

# Harvesting the genetic value of interspecific wheat introgressions



Toby Barber\*<sup>1,2</sup> Keith Gardner<sup>1</sup> Jaroslav Doležal<sup>3</sup> Chris Wright<sup>4</sup> Alison Bentley<sup>1</sup>

1. The John Bingham Laboratory, NIAB, Huntingdon Road, Cambridge, UK  
2. Department of Plant Sciences, University of Cambridge, Cambridge, UK  
3. Centre for Plant Structural and Functional Genomics, Olomouc, Czech Republic  
4. Earlham Institute, Norwich Research Park, Norwich, UK  
\* corresponding author: toby.barber@niab.com



## Background

Wheat breeders have drawn on other grass species, wild relatives of wheat, to introduce genes with advantageous traits such as:

- disease resistance
- yield improvements
- drought tolerance

### Historically:

- Achieved through phenotypic selections
- resulting in genes with negative effects, along with beneficial traits.

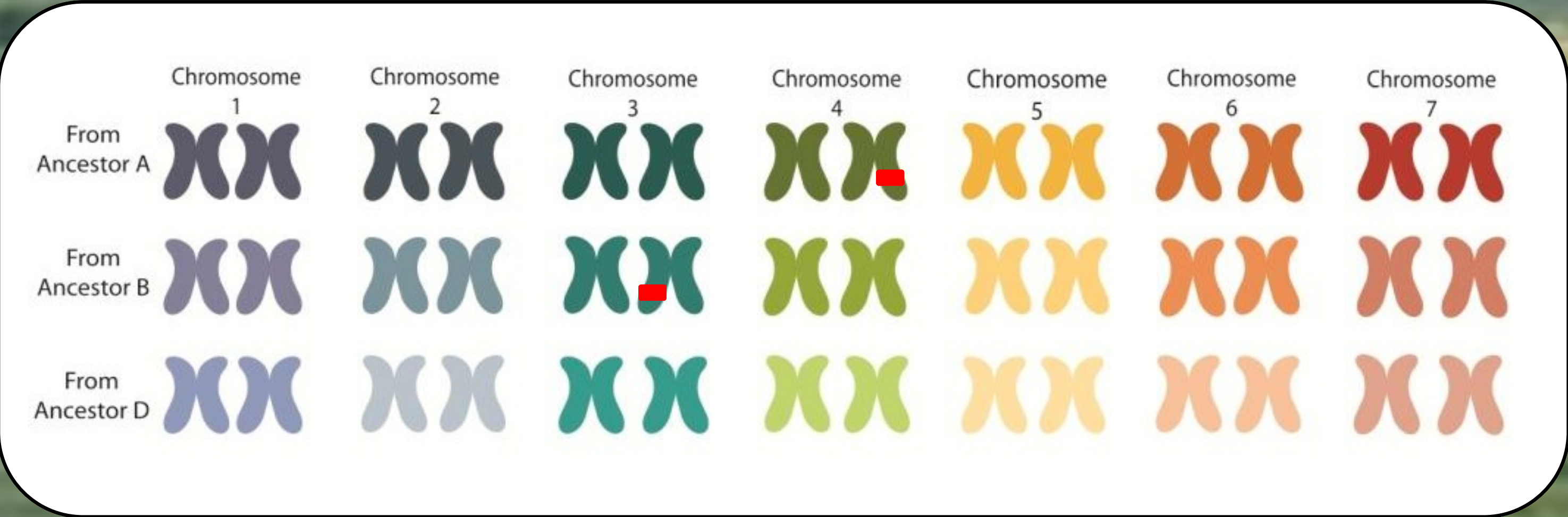
### High density genomics:

- Locate these introgressions on the chromosomes
- Find the specific genes responsible for the traits
- Disentangle the advantageous from the deleterious.

The UK winter wheat variety **Robigus** contains introgressions from the grass species *Triticum dicoccoides* which through phenotypic analysis have been shown to contain:

- + resistance to four major UK wheat pathogens
- + a contribution to yield increases
- susceptibility to yellow rust.

Robigus has become an important variety for wheat breeders and has become the backbone of many breeding programmes.

