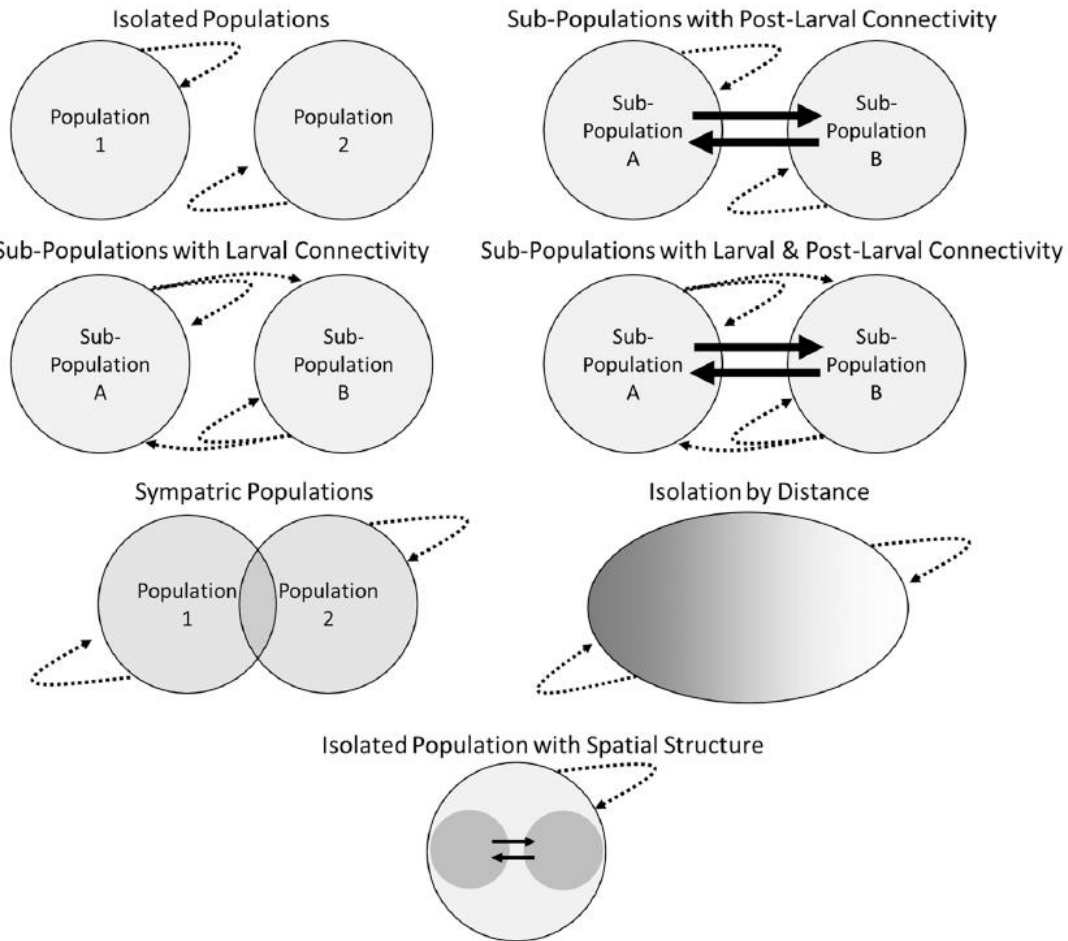
Natalia Díaz-Arce, Iraide Artetxe-Arrate, Campbell R. Davies, Peter Grewe, Igaratza Fraile, Francis Marsac, Gorka Merino, Hilario Murua, Jessica Farley, Naiara Rodriguez-Ezpeleta

Working party on Tropical Tuna 25

November, San Sebastian

[ndiaz@azti.es](mailto:ndiaz@azti.es)

