

## Marker assisted breeding and mass selection of wheat composite cross populations

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### Introduction

*Utilising diverse populations instead of single line varieties is expected to lead to a number of advantages in cereal production. These include reduced epidemics of plant diseases, improved weed competition and better exploitation of soil nutrients, resulting in improved yield stability. However, a number of challenges must be met before diverse wheat populations can be introduced into commercial wheat production: one of these is the development of breeding technologies based on mass selection which enable breeders and farmers to improve specific traits in populations and maintain diversity at the same time.*

BIOBREED is a project started in Denmark in 2011 to meet these challenges for wheat population breeding. The project is focusing on the development of tools and methods for mass selection of traits relevant for organic and low input production, as it is expected that the highest benefits by utilizing diverse populations can be achieved there. These tools and methods include the development of genetic markers for common bunt (*Tilletia caries*) resistance and for traits affecting baking quality, such as gluten content and seed hardness, as well as for the content of nutritive components like anthocyanin and phytate. The development of a composite cross population both with and without common bunt stress will be observed by means of molecular markers and disease readings.

### Resistance to common bunt

The project is screening a selection of 300 wheat varieties for resistance to common bunt in the framework of an association analysis based on field data and DArT marker data. A specific study in a doubled haploid population from the cross between PI 554099 (carrying the *Bt-9* gene of resistance) and the susceptible variety Cortez (Wiersum, Netherlands) segregating for the common bunt resistance gene *Bt-9* aims at the localisation of this gene.

### Composite crosses

A number of 218 crosses have been made between 30 varieties with a moderate to high degree of bunt resistance. These crosses are now in F<sub>2</sub> (169 crosses) or F<sub>3</sub> generation (49 crosses). The F<sub>3</sub> generations are grown as a bulk population both with and without bunt infection. The diversity of the composite cross population will be assessed by molecular markers, and changes in population structure when growing the populations with and without common bunt infection will be followed using these markers. Head rows of the crosses will also be grown separately, and so far 20 heads of 44 of the F<sub>3</sub> generation have been grown with bunt infection. The distribution of bunt resistance between the head rows will give some hints to the underlying genes determining common bunt resistance.

The seed of the populations will be sorted prior to sowing on a gravity separator and by single seed separation based on near infrared transmission (NIT) in order to remove lines with inferior quality traits like low seed hardness and low gluten content. The genetic markers developed in the association analysis will be applied to the composite cross population.

This work is supported by The Danish Food Industry Agency, Ministry of Food, Agriculture and Fishery 2010-14.

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