



Short communication

Molecular characterization of three IRF1 subfamily members reveals evolutionary significance of IRF11 in miyu croaker



Chang Shu, Yueyan Sun, Tianjun Xu*

Laboratory of Fish Biogenetics & Immune Evolution, College of Marine Science, Zhejiang Ocean University, Zhoushan, 316022, China

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ABSTRACT

The interferon regulatory factors IRF1 and IRF2 of the IRF1 subfamily play essential roles in immune responses against viruses. IRF11 is a novel IRF gene of the IRF1 subfamily; IRF11 genes share almost the same evolutionary distance with IRF1 and IRF2 genes. However, the structure and characteristics of IRF11 gene in fish have been rarely reported. In our study, IRF1, IRF2 and IRF11 genes were identified and characterized from miyu croaker genome. Results showed that the IRF1, IRF2 and IRF11 genes contain the same domains; each of these genes is composed of conserved gene organizations and characterized by gene synteny with the orthologous genes. Interestingly, IRF11 was likely found only in fish (but not specific to teleost fish). Evolutionary analysis results showed that IRF1 gene in mammals, IRF2 and IRF11 gene in fish underwent positive selection. IRF1, IRF2 and IRF11 were expressed in a wide range of miyu croaker tissues. These genes also exhibited the same expression patterns after miyu croaker was infected with poly(I:C). Therefore, our data enhanced our understanding of the functions and evolution of IRF11 in fish.

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1. Introduction

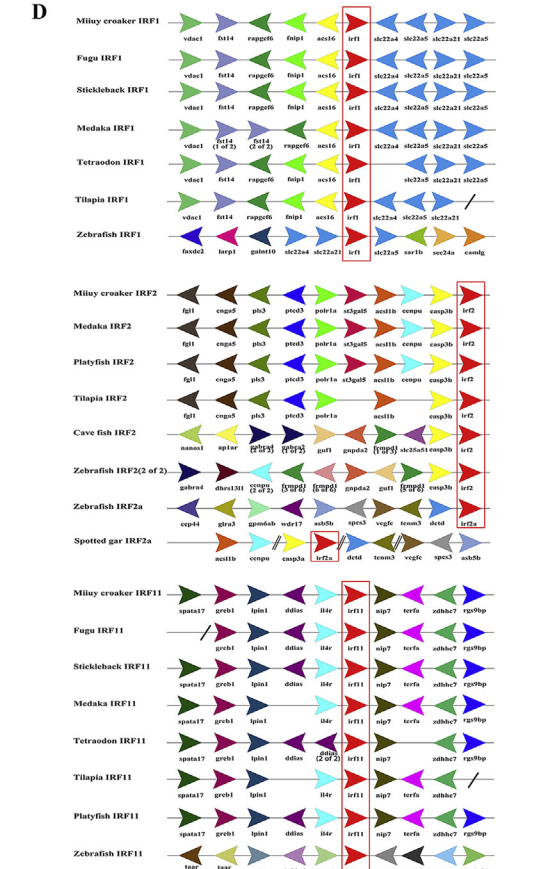
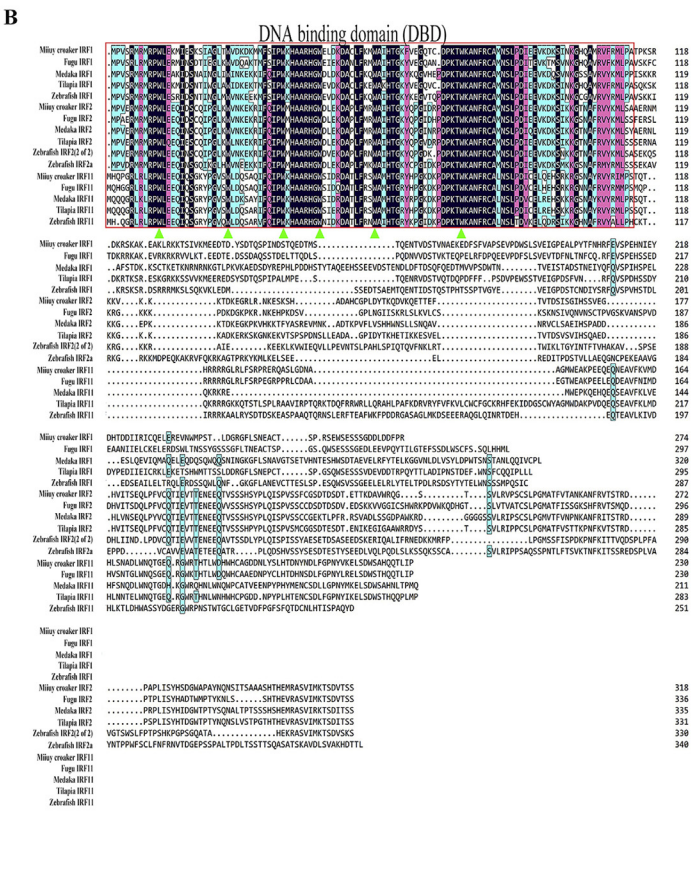
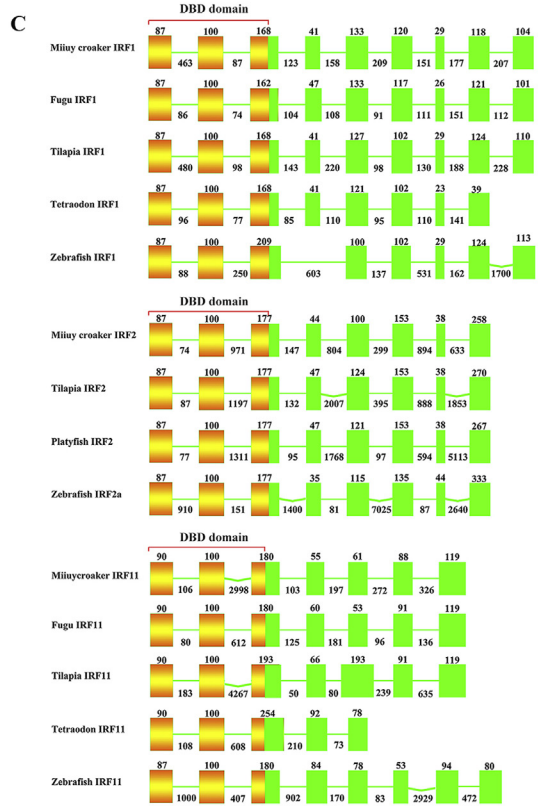
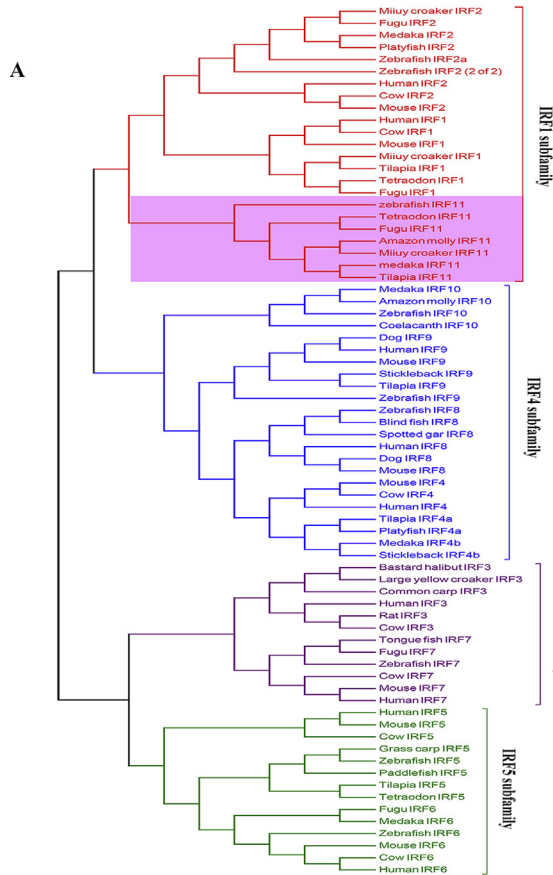
Interferon (IFN) regulatory factors (IRFs) are a family of transcription factors, which were originally identified in the regulation of IFN expression; IRFs can regulate the IFN genes and IFN-stimulated genes (ISGs) (Mamane et al., 1999; Zhang and Gui, 2012), such as Mx, ISG15 and Vig-1 (Robertson, 2006). As critical transcription mediators, IRFs play important roles in antiviral defense, immune response, cell growth regulation and apoptosis (Tamura et al., 2008). Some IRFs have been investigated in fish, for instance, IRF3 and IRF7 have been identified in crucian carp (Sun et al., 2011, 2010), IRF9 has also been detected in crucian carp (Shi et al., 2012) and zebrafish (Shi et al., 2013). Likewise, IRF10 has been found in zebrafish (Li et al., 2014). These IRFs are implicated in the regulation of IFN genes and ISGs in different signal pathways. Thus far, twelve IRFs, namely, IRF1 to IRF11, have been identified in vertebrates (Huang et al., 2010). These genes are classified into four subfamilies: IRF1 subfamily (IRF1, IRF2, and IRF11), IRF3 subfamily (IRF3 and IRF7), IRF4 subfamily (IRF4a, IRF4b, IRF8, IRF9, and IRF10), and IRF5 subfamily (IRF5 and IRF6) (Günthner and Anders, 2013).