# MANAGEMENT UNITS OR FISH STOCKS

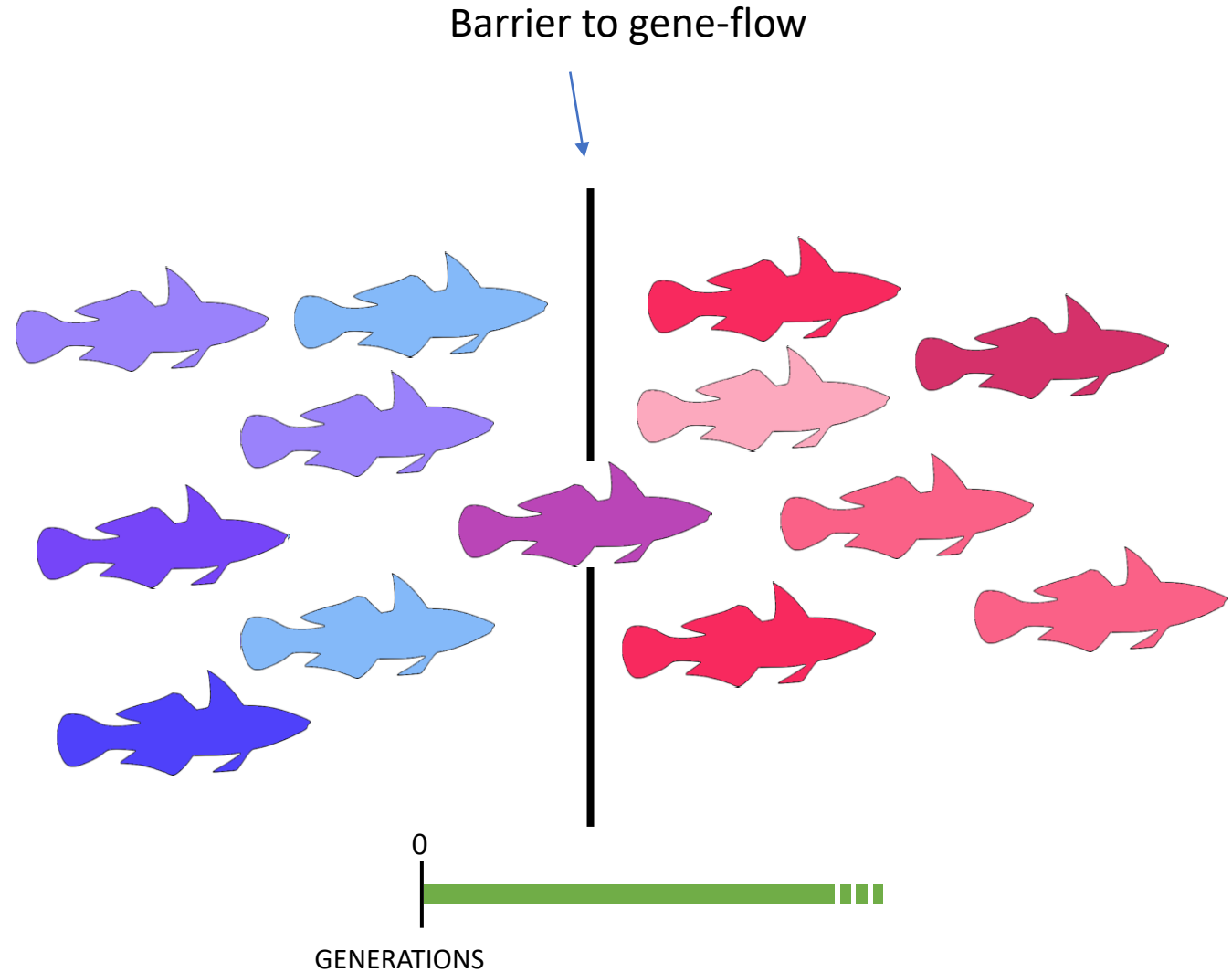


Should correspond with **natural populations**, but population structure and connectivity are often ignored

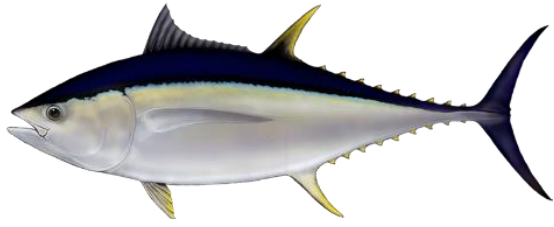
Leading to **overfishing, stock depletion, ...**

## Fish Stock identification and traceability based on genetic markers

- Panmictic populations show homogeneous genetic diversity, while isolated populations become genetically distinguishable
- Genetic markers reflect those differences



# Bigeye (*Thunnus obesus*)



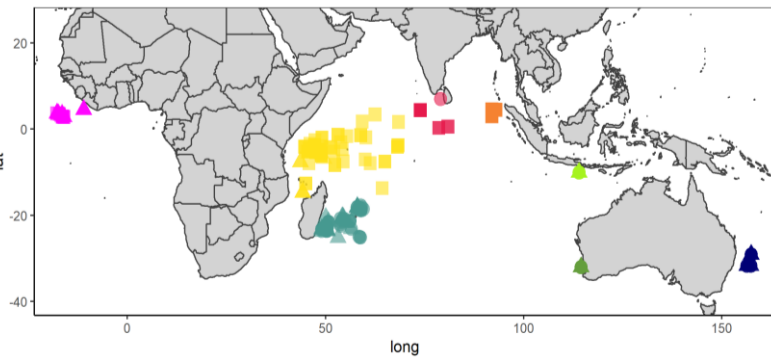
## POPULATION STRUCTURE

Reduced representation sequencing, ddRAD– 15,000 SNPs

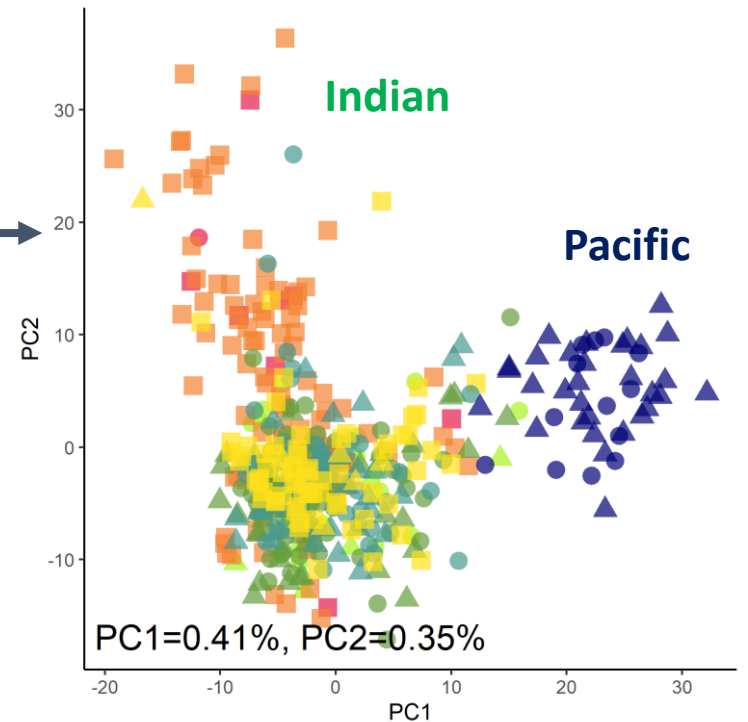
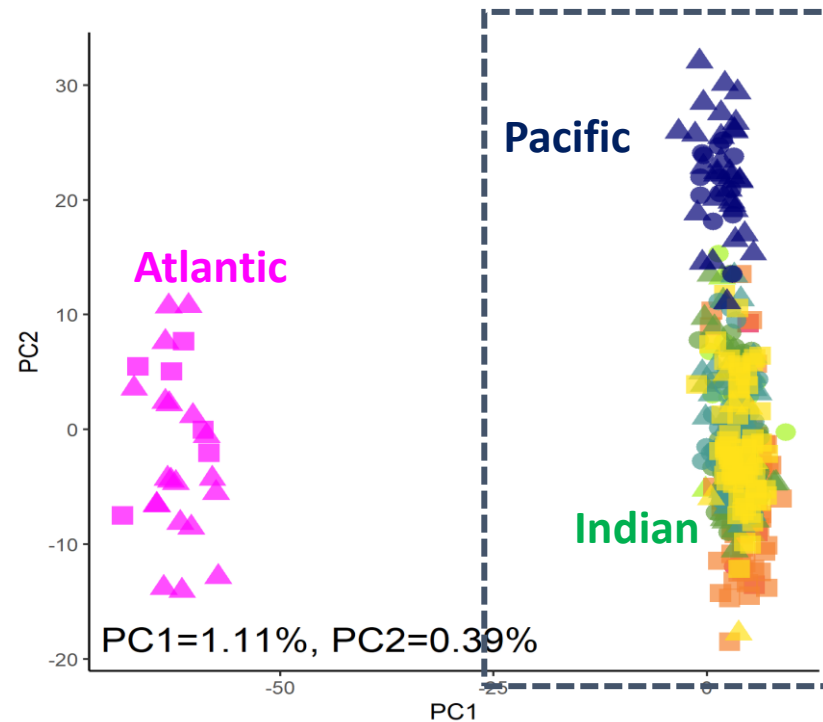
496 SAMPLES

