



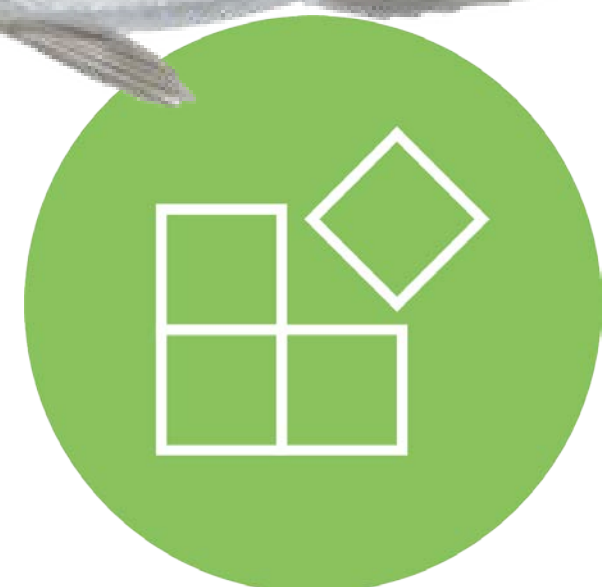
QUESTIONS AND ANSWERS ABOUT THE USE OF GENETICS FOR STOCK ASSESSMENT AND MANAGEMENT. EUROPEAN HAKE AS AN EXAMPLE.

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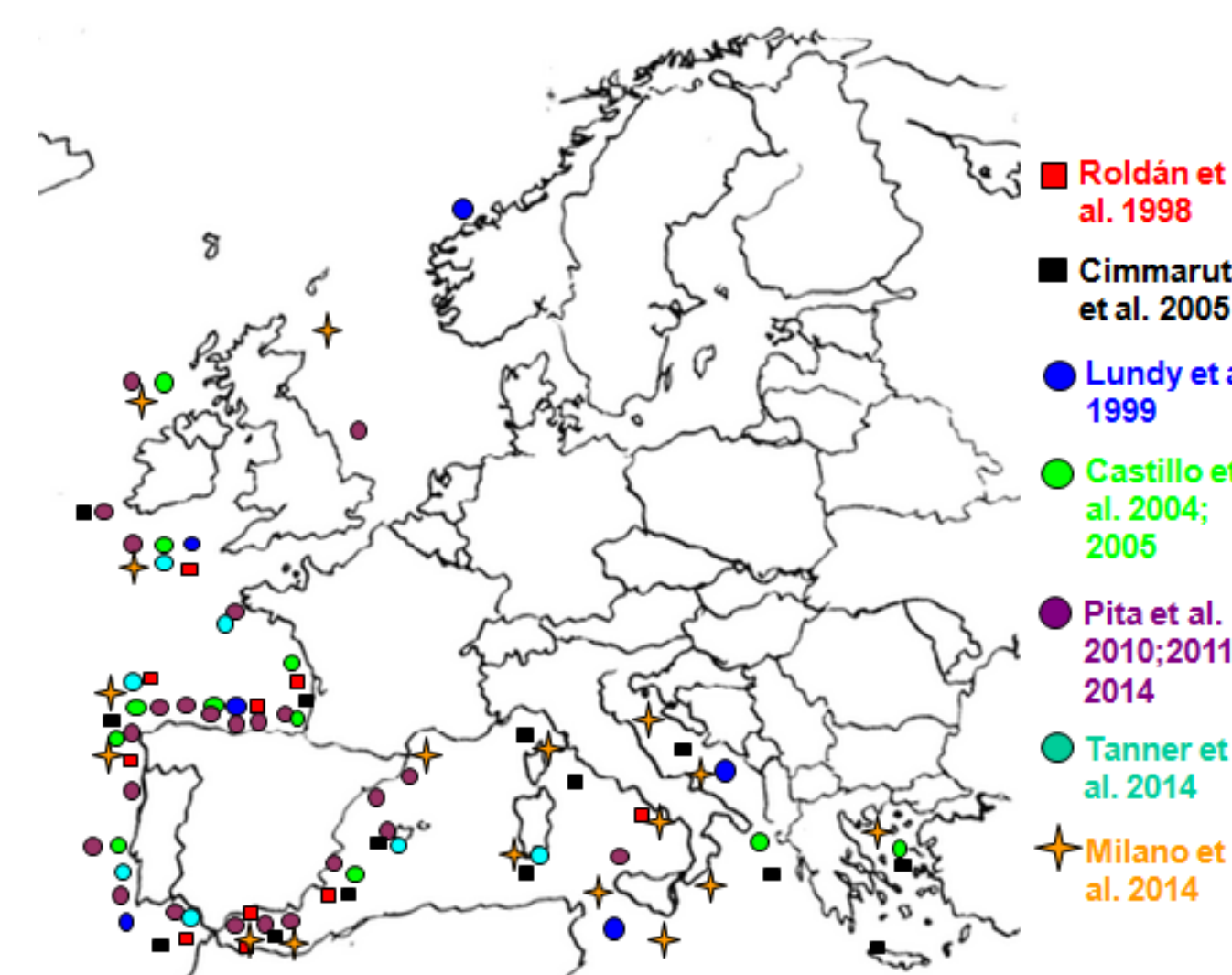


