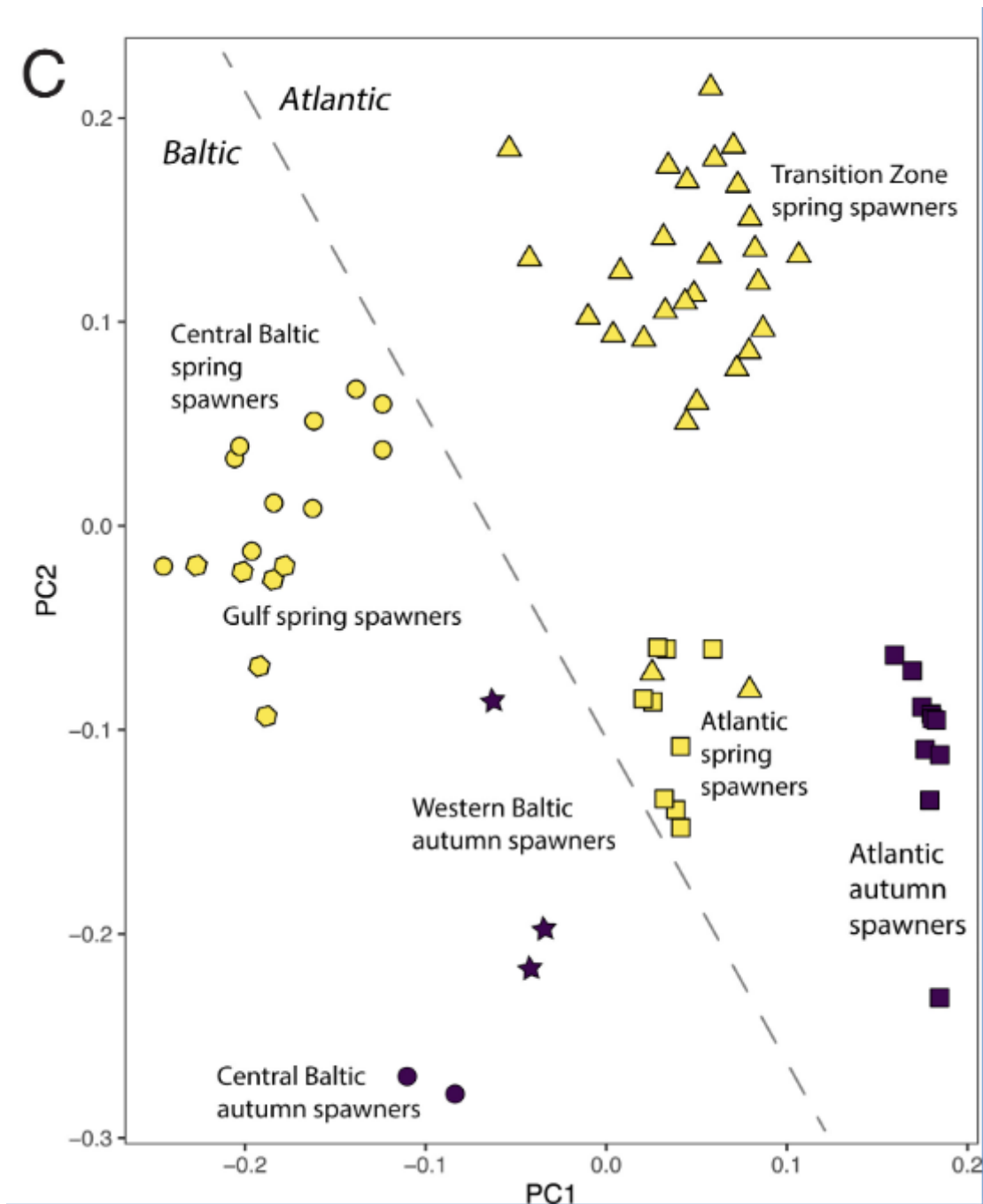


# 1- Dataset Clupea | Atmore et al., 2022