Inter-oceanic differentiation

Intra-oceanic structure

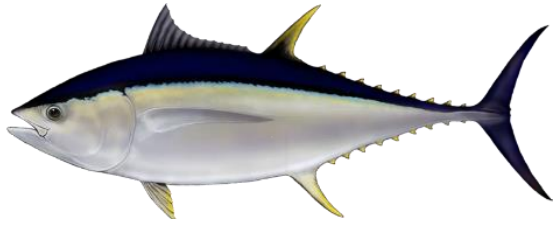


- Adults (>120cm)
- ▲ Juveniles (45-120cm)
- Young of the Year (<45cm)





Bigeye (*Thunnus obesus*)



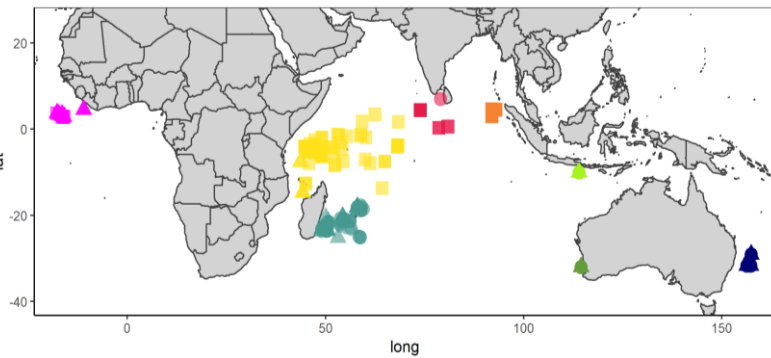
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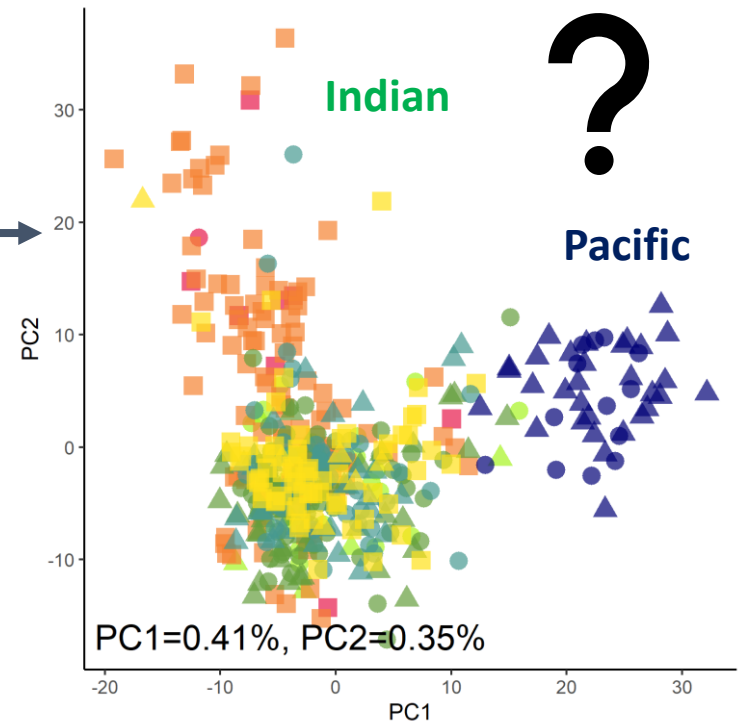
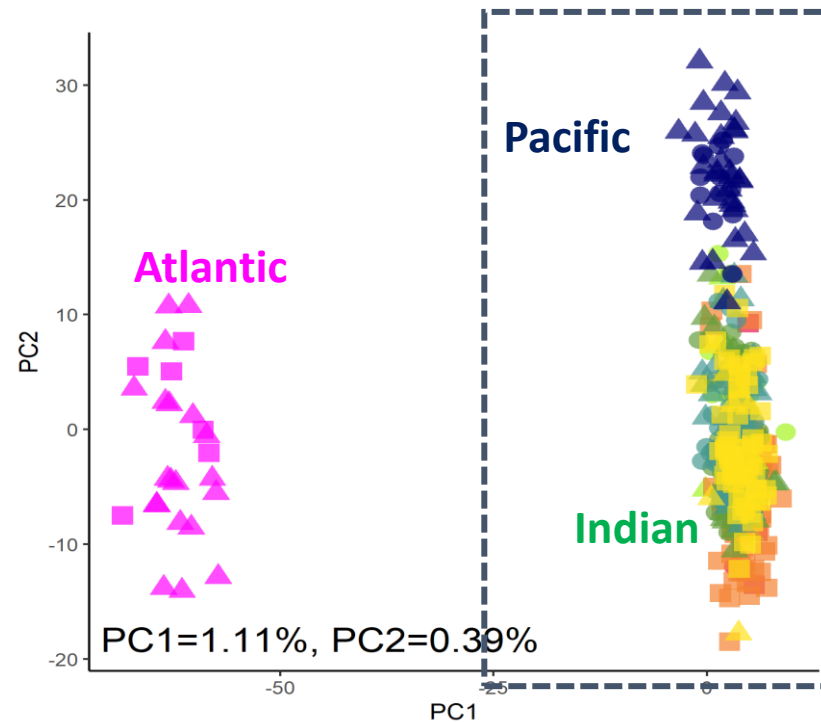
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# NEUTRAL VS ADAPTIVE VARIANTS

