

# Acetylcholinesterase Point Mutations putatively Associated with Organophosphate Resistance in *Tetranychus urticae*

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To screen point mutations associated organophosphate resistance in *Tetranychus urticae* (TSSM), sequence analysis of the cloned TSSM acetylcholinesterase gene (*tssmace*) was conducted. Sequence comparison between the susceptible (UD) and monocrotophos-resistant (AD) strains revealed a total of 6 different point mutations. Three mutations (N32S, R39S and I44T) were located on the signal peptide region of the *tssmace*. The G228S and F439W mutations were located close to one of the aromatic residues in the lining of catalytic gorge and to the glutamic acid forming the catalytic triad, respectively, and appeared to exist as heterogeneous alleles. The last A391T mutation located right next to an aromatic residue in the lining of catalytic gorge was found solely in the AD strain as a homogeneous allele. To investigate the functional significance of the individual mutations in resistance, the AD strain was further selected 4 times with LC<sub>75</sub> dose of monocrotophos, and the frequency change of each mutation was evaluated by sequencing of PCR-amplified *tssmace* cDNA fragment. Among the heterogeneous mutations, the frequency of the F439W was slightly increased whereas the G228S frequency was little changed. Taken together, our findings suggest that the A391T play an essential role and the F439W a supplementary role in conferring monocrotophos resistance. We are currently conducting crossing experiments followed by genotyping to confirm our notion.