# Transcriptional Evidence for the Involvement of MyD88 in Flagellin Recognition: Genomic Identification of Rock Bream MyD88 and Comparative Analysis 

N. Umasuthan, S. D. N. K. Bathige, W. S. Thulasitha, I. Whang, J. Lee


#### Abstract

The MyD88 is an evolutionarily conserved hostexpressed adaptor protein that is essential for proper TLR/ IL1R immune-response signaling. A previously identified complete cDNA ( 1626 bp ) of OfMyD88 comprised an ORF of 867 bp encoding a protein of 288 amino acids ( 32.9 kDa ). The gDNA ( 3761 bp ) of OfMyD88 revealed a quinquepartite genome organization composed of 5 exons (with the sizes of $310,132,178,92$ and 155 bp ) separated by 4 introns. All the introns displayed splice signals consistent with the consensus GT/AG rule. A bipartite domain structure with two domains namely death domain (24-103) coded by $1^{\text {st }}$ exon, and TIR domain (151-288) coded by last 3 exons were identified through in silico analysis. Moreover, homology modeling of these two domains revealed a similar quaternary folding nature between human and rock bream homologs. A comprehensive comparison of vertebrate MyD88 genes showed that they possess a 5-exonic structure. In this structure, the last three exons were strongly conserved, and this suggests that a rigid structure has been maintained during vertebrate evolution. A cluster of TATA box-like sequences were found 0.25 kb upstream of cDNA starting position. In addition, putative $5^{\prime}$-flanking region of OfMyD88 was predicted to have TFBS implicated with TLR signaling, including copies of NFкB1, APRF/ STAT3, Sp1, IRF1 and 2 and Stat1/2. Using qPCR technique, a ubiquitous mRNA expression was detected in liver and blood. Furthermore, a significantly up-regulated transcriptional expression of $O f M y D 88$ was detected in head kidney ( $12-24 \mathrm{~h}$; >2-fold), spleen ( $6 \mathrm{~h} ; 1.5$-fold), liver ( $3 \mathrm{~h} ; 1.9$-fold) and intestine ( $24 \mathrm{~h} ; \sim 2$-fold) post-Fla challenge. These data suggest a crucial role for MyD88 in antibacterial immunity of teleosts.


Keywords-MyD88, Innate immunity, Flagellin, Genomic analysis.

## I. INTRODUCTION

T'HE innate immune system recognizes 'non-self' molecular patterns expressed on the surface of pathogens through the pattern recognition receptors (PRRs). Toll-like receptor (TLR) family members are one of the well-studied
N. Umasuthan, S.D.N.K. Bathige, and W. S. Thulasitha are graduate research assistants with the Department of Marine Life Science, School of Biomedical Sciences, Jeju National University, Jeju Special Self-Governing Province, 690-756, Republic of Korea (e-mail: navaumasuthan@gmail.com).
I. Whang is a post-doctoral researcher with the Department of Marine Life Science, School of Biomedical Sciences, Jeju National University, Jeju Special Self-Governing Province, 690-756, Republic of Korea.
J. Lee is a professor with the Department of Marine Life Science, School of Biomedical Sciences, and the Director, Fish Vaccine Development Center, Jeju National University, Jeju Special Self-Governing Province, 690-756, Republic of Korea (Tel.: +82 64754 3472; fax: +8264756 3493; e-mail: jehee@jejunu.ac.kr).

This work was supported by the Fish Vaccine Research Center of the Ministry of Oceans and Fisheries (PJT200599).

