Maternal effects shape the alternative splicing of parental alleles in reciprocal cross hybrids of Megalobrama amblycephala x Culter alburnus

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Abstract

Background Maternal effects contribute to adaptive significance for shaping various phenotypes of many traits. Potential implications of maternal effects are the cause of expression diversity, but these effects on mRNA expression and alternative splicing (AS) have not been fully elucidated in hybrid animal. Results Two reciprocal cross hybrids following hybridization of Megalobrama amblycephala (blunt snout bream, BSB) and Culter alburnus (topmouth culter, TC) were used as a model to investigate maternal effects. In a comparison of BSB and TC homoeolog expression from the two reciprocal cross hybrids, we identified 49–347 differentially expressed BSB-homoeologous genes and 54–354 TC-homoeologous genes. 2402, 2959, and 3418 AS events between the two reciprocal cross hybrids were detected in Illumina data of muscle, liver, and gonads, respectively. Moreover, 21,577 (TC-homoeologs) and 30,007 (BSB-homoeologs) AS events were found in the 20,131 homoeologous gene pairs of TB F3 based on PacBio data, while 30,561 (TC-homoeologs) and 30,305 (BSB-homoeologs) AS events were found in BT F3 homoeologous gene pairs. These results further improve AS prediction at the homoeolog level. To analyze body shape traits, bmpr2a of the bone morphogenetic protein family was selected as an AS model to investigate expression diversity. Conclusions The distribution of differentially expressed genes and AS in BSB- and TC-subgenomes exhibited various changes between the two reciprocal cross hybrids, suggesting that maternal effects are the cause of expression diversity. These findings provide a novel insight into mRNA expression changes and AS under maternal effects in lower vertebrates.

Full Text

This preprint is available for download as a PDF.

