Is extensive MHC class II diversity in striped dolphin (Stenella

coeruleoalba) in the Mediterranean Sea shaped by recent epizootics?

Arbanasić H¹, Medrano-González² L, Svetličić I¹, Gomerčić T³, Đuras M³, Galov A¹

¹Faculty of Science, University of Zagreb, Rooseveltov trg 6, 10000 Zagreb, Croatia, ² Departamento de Biología Evolutiva, Facultad de Ciencias, Universidad Nacional Autónoma de México, Avenida Universidad 3000, Ciudad Universitaria, México 04510, México

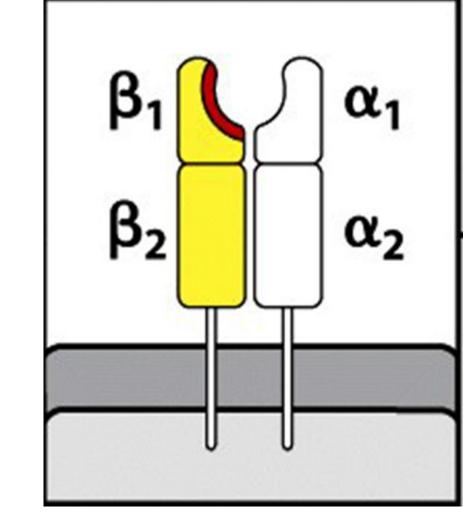
³Faculty of Veterinary Medicine, University of Zagreb, Heinzelova 55, 10000 Zagreb, Croatia

INTRODUCTION

The major histocompatibility complex (MHC) are highly polymorphic genes important for adaptive immunity. Due to their association with adaptation and fitness traits, MHC genes have been largely explored in evolutionary ecology and conservation genetics. The maintenance of high genetic diversity on MHC genes is attributed to the action of balancing selection driven by pathogens.

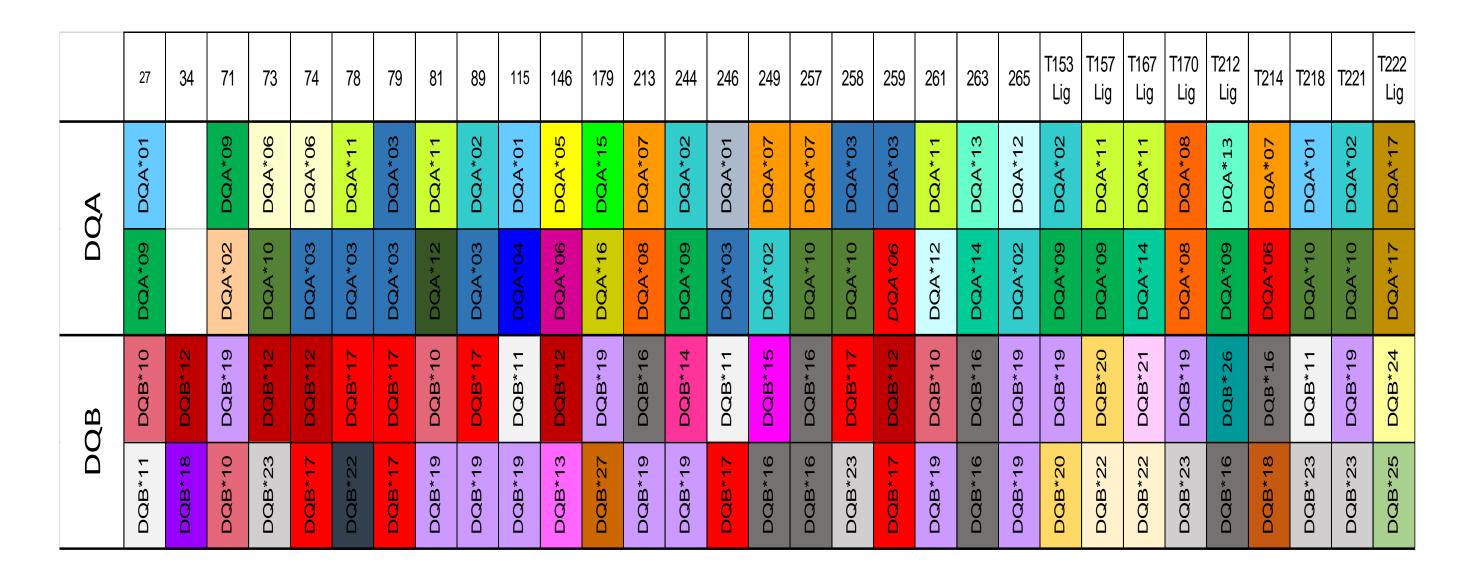
METHODS

The analysis was performed on MHC class II DQA and DQB genes that code for antigen binding subunits of the membrane receptor.