IRF members can be divided into two groups on the basis of the different functions of IRFs: transcriptional activators (e.g., IRF1, IRF3, IRF7, IRF9 and IRF10) and bi-functional factors (e.g., IRF2, IRF4, IRF5 and IRF8) that function as activators and repressors (Nehyba et al., 2002; Hu et al., 2013). These transcription factors contain highly homologous N-terminal DNA binding domains (DBD), which can bind to DNA to perform diverse biological functions (Taniguchi et al., 2001). The IRF association domain (IAD) in the C-terminal region of IRFs exists in IRF3, IRF4 and IRF5 subfamilies; IAD2 is present in the IRF1 subfamily (Tamura et al., 2008). The IRF1 subfamily is an important group with three IRF members: IRF1, IRF2, and IRF11. IRF1 and IRF2, which have been identified in several fishes, are transcriptional factors of the type I IFN gene and are involved in cell growth regulation and apoptosis (Cuesta et al., 2003; Collet et al., 2003; Gan et al., 2012). IRF11 is a novel IRF gene that was first identified in zebrafish (Stein et al., 2007). IRF11 genes are specific to teleost fish (Huang et al., 2010). Although IRF11 in zebrafish has been analyzed through bioinformatics (Feng et al., 2015), in-depth studies on teleost IRF11 genes, including genomic structure, characteristics and expression patterns, have yet to be performed.

IRF family members have been extensively investigated in mammals; however, IRF family members in lower vertebrates have been rarely investigated. IRFs have also been widely studied in

* Corresponding author.

E-mail address: tianjunxu@163.com (T. Xu).



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