

Primers for the amplification of the MHC II β chain exon 2 in the Atlantic goliath grouper (*Epinephelus itajara*)

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Abstract In the present study we designed a pair of primers to amplify the exon 2 of the MHC II β chain of the Atlantic goliath grouper, which is responsible for the recognition of pathogenic molecules and the regulation of the immune system. Future analyses of this region may provide an important database to understand the evolutionary processes affecting the populations of the goliath grouper, and to predict the conservation perspectives in the species.

Keywords *Epinephelus itajara* · Genetic diversity · *MhcEit-DAB*

The formation of spawning aggregations in fishes presents opportunities for efficient fishing and removal of significant proportions of a population within short time frames, however such practice might impact negatively these populations, collapsing them through overexploitation (Sadovy and Eklund 1999; Tobin et al. 2013). Collapsed populations are

likely to reduce their evolutionary fitness towards changes in the environment, e.g. the raise of new pathogens, making those more susceptible to illnesses (Eizaguirre and Lenz 2010).

Family Epinephelidae is an example of collapsed populations in a global scale, due to its directioned fisheries activities to the spawning aggregations (Sadovy de Mitcheson et al. 2012). The goliath grouper (*Epinephelus itajara*, Lichtenstein, 1822) is the largest bony fish and it is found in the tropical Atlantic Ocean, reaching 25 m in length and over 400 kg in weight (Sadovy and Eklund 1999). As a prominent sport angling species, which is also targeted by commercial fishermen, *E. itajara* has been exploited intensively over the past 30 years, and its populations are now in sharp decline (Aguilar-Perera et al. 2009). The docile behavior, slow growth, formation of spawning aggregations and current genetic data (low variation) seem to make its populations truly vulnerable to extinction (Frias-Torres 2006; Gerhardinger et al. 2006; Koenig et al. 2007; Silva-Oliveira et al. 2008; Mann et al. 2009).

The genes responsible for the recognition of peptides molecules and the regulation of the immune system form part of the major histocompatibility complex (MHC), which is the most polymorphic region of the vertebrate genome (May and Beebe 2009). The region of the MHC, which recognizes and binds to antigens (Peptide Binding Region—PBR), is located in MHC class II. This region of the genome is responsible for increasing the host's capacity to identify specific invasive agents (Eizaguirre and Lenz 2010). Therefore, many molecular studies of vertebrates have focused on the amplification of exon 2 of the DQB genes of the β chain of the molecules of MHC class II, given the importance of this sequence for the immune response and its high degree of polymorphism (Sonsthagen et al. 2014; He et al. 2014).

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