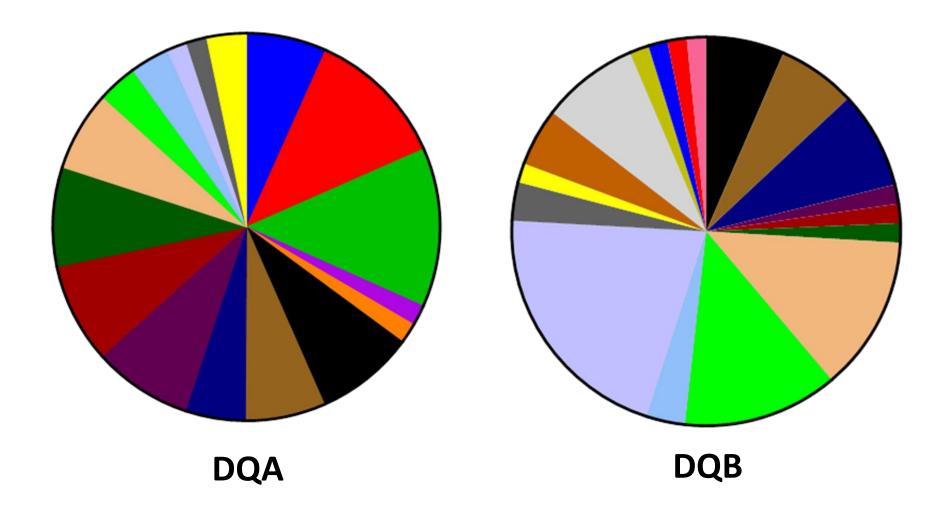


RESULTS

1. Extraordinary variability with 17 DQA and 18 DQB alleles. There are 29 unique **genotypes** detected in 31 individuals

