

Applications

Date: Tuesday 30 August

Time: 15:10/ 17:45

Room: Pentlands (East/West)
Prestonfield

Abstract 6

Speed talk & poster

Is extensive MHC class II diversity in striped dolphin (*Stenella coeruleoalba*) in the Mediterranean Sea shaped by recent epizootics?

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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. Here, analysis of MHC class II DQA and DQB loci in striped dolphin from the Mediterranean Sea revealed extraordinary diversity, with 29 unique genotypes detected in 31 individuals. Allelic diversity represented by 17 DQA and 18 DQB alleles, which form 27 two-locus haplotypes, 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. The acting of balancing selection on both genes was indicated by homogenised allele and supertype frequencies, presence of rare alleles, and several tests of long-term positive selection. We have found intriguing results on DQA diversity comparable to DQB locus, which is atypical for usually less polymorphic MHC alpha genes. Moreover, Ewens-Watterson test provided compelling evidence of recent selective pressure acting on the striped dolphin's DQA gene. Indeed, the Mediterranean striped dolphin population faced severe recurrent morbillivirus epizootics over the last decades, of which the first one recorded during 1990-1992 was particularly severe. We hypothesize that morbillivirus exerted selective pressure that shaped extensive MHC class II DQ genes diversity in striped dolphin, which potentially might be an interesting model to observe contemporary adaptation to environmental challenges.

European Conservation Genetics Meeting



August 30 – September 1
Edinburgh