Adaptation mechanisms alter genotype and allele frequencies

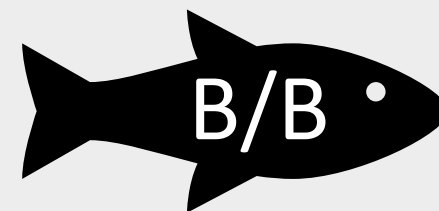
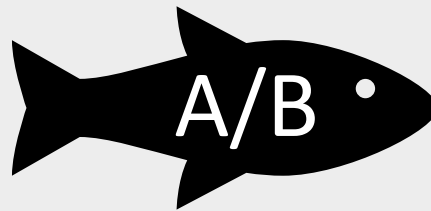


Nuclear



- Neutral genetic variants don't affect individuals' fitness
- Adaptive genetic variants affect individuals' fitness

Possible genotype versions



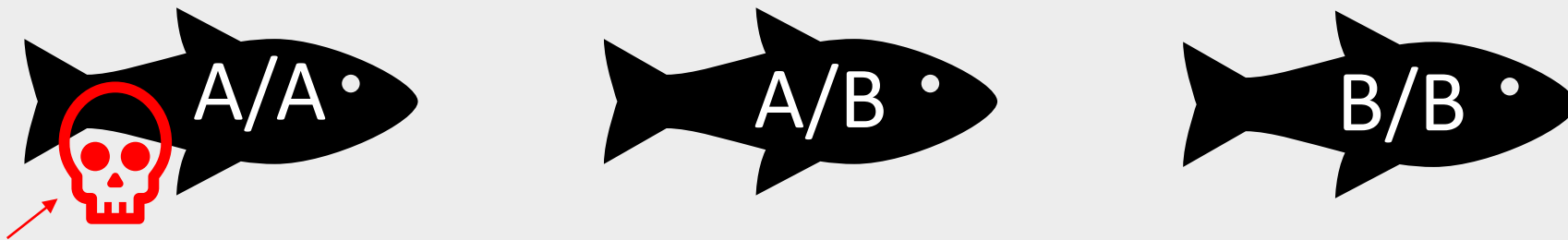
Negative selection

Natural selection alters genotype and allele frequencies in the population

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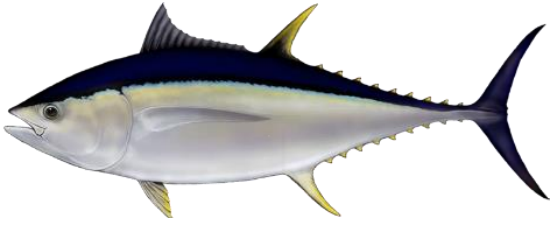
- We can identify potential adaptive markers by analyzing allele and genotype frequencies



Negative selection

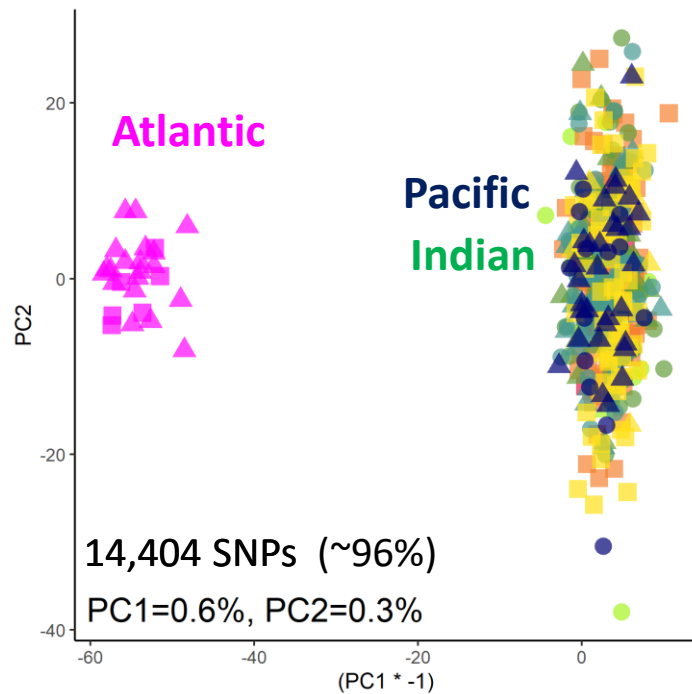
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Bigeye (*Thunnus obesus*)



