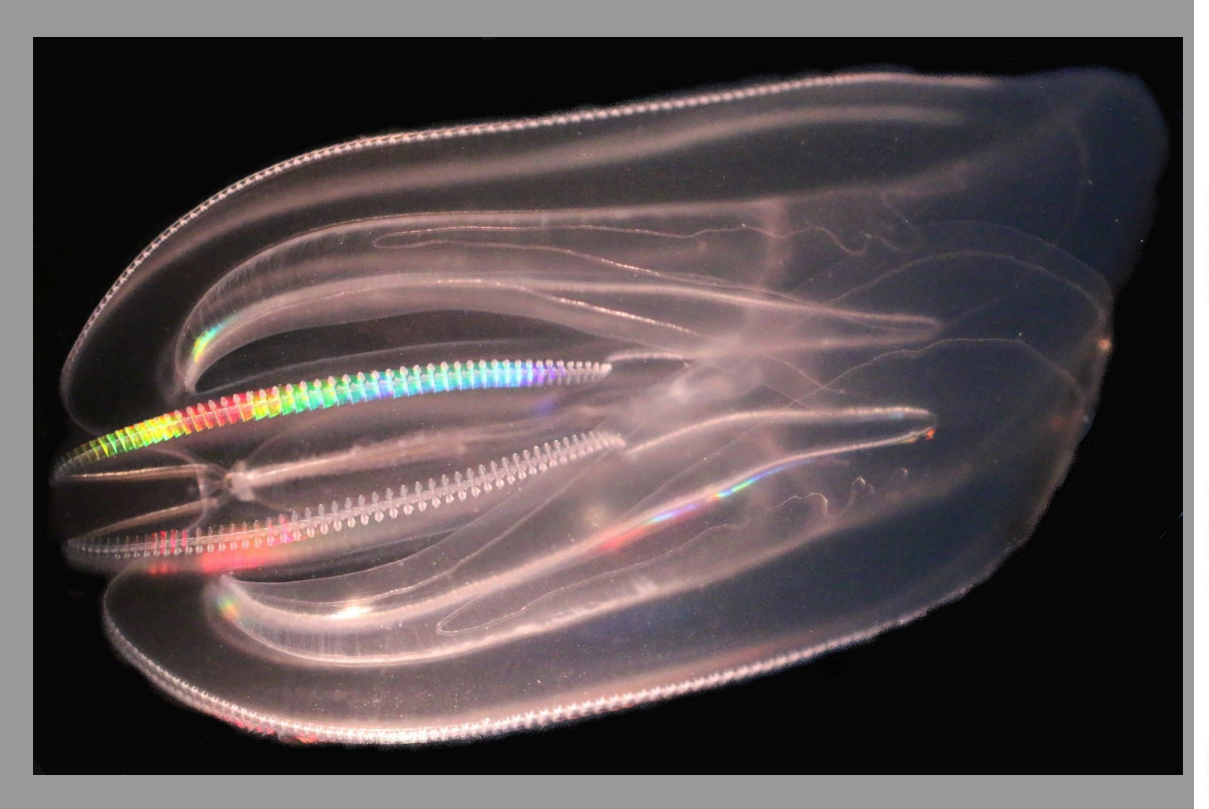


Presence of hybrids in a highly variable environment

