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عنوان مقاله:

PHYLOGENETIC STUDY OF ZAR1 GENE IN DIFFERENT ANIMAL SPECIES

محل انتشار:

اولین کنفرانس بین المللی ایده های نو در کشاورزی (سال: 1392)

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خلاصه مقاله:

Zygote Arrest1, Zar1, is the first identified oocyte-specific maternally-expressed gene that functions at the oocyte-to-embryo transition and encodes a protein that is thought to function in the initiation of embryogenesis. Studying the maternal genes, including oocyte-specific ones, in farm species is a valuable model for the study of the mechanisms that affect oocyte quality and its implication in the success of embryo development and survival. Therefore the aim of this study was to identify different fractions of protein and phylogenetic of ZAR1 gene in different species of animal.Material and Methods: In this study, we used bioinformatics studies and NCBI databases, for awareness of the phylogenetic of ZAR1 genes. For human, cow, sheep, goat and other species, mRNA and protein sequences of gene ZAR1, obtained from the NCBI and Uniport database. Drawing phylogenic tree by Neighbor-Joining (NJ) method base on mRNA sequences and calculation of the percentage of nucleotides replacement by maximum likelihood method was performed using MEGA4 software. The InterPro and Conserved domain database (CDD) software was used for detection of different fractions of protein.Result: Comparison of mRNA sequences showed that phylogenic tree is rooted for this gene, as an orthologous gene, which is derived from a common ancestor. The sequence of sheep and goat is placed in a sub-branch which forms a clade beside cow and then pig sequence. This result could be a clue for similar performance of this gene among different species, making difference timing of the oocyte-to-embryo transition from species to species. Also, the results illustrated that, the average ratio of substitutions to replacement is more than one, suggesting a higher percentage of nucleotides substitution in comparison with nucleotides replacement. Furthermore, scrutiny of different fractions of ZAR1 proteins, revealed presence of a zinc finger domain (Znf-3CxxC domain) which is connected to two-His and two-Cys amino acids. These findings indicate that, this protein belong to a component of DNA-binding proteins that involved in protein-protein interactions, suggesting its role in transcription regulation. So, these ZAR1 proteins contain an important functional domain that is conserved through vertebrate .evolution

کلمات کلیدی:

ZAR1 gene, Phylogenetic tree, Zinc-finger domain, Oocyte-to-embryo transition

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