PRRs. These single membrane-spanning non-catalytic receptors recognize structurally conserved pathogenassociated molecular patterns (PAMPs) [1]-[4]. Different TLR subfamily members are involved in recognizing specific PAMPs derived from various microbial pathogens. TLR5 recognizes a substituent of bacterial flagellum called flagellin (FLA). The myeloid differentiation factor 88 (MyD88) is an evolutionarily conserved host-expressed adaptor protein required for the TLR/ IL-1R immune-response signaling [5]. It modulates the TLR signaling which culminate in the NF- KB activation and production of TNF and other inflammatory cytokines [6]. MyD88 has a bi-partite structure composed of an N-terminal death domain (DD) and C-terminal TIR domain. While the TIR domain interacts with its cognate domains located in the cytoplasmic tails of activated TLRs or IL-1R, DD mediates the interaction with the corresponding domain in IL-1R-associated kinase (IRAK) family members. Functional evidences indicated that MyD88 is a vital component of the innate immunity playing a critical role in initiating and activating the immune response, especially in the MyD88-dependent TLR/IL-1R signaling pathway [6], [7].

MyD88 has been reported from many species including several teleosts such as zebrafish [8], Japanese flounder [9], large yellow croaker [10] and rainbow trout [11]. Our previous documentation of MyD88 from rock bream (OfMyD88) was limited to its cDNA identification and mRNA expression in healthy fish, and animals challenged with LPS and Edwardsville tarda[12]. However, the gene structure and genomic evolution of MyD88, and its involvement in flagellin induced TLR5 signaling in fish was not studied. The current study was designed to evaluate its exon-intron structure, and to examine its transcription upon flagellin challenge.

## II. Materials and Methods

## A. Identification of $c D N A$ and $g D N A$

Full-length cDNA of MyD88 was identified from a previously characterized transcriptome library [13], and characterized (HM035064) [12]. A bacterial artificial chromosome (BAC) library was screened using gene-specific oligos (F1, 5'-AATCCTGACGCAGGTGGAGAGAAA-3' and R1, 5'-AGCTGTCAACCTCTGGAACCTGAA-3') designed for the above cDNA, as described previously [14], and gDNA of $M y D 88$ was retrieved from the positive BAC clone located, by GS-FLX sequencing.

# International Journal of Biological, Life and Agricultural Sciences 

ISSN: 2415-6612
Vol:8, No:5, 2014

## B. Molecular and Genomic Characterization

The gDNA and cDNA sequences of $O f M y D 88$ were aligned and gene-structure was determined. Putative 5 '-flanking region was obtained by genome walk approach (R2, 5'-GCTTCAGGCGTCCACAGGTTAC-3') and subjected to prediction of transcription factor binding sites (TFBS) using in silico tools. Molecular models of DD and TIR domain were generated based on human MyD88 (3mopC and 2z5vA) by homology modeling approach. Protein sequences of MyD88 homologs were compared using ClustalW and MatGAT matrix analyzer.

## C. Animals, Challenge and Tissue Collection

Details of animal rearing, tissue collection and processing have been described elsewhere [14]. For the FLA challenge, healthy $O$. fasciatus fish ( $\sim 96 \mathrm{~g}$ ) were acclimatized to laboratory conditions in our Fish Vaccine Development Center, Jeju National University (Republic of Korea). $100 \mu \mathrm{~L}$ of PBS containing FLA (Invivogen) at $2.4 \mu \mathrm{~g}$ fish ${ }^{-1}$ was injected by intraperitoneal (i.p.) injection ( $\mathrm{n}=20$ ). An untreated control group ( $\mathrm{n}=10$ ) was established as negative control. A group ( $\mathrm{n}=20$ ) which was injected with $100 \mu \mathrm{~L}$ of PBS only was considered as the control. Different tissues including head kidney, spleen, intestine, liver, were collected from four fish $(\mathrm{n}=4)$ at time points of $3,6,12$, and 24 h post-injection.

## D.Transcriptional Analysis

Total RNA extraction, cDNA synthesis and transcriptional analysis were performed as described earlier [14]. Quantitative real-time PCR (qPCR) was conducted to investigate the OfMyD88 mRNA levels. Briefly, the cDNA synthesized from RNA samples of FLA- or PBS-injected and unchallenged animals was used as template in standard SYBR Green qPCR (TaKaRa), using OfMyD88 (F1 and R1) and $\beta$-actin (internal control; F2, 5'-TCATCACCATCGGCAATGAGAGGT-3' and R3, 5'-TGATGCTGTTGTAGGTGGTCTCGT-3') genespecific oligos. Data was analyzed by Livak-comparative Ct $\left(2^{-\Delta \Delta C t}\right)$ method.