Figures

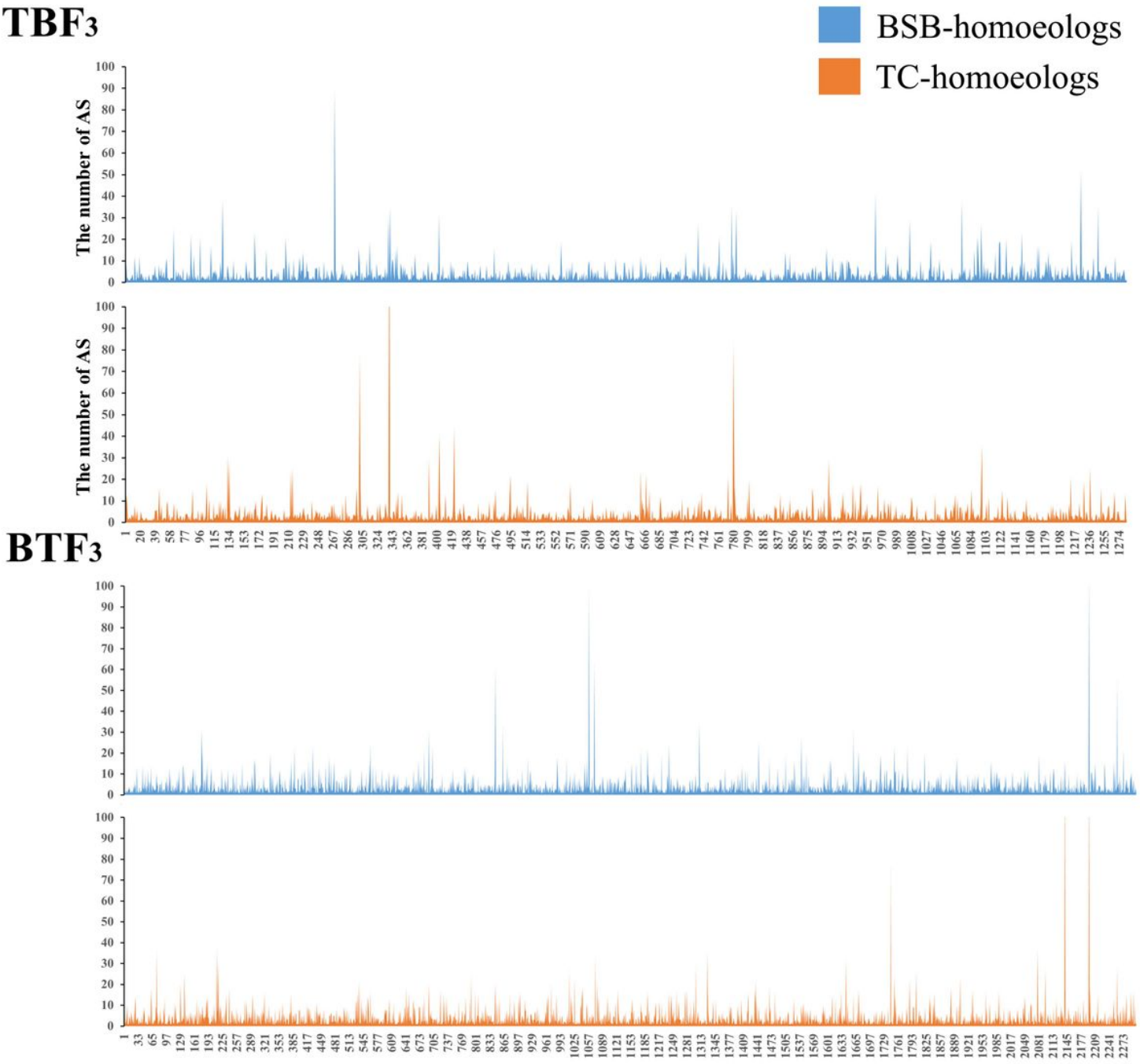

Figure 1

Distribution of AS events observed in each gene of the two reciprocal cross hybrids.

