

# A ROUGH STATE for the STARRY SMOOTH-HOUND

Nanopore sequencing of 6kb amplicons reveal potential population bottleneck in demersal shark species *Mustelus asterias*

Daniël van Berkel<sup>1</sup>, Joost van den Heuvel<sup>2</sup>, Niels Brevé<sup>3</sup> & Reindert Nijland<sup>1</sup>

<sup>1</sup> Marine Animal Ecology Group, Wageningen University, the Netherlands, <sup>2</sup> Laboratory of Genetics, Wageningen University, the Netherlands, <sup>3</sup> Sportvisserij Nederland (Dutch Angling Society), Bilthoven, the Netherlands



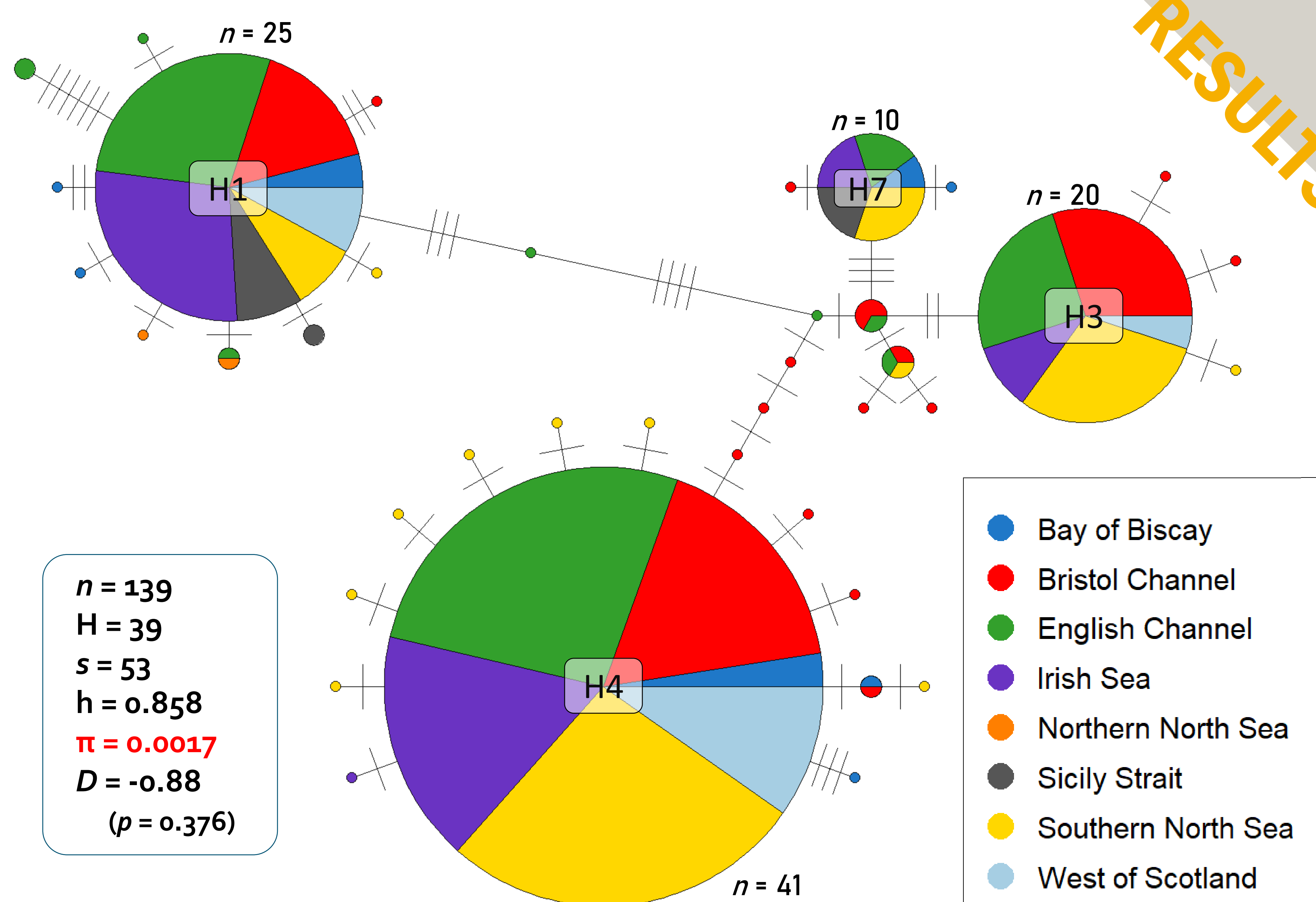
## INTRODUCTION

- North Sea elasmobranchs are under heavy **anthropogenic pressure**. [1]
- The demersal starry smooth-hound, *Mustelus asterias*, has **decreased** in the **northeast Atlantic**, and is **extremely vulnerable** in the Mediterranean. [2]
- Currently, **no measures** are in place for fisheries.
- Differences in **life-history traits** indicate the existence of **two subpopulations** in the northeast Atlantic. [3,4]
- Tag-recapture studies emphasize **strong natal philopatry**. [5,6]
- Molecular tools could provide valuable insight in the **genetic diversity** and **population structure** of *Mustelus asterias*.

## HYPOTHESIS

At least two **subpopulations** are present, one residing in the **southern North Sea and English Channel**, the other residing in the **Irish Sea and Celtic Sea**.

## RESULTS



## CONCLUSIONS

1. **No correlation** between location and haplotypes
2. Low overall **nucleotide diversity**
3. Remarkable haplotype structure, with **three distinct haplo-groups**

## METHODS

- Collected finclips of **139 pups and large females**.
- Amplified a **6000 bp** region of the mitochondrial DNA using PCR.
- Sequenced with R10.3 and R10.4.1 flow cells.
- Clustered reads using **decona** tool. [7]

## CONTACT



WAGENINGEN  
UNIVERSITY & RESEARCH



daniel.vanberkel@wur.nl