

Modified Genome-Scale Metabolic Model of Escherichia coli by Adding Hyaluronic Acid Biosynthesis-Related Enzymes (GLMU2 and HYAD) from Pasteurella multocida

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Abstract : Hyaluronic acid (HA) consists of linear heteropolysaccharides repeat of D-glucuronic acid and N-acetyl-D-glucosamine. HA has various useful properties to maintain skin elasticity and moisture, reduce inflammation, and lubricate the movement of various body parts without causing immunogenic allergy. HA can be found in several animal tissues as well as in the capsule component of some bacteria including *Pasteurella multocida*. This study aimed to modify a genome-scale metabolic model of *Escherichia coli* using computational simulation and flux analysis methods to predict HA productivity under different carbon sources and nitrogen supplement by the addition of two enzymes (GLMU2 and HYAD) from *P. multocida* to improve the HA production under the specified amount of carbon sources and nitrogen supplements. Result revealed that threonine and aspartate supplement raised the HA production by 12.186%. Our analyses proposed the genome-scale metabolic model is useful for improving the HA production and narrows the number of conditions to be tested further.

Keywords : *Pasteurella multocida*, *Escherichia coli*, hyaluronic acid, genome-scale metabolic model, bioinformatics

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