



Finding genes involved in HA production a Systems Biology Approach

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Abstract: Hyaluronic acid is a very important and vital polysaccharide. It is very important in the human body and various industries[1]. The study of genes and main proteins in the production pathway of hyaluronic acid through data from biological databases showed multiple alignment of amino acid sequences of *hasA*, *hasB* and *hasC* genes in *Streptococcus Pyogenes* bacteria with other bacteria producing this substance[2], there is a distinct and repetitive amino acid sequence retained in all bacteria, and in the case of the *hasC* gene, this sequence contains almost the entire sequence of the amino acid sequences of the *hasC* gene. Studies have also shown that the functional units of these proteins are exactly within these retained sequences, and these same issues increase the importance of the sequences. The study of the phylogenetic tree of these genes shows that compared to other genes, the *hasA* gene, as a very important gene, has a more evolutionary distance in the production pathway of hyaluronic acid. In the interaction of HASA, HASB and HASC proteins, it was found that the simultaneous presence of these 3 genes in bacteria is very important. Also, the well-known and accurate relationship between HASA and HASB proteins in bacteria is more than the relationship between HASA and HASB proteins. Using analyzed data can help us produce more hyaluronic acids in laboratory studies and make industrial strains.

Keywords: Hyaluronic acid; system biology; Streptococcus Pyogenes; has

References

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