## III. Results and Discussion

A putative coding sequence of 867 bp encoding a peptide of 288 residues ( $\sim 33 \mathrm{kDa}$ ) and untranslated regions (UTRs) at $5^{\prime}$ ( 122 bp ) and $3^{\prime}$ ( 637 bp ) terminals of coding sequence were identified. Domain analysis revealed the presence of a death domain (DD; 24-103) and a TIR domain (151-288) in OfMyD88 protein (Fig. 1).

The DD of OfMyD88 was composed of six helices and TIR was composed of five helices and four major sheets. The homology modeling analysis revealed a similar folding pattern between MyD88 domains of human and rock bream homologs (Fig. 2). In addition, pairwise homology analysis revealed that teleost homologs share a tight conservation among them, and OfMyD88 shares a higher overall homology with its Mandarin fish homolog (Table II). This comparison further showed that relative homology in TIR domain is higher than that of DD.


Fig. 1 The schematic diagram of rock bream MyD88 (OfMyD88) transcript and comprehensive domain architecture of OfMyD88 protein. OfMyD88 is composed of DD and TIR domain. In TIR domain, three conserved motifs are found.

TABLE I
Properties of Rock Bream MYD88 (OFMYD88) at Different Molecular Levels

| MoLECULAR LEVELS |  |  |
| :--- | :--- | :--- |
| Characteristics |  | OfMyD88 |
| Nucleotide (cDNA) | Length of cDNA | 1626 |
|  | $5^{\prime}$ UTR | 122 |
|  | CDS (bp) | 867 |
|  | 3' UTR | 637 |
|  | Polyadenylation signal | ${ }^{1608}$ AATAAA $^{1613}$ |
|  | Peptide (aa) | 288 |
|  | Death domain | $24-103$ |
|  | TIR domain | $151-288$ |
|  | $N$-glycosylation site | $1\left({ }^{19}\right.$ NMSV) |
|  | Length of gDNA (bp) | 3761 |
|  | Number of exons | 5 |
|  | Number of introns | 4 |
|  | TFBS in putative | Sp1, NF-kB1, STAT1/2, |
|  | promoter ${ }^{\text {a }}$ | IRF1/2 and APRF |
|  | Dominant mRNA | (STAT3) |
|  | expression (qPCR) | Liver |

${ }^{\text {a Predicted using AliBaba2.1, JASPAR and PROMO servers. }}$


Fig. 2 Homology modeling of rock bream MyD88 (OfMyD88) (A) TIR domain and (B) DD. Conserved residues in TIR domain are shown

These in silico data confirmed that OfMyD88 essentially features the common properties of other MyD88s, in particular, those identified from teleosts. Similar to TLRs, the key adaptor proteins in TLR signaling pathways, including MyD88, have been conserved among different vertebrate classes [15], [16]. Hence, teleost MyD88 could be assumed to have similar biological roles as demonstrated in mammals.

TABLE II
Homology Indices of the Rock Bream Myd88 (OFMYD88) with the other Homologs