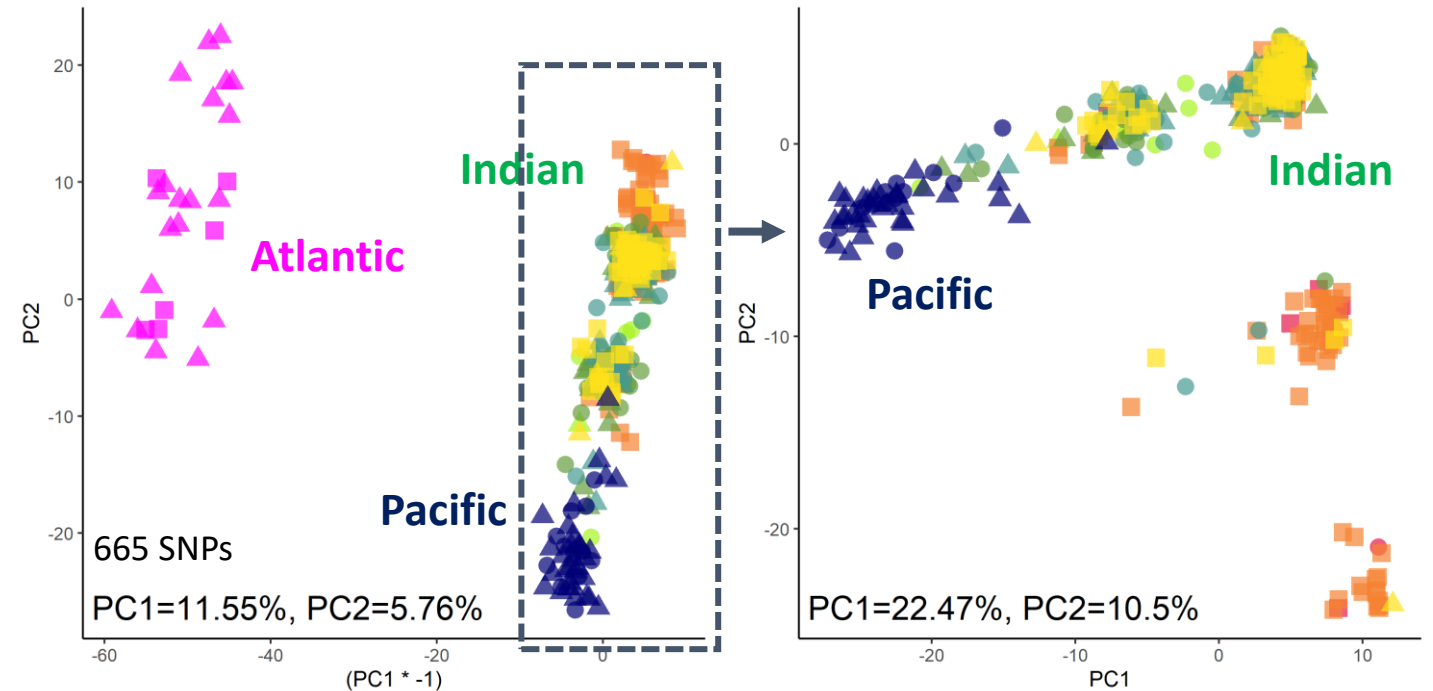
## NEUTRAL markers

support Indo-Pacific pan-population



## OUTLIER markers

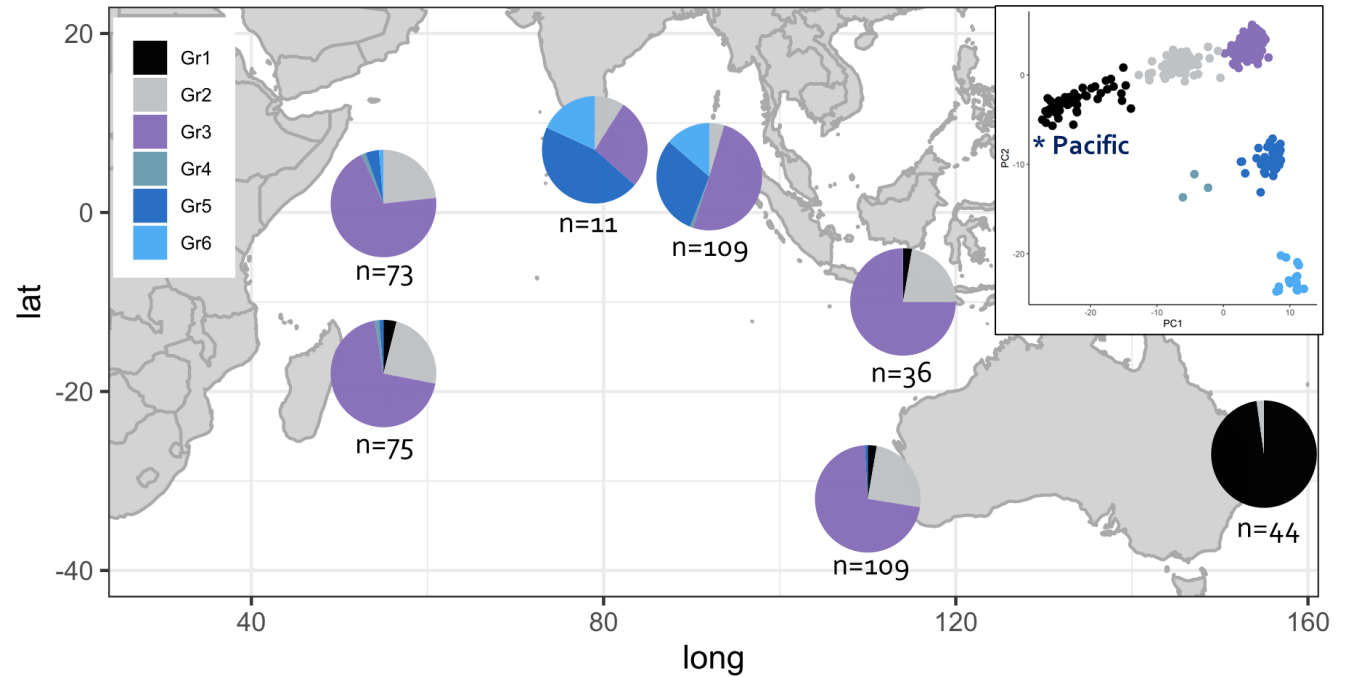
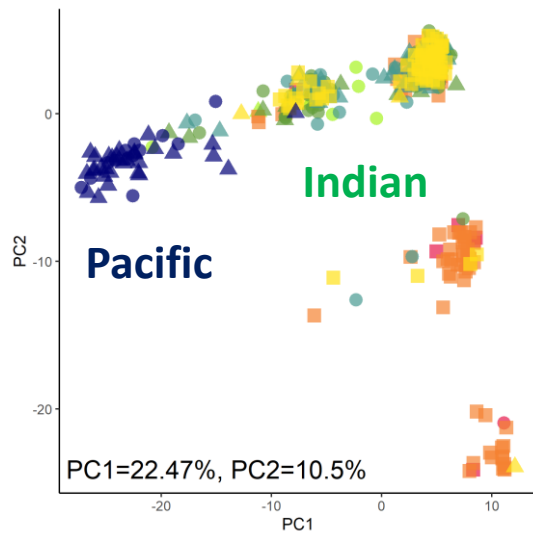
support structure: co-occurring genetic groups





