

# The impact of rapid environmental change on the evolution of immunogenetic diversity in coral reef fishes

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## Introduction

\*Coral reef fishes rely on a diverse array of innate immune receptors as a front-line of defense against pathogens, in particular for ensuring the survival of developing embryos and larvae in the environment during their pelagic phase.

\*However, the diversity and evolutionary history of these receptors in coral reef fishes remain poorly understood.

\*These knowledge gaps are problematic, as they form the basis for functional work and the critical historical context for accurately forecasting the response of lineages to environmental changes over the next century.

\*Here we investigate the impact of shifts in biodiversity hotspots on the genetic diversification of two families of innate immune receptors in an iconic clade of tropical reef fishes: Holocentridae (squirrelfishes and soldierfishes)

## Methods

\*RNA was sequenced from pooled gill, heart, spleen, and liver tissues from fishes collected in Okinawa, Japan.

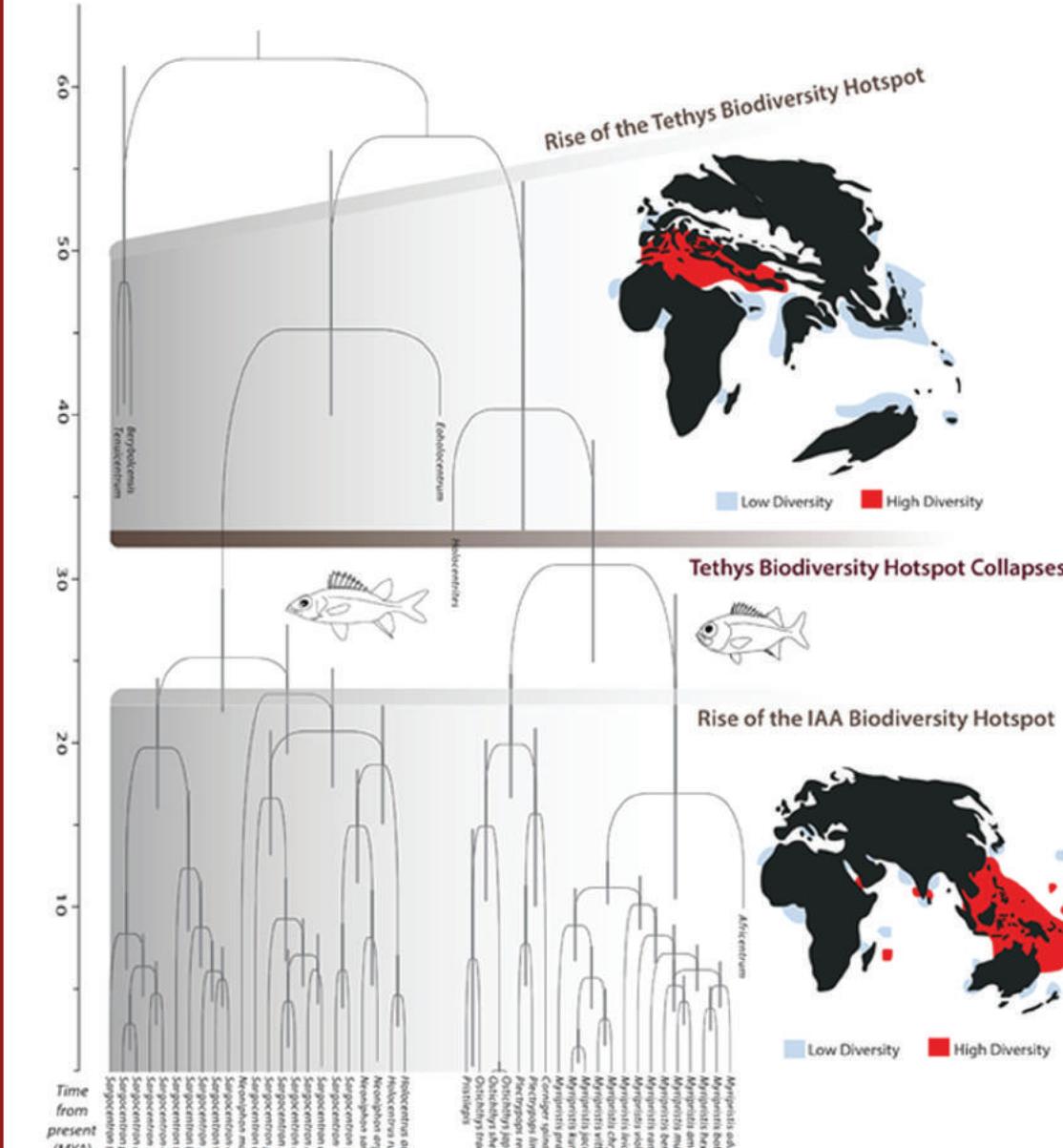
\*Transcriptomes were assembled using TRINITY and translated using TransDecoder