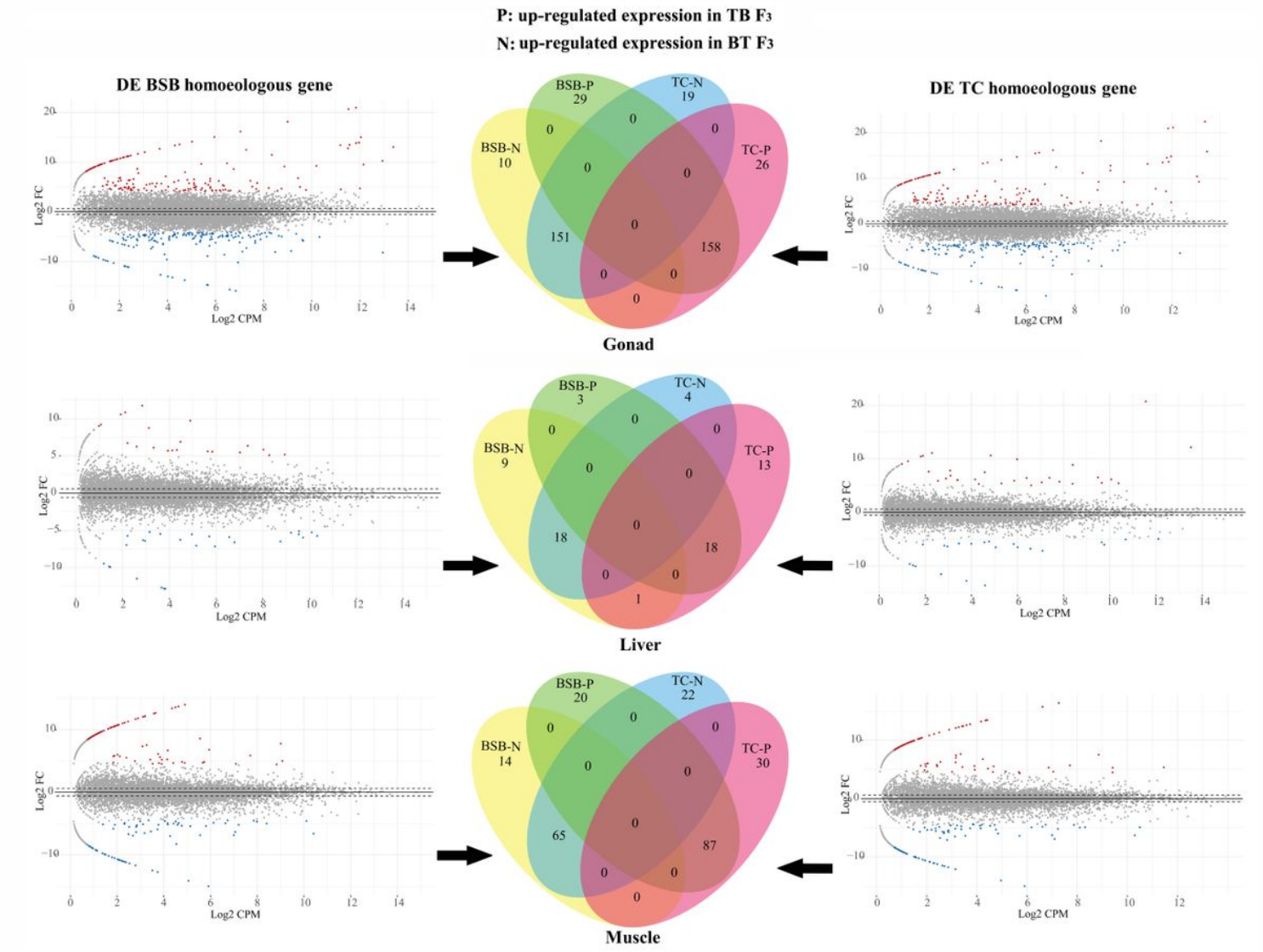

Figure 2

DEGs detected in homoeolog expression levels between the two reciprocal cross hybrids (BT F3 and TB F3). Shared DEGs are listed in the Venn diagram. The same differential expressed trends were always found in respective BSB- and TC- homoeologous genes. The values of log2 fold change (FC) and log2 counts per million (CPM) were used to assess significant DEGs.

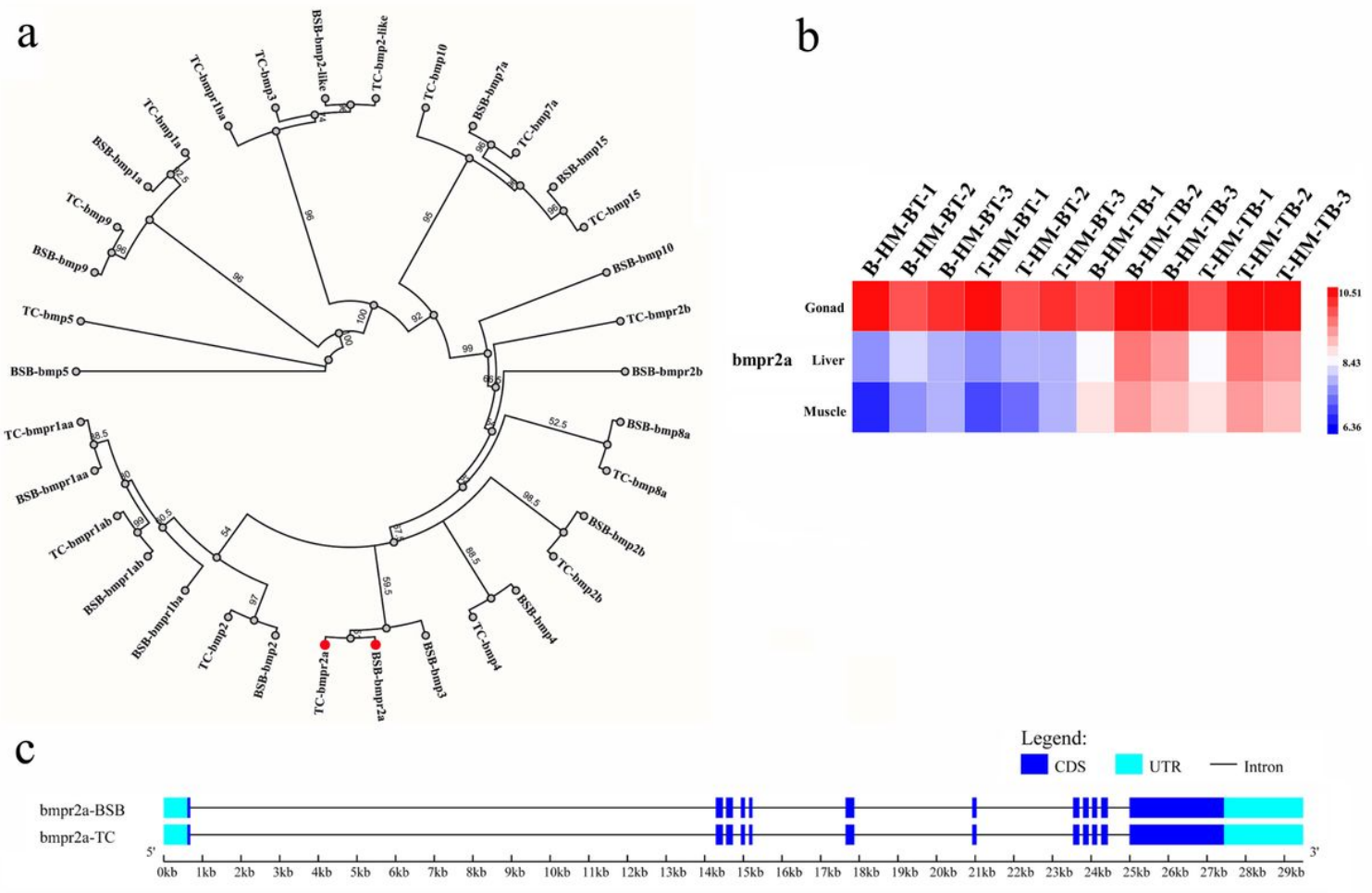

Figure 3

Phylogenetic tree of the bone morphogenetic protein (BMP) family and homoeolog 19 expression of bmpr2a. (A) Phylogenetic neighbor-joining tree of the BMP family between M. amblycephala (BSB) and C. alburnus (TC). The genetic distance model was used with the Tamura–Nei method [39] and bootstraps were shown around corresponding branches. (B) Heatmap showing the homoeolog expression of bmpr2a, which was not significant different between TB F3 and BT F3 in all three tissues. (C) The gene structure of bmpr2a.

