Data Article

Data in support of the discovery of alternative splicing variants of quail LEPR and the evolutionary conservation of qLEPRl by nucleotide and amino acid sequences alignment

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ABSTRACT

Leptin receptor (LEPR) belongs to the class I cytokine receptor superfamily which share common structural features and signal transduction pathways. Although multiple LEPR isoforms, which are derived from one gene, were identified in mammals, they were rarely found in avian except the long LEPR. Four alternative splicing variants of quail LEPR (qLEPR) had been cloned and sequenced for the first time (Wang et al., 2015[1]). To define patterns of the four splicing variants (qLEPR₁, qLEPR-α, qLEPR-β and qLEPR-γ) and locate the conserved regions of qLEPR₁, this data article provides nucleotide sequence alignment of qLEPR and amino acid sequence alignment of representative vertebrate LEPR. The detailed analysis was shown in [1].
Value of the data

- qLEPR is a potentially important factor with multifunctional features, but qLEPR is completely not characterized in the literature.
- Future studies concerning effects of qLEPR in biological systems would require its characterization, which will be facilitated by the alternative splicing data in here.
- Nucleotide sequence alignment of qLEPR defines patterns of the splicing variants.
- Amino acid sequence alignment locates the conserved regions of LEPR in vertebrates.

1. Data, experimental design, materials and methods

The data shown here are two figures of sequence analysis of Japanese quail LEPR (qLEPR). Supplementary Fig. S1 is a comparison of the nucleotide sequences of four alternative splicing variants of qLEPR including qLEPRl, qLEPR-a, qLEPR-b and qLEPR-c. Supplementary Fig. S2 is an alignment of amino acid sequences of qLEPR with that of some other vertebrates.

1.1. Nucleotide sequences alignment of four qLEPR variants

qLEPRl (a long variant of qLEPR, GenBank: KJ639903) we first cloned was implemented a nucleotide blast in public database NCBI. The nucleotide sequence identify between qLEPRl and chicken LEPR reached 92%. Therefore, the exons and the canonical GT–AG donors and acceptor sites of qLEPRl were defined according to chicken genomic LEPR (GenBank: NC_006095). Other three variants were aligned with qLEPRl by ClustalW. Based on the alignment in this data, Supplementary Fig. S1 was made and its detailed analysis was shown in Ref. [1].
1.2. Amino acid sequences alignment of LEPR in vertebrates

The signal peptide and transmembrane regions of the predicted amino acid sequence of qLEPRl were detected with the SMART program (http://smart.embl-heidelberg.de/). The amino acid sequences of LEPR in other species were retrieved from public databases (including NCBI and Ensembl). The predicted amino acid sequence of qLEPRl was aligned with that of other vertebrates by ClustalW. Supplementary Fig. S2 was made according to the alignment of LEPR in vertebrates. The analysis was also shown in Ref. [1].

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2015.11.025.

Reference