

# Weed Science Society of America

## FACT SHEET

# The Genetic Mapping of Weeds



The 2020 annual meeting of the Weed Science Society of America (WSSA) featured a special symposium on *Genomics of Weedy and Invasive Species: 2025 and Beyond* – a session that inspired this backgrounder. Our thanks go to the many weed scientists below who shared their work during the symposium and are spearheading important genomics initiatives reflected in this document:

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## **1. What are weed genomes, and why do weed scientists want to map them?**

A genome is the genetic material that carries the traits of an animal, plant or single-celled life form that can be inherited by subsequent generations. When an international team of scientists mapped the *human* genome, they unleashed a new wave of healthcare innovation. As a result, we now have a better understanding of the genetic basis for disease and of how treatments can be tailored to produce better outcomes. Genomics has even given us the ability to discover the geographic and ethnic origins of our ancestors and to track their migration across country borders and continents.

Genome mapping holds similar promise in the field of weed science. Examples of its potential include:

- Understanding which aspects of a weed’s genetics make it “weedy.”
- Identifying the genetic basis for herbicide resistance and how we might make it more difficult or slower to evolve.
- Determining new and more targeted weed management strategies.
- Determining how we might alter weed populations to reduce their competitiveness and make them easier to control.
- Understanding how to improve a crop’s ability to compete more effectively against weeds.
- Uncovering patterns related to when and where invasive weeds have been introduced and using the information to develop strategies that can limit new introductions.

## 2. How many weeds have been mapped so far and what are they?

Partial, draft genome sequences are available for at least 35 weed species. As of the publishing of this fact sheet, complete reference-grade genomes have been published for six weeds – each with a reputation for causing significant agricultural crop losses:

- Horseweed (*Erigeron canadensis*, also known as *Conyza canadensis*)
- Palmer amaranth (*Amaranthus palmeri*)
- Waterhemp (*Amaranthus tuberculatus*)
- Smooth pigweed (*Amaranthus hybridus*)
- Red rice/feral rice (*Oryza sativa*)
- Kochia (*Kochia scoparia*, also known as *Bassia scoparia*)

## 3. What is the difference between a draft genome and a reference genome?

The goal of genome mapping is to understand how the various components of the genome (nucleotides) are arranged. With a draft genome, there might be thousands of small, assembled fragments, but how they fit together remains unknown. This fragmentation limits the mapping’s usefulness. In reference genomes, the sequence has been determined. There are uninterrupted segments of DNA with few gaps or errors.

Draft genomes with partial assemblies may be sufficient to understand population biology or the evolutionary relationships among weed species. They may also be sufficient to develop molecular-level tools for identifying specific weed species. Reference genomes, though, are needed to tackle

more complex questions, such as the biology underlying weedy traits and how complex factors interact to produce herbicide resistance.

#### 4. What have we learned so far from draft and reference weed genomes?

Scientists have uncovered a wide range of new insights from genome sequencing projects. Here are a few examples:

##### **Genetics can aid in the early detection of troublesome weeds.**

When Midwest farmers discovered that seed mixes used on Conservation Reserve Program (CRP) acreage contained Palmer amaranth, alarm bells went off. The weed is extremely aggressive and hard to treat. Seed growers needed a way to ensure their mixtures were Palmer amaranth free. [Researchers at the University of Illinois](#) were able to use their understanding of genetics to develop a rapid screening test that can detect the presence of Palmer amaranth DNA in seed mixtures – helping to prevent the introduction of this problematic weed into CRP acreage across the country.

Another example: Glyphosate-resistant horseweed has caused yield losses of up to 83% in soybean and up to 46% in cotton. [Researchers have used genomics](#) to understand how some populations of horseweed in Canada evolved very high levels of glyphosate resistance. They used the information to document the first populations of horseweed in the U.S. that exhibit the same high levels of resistance. It is hoped this early detection can lead to integrated controls that prevent the spread of herbicide-resistant horseweed and protect crops.

##### **There isn't a single genetic "cause" for herbicide resistance.**

Before gene sequencing, it was hard for scientists to understand the mechanisms involved in the evolution of herbicide resistance. Now, though, they have learned there is no single genetic "cause." Instead, there are multiple pathways for the evolution of resistant traits, making genetic analysis of troublesome weeds especially important.

[Researchers have identified](#) five "superfamilies" of genes that are likely involved. They are large, diverse and part of the underlying pathways weeds use to survive the stresses they encounter in their environment. These pathways include:

- cytochrome P450 monooxygenase enzymes
- glutathione S-transferase enzymes
- ATP-binding cassette transporter proteins
- major facilitator superfamily transporter proteins
- glycosyltransferases enzymes

## Genetic differences between male and female weeds can influence the spread of herbicide resistance.

[Researchers at the University of Illinois](#) have successfully sequenced the DNA for male and female Palmer amaranth and waterhemp plants to identify the genetic basis of sex determination. This reproductive difference promotes outcrossing and genetic diversity, which can promote the evolution and spread of herbicide-resistant populations.