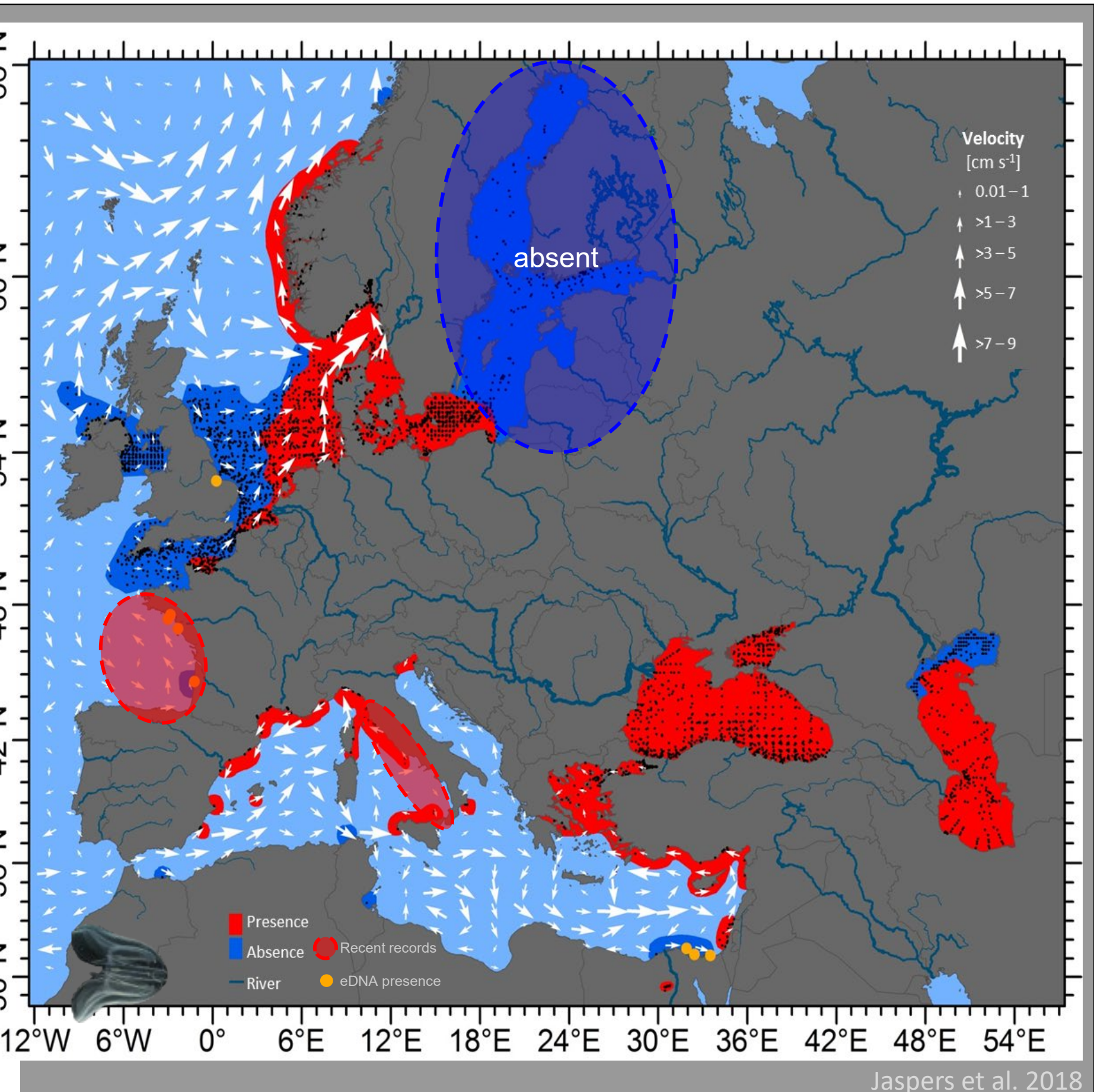
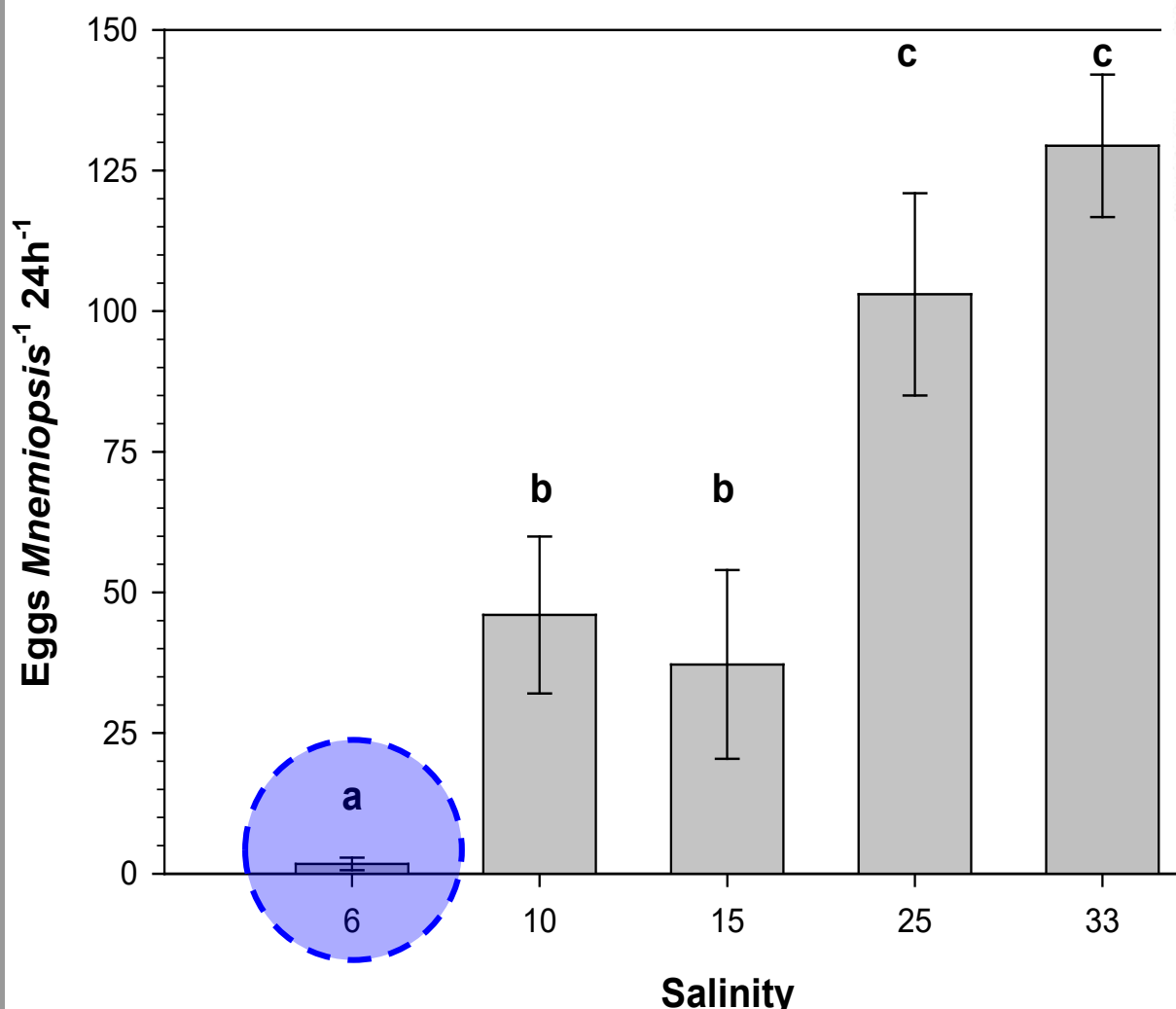