\*A pipeline was developed using a combination of Unix, Python, and SLURM to identify and retrieve target sequences using a combination of HMMER, MAFFT, and IQTREE2 from translated transcripts and publicly available data

\*Searches were conducted in conjunction with existing ray-finned fish NITR and TLR databases

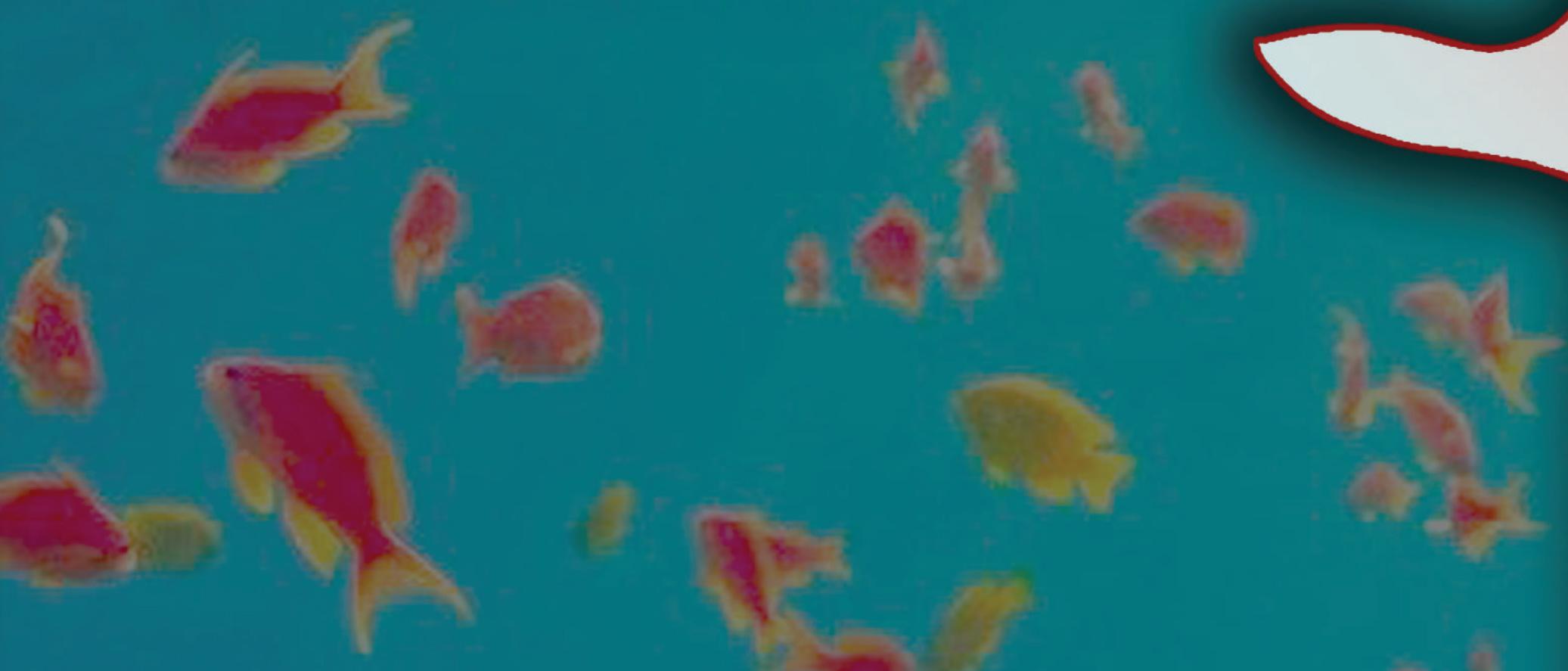
\*A time-calibrated molecular phylogeny of living and fossil holocentrids was estimated using Beast 2.7.1 and data from Dornburg et al (2014)

## Results:



\*A superimposition of holocentrid evolutionary history and shifts in biodiversity. Holocentrids arose like most modern reef fishes during the early Cenozoic, a time when coral reef biodiversity was highest in the Tethys biodiversity hotspot.

\*Oceanic and plate tectonic changes led to the collapse of the hotspot and widespread extinction beginning in the early Oligocene. Following the rise of Indo-Australian Archipelago (IAA) hotspot, holocentrids began a second phase of species diversification.

