

# Understanding Genetics of Herbicide Resistance in Weeds: Implications for Weed Management

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## Abstract

Herbicide-resistant weeds pose a serious threat to weed management. Several factors govern the rate at which the resistant individuals (alleles) become dominant in the population [3]. Genetic factors, such as the initial frequency of resistant alleles present in the population, the dominance relationships among the alleles and fitness cost of the resistance gene(s) can significantly influence evolution of resistance to herbicides. Other factors, such as biology of weed species (e.g. life cycle, [seed production](#) capability, mating system), the herbicide and target site properties (chemical structure, herbicide-target site interactions and residual activity), herbicide dose and application performance can impact dynamics of herbicide resistance evolution, as well. This review focuses on how genetic factors influence the evolution and spread of herbicide resistance in weeds and how herbicide use pattern can determine the genetics of herbicide resistance. Additionally, how this information can be useful in both proactive and reactive management of herbicide-resistant weeds is also discussed. management across the globe. Weeds evolve resistance to herbicides as a result of herbicide selection pressure. Under continuous herbicide selection, the resistant individuals dominate in a population

Understanding the genetics of herbicide resistance will help assess frequency and spread of herbicide resistance allele(s) in a population, which will assist in formulating prudent weed management practices to delay the evolution of resistance.

Dominant expression of the resistance allele also accelerates the process. Target-site resistance (TSR) is determined by a single gene, and is more likely a result of strong selection pressure. Although, non-target site resistance (NTSR) usually results under moderate selection pressure accumulating multiple alleles with minor effects imparting resistance, it may also involve a single gene when evolved under high selection pressure. Such monogenic resistances evolve and spread quickly, especially when the resistance is dominant and nuclear-inherited. Herbicide mixtures with different modes of action when applied at recommended doses can effectively delay the evolution of both TSR and NTSR.

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