

DIVERSITY OF TWO GENES FROM CHEWING PEST *PLUTELLA XYLOSTELLA* (L.) POPULATIONS NATIVE TO DIFFERENT GEOGRAPHICAL REGIONS OF KARNATAKA, INDIA

B. N. CHAITANYA¹, R. ASOKAN² & T. SITA³

^{1, 2}Division of Biotechnology, Indian Institute of Horticultural Research (IIHR),
Bangalore, Karnataka, India

³Head Division of Biotechnology, St. Martin's College of Engineering, Dollapally, Hyderabad, Telangana, India

ABSTRACT

Plutella xylostella (L.), the Diamondback Moth (DBM), is a serious pest of cruciferous crops across the world, resulting in crop damage. To evaluate the extent of genetic variation in this species, five populations were collected across Karnataka, India. Two important genes: Ecdysteroid receptor (EcR) and Juvenile hormone epoxidase hydrolase (JHEH) were considered for the same. The former is involved in molting process wherein, the later in reproduction and development. In the present study, we have successfully cloned and sequenced both the genes which resulted in 671 and 798 bp amplicons for both EcR and JHEH gene respectively. Further, on sequence alignment with Bioedit, neither nucleotide variation nor parsimony regions for EcR were reported. In case of JHEH, 56 (7.01 %) nucleotide variations along with 43 parsimony informative sites were chronicled. Further, translating nucleotides, 223 and 266 amino acids were generated respectively. Phylogenetic analysis supported that, populations of DBM under study clustered into a single clade, deciphering perseverance of low genetic variations. The data generated with this study aids in designing a safe and effective management strategy like Ribonucleic acid interference (RNAi).

KEYWORDS: Ecdysteroid Receptor, Juvenile Hormone Epoxidase Hydrolase, RNAi, Genetic Diversity

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