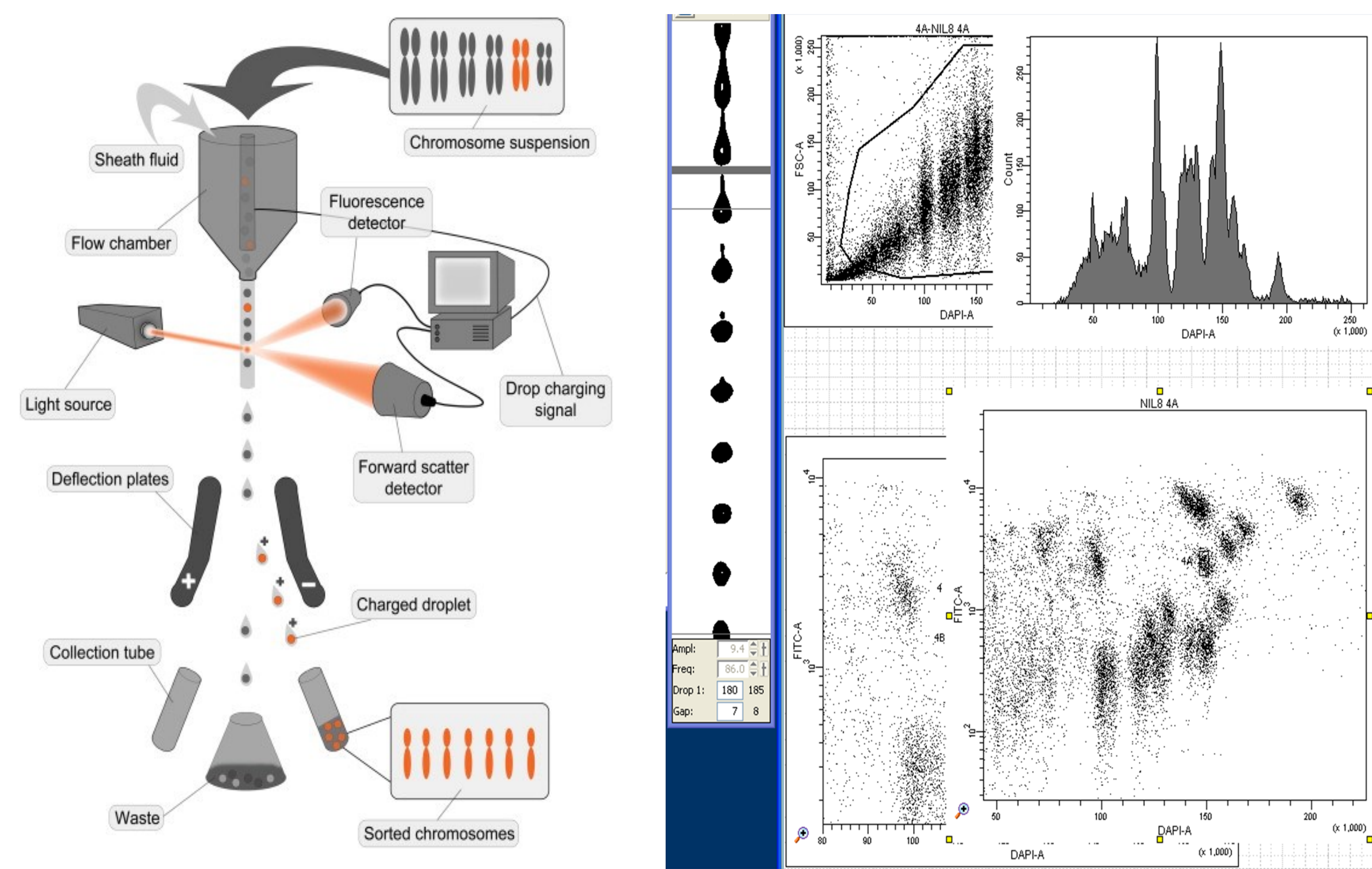


## Germplasm

Through genetic mapping using the NIAB 8-way MAGIC population, 2 alien introgressions derived from Robigus were located on chromosomes 3B and 4A. Sibling lines or NILs (Near Isogenic Lines) have been generated which differ only in the region of the introgression. These are being grown in the field to allow direct testing of the phenotypic effects of the introgressions along-side the Oakley x Gatsby population, which is segregating for the Robigus introgressions.

The introgression on **chromosome 4A** has been linked to brown rust resistance, yellow rust susceptibility and a yield effect.

## Chromosome flow sorting



## Genetic analysis

4A NIL pair chromosome flow sorted by Doležal lab in Czech Rep.

Next-Generation-Sequencing of flow sorted chromosomes at Earlham Institute.

Develop tools to track and maintain beneficial genes in modern wheat.

Bioinformatic analysis to annotate and characterise the unique genes present in the introgression.

This project represents a novel approach of detecting and dissecting interspecific introgressions in wheat using a combination of modern genomic technologies with germplasm resources derived from a multiparental population, with the aim of maximizing the potential benefits of interspecific introgressions in the wheat gene pool for breeders and farmers.