European hake is a main fisheries resource in Atlantic waters. Currently there are two different stocks for management purposes: Northern and Southern stock. However, as ICES recognize, there are serious doubts about the scientific basis for this separation. Wrong stock definitions can drive to wrong management decisions. The **goal of this work** was to review, analyze and evaluate the available genetic information and their usefulness for hake assessment and management.

We have made an extensive analysis of all genetic data of European hake published up to date. The approach of the genetic studies has been different regarding the genetic markers, spatial coverage, time series, sampling procedure or statistical tests used. In general, all the genetic information shows a pattern of connectivity among Atlantic populations of hake regardless of the subdivision in stocks by the ICES, although the level of connectivity is different depending on the type of data.



The GADGET (Globally applicable Area-Disaggregated General Ecosystem Toolbox), is a powerful framework developed to model marine ecosystems within a fisheries management and biological context. There is a high degree of flexibility in the use of different data sources and interactions applied on the models (predation, recruitment, migration, etc).



The GADGET model

Genetic Data



Problems detected

1. Can not compare the results obtained for different types of markers: neutral vs. selective
2. There are not, in general, a spatial and/or temporal sampling design focused to test demographic hypothesis (not the genetic ones)
3. There is no information about the age of individuals sampled in any of the analyzed papers.
4. Limitations of the use of hierarchical indexes as Wright' F_s
5. The models are based on the real population size not in the effective size



- ✓ What are the most suitable genetic markers to infer connectivity? What is the impact of using neutral or selected markers?
- ✓ How the age of the individuals sampled can impact on a dynamic model?
- ✓ Is the sampling design (spatial and temporal) focused to test demographic hypothesis, not only the genetic ones?
- ✓ What are the limitations of the use of hierarchical indexes as Wright' F_s to decipher the genetic structure of European hake populations?

- ✓ Neutral markers are the best choice to investigate gene flow, migration or dispersal, which means connectivity. Non-neutral or adaptive genetic variation must be analysed in quantitative genetic experiments under controlled environmental conditions (Holderegger et al. 2006).
- ✓ Sampling by size for a dynamic model: differential impact according to age of migration. Migration of larvae and or juveniles has a less relevant impact in the modeling than adults migration.
- ✓ In spite of the fact that F_{st} is a good index for estimating demographic inferences, its reliability is constrained by subpopulations heterozygosity (Meirmans & Hedrick, 2011).



Our recommendations are:

- i) use neutral markers to estimate connectivity,
- ii) detect significant changes in abundance of population and structure instead of sampling error and environmental noise by analyzing long-term data sets,
- iii) Combine both, structural genetic criteria and genetic metrics such as N_e into management can provide more precision on the rate of genetic erosion and improving assessing risks of extinction by genetic factors (Pita et al., 2017).



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