Using data sets compiled from sex-specific and sex-biased genome sequences, researchers were able to distinguish between male and female plants from multiple, geographically distinct Palmer amaranth and waterhemp populations with a 95 percent or greater accuracy.

What does this mean for the future of weed control? Both Palmer amaranth and waterhemp are resistant to multiple herbicides and can cause devastating yield losses in food crops. It is possible to imagine how genes might be modified to ensure all offspring from Palmer amaranth and waterhemp plants growing in a given location would be of the same sex – causing the population to collapse.

## Pollen can contribute to the dispersal of herbicide-resistant traits.

Though gene flow is an important component in evolutionary biology, its role in dispersal of herbicide-resistant gene variants among weed populations has been poorly understood. [Field experiments conducted](#) at the University of Nebraska-Lincoln explored whether pollen was a factor. The research showed that the mechanism of glyphosate resistance could be transferred by pollen from glyphosate-resistant to glyphosate-susceptible waterhemp. This finding helps to explain the rapid dispersal of glyphosate-resistant waterhemp across the Midwestern United States.

## Understanding the genetics of resistant weeds can shape innovations in weed management.

Scientists mapping the genomes of some of the world's most troublesome weeds are building a foundation that can be used to understand weed characteristics and to develop better controls. Examples include:

### **Horseweed (*Erigeron canadensis*)**

Also known as marestail, horseweed was the first broadleaf weed to evolve resistance to glyphosate in a U.S. cropping system. And those resistant weeds have led to significant yield losses in soybean and cotton crops.

Researchers working on the horseweed genome have determined that repeated use of glyphosate has led to multiple mutations that have caused an increased expression of transporter genes and of glutathione S-transferase and glycosyltransferases enzymes. [Understanding the genetic basis of](#)

[resistance](#) may pave the way for using CRISPR/Cas technology to insert a new gene sequence that would replace those herbicide-resistant traits.

### **Kochia (*Bassia scoparia*)**

Scientists [have mapped the genome of kochia](#), a major weed in North American crops. Their research points to *mobile genetic elements* (MGEs) as a possible “trigger” for the evolution of resistance to glyphosate. This genetic fingerprint has helped the team identify multiple glyphosate-resistant populations of kochia that have evolved independently in the Pacific Northwest and in Canada. Researchers say this level of understanding is an important step towards developing more sustainable approaches to weed control.

### **Blackgrass (*Alopecurus myosuroides*)**

Blackgrass is the most problematic weed for winter-cereal farmers in the United Kingdom and is considered a very real threat to food security. [Scientists at Rothamsted Research](#) are now exploring how to use what they know about the black-grass genome to silence specific genes that make the weed so successful. In the lab, for example, they were able to use virus-induced gene silencing to make herbicide-resistant blackgrass weeds susceptible to treatment.

### **Goosegrass (*Eleusine indica*)**

Goosegrass is one of the most common and destructive agricultural weeds in the world. It is incredibly resilient, with the ability to survive extreme drought, heat and low mowing. It also has evolved resistance to at least seven classes of herbicides.

An international team of researchers [mapped the weed’s genome](#) – an important first step in understanding why goosegrass is so successful and can adapt so quickly. They were able to identify multiple goosegrass genes associated with herbicide resistance. The same team uncovered genetic markers related to disease resistance, drought resistance and other goosegrass traits. Understanding these important pathways may suggest new molecular targets for herbicide development and for other novel weed management strategies.

## **5. What is the state of weed genomics today?**

Though important work has been done, to date weed genomics has lagged well behind genome mapping for other plant pests and pathogens. One predominant reason is that weed genomes contain a high level of repetition – typically more than half of their DNA. That repetition makes them tough to map. Imagine trying to work on a puzzle made up largely of pieces that were precisely the same, but each occupying a unique place in the total picture. How would you determine which piece goes where?

Sorting out the repetitive content in weed genomes can be time consuming and expensive, and it requires the right expertise and tools. Today, though, new technologies are beginning to reduce the cost of genome assembly and are helping weed scientists deliver the more complete and accurate sequencing results needed to advance weed management.

## **6. What resources are available to help weed scientists who want to conduct genetic research?**

### **International Weed Genomics Consortium:**

Weed scientists have launched a new [International Weed Genomics Consortium \(IWGC\)](#) to promote a community-based approach to weed genomics. Scientists from academia and industry have begun to collaborate, set priorities and build reference genomes for the world's most troublesome weed species. The consortium provides researchers [with user-friendly analytical tools and training](#), facilitates discussion and collaboration, and [publishes reference genomes](#) for broad use after the mapping work has been completed.

### **GenBank:**

Another resource is [GenBank](#), a database of genetic sequences maintained by the National Center for Biotechnology Information – part of the National Institutes of Health. The GenBank database contains an annotated collection of *all* publicly available DNA sequences, including those for weeds. GenBank participates in an [international collaborative](#) that includes the DNA DataBank of Japan and the European Nucleotide Archive. The three databases exchange genetic sequencing data daily.