عنوان مقاله:

(In silico Discovery of Conserved and Novel miRNAs from Expressed Sequence Tags in the Chicken (Gallus gallus

محل انتشار:

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خلاصه مقاله:

MicroRNAs (miRNAs) and other types of small non-coding RNAs play a crucial role in the regulation of gene expression in eukaryotes either by post-transcriptional degradation or attenuating translation of messenger RNAs. In the case of the chicken (Gallus gallus), knowledge regarding miRNAs is still limited. In the present study, a computational approach was employed to screen miRNAs from the Expressed Sequence Tags (ESTs) of the chicken. A total of ۲۱,۲۹۸ known miRNAs belonging to ۱۱۴ metazoan species were searched for homology against more than ۱۹۲,۰۲۰ EST sequences of the chicken. Consequently, ۶۰ potential miRNA candidates were identified according to a range of filtering criteria. As a result, four novel miRNAs were found among the identified miRNAs including gga-miR-۹۲a, gga-miR-۲۴۳۸, gga-miR-۲۹۷۰-۵p, and gga-miR-۲۹۷۰-۳p belonging to miR-۹۲, miR-۲۴۳۸ and miR-۲۹۷۰ families. To predict their targeted genes, a BLAST search was done against the chicken ۳' UTR mRNA database. As a result, ۶۷۸, ۴۲۲, ۱۷۱ and ۱۱۰ targets were determined for gga-miR-۹۲a, gga-miR-۲۴۳۸, gga-miR-۲۹۷۰-۵p, and gga-miR-۲۹۷۰-۳p, respectively. Most of the predicted target genes participate in multiple biological processes, including immune system, regulation of cAMP biosynthesis, regulation of cyclase activity and regulation of lyase activity. Finally, a phylogenetic analysis of gga-miR-۲۹۷۰ and gga-miR-۹۲a sequences revealed a close relationship between the chicken and Taeniopygia guttata, while gga-miR-۲۴۳۸ shares maximum percentage sequence similarity with bta-miR-۲۴۳۸ in Bos taurus. The present study is the first attempt to screen microRNAs from ESTs originating from the .chicken leading to the identification of novel miRNAs

کلمات کلیدی:

Computational approach, Filtering criteria, Phylogenetic analysis, Screening miRNAs., میکرو آر ان ای, جوجه, پیش بینی

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