

ASSESSING THE RISK OF GENE FLOW BETWEEN WHEAT AND JOINTED GOATGRASS

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Abstract

Jointed goatgrass (*Aegilops cylindrica*) is a noxious weed in most wheat (*Triticum aestivum*) growing regions. Both species are polyploid with one genome (D) in common which allows successful hybridization to occur in the field. In the early 1990's, seed was found on hybrids which raised the question on whether genes from wheat could move into jointed goatgrass. Research by the University of Idaho and Oregon State University addressed this question which became more important with the advent of herbicide resistant wheat. Results of this collaborative research include (1) Hybrids were partially female fertile and seed on hybrids were due to backcrossing, (2) Either species could serve as the recurrent backcross parent, (3) Partial self-fertility could be restored after two backcrosses to jointed goatgrass, (4) Backcrossing occurred in the field to produce BC₁ and BC₂ plants, (5) Recurrent backcross parent could be determined using genomic in situ hybridization and/or molecular markers, (6) Female parent of hybrid was primarily jointed goatgrass based on chloroplast molecular markers, (7) Introgression of genes on the D genome could occur with or without selection pressure, and (8) Placement of a transgene on the non-shared A or B genomes did not insure that gene movement would not occur. To minimize the risk of gene flow between the two species, it is critical to prevent the production of the BC₂ generation to prevent the restoration of self-fertility that would allow stable introgression of a wheat gene in jointed goatgrass. Management strategies were developed to achieve this goal.

Introduction

Jointed goatgrass (*Aegilops cylindrica*) is a noxious weed in wheat (*Triticum aestivum*) production areas of the Western United States. Since wheat (ABD genomes) and jointed goatgrass (CD genomes) are closely related natural hybridization can occur between the two species. In 1991, seed was found on hybrids in a field in Northern Idaho and questions were raised concerning the source of the seeds since the hybrids were considered sterile. The seed was found to be due to backcrosses to either jointed goatgrass or wheat. This raised the question as to whether genes from wheat could move to jointed goatgrass. This question became more important with the advent of herbicide resistant wheat. Collaborative research by the University of Idaho and Oregon State University over the past 17 years has investigated this and multiple aspects of the genetics of jointed goatgrass and the potential for gene flow between the two species. Research included determining the source of the seed found on the hybrids, the potential for jointed goatgrass to serve as a backcross parent, restoration of fertility in backcrosses to jointed goatgrass, methods to determine the recurrent backcross parent of field derived backcrosses, potential for introgression of wheat genes from the shared D genome and potential for gene transfer from the unshared A and B genomes of wheat.

Potential for jointed goatgrass or wheat to be the backcross parent

For gene flow to occur jointed goatgrass had to be able to serve as the backcross parent. It was determined that both jointed goatgrass and wheat could serve as the backcross parent in crosses to hybrids in the greenhouse. It was also shown that backcrossing to both jointed goatgrass and/or wheat could occur naturally in the field (Figure 2).



Figure 2. Jointed goatgrass x wheat hybrids planted in jointed goatgrass to determine rate of backcrossing in the field.

Snyder, J., C. Mallory-Smith, J. Hansen, S. Balter, and R.S. Zemetra. 2000. Seed production on *Triticum aestivum* by *Aegilops cylindrica* hybrids in the field. *Weed Sci.* 48:588-593.

Source of viable seeds on hybrids

Genetic analysis of wheat x jointed goatgrass hybrids showed that the hybrids were not sterile but partially female fertile (2%) allowing for the potential for backcrossing to occur. The partial fertility was most likely due to the two species sharing the D genome which allowed for bivalent formation of the D genome chromosomes during meiosis in the hybrids (Figure 1). Cytogenetic analysis of the seeds found on the wheat x jointed goatgrass hybrids indicated that the seeds were the result of backcrosses to either jointed goatgrass or wheat.



Figure 1. Meiotic preparation of jointed goatgrass x wheat hybrid showing D genome bivalents.

Zemetra, R.S., J. Hansen, and C.A. Mallory Smith. 1998. Potential for gene transfer between wheat (*Triticum aestivum*) and jointed goatgrass (*Aegilops cylindrica*). *Weed Sci.* 46:313-317.

Restoration of self-fertility of jointed goatgrass backcrosses

For gene flow to occur from wheat to jointed goatgrass, self-fertility would need to be restored to allow for the potential for stable gene introgression into the jointed goatgrass genetic background. In a greenhouse study it was found that female fertility increased with each backcross (Figure 3) and that partial self-fertility was restored after only two backcrosses to jointed goatgrass and that the level of self-fertility would increase with each subsequent generation of selfing.

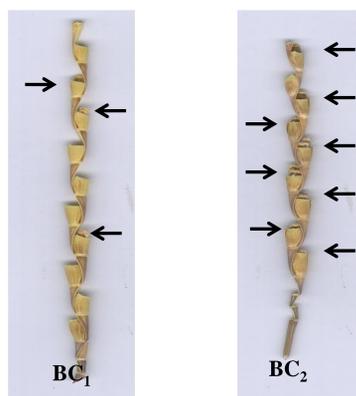


Figure 3. Seed set on BC₁ and BC₂ with jointed goatgrass as the recurrent parent indicating the increase in fertility with each subsequent backcross. Arrows indicate seed.

Wang, Z., R.S. Zemetra, J. Hansen and C.A. Mallory-Smith. 2001. The fertility of *Triticum aestivum* X *Aegilops cylindrica* hybrid and its backcross progenies and the implication for gene flow between the two species. *Weed Sci.* 49: 340-345.