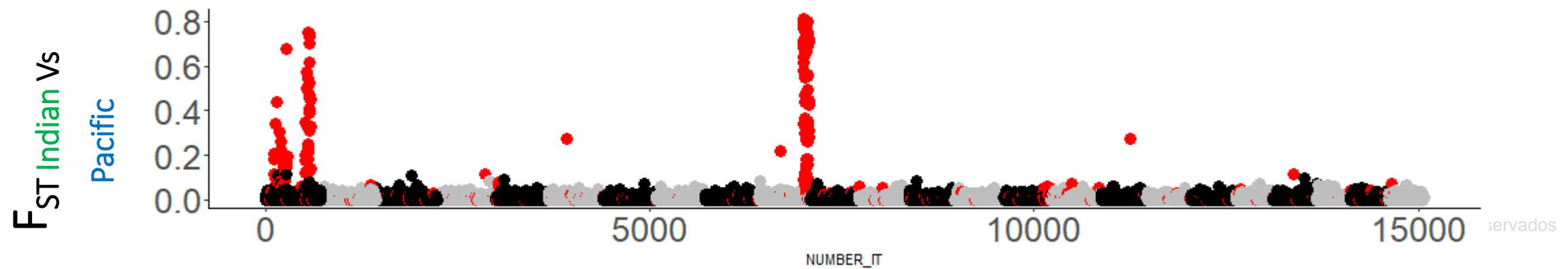
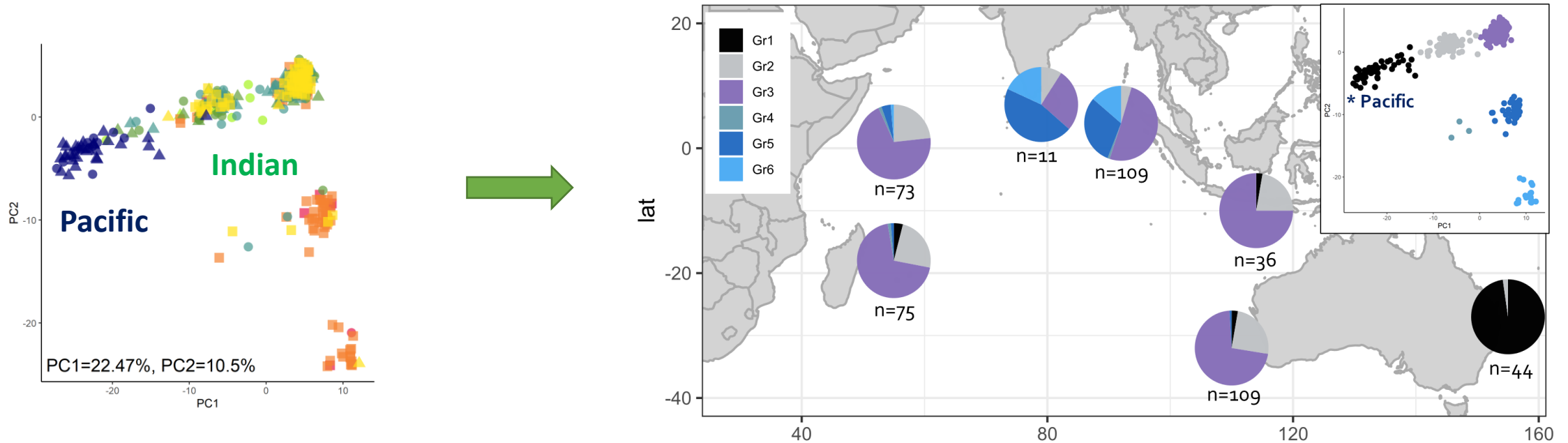
# OUTLIER MARKERS