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Problem

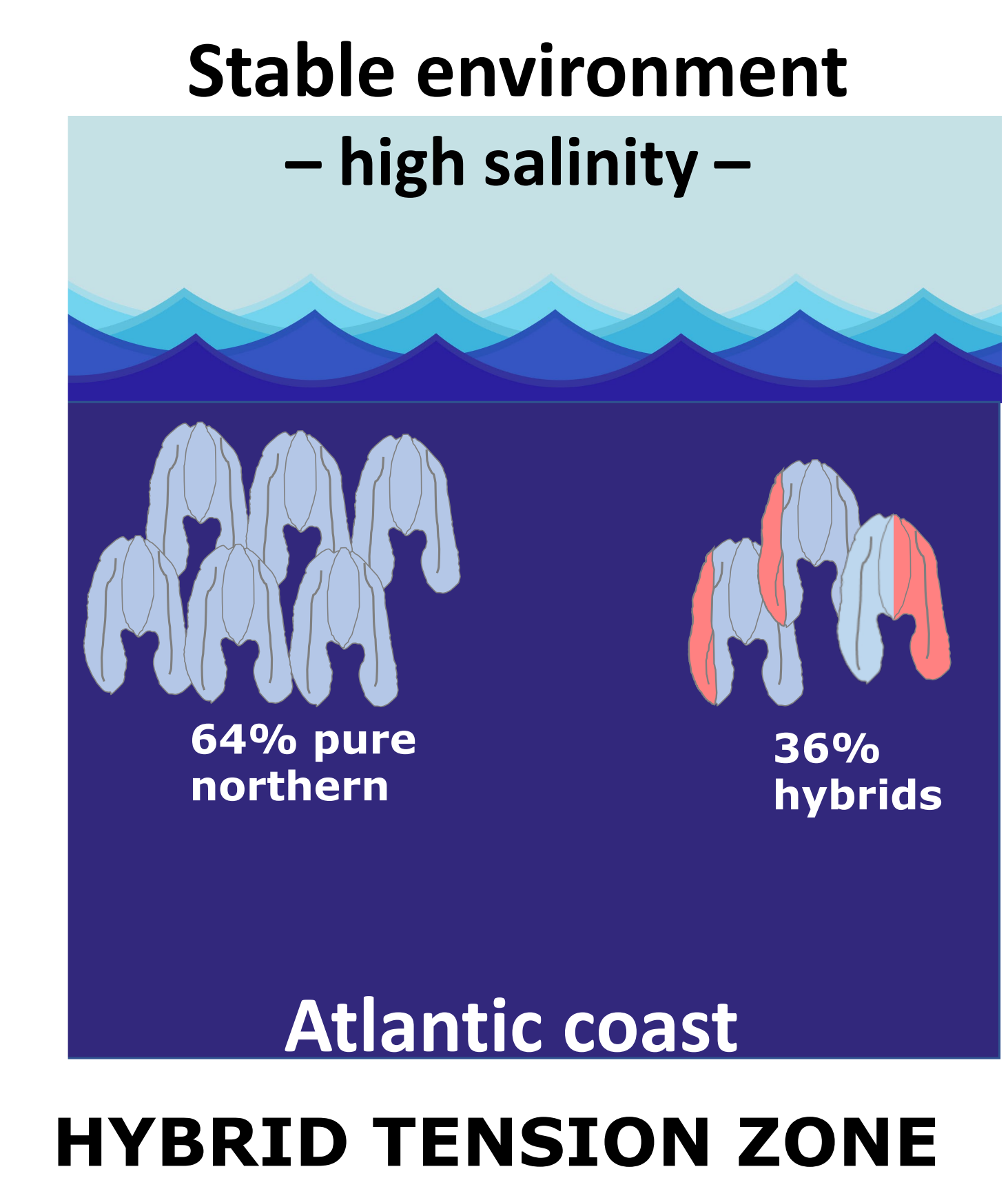
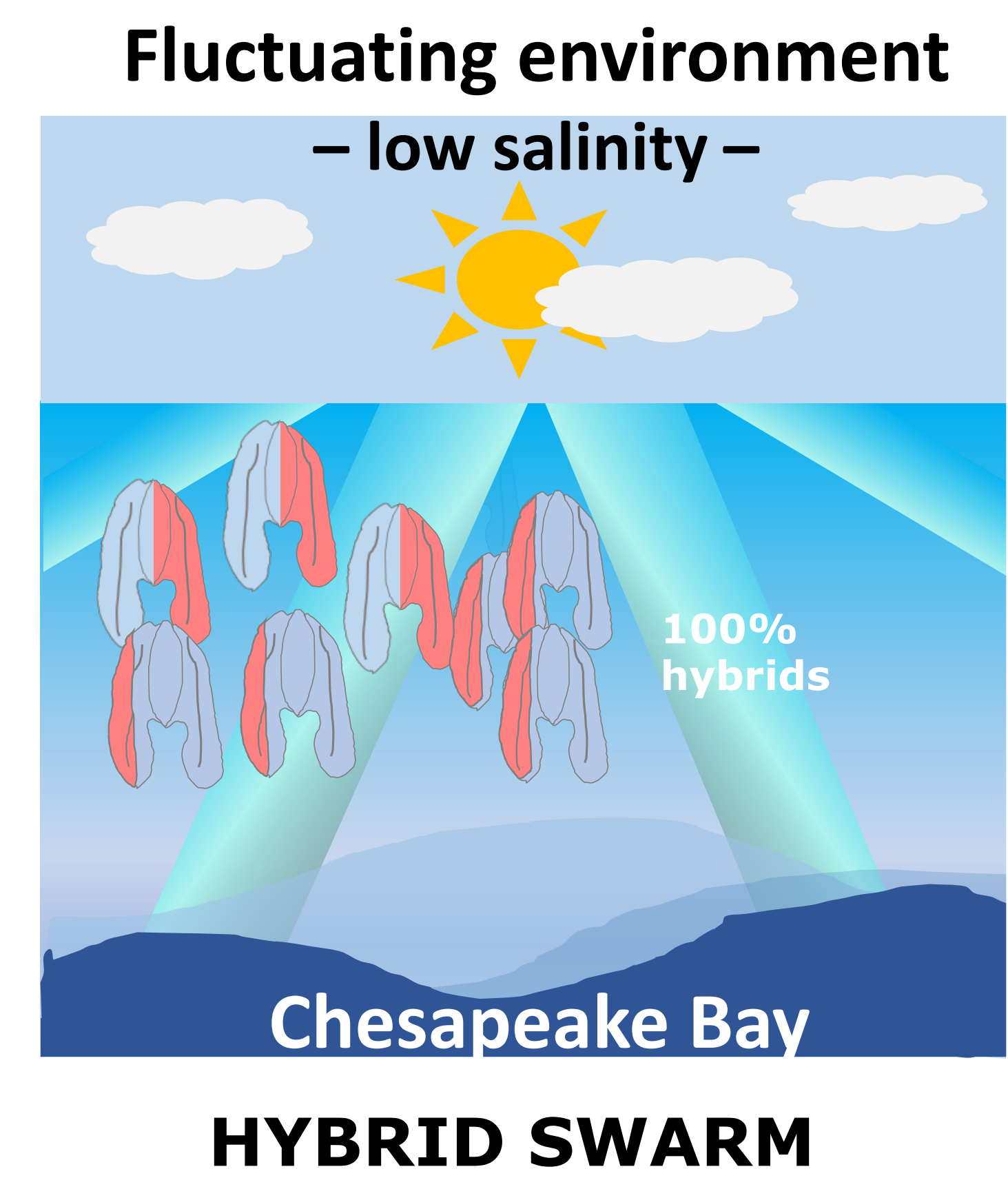


Wide distribution of invasive *Mnemiopsis leidyi* (ctenophore) in western Eurasia.