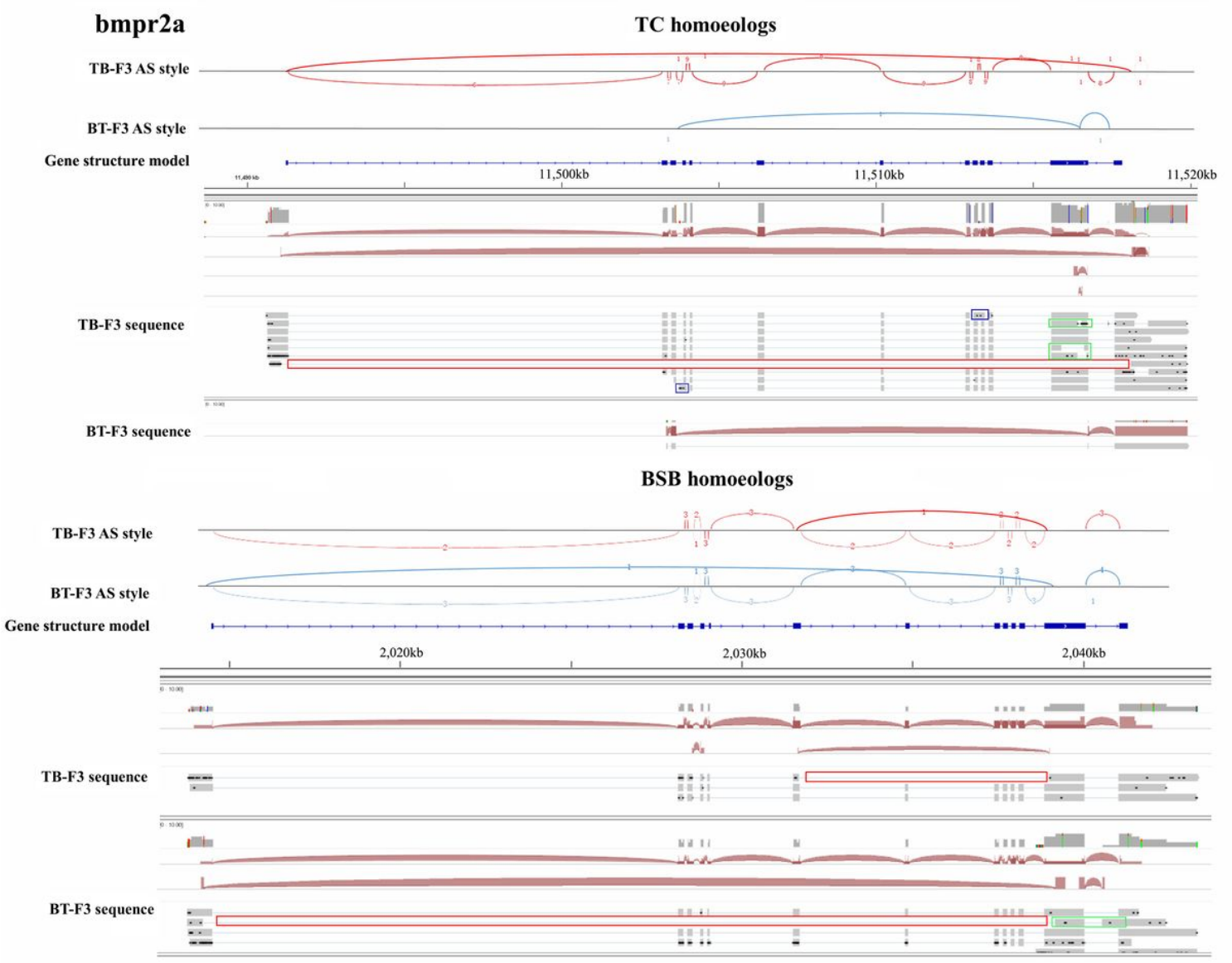

Figure 4

Various AS events detected in BSB- and TC- homoeologs of bmpr2a. Red box represents skipped exons (SE), blue box represents retained introns (RI), and the green box represents alternative 3' splice site (A3SS) events.

Supplementary Files

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- supplement1.pdf