

Jointed Goatgrass Genetics



Jointed goatgrass (*Aegilops cylindrica*) is a weed that causes serious problems in winter wheat fields in the western United States. Jointed goatgrass and wheat have a close genetic relationship and share many traits. To date, no herbicide has been developed that can selectively remove jointed goatgrass from conventional wheat. However, current herbicide-resistant wheat technology will provide producers with a tool to control jointed goatgrass in the crop. Concerns remain, though, that the resistance gene could move from wheat into jointed goatgrass populations. Understanding the genetic relationship between wheat and jointed goatgrass will help with the development of management strategies that minimize the potential for gene flow between the two species.

Origin of Wheat and Jointed Goatgrass

The close relationship between wheat and jointed goatgrass can be traced back to a common ancestor of the two species. Most plant species have two sets of chromosomes and are called diploids. However, jointed goatgrass has four sets of chromosomes and wheat has six sets. Two sets in jointed goatgrass are from one ancestor (designated CC) and two sets are from another ancestor (designated DD). Jointed goatgrass is then designated CCDD to indicate two sets of C and D chromosomes. Each set contains seven chromosomes for a total of 28 chromosomes (Figure 1). Wheat has three ancestors and therefore contains six sets of seven chromosomes. Using capital letters to describe wheat chromosomes gives a designation of AABBDD for a total of 42 chromosomes. Both jointed goatgrass and wheat have two sets of D chromosomes, indicating they share a common ancestor. This common ancestor helps explain why jointed goatgrass is difficult to control in wheat and why there is a potential for gene flow between the two species.

Problems with Genetic Similarity

The shared ancestor and similar genetic background of winter wheat and jointed goatgrass results in the two species having similar growth habits. Both species germinate in the fall, overwinter, and then flower and produce seed in the late spring and summer of the subsequent year. This similarity of growth habits is one reason why jointed goatgrass control is difficult in conventional winter wheat.

The similar genetic background also means that jointed goatgrass and wheat have similar physiological and biochemical pathways. These similarities make developing a selective herbicide for jointed goatgrass control difficult without injuring the conventional (not herbicide-resistant) wheat. The recent development of herbicide-resistant wheat allows the selective control of jointed goatgrass in wheat because the wheat has been modified to no longer be sensitive to the herbicide.

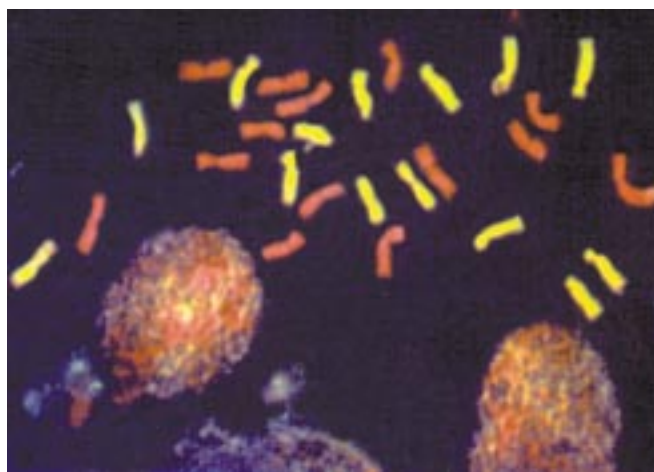


Figure 1. Mitotic chromosome spread of jointed goatgrass showing two sets of seven C genome chromosomes (yellow) and two sets of seven D genome chromosomes (red), resulting in 28 total chromosomes in jointed goatgrass.

The problem with this approach is that the genetic similarity between jointed goatgrass and wheat allows hybridization between the two species, with the potential for movement of the resistance gene into a jointed goatgrass population, resulting in herbicide-resistant jointed goatgrass.

Producing Wheat by Jointed Goatgrass Hybrids

The production of wheat by jointed goatgrass hybrids in wheat fields has occurred naturally for many years wherever the two species co-exist. The hybrids are usually easy to spot in wheat fields because their seed heads are intermediate in appearance between wheat and jointed goatgrass (Figure 2). When pollen from winter wheat fertilizes a jointed goatgrass flower or when jointed goatgrass pollen fertilizes a winter wheat plant a hybrid seed can be produced. Studies indicate that hybrid production in the field is primarily by wheat pollen fertilizing jointed goatgrass. The hybrids are vigorous plants with many tillers but produce extremely low numbers of viable seed. The hybrid has five sets of seven chromosomes, designated ABCDD (Figure 3). The lack of two chromosome sets for the A, B, and C genomes is the primary cause of the sterility observed in the hybrids. However, the presence of two sets of D chromosomes allows for chromosome pairing of the D genome and for partial female fertility of the hybrid and seed formation (Figure 4). Pollen must be provided by either a wheat or jointed goatgrass plant for hybrids to produce seeds. Such a mating is called a backcross. A successful backcross with jointed goatgrass would be the first step needed for movement of a herbicide resistance gene from wheat to jointed goatgrass.