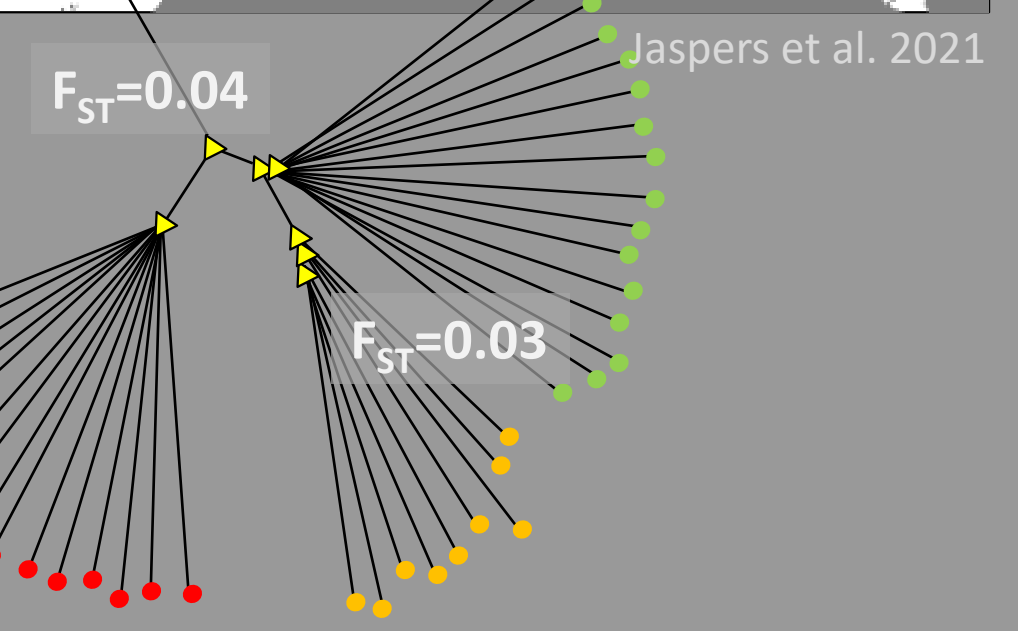
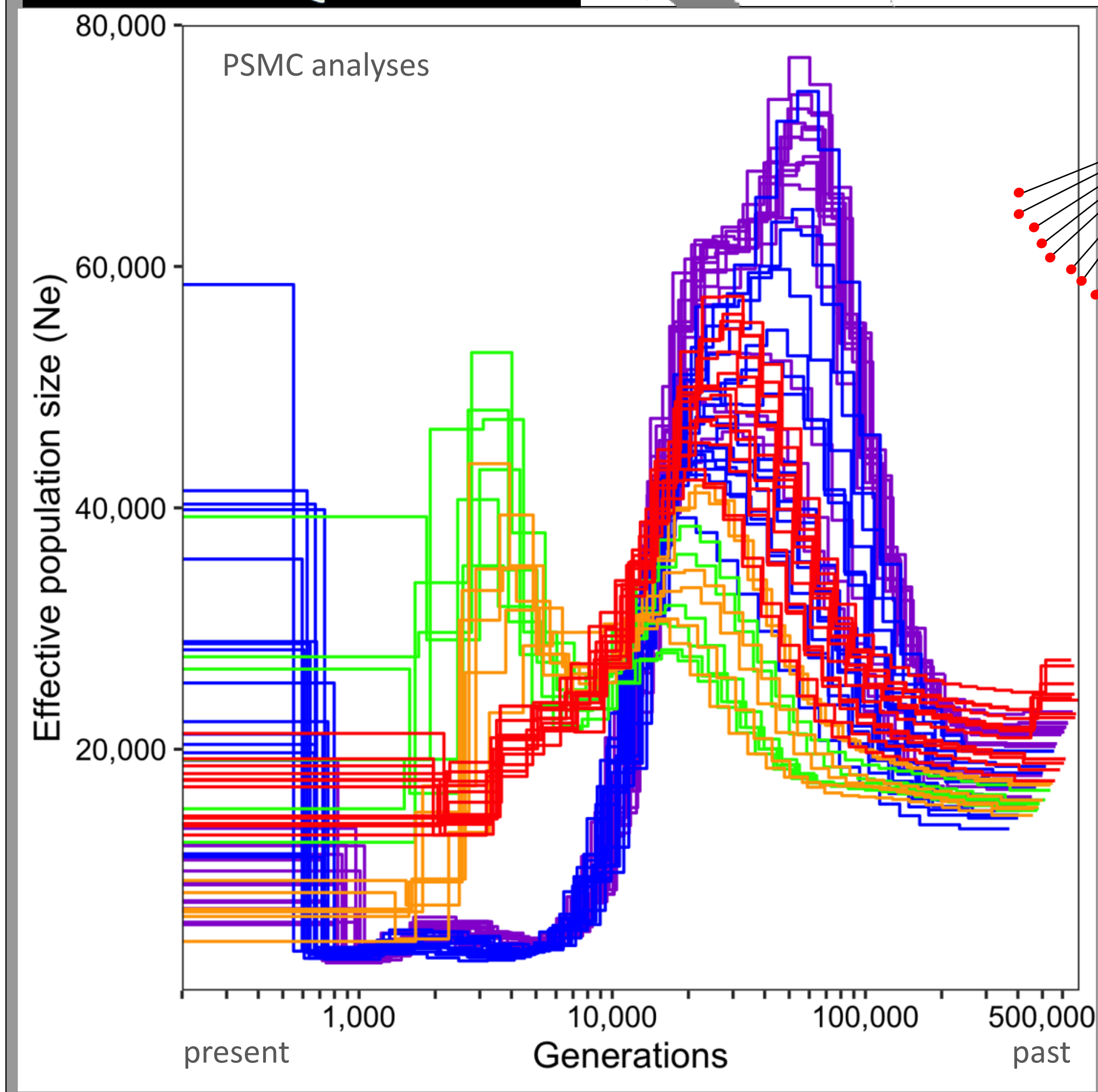
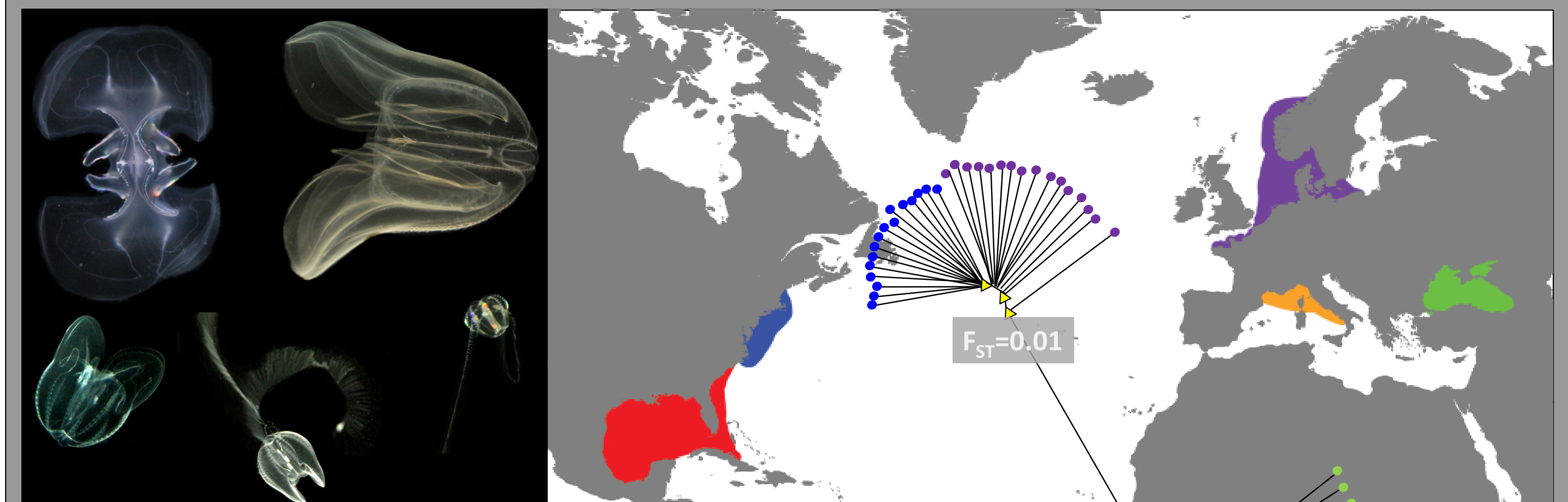
Salinity restricts range expansion of *M. leidyi* in northern Europe (Baltic Sea), while they are present in