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A Dynamic Model for Assessing the Advanced Glycation End Product Formation in Diabetes

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Abstract : Advanced Glycation End (AGE) products are the end products due to the reaction between excess reducing sugar present in diabetes and free amino group in protein lipids and nucleic acids. Thus, non-enzymic glycation of molecules such as hemoglobin, collagen, and other structurally and functionally important proteins add to the pathogenic complications such as diabetic retinopathy, neuropathy, nephropathy, vascular changes, atherosclerosis, Alzheimer's disease, rheumatoid arthritis, and chronic heart failure. The most common non-cross linking AGE, carboxymethyl lysine (CML) is formed by the oxidative breakdown of fructosyllysine, which is a product of glucose and lysine. CML is formed in a wide variety of tissues and is an index to assess the extent of glycoxidative damage. Thus we have constructed a mathematical and computational model that predicts the effect of temperature differences in vivo, on the formation of CML, which is now being considered as an important intracellular milieu. This hybrid model that had been tested for its parameter fitting and its sensitivity with available experimental data paves the way for designing novel laboratory experiments that would throw more light on the pathological formation of AGE adducts and in the pathophysiology of diabetic complications.

Keywords : advanced glycation end-products, CML, mathematical model, computational model
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