IMPORTANCE OF THE P106S TARGET SITE MUTATION IN CONFERRING RESISTANCE TO GLYPHOSATE IN AN ELEUSINE INDICA BIOTYPE FROM THE PHILIPPINES. Shiv S. Kaundun, Ian A. Zelaya, Richard R. Dale, Amy Lycett, Patrice Carter, Kate Sharples, and Eddie McIndoe, Syngenta Ltd., Weed Control Research, Jealott's Hill International Research Centre, Bracknell, Berkshire, RG42 6EY, UK.

Few studies on herbicide resistance report co-segregation analysis to unambiguously establish the correlation between genotype and phenotype. Herein we report on the importance of the EPSPS prolyl ${ }^{106}$ point mutation to seryl (P106S) in conferring resistance to glyphosate in a goosegrass (Eleusine indica) population from Davao, Island, The Philippines. The resistance factor estimated when comparing the Davao population to a known susceptible E. indica biotype was 4.4 fold. Evaluation of potential resistance mechanisms identified the presence of P106S in EPSPS whilst no consistent differences were observed in glyphosate absorption or translocation patterns. PCR amplification of specific alleles (PASA) analysis established that the mixed-resistant Davao population was comprised of $39.1 \%$ homozygous proline wild-type (PP106), $3.3 \%$ heterozygous serine mutant (PS106) and 57.6\% homozygous serine mutant (SS106) genotypes. Rate response estimate of plants with a predetermined genotype confirmed that Davao SS106 individuals were at least 2 fold more resistant to glyphosate compared to Davao PP106 individuals. Further, extensive co-segregation analysis at different growth stages and glyphosate rates confirmed a strong correlation ( $P<0.01$ ) between presence of SS106 and the resistant phenotype. Bioinformatics evolutionary conservation analysis of proly ${ }^{106}$ indicated that the residue is less conserved compared to highly-conserved structural or functional residues in EPSPS; the potential structural implications of P106S mutation on vicinal residues in EPSPS are discussed.