Use of genomic in situ hybridization to determine the recurrent backcross parent of BC₁ and BC₂ plants

For gene migration to occur from wheat to jointed goatgrass through backcrossing to hybrid plants the recurrent parent must be jointed goatgrass. Since chromosome numbers can be variable in the backcross generations another method was needed to determine if the recurrent parent was wheat or jointed goatgrass. Genomic in situ hybridization (GISH) allowed for the visualization of the C genome chromosomes in the BC₁ generation and the number of C genome chromosomes could be used to identify the recurrent parent. It was found that the majority of BC₁ plants had wheat as the recurrent parent though BC₁ plants were found that had jointed goatgrass as the recurrent parent.

GISH was also found to be useful in detecting the presence of wheat chromosomes from either the A or B genomes in BC₂S₁ plants where partial self-fertility had been restored (Figure 4). The presence of the A or B genome chromosomes would allow for the introgression of wheat genes even from the unshared genomes of wheat.

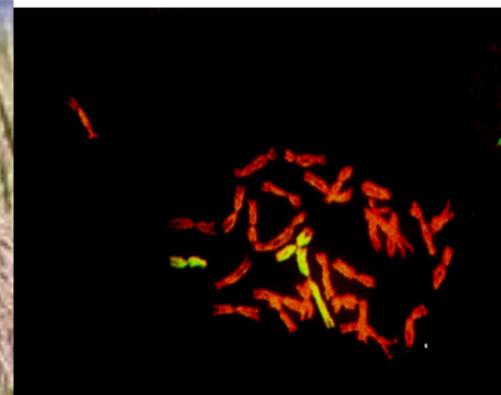


Figure 4. BC₂S₁ plant carrying three chromosomes from either the A or B genome of wheat.

Wang, Z., A. Hang, J. Hansen, C. Burton, C.A. Mallory-Smith, and R.S. Zemetra. 2000. Visualization of the A and B genome chromosomes in wheat (*Triticum aestivum* L.) x jointed goatgrass (*Aegilops cylindrica* Host) backcross progenies. *Genome* 43: 1038-1044.

Wang, Z., R.S. Zemetra, J. Hansen, A. Hang, C.A. Mallory-Smith, and C. Burton. 2002. Determination of the paternity of wheat (*Triticum aestivum* L.) x jointed goatgrass (*Aegilops cylindrica* Host) BC₁ plants using genomic in situ hybridization technique. *Crop Sci.* 42: 939-943.

Determination of the female parent of field derived hybrid plants

To determine the source of hybrids in the field information on the female parent of the hybrid would be useful. This would aid in determining methods to minimize the spread of the hybrid seed from jointed goatgrass infested fields. Chloroplast molecular markers were used to determine whether the female parent was either jointed goatgrass or wheat. In the majority of hybrids studied it was found that the female parent was jointed goatgrass.

Ghandi, H., M.I. Vales, C. Watson, C. Mallory-Smith, N. Mori, M. Rehman, R.S. Zemetra, and O. Riera-Lizarazu. 2005. Chloroplast and nuclear microsatellite analysis of *Aegilops cylindrica*. *TAG* 111:561-572.

Introgression of genes from the D genome of wheat into jointed goatgrass

As partial self-fertility was restored in the BC₂ generation evaluation was possible on subsequent generations for the introgression and retention of genes from the D genome of wheat into jointed goatgrass. Using molecular markers associated with the D genome in wheat (Figure 5) it was determined that recombination could occur between all the D genome chromosomes.

Evaluation for specific genes on the D genome of wheat, imazamox resistance (*Imi 1*) and resistance to Pseudocercospora foot rot resistance (*Pch 1*) in BC₂S₁ and BC₂S₂ plants found that introgression had occurred either with or without selection.

Kroiss, L.J., P. Tempalli, J. L. Hansen, M. I. Vales, O. Riera-Lizarazu, R. S. Zemetra, C. A. Mallory-Smith. 2004. Marker-assessed retention of wheat chromatin in wheat (*Triticum aestivum*) by jointed goatgrass (*Aegilops cylindrica*) backcross derivatives. *Crop Sci* 44:1429-1433.

Perez-Jones, A., C. A. Mallory-Smith, O. Riera-Lizarazu, C. J. W. Watson, Z. Wang, M. Rehman, and R. S. Zemetra. 2006. Introgression of a foot rot resistance gene from winter wheat (*Triticum aestivum*) into jointed goatgrass (*Aegilops cylindrica*). *Crop Sci* 46: 2155-2160.

Perez-Jones, A., C.A. Mallory-Smith, J. Hansen, and R. S. Zemetra. 2006. Introgression of an Imidazolinone-resistance gene from winter wheat (*Triticum aestivum* L.) into jointed goatgrass (*Aegilops cylindrica* Host). *TAG*. 114: 177-186.

Impact of placement of transgenes on the A or B genome of wheat on the potential for gene migration

A study was conducted using the gene for glyphosate resistance on either the A, B or D genome of wheat to determine if genome placement could prevent the movement of a transgene from wheat to jointed goatgrass. The study was conducted with and without selection for glyphosate resistance. Based on the results of the study it does not appear that placement of a transgene on an unshared genome would prevent gene migration from wheat to jointed goatgrass. In the case of glyphosate resistance it appeared that selection pressure could enhance the potential for migration due to gametophytic selection for gametes carrying the resistance gene, decreasing the number of seed set on each backcross generation but increasing the number of backcross progeny carrying the gene for resistance. Introgression of the wheat gene appears to have occurred in the BC₂S₁ or BC₂S₂ generation but confirmation of the presence of translocations needs to be done using GISH.

Rehman, Maqsood. 2006. "Effect of genome location on transmission and retention of wheat (*Triticum aestivum*) genes in jointed goatgrass (*Aegilops cylindrica*)". Ph.D. dissertation. University of Idaho.

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