

Development of cost – effective technology for mass multiplication and delivery of *Beauveria bassiana* and *Metarhizium anisopliae* biocontrol agents

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Plant protection against *H. armigera* has been progressively reoriented from a therapeutic approach to a rational use of pesticide chemicals in which consumer health and environmental preservation prevail over any other productive or economic considerations. *Beauveria bassiana* and *Metarhizium anisopliae* are the most widely used biocontrol agents and their application on plants is foliage spray. Unlike chemicals these biocontrol agents need support even after their application to get established in targeted niche. To ensure the sustained availability of biocontrol agent's requires several steps addressed to its isolation in pure culture and screening by means of efficacy bioassays performed in vitro and in vivo trials under real conditions of application and standardization of abiotic factors. For the commercial delivery of *B.bassiana* and *M.anisopliae*, these were produced on Agricultural wastes like wheat bran flakes supported excellent growth of both *B.bassiana* and *M.anisopliae*. Population of *B.bassiana* and *M.anisopliae* in colonized wheat bran are as $>10^8$ cfu/gm of the fermented substrate. The developed fungi are formulated by means of biocompatible additives to increase survival and to improve the application and stability of the final product. This study led to test the efficacy of developed final product under laboratory and field trials for control of *H. armigera*. Cost –effective Technologies of colonization of biocontrol agents on agricultural wastes are becoming popular and to improve plant health and yield, irrespective of crop.

Keywords: Delivery system, Mass multiplication, *B.bassiana* and *M.anisopliae*.

Structure-function based study in ns-synonymous SNPs of MMP3 and MMP13 genes responsible for cardiovascular disease - A computational approach

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Human genome project paved the way to understand and predict molecular basis of disease. Single-nucleotide-polymorphisms (SNPs) are the predominant mutation, may be as a result of biochemical abnormalities. The Matrix-metalloproteinase MMP 3 and MMP 13 genes inspected in the study accounts for various forms of Cardiovascular Diseases (CVD). The deleterious effect of non-synonymous (ns-SNPs) were analyzed using computational tools such as SIFT and PolyPhen 2. iMutant, PANTHER and PROVEAN tools were also used to analyze the phenotypic and evolutionary prospects. Further, Root Mean Square Deviation (RMSD) was calculated using SWISS-PDB viewer for the 50% of SNPs that were predicted to be deleterious by SIFT and PolyPhen 2.0 together. Accordingly, the point mutations P187S, P276S, R316C, and W333R in MMP 3 and Y42H, F74S, M91T, D100N, D198V, W207G, P281L, T323M, and G446R in MMP 13 had $RMSD \geq 1.0 \text{ \AA}$. The deviation between native and mutant type structures will be more if the RMSD value are more and this deviation may reflect on their function. Thus we conclude that the study helps us in better understanding of the variation in the perspective of in-silico structure and function and also showed that the above mutation as major targets which may lead to CVD.

Keywords: MMP3, MMP113, computational tools, RMSD, Cardiovascular Disease.

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