the low saline Black & Caspian Seas. Concern that northern populations develop tolerance to low salinity!

Conclusions



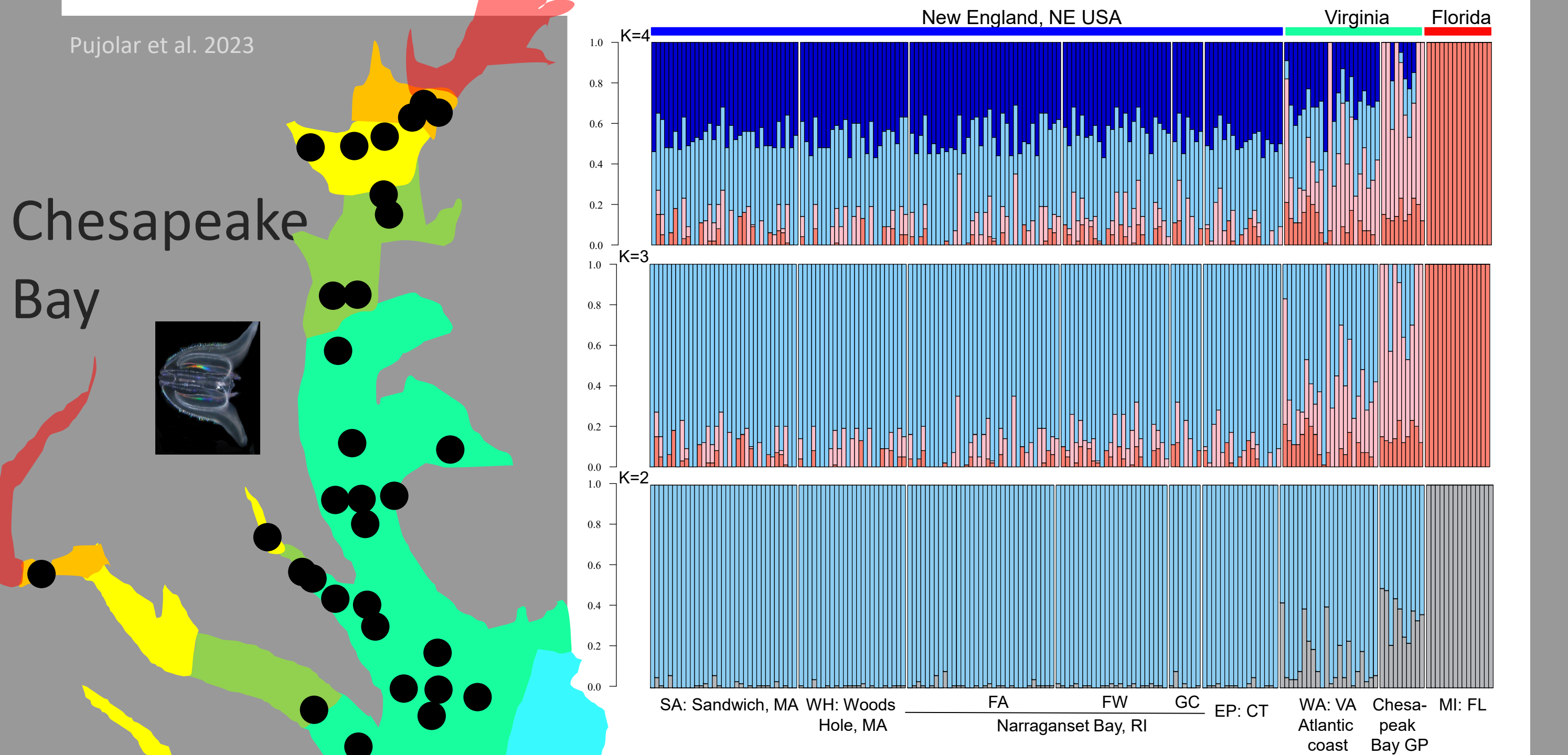
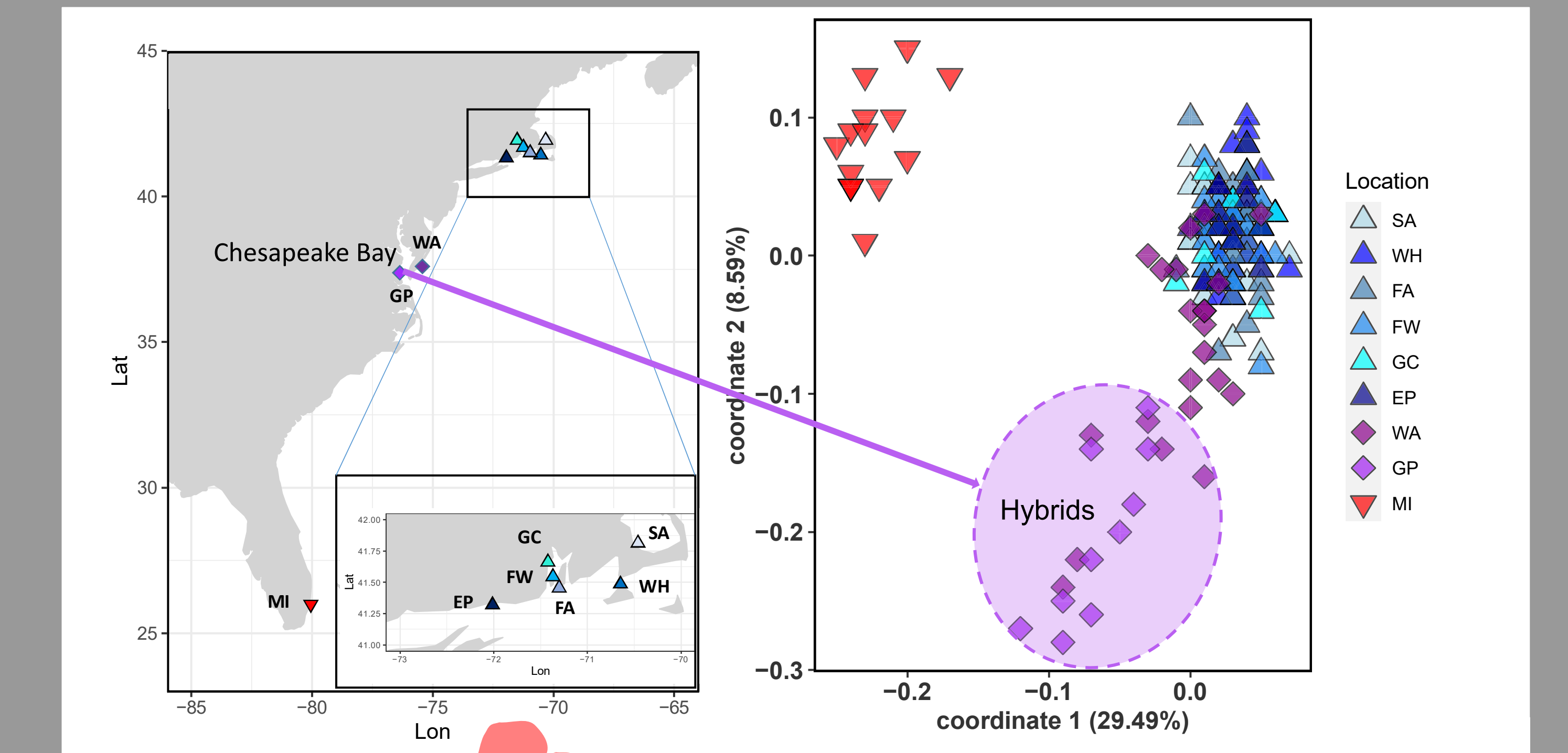
Selection for hybrids in variable low saline environments of Chesapeake Bay. Translocation of hybrid *M. leidyi* from Chesapeake Bay into Northern Europe should be prevented by all means, especially as we find ongoing gene flow between NE USA and Northern Europe.

