

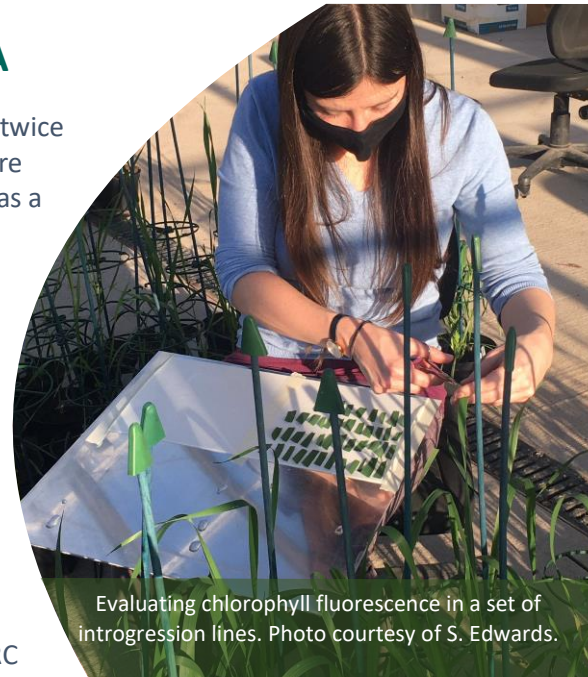
Community Screening of Wheats Containing Exotic DNA

Wheat used in various forms as a domesticated food crop evolved only once or twice more than 10,000 years ago. Its progenitors and wild relatives, of which there are many genetically diverse accessions, evolved over several millions of years and as a consequence contain a vast reservoir of genetic variation absent in modern cultivated wheats. This variation can be used to greatly expand the genetic diversity in today's crops, thereby aiding the discovery of new superior traits to increase productivity for farmers in the climates of the future.

Genetic variation from wild relatives has already had major impacts on wheat production (see [IWYP Science Brief No. 36](#)). However, several bottlenecks have to be overcome to fully exploit this huge genetic resource. The low frequency of successful transfer of chromosome pieces (introgressions) from wild relatives into wheat, the removal of deleterious genes after introgression and the detection, characterization and tracking of the introgressed pieces of DNA are all technical challenges that have been overcome at the Wheat Research Centre (WRC) at Nottingham University, UK. Over many years, the WRC has created a “[Wheat/Wild Relative Toolkit](#)” with 330 stable lines carrying introgressions from several wheat wild relative species. A further 600+ heterozygous introgressions have also been produced and will be made available once stable homozygous introgressions have been generated. This work has been achieved in collaboration with colleagues at the University of Bristol, Rothamsted Research, the John Innes Centre (JIC) and the National Institute of Agricultural Botany (NIAB) with support provided by the Biotechnology and Biological Sciences Research Council (BBSRC). This resource has been valuable in several IWYP Research Projects and Prof. J. King and colleagues at the WRC currently have an active IWYP Research Project screening this resource (see [IWYP Science Brief No. 20](#)). Over the past few years other groups have also explored the value of introducing novel genetics into wheat (see [IWYP Science Brief No. 36](#)). Chromosomal segments from these introgressions can now be tracked in wheat using robust diagnostic KASP™ assays ([Grewal et al., 2020](#); [2021](#); [2022](#); [King et al., 2022](#)). These permit easy identification of the position and size of the introgression and can differentiate between homozygous and heterozygous introgressions.

These valuable introgression lines now need to be screened for as wide a range of traits as possible to identify the useful genetic traits they carry. Pilot screening for several phenotypic traits on small samples of the introgression lines has revealed unique variation for most of the traits sought, including economically important traits for fungal and viral disease resistance, yield components, abiotic stress tolerance, grain nutrition, flowering morphology, photosynthesis and biomass. The IWYP Hubs at CIMMYT, Kansas State University and NIAB are backcrossing selected introgression lines with novel floral and photosynthetic characters into spring and winter wheats, while several other institutions, universities and companies are also exploring interesting features of these introgression lines.

Additional partners with the expertise to phenotypically screen large number of introgression lines for important traits are needed to fully exploit the value held in this collection and generate novel resources for the global wheat research and breeding communities. For inquiries to join this endeavor, please contact Prof. Julie King at Julie.king@nottingham.ac.uk. For those interested in acquiring seed of the first set of introgression lines, lots are available from the [SeedStor](#) at the Germplasm Resource Unit (GRU) at John Innes Centre, Norwich, UK. Over time the range of seed types available carrying different sources of introgressed DNA will expand and will also be deposited at this facility for distribution.



Evaluating chlorophyll fluorescence in a set of introgression lines. Photo courtesy of S. Edwards.

Genomic in situ hybridization showing introgressions from *Aegilops muticum*. Photo courtesy of J. King.