Backcrossing Wheat by Jointed Goatgrass Hybrids

In greenhouse and field studies, seed was produced on hybrid plants using pollen from jointed goatgrass, resulting in the first backcross generation (BC_1). A low amount of seed (1–2% seed/florets) was produced and this level occurred both with controlled crosses in the greenhouse and with natural pollination in the field. The BC_1 plants that grew from these seeds produced very

little viable pollen because of imbalances in the number of A, B, and C genome chromosomes. An increasing number of C genome chromosome pairs to compliment the seven pairs of D genome chromosomes in the BC_1 plants resulted in 4% average female fertility and allowed for an increase in seed production on BC_1 plants when pollinated by jointed goatgrass. The second backcross generation (BC_2) produced in the greenhouse showed an additional increase in female fertility plus the restoration of partial male fertility (viable pollen) and resulted in plants that could self-pollinate. This production of self-fertile plants indicated that only two generations of backcrossing would be required for a herbicide-resistant gene to move from wheat to jointed goatgrass, and this could take as little as three years from when the herbicide-resistant crop was first planted. With each generation of



Figure 2. Wheat by jointed goatgrass hybrids in a wheat field.

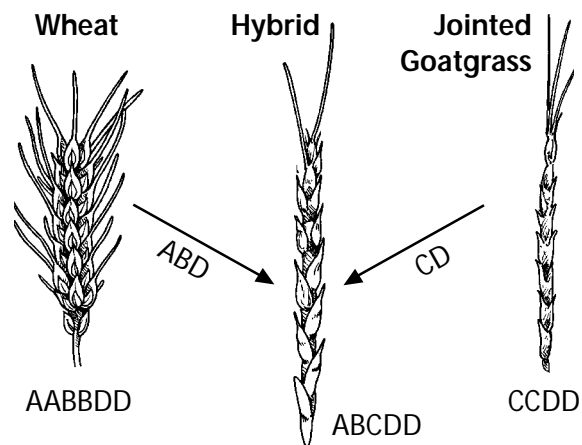


Figure 3. Formation of wheat by jointed goatgrass hybrids (ABCDD) by crossing wheat (AABBDD) by jointed goatgrass (CCDD).

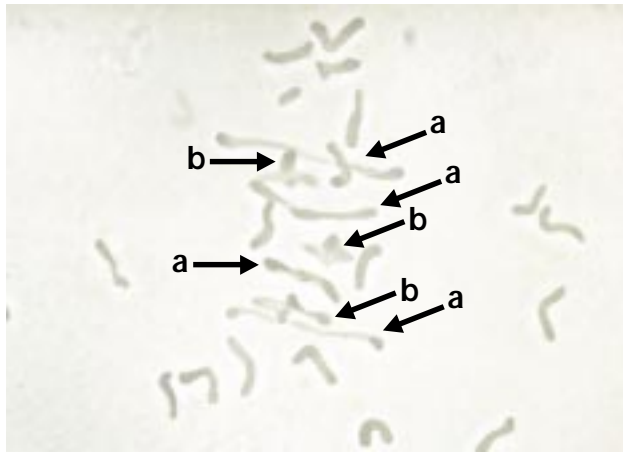


Figure 4. Meiotic preparation of a wheat by jointed goatgrass hybrid showing chromosome pairing of the D genome chromosomes of the two species. A total of seven rod (a) and ring (b) bivalents involving the D genome chromosomes from wheat and jointed goatgrass are shown. The remaining chromosomes are from the A, B, and C genomes and do not have a chromosome to pair with in the hybrid.

backcrossing to jointed goatgrass and subsequent generations of self-pollination, the number of A and B genome chromosomes will decrease until the original number of chromosomes found in jointed goatgrass (28) is restored.