Co-occurring genetically distinguishable groups



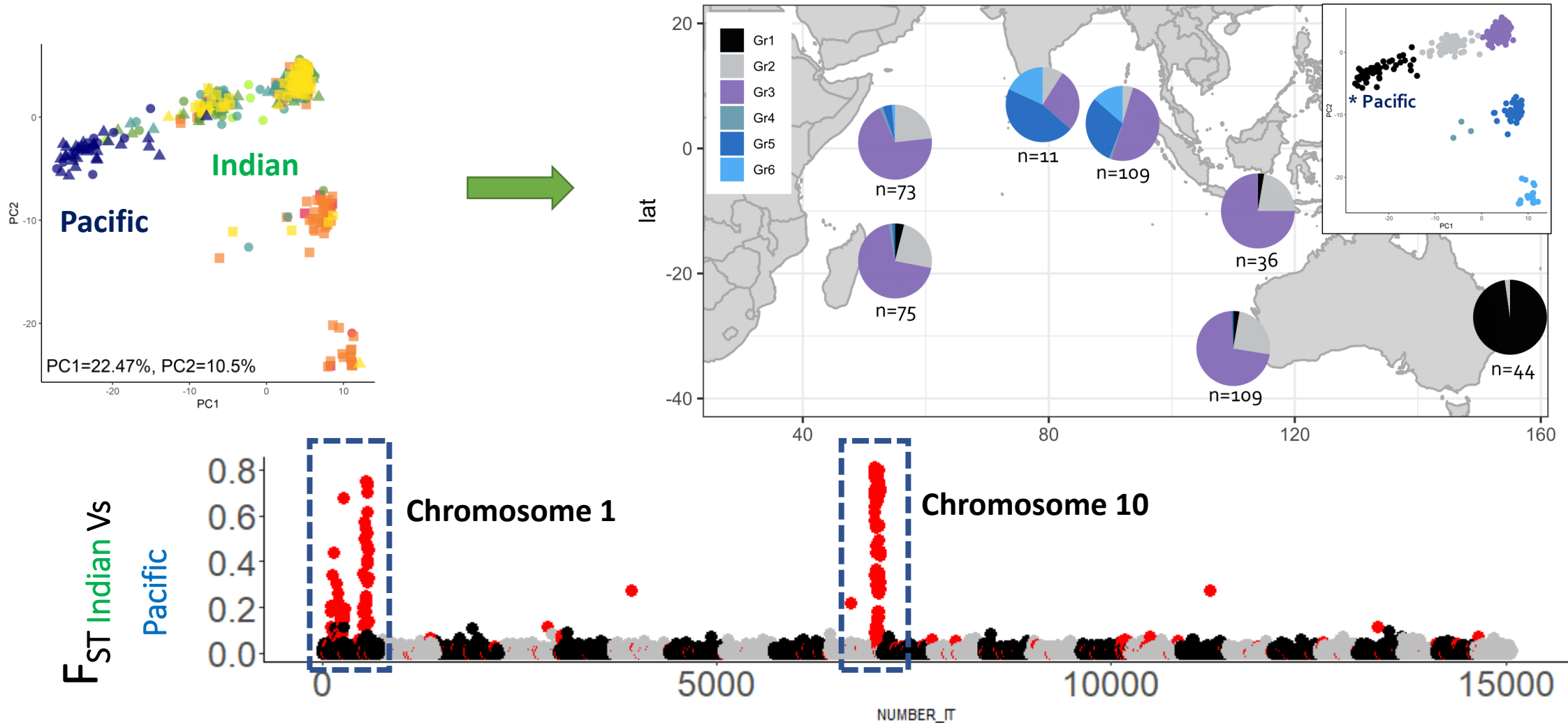
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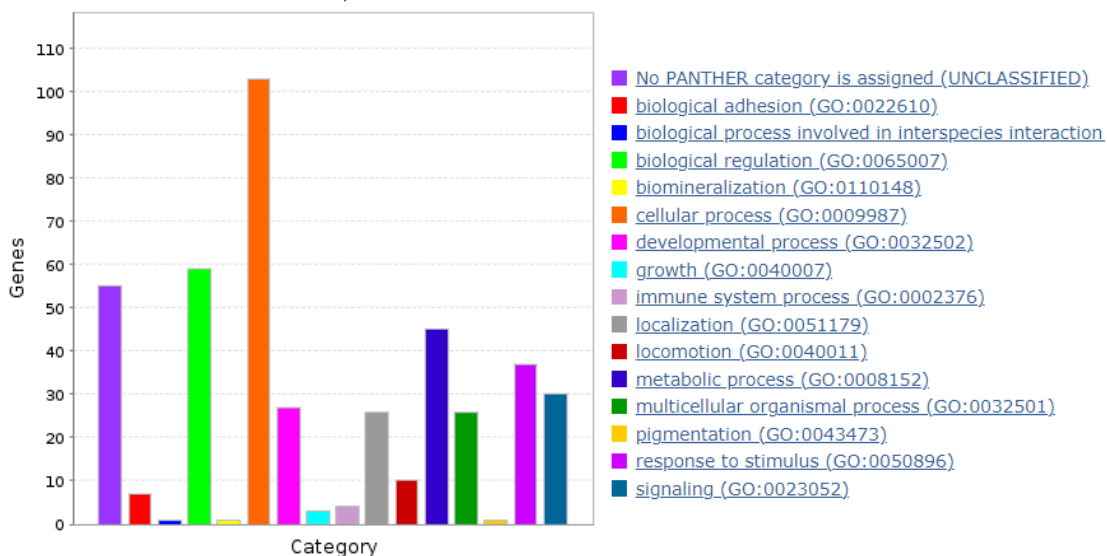


## OUTLIER markers

Are located within genes involved in different biological processes (potentially adaptive)

