



## Predicting RNA Secondary Structures of *ADC* and *ODC* Genes Involved in Putrescin Biosynthesis in Fenugreek (*Trigonella foenum-graceum* L.)

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**Abstract:** Knowledge about the structure of biological molecules and knowing that how they interact when generating new compositions can be very useful for medicinal purposes. Fenugreek (*Trigonella foenum-graceum*) is a valuable medicinal plant of fabaceae family that has medicinal properties and has the ability to stabilize nitrogen. Ribonucleic acid (RNA) has various functions in cells. The structure of the RNA determines its functions. Unfortunately, the prediction of RNA structure is more difficult than predicting the second and third structures of proteins. Over the past few decades, several methods have been designed to predict the second structure of the RNA. Some of these methods predicted the secondary structure for our sequence by receiving the input RNA sequence and then maximizing of base pairs or minimizing the free energy of one or more sequences. In this study, we used Sfold, Mfold and RNAfold software to predict the secondary structure of the RNA of *ADC* and *ODC* genes which are involved in Arginine decarboxylase and Ornetin decarboxylase biosynthetic pathway and contributing in Putrescin biosynthetic pathway. The minimum free energy for *ADC* and *ODC* genes in RNAfold software was -165.14 and -167.2, respectively. The number of hairpins was 11 and 13, number of multi-loop was 6 and 5 respectively. In Sfold software, the free energy was -166 and -201.6, respectively, the number of hairpins was 13 and 12, and the number of multi-loop was 9 and 8, and minimum free energy in Mfold was -166 and -202.8, the number of hairpins was 12, 11, and The number of multi-loops was 10 and 9. This data can be use for gene expression and turn off gene at RNA level.

**Keywords:** Fenugreek; Mfold, RNAfold; Secondary structure RNA; Sfold,