Results – invasion dynamics

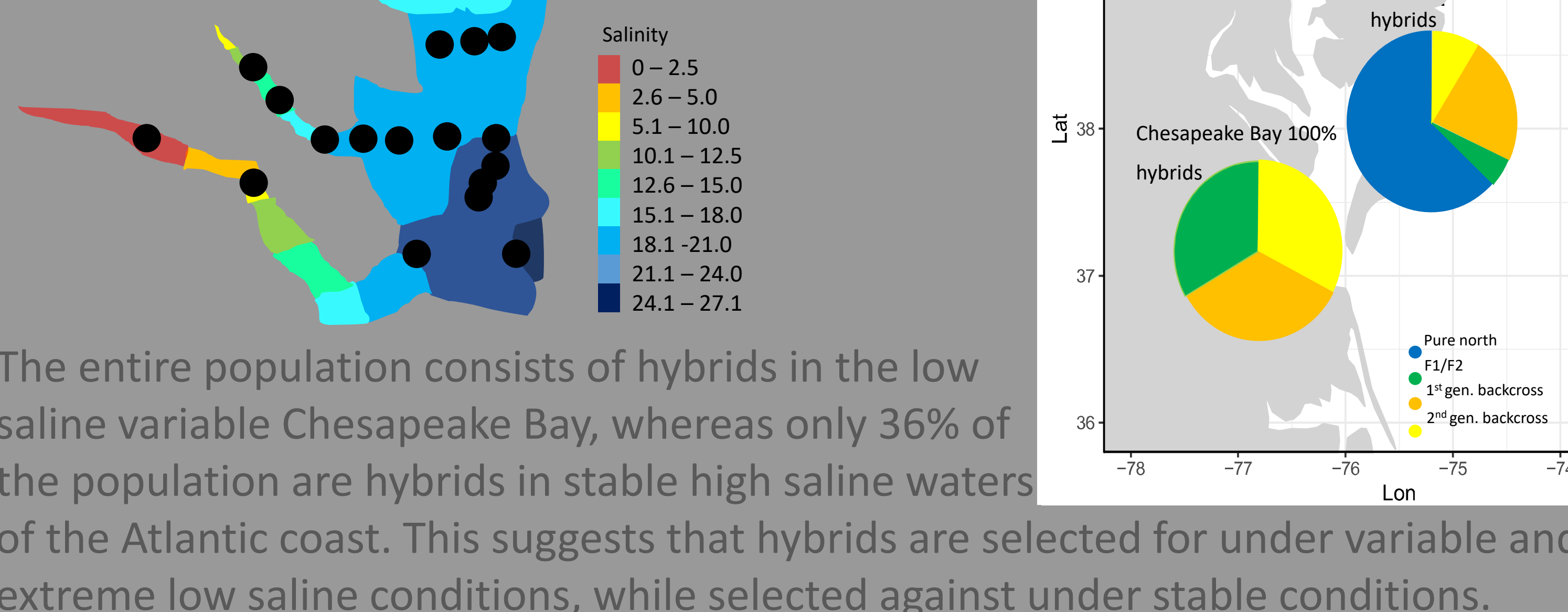


Whole genomes allow to reconstruct the demographic history of populations, their growth (expansion), contractions and ancestry. This hints to understand invasion dynamics, the origin of invasive populations, time and magnitude of introduction events.

Results – native hybrids in low salinity



Hybrids are found in Chesapeake Bay. This is a highly fluctuating environment and includes extreme low salinity where *M. leidyi* is present (black dots).



The entire population consists of hybrids in the low saline variable Chesapeake Bay, whereas only 36% of the population are hybrids in stable high saline waters of the Atlantic coast. This suggests that hybrids are selected for under variable and extreme low saline conditions, while selected against under stable conditions.