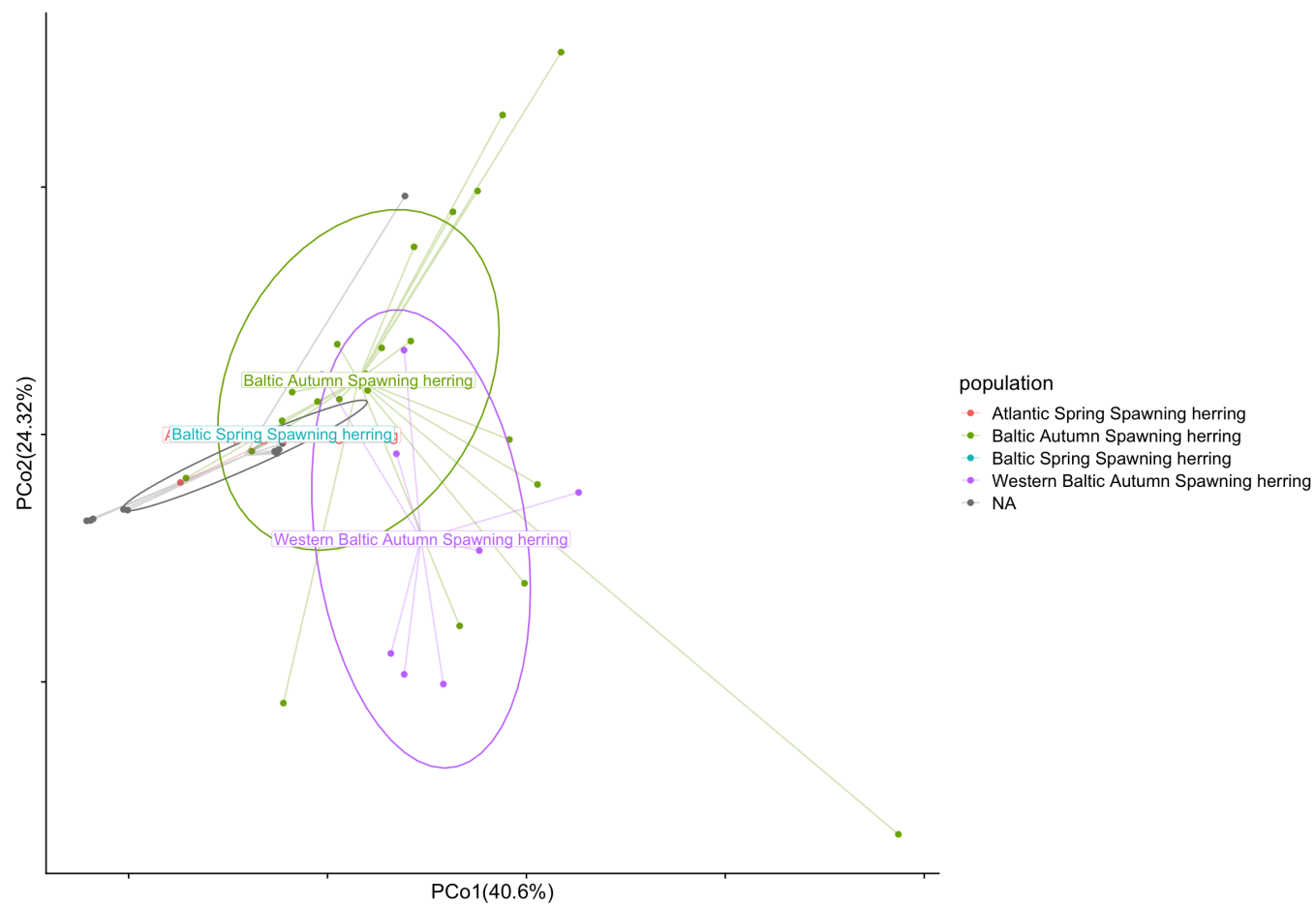
<https://www.pnas.org/doi/10.1073/pnas.220870311>