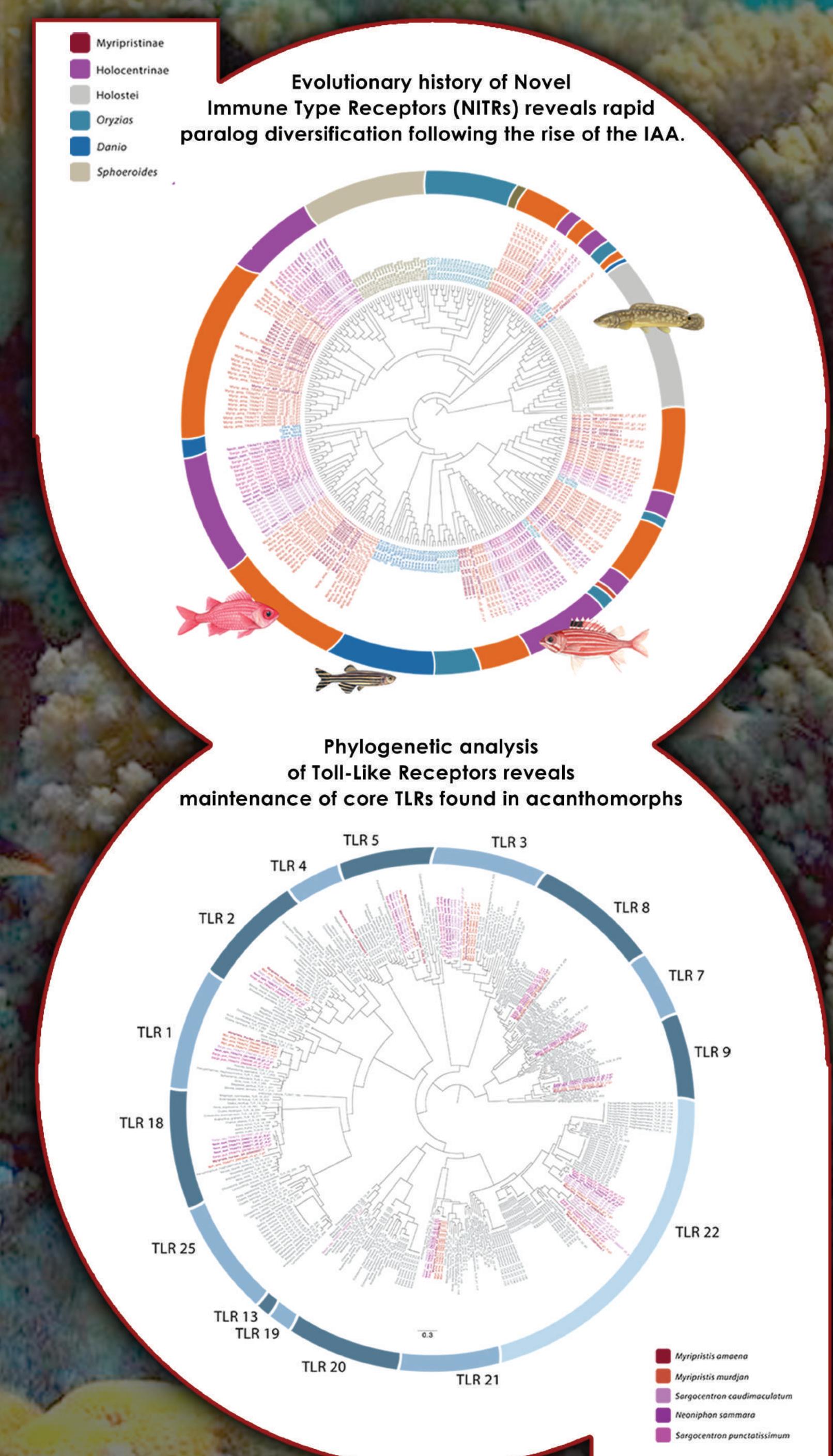


## Discussion

\*Our work is the first description of these receptors in Holocentrids. We expand the scope of NITRs known from the group from 4 to nearly 200 unique sequences and provide the first evidence of TLR 13 in an Acanthomorph.

\*We find a decoupling of diversification dynamics between TLRs and NITRs. TLRs are characterized by a low level of paralog evolution and maintenance of core receptors. In contrast, NITRs are characterized by rapid paralog diversification, particularly in *Myripristis*.

\*NITRs are analogous to human natural killer cell receptors, suggesting that the rise and fall of biodiversity hotspots may have played a large role in shaping the molecular basis of the killer-cell response in coral reef fishes



## Future work

\*We are adding publicly available sequences from non-reef myripristines to better characterize the diversification of these receptors in the clade.

\*We are also expanding analyses to characterize the predicted functional diversity of these receptors based on sequence motifs and protein models.

## Data Availability:

[https://github.com/rajasangeetha/Immunogenetic\\_diversification\\_Squirrel-fishes](https://github.com/rajasangeetha/Immunogenetic_diversification_Squirrel-fishes)