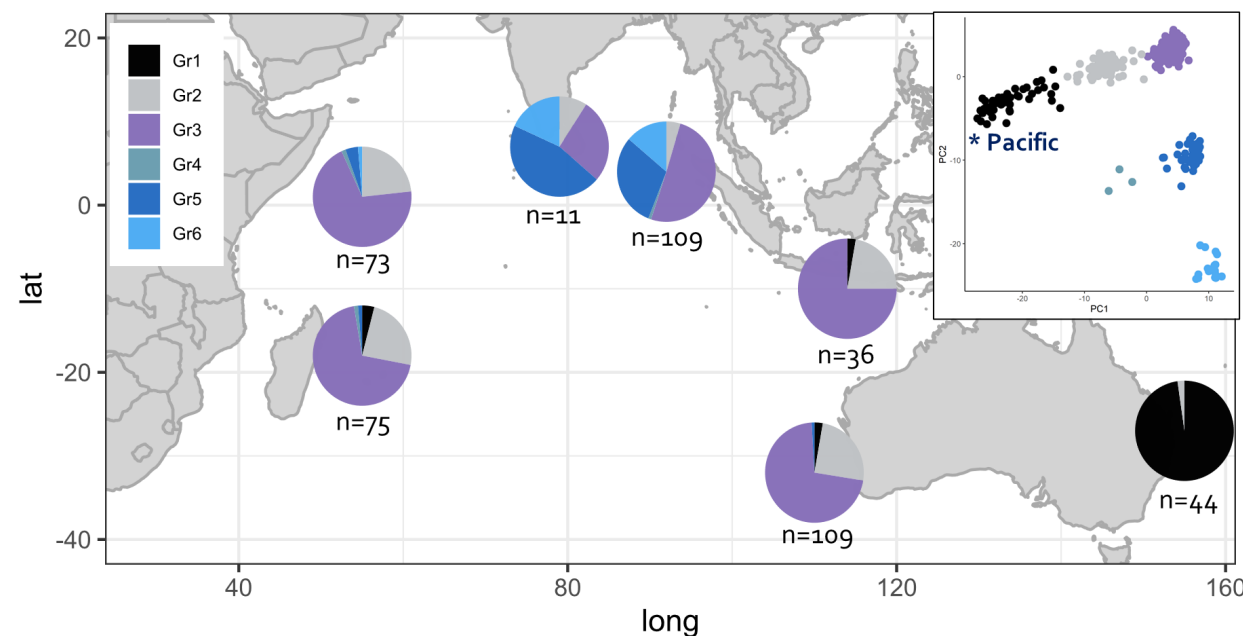
PANTHER GO-Slim Biological Process

Total # Genes: 160 Total # process hits: 435



Can be used to:

- ❖ distinguish between locally adapted populations (even if partially connected)
- ❖ understand geographic connectivity



# CONCLUSIONS

- The **Atlantic** is isolated from **Indian** and **Pacific** oceans
- Between **Indian** and **Pacific** and within **Indian**:
  - There is **connectivity** and **gene flow**, but **selection** is occurring:
    - Individuals with given genomic variants are prevalent in some areas
    - These variants provide advantages or disadvantages to area-specific variables

# Thank you for your attention

Participate to gene-flow



## Funding



## Contact



Natalia Diaz-Arce

✉ [ndiaz@azti.es](mailto:ndiaz@azti.es)

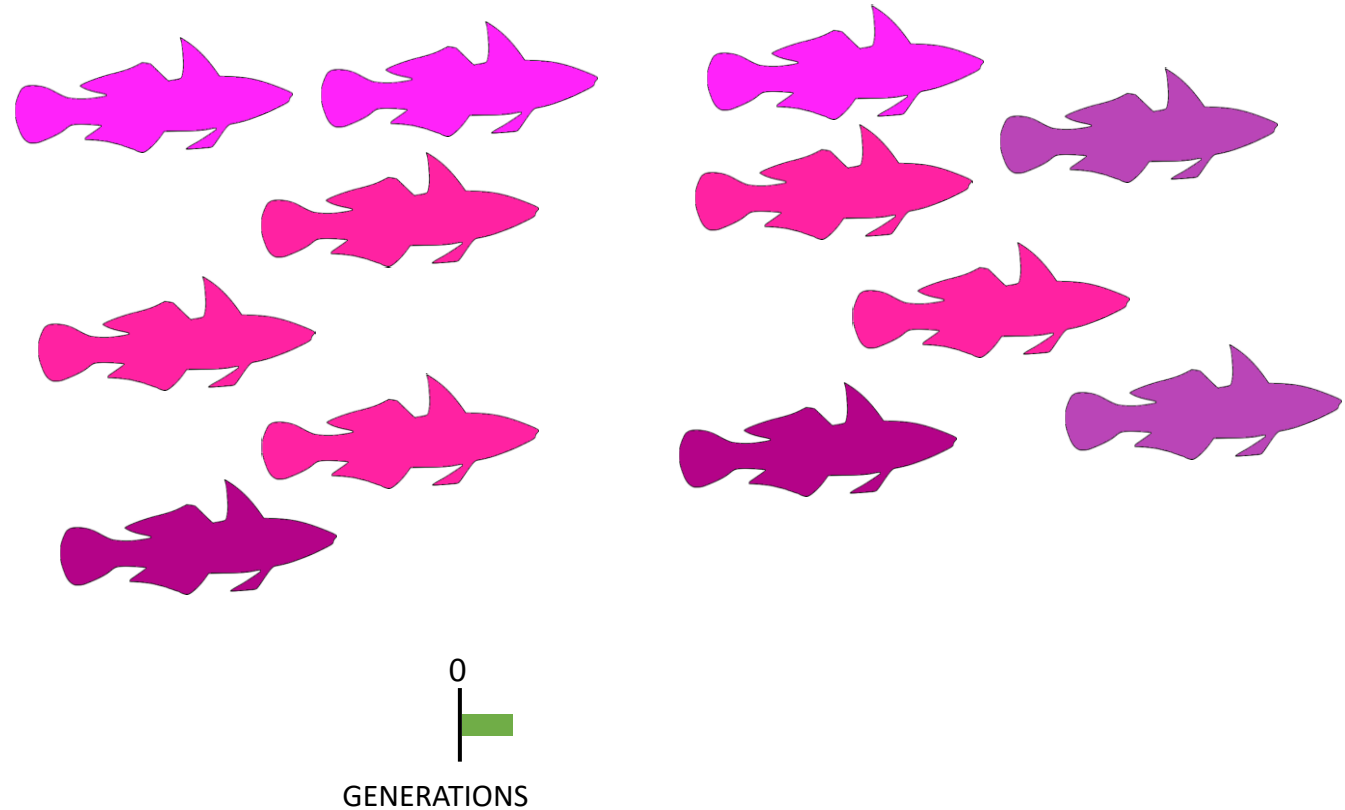






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