

## **Performance and variability of thirteen winter wheat composite cross populations (CCP) with differing cultivation histories.**

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Alternative breeding approaches in organic agriculture have started to address pressing issues such as the lack of appropriate plant varieties particularly suited to cope with higher biotic and abiotic stresses, generally found in low-input and organic production systems. This challenge, coupled with the additional pressure of loss of plant genetic diversity, has driven novel breeding approaches such as Composite Cross Populations (CCPs) and other genotype mixtures, thereby increasing both intra- and inter-varietal diversity. This High genetic Diversity (Hi-D) approach is relevant to organic agricultural systems for two reasons; firstly the availability of diverse germplasm improves chances of finding germplasm suited for low-input conditions as found in organic agriculture. Secondly, the comparatively large environmental variability in organic systems needs to be buffered with higher levels of in-field diversity. COBRA (Coordinating Organic plant Breeding Activities for Diversity) aims to support and develop plant breeding and seed production in Europe by increasing the use of plant material with High genetic Diversity (Hi-D) through coordinating, linking and expanding existing breeding and research in cereals (wheat and barley) and grain legumes (pea and faba bean).

Three winter wheat (*Triticum aestivum* L.) CC populations were created in 2001, through collaboration with the Elm Farm Research Centre and the John Innes Institute. In 2005, seed batches of the F<sub>4</sub> of these populations were equally divided and distributed to three additional partners (France, Hungary and the University of Kassel). In 2007, it was decided to submit one of the CC populations to changes in environments every year. A pattern was developed between eight partners whereby these “cycling” populations would be grown in a plot of >100m<sup>2</sup> and sent to the next cycling partner the following year. The original partners (UK, Hungary and Germany) have also maintained their original “non-cycling” populations for comparison. The aim of the project is to be able to compare populations that all originated from the same seed batch in 2005, but that have been exposed to vastly different climates in one site (Germany) for their performance and diversity (phenotypic diversity, yield and disease occurrence). In 2013, seed from each of the eight “cycling” and three “non-cycling” populations were planted at the University of Kassel. Information regarding yield, foot and foliar diseases and phenotypic variation recorded. The wheat varieties Achat, Akteur and Capo were included for comparison.

Observations in the field during the growing period showed noticeable phenotypic differences between the populations in terms of plant height, ear length and colour and whether the ears were awned or awnless. In 2014, a severe epidemic of yellow rust, caused by *Puccinia striiformis*, occurred in the region with many varieties being severely diseased. During flowering, the average diseased leaf area for the populations was 8 % (SD 2.7), while diseased leaf area for the reference variety Akteur was 17 % (SD 6.2). The average yield for the reference varieties was 4.44 t/ha and 4.47 t/ha for the populations. Although there were no statistically significant differences regarding a number of agronomic traits, the populations varied significantly in morphological characteristics such as stem and ear length. Thus, although the populations have the same origin they have evolved differently since they were separated and they maintained a high degree of diversity through the different climates and locations and over time. Molecular analysis of the populations is currently being completed

and this should give further insight into the genetic differences between the populations. In addition saved seed of the populations received in 2013 has been planted with seed harvested in 2014 in order to ensure that the differences observed between the populations were due to actual genotypic differences and not due to differing seed weight and health.

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