

## **In the Weeds: Genomic Analysis of Glyphosate Resistance in Crop Fields**

### **Assessment**

By the end of the study, students will be able to:

1. Use NCBI data and tools and a biologically real example to test hypotheses about herbicide resistance.
2. Use BLAST to compare DNAs of EPSP genes from glyphosate sensitive and glyphosate resistant strains of the same weed species.
3. Determine whether a single mutation (SNP) at the DNA level would cause a silent, synonymous or nonsynonymous amino acid change
4. Use a protein structure 3-dimensional rendering program to make inferences about possible mechanisms of EPSP glyphosate resistance.
5. Develop a hypothesis that you could test to determine how glyphosate affects the EPSP synthase enzyme.
6. How can PubMed help you answer a research question?

**Answer the following questions related to what you just learned in the genomic analysis activity.**

1. What do the various forms of BLAST do? BLAST stands for Basic Local Alignment Search Tool.
2. What is a cDNA?
3. Do all DNA mutations change the protein?
4. In which codon positions are mutations more likely to cause protein change?
5. What codon position has been altered in the Glyphosate resistant gene?
6. Had there been a mutation in the third codon position of E, would that have changed the amino acid to an A?

7. In what type of protein primary structure does the non synonymous amino acid substitution from E to A take place?
8. Could a change at the protein level be detectable at the mRNA level?
9. What amino acids is ESSPs involved in synthesizing?
10. Could a mutation in this gene cause glyphosate resistance?