| Species | Identifier | Acc. No. | Length | Degree of identity [I\%] |  | Degree of similarity [S\%] |  |  |  |
| :--- | :--- | :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | (aa) | Whole | DD | TIR | Whole | DD | TIR |
| Mandarin fish | ScMyD88 | ADM25313 | 288 | 91.3 | 86.3 | 96.4 | 95.5 | 92.5 | 99.3 |
| Large yellow croaker | LcMyD88 | ACL14361 | 287 | 86.2 | 82.5 | 94.9 | 93.4 | 91.3 |  |
| Zebrafish | DrMyD88 | AAZ16494 | 284 | 70.9 | 55.0 | 87.7 | 81.3 | 71.3 | 98.6 |
| Frog | XlMyD88A | NP_001081001 | 283 | 59.5 | 50.0 | 74.6 | 74.0 | 67.5 | 84.8 |
| Chicken | GgMyD88 | A5HNF6 | 299 | 61.2 | 49.4 | 78.3 | 75.3 | 69.1 | 88.4 |
| Mouse | MmMyD88 | NP_034981 | 296 | 61.6 | 50.0 | 77.5 | 78.0 | 75.0 | 88.4 |
| Human | HsMyD88 | AAP36509 | 297 | 60.4 | 47.5 | 76.3 | 73.7 | 67.5 | 86.3 |

Degree of identity [ $\mathrm{I} \%$ ] and similarity [S\%] was calculated by the MatGAT program using BLOSUM62 scoring matrix maintaining first gap penalty and extending gap penalty levels at 12 and 1 , respectively. MotifScan was employed in determining the domain span in each species.


Fig. 3 Genomic organization of rock bream MyD88 (OfMyD88).Gene-structure and domain coding regions of $O f M y D 88$. Exons and introns are shown by box (white, UTR and black, CDS) and lines, respectively

Previously reported $O f M y D 88$ sequence and the gDNA sequence ( 3761 bp ) of current study varied by a single bp in the CDS causing a single amino acid variation. The OfMyD88 exhibited a quinquepartite genome organization composed of five exons split by four introns. All the introns displayed splice signals consistent with the consensus GT/AG rule. While the DD was encoded by first exon, the TIR domain was encoded by last three exons (Fig. 3).

Comparison of vertebrate MyD88 genes led us to propose a common quinquepartite gene structure for $M y D 88$. The last three exons coding the TIR domain were equal in size (181, 92 and 155 bp ) in all the vertebrate classes, except the third exon of teleost MyD88 which slightly varied ( 178 bp ), revealing the rigid conservation of its TIR domain and its functional importance. This is in agreement with the amino acid homology data. In contrast, first two exons broadly varied in their sizes in different classes (Table III).

Furthermore, inspection of OfMyD88 gDNA indicated a putative cluster of TATA box-like sequence quite far away from the TIS. Several potential TFBS were predicted to be located in this 5 '-flanking region including sites for Sp 1 , NF$\kappa$ B1, STAT1/2, IRF1/2 and APRF (STAT3), all of which have been demonstrated to impact the transcriptional expression of MyD88 [17]. This suggests that $O f M y D 88$ is also might be regulated by various transcription factors.

The levels of $O f M y D 88$ were quantified by qPCR technique and found that it is ubiquitously expressed with higher levels in liver and other immune relevant tissues. Both LPS and $E$. tarda up-regulated its expression in blood, liver and head kidney [12]. In the current study, involvement of $O f M y D 88$ in TLR5 mediated signaling was tested. Data revealed a significantly induced expression of $O f M y D 88$ in head kidney
(12-24 h; >2-fold), spleen ( $6 \mathrm{~h} ; 1.5$-fold), liver (3 h; 1.9-fold) and intestine ( $24 \mathrm{~h} ; \sim 2$-fold), in response to FLA-challenge.
However, FLA-mediated induced, highest expression occurred in a tissue-specific manner as shown in Fig. 4. Our results were in consistent with the report in Indian major carp, mrigal [18], in which FLA induced the expression of MyD88 (along with TLR5 and TRAF6) in multiple tissues examined.


Fig. 4 OfMyD88 expression analysis after FLA-challenge. Transcriptional expression was analyzed in head kidney (HK), spleen (SP), liver (LV), and intestine (IT) post-FLA challenge using qPCR.

Relative mRNA expression was calculated by the $2^{-\Delta \Delta C t}$ method relative to PBS-injected controls and normalized with the same, using the $\beta$-actin as the reference gene.