Methods to Prevent Gene Flow

The results of backcross experiments on wheat by jointed goatgrass hybrids were used to develop methods that wheat producers could use to minimize the potential movement of the herbicide resistance gene from wheat to jointed goatgrass. A simple way to eliminate gene flow is to prevent the restoration of self-fertility by eliminating the production of BC_1 and BC_2 seed in the field. Prevention of BC_1 seed production requires only the absence of hybrids in the field. This can be accomplished by using wheat seed certified free of jointed goatgrass. If the hybrid seed was already in the field and BC_1 seed was produced, harvesting the seed and not saving it to plant in subsequent years would reduce the number of BC_2 seeds being planted. Cleaning combines between fields is necessary to reduce the risk of contaminating seed with BC_2 seed.

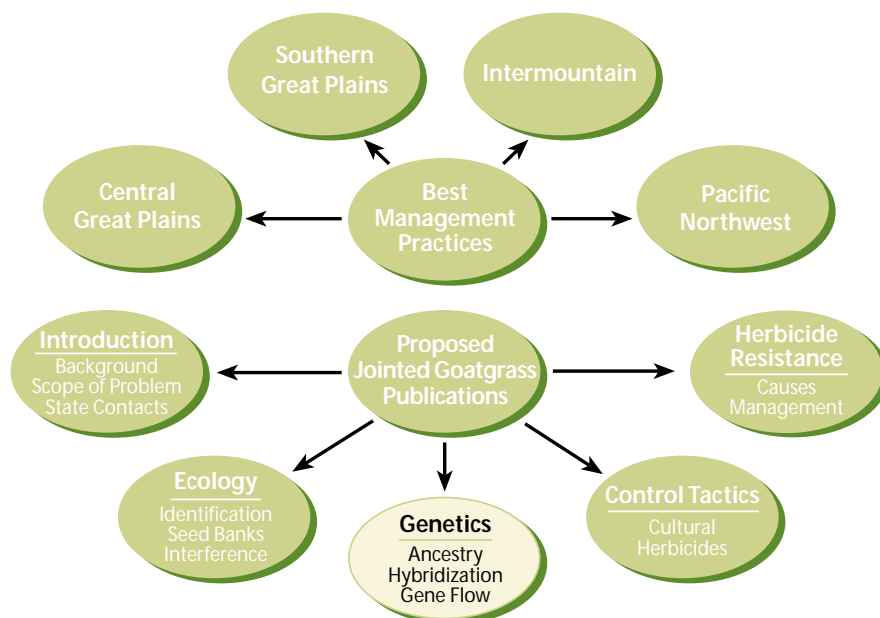
Since self-fertility is primarily restored in the second backcross generation, the absence of the

BC_2 generation will prevent the production of self-fertile, herbicide-resistant plants in the field. Elimination of a BC_2 generation can be achieved by using integrated methods of weed control, including seed certified free of jointed goatgrass, crop rotation, and herbicides with alternate modes of action. Methods to minimize the spread of jointed goatgrass, wheat by jointed goatgrass hybrids, and any backcross generations are described in more detail in EB1935 “Jointed Goatgrass Control Tactics.”

A second method to prevent gene flow is to reduce the potential for retention of the herbicide-resistance gene in the self-fertile BC_2 progeny by placing the gene on a chromosome of one of the unshared genomes. Scientists discovered that wheat genes on the shared D genomes are retained in the self-fertile BC_2 progeny, indicating that a herbicide resistance gene from wheat would be retained in some of the BC_2 progeny. As self-fertility was restored the number of chromosomes in the hybrid plant approached that of jointed goatgrass (28), indicating that the chromosomes of the unshared A and B genomes were gradually lost. If a herbicide resistance gene is on the A or B genome chromosome, the gene will not likely be retained as the normal chromosome number of jointed goatgrass is restored. This concept is currently being tested using three herbicide-resistant wheat lines with a herbicide resistance gene on either the A, B, or D genome.

Summary

The common genetic background of wheat and jointed goatgrass makes jointed goatgrass control in winter wheat difficult and increases the chance of successful gene flow, including resistance genes transferring from herbicide-resistant wheat to jointed goatgrass. Gene flow activity can be greatly decreased by reducing the occurrence of wheat by jointed goatgrass hybrids and BC_1 plants in the field. The production of hybrids and backcross generations can be reduced by using certified wheat seed free of jointed goatgrass, crop rotation, herbicide rotation, and perhaps by placing the herbicide-resistant gene in an unshared wheat genome. Using these practices will increase the longevity of the herbicide resistance technology and maintain use of herbicides as an effective jointed goatgrass management tool.



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