



Collaboration for Environmental Evidence

Systematic Review No. 65

DOES REDUCED MHC DIVERSITY DECREASE VIABILITY OF VERTEBRATE POPULATIONS?

Review Report

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Cover Sheet

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Summary

1. Background

Pathogens are considered as one of the major extinction factors (Smith et al. 2009; Wilcove et al. 1998). Arguably, depletion of genetic diversity within populations may make them more vulnerable to pathogen assault (Altizer et al. 2003; de Castro and Bolker 2005; O'Brien and Everman 1988). First, inbreeding depression associated with population bottlenecks (Keller and Waller 2002) may limit the ability of individuals to mount an effective immune response. Indeed, inbreeding has been demonstrated to increase susceptibility to infections (Acevedo-Whitehouse et al. 2003; 2005; Coltman et al. 1999; Ilmonen et al. 2008; Reid et al. 2007; Ross-Gillespie et al. 2007; Spielman et al. 2004). Second, the loss of variation at genes responsible for resistance to parasites may render populations more susceptible to infection. This argument applies to highly polymorphic vertebrate Major Histocompatibility Complex (MHC) genes, coding for proteins presenting pathogen-derived antigens to T-cells, thus initiating the adaptive immune response (Janeway et al. 2004). Hughes (1991) suggested that retention of variation in these genes is an essential element of effective conservation programmes, but this argument remains controversial (Hedrick 2001). Apart from MHC, other polymorphic genes can influence the effectiveness of defences against pathogens (Acevedo-Whitehouse and Cunningham 2006). Here however we concentrate on MHC genes only, as they are the most polymorphic genes known in vertebrates, and their function and evolution is better understood than that of other genes involved in the immune response.

2. Objectives

To answer the major question: whether reduced MHC diversity decreases viability of vertebrate populations? This question has three components which can be formulated into more specific questions: (1) can drift render MHC loci effectively neutral and thus reduce their diversity in populations? (2) can reduced variation at MHC increase population-level parasite load or prevalence of disease? (3) does reduced variation at MHC increase probability of population extinction?

3. Methods

Multiple electronic sources were searched using several Boolean expressions. The relevance of a study was first assessed by reading the title and abstract, and then by reading full texts of the papers considered relevant. Two reviewers reached consensus regarding which data should be included. Searches were performed only in English. Meta-analysis, tabulation and qualitative synthesis of results were performed.

4. Main results

The majority of studies comparing levels of MHC diversity across populations with that of neutral variation have found a significant correlation. This indicates that on the short time scale MHC variation is shaped predominately by demographic processes rather than by selection. Nevertheless, some tests of selection suggest the role of selection in shaping MHC allele frequencies. In two of twelve species included in Table 1, evidence of balancing selection and not of drift shaping MHC variation was found. In five species the

evidence was mixed, indicating that both drift and selection may have an impact, and five studies found evidence of drift only. In one of the two positive studies the evidence of positive selection was found only in a fraction of populations.

We have found only a single study relating infection to MHC diversity across populations; no evidence that MHC variation was associated with mortality caused by the bacterial pathogen was found in this study.

We have not found any studies reporting populations or species that have gone extinct following reduction of MHC variations.

5. Conclusions

Implications for conservation. Given the uncertainty about the role of MHC variation for population viability, avoidance of inbreeding as the main aim of genetic restoration programmes seems reasonable, especially since inbreeding depression has well documented detrimental effects on fitness, including impairment of the immune response. Thus, it seems rational to recommend inbreeding avoidance as a priority in cases where it would conflict with retention of maximum MHC variation. Natural populations harbouring the most MHC variation will also usually have more genome-wide diversity; therefore the protection of both types of genetic diversity can be achieved simultaneously.

Implications for research. Despite balancing selection shaping MHC polymorphism in the long term, MHC variation is often substantially reduced due to genetic drift acting in bottlenecked and fragmented populations. However, whether such a loss poses a threat to the survival of populations remains unclear. The scarcity of direct evidence for the impact of MHC diversity on the survival prospects of populations, coupled with examples of long-term survival of populations despite reduced MHC polymorphism may suggest that MHC diversity is not as serious a concern in conservation as some authors have suggested. However, as the causes of past extinction events are usually uncertain, the evidence is likely to be unbalanced: it is easier to document survival, than extinction of species with depleted MHC diversity. There is thus an imperative need for data that could indirectly reveal the possible consequences of MHC diversity for population viability. In particular, we need more data on the impact of MHC allelic richness on the abundance of parasites and prevalence of disease in populations. Such data, although indirect, are much easier to obtain than the data relating MHC variation to actual extinction events. Efforts should be made to control for genome-wide inbreeding. Complementary research should assess the role of pathogens in shaping population dynamics.