The up-regulated expression of MyD88 in E. tarda treated animals [12] might have occurred due to the FLA-mediated transcriptional induction, at least in part. Although these lines of evidence suggested an involvement of MyD88 in TLR(5) signaling, the significance of increased MyD88 mRNA and its
association with TLR5-mediated responses, such as cytokine production needs further experiments. In addition, functional
aspects of teleost MyD88 remains to be elucidated.

TABLE III
Comprehensive Gene-Structural Comparison of Vertebrate Myd88S

| Lineage | Species |  | E1* |  | I1 | E2 | I2 | E3 | I3 | E4 | I4 | E5* |  | Accession no. |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | (bp) | 5' | CDS |  |  |  |  |  |  |  | CDS | 3' |  |
| Mammalia | H. sapiens | 4545 | 184 | 367 | 835 | 135 | 389 | 181 | 188 | 92 | 283 | 155 | 1736 | ENST00000396334 |
|  | M. musculus | 2707 | 82 | 328 | 921 | 135 | 389 | 181 | 160 | 92 | 243 | 155 | 21 | ENSMUST00000035092 |
| Aves | G. gallus | 12685 | - | 340 | 3600 | 132 | 1958 | 181 | 836 | 92 | 1888 | 155 | 3503 | ENSGALT00000044477 |
| Reptilia | C. pictabellii | 17469 | 5 | 346 | 7275 | 120 | 1430 | 181 | 1525 | 92 | 2408 | 155 | 3932 | XM_005297139 |
| Amphibia | X. tropicalis | 5537 | 147 | 316 | 1267 | 111 | 1026 | 181 | 772 | 92 | 927 | 152 | 546 | NM_001016837 |
| Pisces | D. rerio | 3941 | 136 | 304 | 785 | 123 | 80 | 181 | 414 | 92 | 1319 | 155 | 352 | NC_007135 |
|  | P. olivaceus | 3120 | - | 310 | 974 | 123 | 808 | 178 | 398 | 92 | 82 | 155 | - | AB221347 |
|  | T. rubripes | 5471 | - | 310 | 3896 | 132 | 389 | 178 | 226 | 92 | 93 | 155 | - | NM_001113195 |
|  | O. fasciatus | 3761 | 122 | 310 | 379 | 132 | 1096 | 178 | 553 | 92 | 107 | 155 | 637 | This study |

E, exon; I, intron; the first (E1) and last (E5) exons ( ${ }^{*}$ ) have been divided into two parts ( $5^{\prime} / 3^{\prime}$-UTRs and CDS).

## IV. Conclusion

Current study evaluated the genomic evolution of MyD88 and its involvement in FLA-mediated TLR5 signaling. Our results suggest that MyD88 is an evolutionarily conserved molecule in terms of gene-structure and protein domain architecture; and therefore, mammals and teleost MyD88 may share similar functional roles. FLA stimulated OfMyD88 expression at transcriptional level in different tissues of challenged fish indicated its important role in FLA-mediated TLR5 signaling.

## AcKNOWLEDGMENT

Authors are grateful to Dr. Bong-Soo Lim and Dr. HyungBok Jung to provide fish rearing facilities and help in FLA challenge experiment.