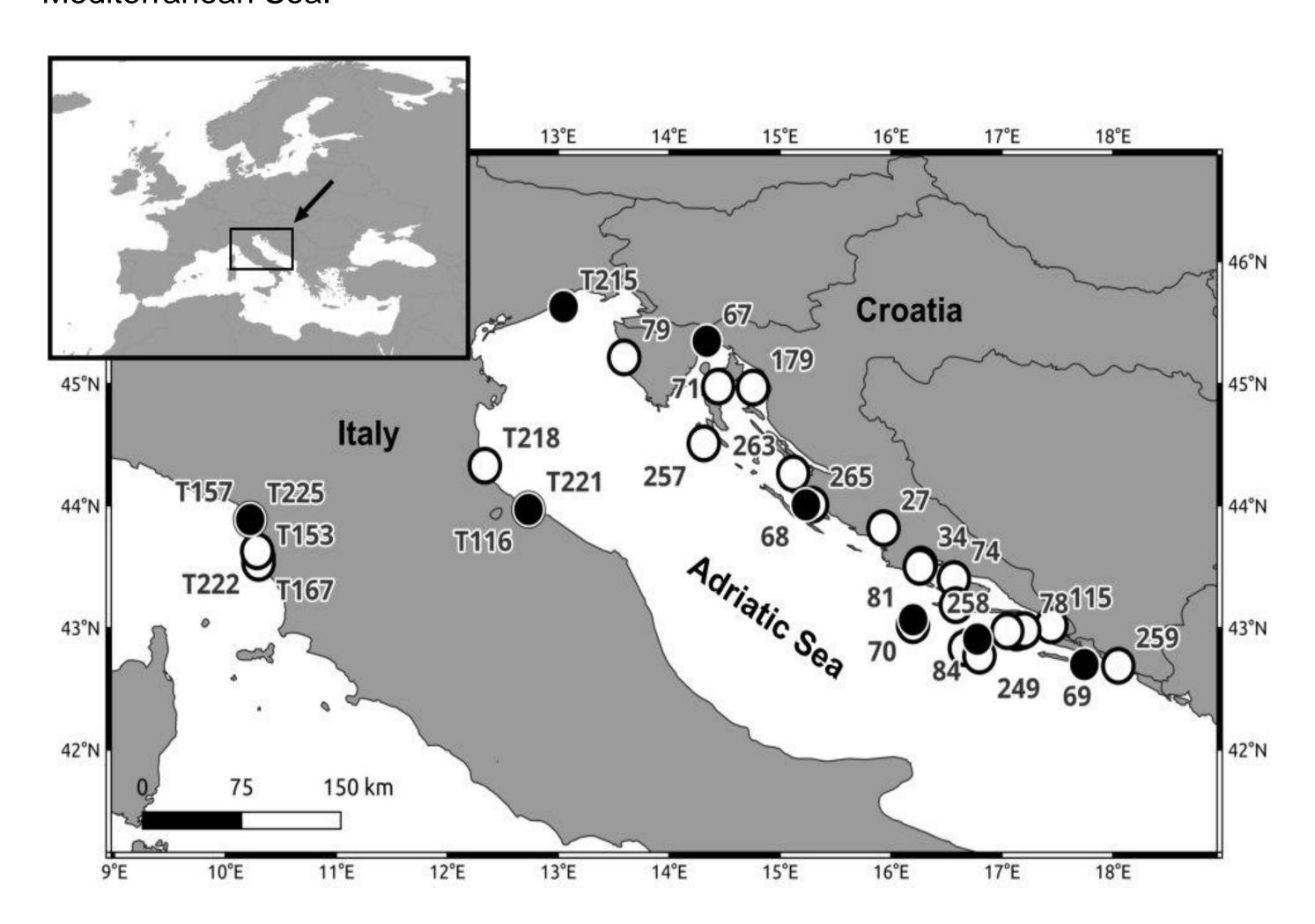


2. Atypically high DQA locus variability comparable to DQB, as demonstrated by allelic richness

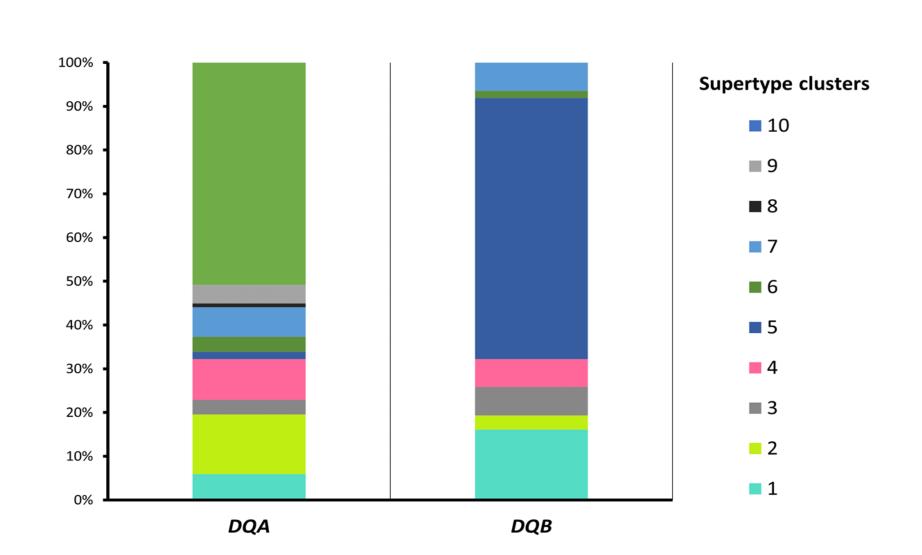


SAMPLE

In this study we analysed MHC class II loci in 31 striped dolphin individuals from the Mediterranean Sea.



3. Genetic diversity was further extended to substantial functional diversity. Namely, translated alleles formed ten DQA and seven DQB **structural supertypes** capable of binding and presenting a broad range of antigens.



- 4. Strong influence of **balancing selection over species evolution** is indicated by homogenised allele frequencies, Tajima's D and tests based on non-synonymous to synonymous substitutions rate ratio (PAML, OmegaMap, HyPhy, MEGA)
- 5. Ewens-Watterson test provided compelling evidence of **recent selective pressure** acting on striped dolphin's DQA gene. The observed homozygosity (0.079)

 was significantly lower (p=0.006) than the expected (0.125).

HYPOTHESIS

We hypothesize that morbillivirus, which recurrently invaded Mediterranean population over last decades, exerted strong selective pressure on MHC class II DQ loci in striped dolphin. Accordingly, striped dolphin MHC class II genes are potentially interesting model to observe contemporary adaptation to environmental challenges.