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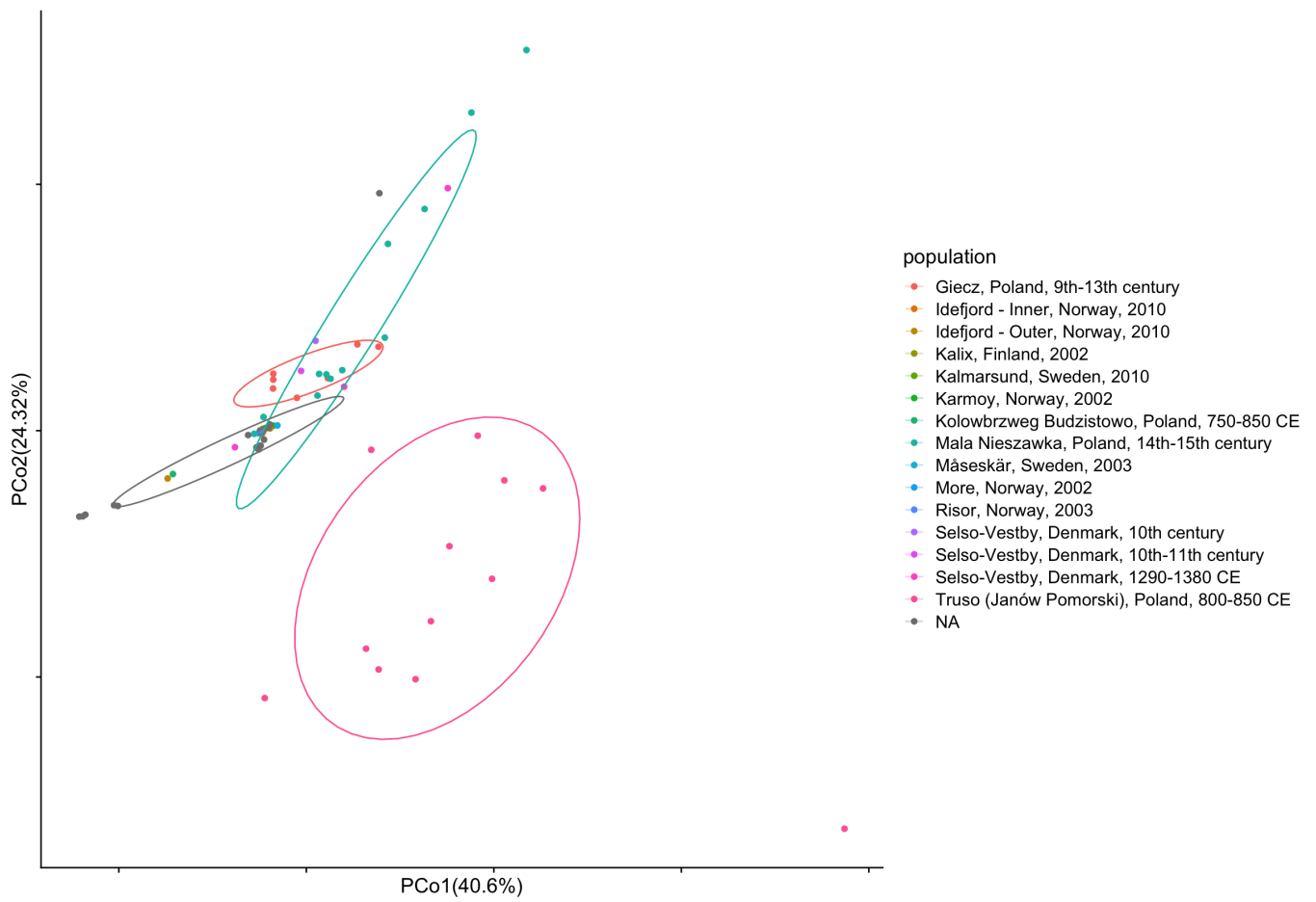


Versus:

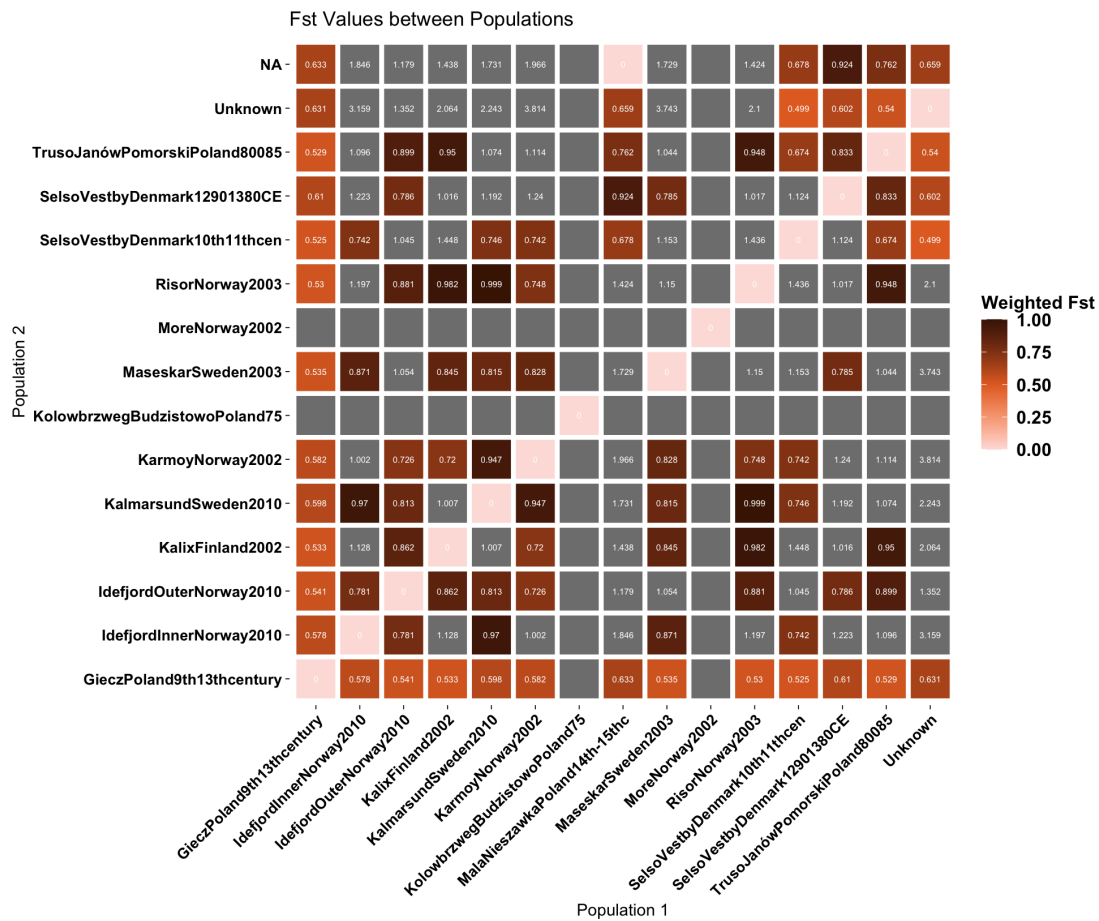
1)



2)



3)



- 1) MDS ecotypes (ancient + modern)
- 2) MDS populations (ancient + modern)
- 3) FST matrix (ancient + modern), **FST equation needs to be fixed.**

## Heterozygosity $\theta$

Location	Period	Value
Giecz, Poland	9th-13th century	<b>0.022</b>
Mala Nieszawka, Poland	14th-15th century	<b>0.062</b>

<b>Location</b>	<b>Period</b>	<b>Value</b>
Truso, Janów Pomorski, Poland	800-850	<b>0.076</b>
Kolowbrzweg, Budzistowo, Poland	75	NA
Selso, Vestby, Denmark	10th-11th century	<b>0.135</b>
Selso, Vestby, Denmark	1290-1380 CE	<b>0.067</b>
Karmoy, Norway	2002	0.002
More, Norway	2002	NA
Risor, Norway	2003	0.006
Maseskar, Sweden	2003	0.003
Kalix, Finland	2002	0.006
Kalmarsund, Sweden	2010	0.006
Idefjord Inner, Norway	2010	0.004
Idefjord Outer, Norway	2010	0.015

## **Conclusions**

-Ancient DNA specimens are not suitable for the current *Skmer* pipeline (order of magnitude higher for heterozygosity  $\theta$ ).

-Modules (FST and MDS plots) need to take into account statistic from *Skmer* to discard individuals and populations that are not into a certain threshold for error rate, coverage, read length genome size, heterozygosity.