## References

[1] Armant MA, Fenton MJ. "Toll-like receptors: a family of patternrecognition receptors in mammals." Genome biology, vol. 3, 2002, pp. reviews 3011 .
[2] Beutler B. "The Toll-like receptors: analysis by forward genetic methods." Immunogenetics, vol. 57, 2005, pp. 385-92.
[3] Bilak H, Tauszig-Delamasure S, Imler JL. "Toll and Toll-like receptors in Drosophila."BiochemSoc Trans, vol. 31, 2003, pp. 648-51.
[4] Krishnan J, Selvarajoo K, Tsuchiya M, Lee G, Choi S. "Toll-like receptor signal transduction." ExpMol Med, vol. 39, 2007, pp. 421-38.
[5] Janssens S, Beyaert R. "A universal role for MyD88 in TLR/IL-1Rmediated signaling." Trends in biochemical sciences, vol. 27, 2002, pp. 474-82.
[6] Medzhitov R, Preston-Hurlburt P, Kopp E, Stadlen A, Chen C, Ghosh S, et al. "MyD88 is an adaptor protein in the hToll//L-1 receptor family signaling pathways." Molecular cell, vol. 2, 1998, pp. 253-8.
[7] Wesche H, Henzel WJ, Shillinglaw W, Li S, Cao Z. "MyD88: an adapter that recruits IRAK to the IL-1 receptor complex." Immunity, vol. 7, 1997, pp. 837-47.
[8] van der Sar AM, Stockhammer OW, van der Laan C, Spaink HP, Bitter W, Meijer AH. "MyD88 innate immune function in a zebrafish embryo infection model."Infection and immunity, vol. 74, 2006, pp. 2436-41.
[9] Takano T, Kondo H, Hirono I, Saito-Taki T, Endo M, Aoki T. "Identification and characterization of a myeloid differentiation factor 88 (MyD88) cDNA and gene in Japanese flounder, Paralichthysolivaceus." Developmental \& Comparative Immunology, vol. 30, 2006, pp. 807-16.
[10] Yao CL, Kong P, Wang ZY, Ji PF, Liu XD, Cai MY, et al. "Molecular cloning and expression of MyD88 in large yellow croaker, Pseudosciaenacrocea." Fish Shellfish Immunol, vol. 26, 2009, pp. 24955.
[11] Rebl A, Goldammer T, Fischer U, Kollner B, Seyfert HM. "Characterization of two key molecules of teleost innate immunity from rainbow trout (Oncorhynchusmykiss): MyD88 and SAA." Vet ImmunolImmunopathol, vol. 131, 2009, pp. 122-6.
[12] Whang I, Lee Y, Kim H, Jung SJ, Oh MJ, Choi CY, et al. "Characterization and expression analysis of the myeloid differentiation factor 88 (MyD88) in rock bream Oplegnathusfasciatus." MolBiol Rep, vol., 2010, pp. 3911-3920.
[13] Umasuthan N, Whang I, Kim J-O, Oh M-J, Jung S-J, Choi CY, et al. "Rock bream (Oplegnathusfasciatus) serpin, protease nexin-1: Transcriptional analysis and characterization of its antiprotease and anticoagulant activities." Developmental \& Comparative Immunology, vol. 35, 2011, pp. 785-98.
[14] Umasuthan N, Bathige S, Revathy KS, NiroshanaWickramaarachchi W, Wan Q, Whang I, et al. "AC1 inhibitorortholog from rock bream (Oplegnathusfasciatus): Molecular perspectives of a central regulator in terms of its genomic arrangement, transcriptional profiles and antiprotease activities of recombinant peptide." Developmental \& Comparative Immunology, vol., 2013, pp. 197-210.
[15] Lynn DJ, Lloyd AT, O’Farrelly C. "In silicoidentification of components of the Toll-like receptor (TLR) signaling pathway in clustered chicken expressed sequence tags (ESTs)." Veterinary Immunology and Immunopathology, vol. 93, 2003, pp. 177-84.
[16] Prothmann C, Armstrong NJ, Rupp RA. "The Toll/IL-1 receptor binding protein MyD88 is required for Xenopus axis formation." MechDev, vol. 97, 2000, pp. 85-92.
[17] Harroch S, Gothelf Y, Revel M, Chebath J. "5' upstream sequences of MyD88, an IL-6 primary response gene in M1 cells: detection of functional IRF-1 and Stat factors binding sites." Nucleic acids research, vol. 23, 1995, pp. 3539-46.
[18] Basu M, Swain B, Maiti NK, Routray P, Samanta M. "Inductive expression of toll-like receptor 5 (TLR5) and associated downstream signaling molecules following ligand exposure and bacterial infection in the Indian major carp, mrigal (Cirrhinusmrigala)." Fish \& Shellfish Immunology, vol. 32, 2012, pp. 121-31.

