

Improving quality and health in diverse populations of wheat

By:

Anders Borgen, Agrológica, Houvej 55, 9550 Mariager, Denmark E-mail: borgen@agrológica.dk

Introduction

Biodiversity is one of the keystones in the concept of organic agriculture, both as a goal in it self, and as a mean to control pests and diseases, and to optimal exploitation of resources. On the other hand, monocultures have advantages in producing a homogeneous crop easy to harvest and process. In cereal production, composite cross populations have been proposed as a compromise between the benefits of biodiversity and monoculture fit for organic farming (Döring *et al.* 2011).

A change from pure line pedigree breeding to population breeding calls for a new set of breeding tools to develop optimal quality and yield compatible with pure line varieties. The aim of this work is to test different population breeding methods, where unfit germplasm are discarded while still maintaining some degree of diversity of adapted plants.

Common bunt (*Tilletia caries*) is a devastating pseudo seed borne disease of wheat intensively controlled by fungicide seed treatment in conventional agriculture. In organic agriculture, control measures are limited to mechanical treatments such as brush cleaning (Borgen 2015) or heat treatments (Kristen and Borgen 2001, Borgen *et al.* 2005), application of natural compounds like acetic acid (Borgen and Nielsen 2001), mustard, milkpowder, Tillekur or bio-agents like Cedomon (Borgen and Kristensen 2001, Borgen and Davanlou 2001). Therefore, control of common bunt in organic agriculture must follow an integrated strategy including several different measures including also genetic resistance. Measures for breeding pure line varieties for resistance to plant diseases are well known, but these cannot be used in population, at least not without adjustments.

Common bunt drastically reduce seed production in infected plants, and natural selection will therefore theoretically reduce susceptible lines within a population. However, a quantification of this effect has not previously been made.

Protein content is an important quality parameter in cereals whether used for baking or feed. It has previously been shown that it is indeed possible to increase protein content in populations by single seed sorting based on Near Infrared Reflection (Borgen *et al.* 2014). However, seed in this trial were sorted and sown directly. Seed sorting will affect not only the genetic composition of the seed, but possibly also the vigour of the seed, potentially affecting the yield and quality of the harvested grain. The longer term genetic effect of NIR seed sorting is therefore still a bit unclear.

Materials and methods

In 2008, 40 crosses were made between 20 parents of winter wheat, and in 2008 another 200 crosses were made between these and additional 11 parents. Each cross were propagated separately. In 2010 samples from each of the crosses from 2008 were merged, and inoculated with spores of common bunt (*Tilletia caries*). Each year onwards, the population were threshed and sown without seed treatment, allowing the pathogen to multiply naturally within the population (Steffan 2014). In 2011, samples of all crosses were merged, following the same procedure. In 2012, each individual cross population were inoculated with bunt spores, and grown separately with bunt in 1m² plots maintaining their own pathogen population. In crosses without infected plants to maintain selection pressure, new spores were added annually.

Each of the parents were in 2013 and 2014 grown in separate micro plots, inoculated both with a blend of new spore, and with propagation of their own spores within each variety (Borgen 2015). The frequency of infected heads were recorded based on macro symptoms in both pure line parents

and the populations.

All winter wheat varieties selected as parents had in one or more publications been recorded as resistant to bunt.

A British CCP (ORC Wakelyns CCP) well described in other papers of this publication was included in 2013 with infection of bunt, and multiplied for one year with infection. The same population had also been grown in Hungary, where it had been naturally infested with bunt.

In 2008, 15 crosses were made between 13 spring wheat varieties, of which 5 had purple bran. Each cross were grown separately each year onwards in 1m² plots. Each year, crosses with a purple wheat parent were colour sorted, discarding light kernels. In 2013, each cross were sorted into 3 fractions based on protein on each kernel using a BoMill IQ Grain Quality Sorter 1002. The highest and lowest protein fraction each contained 20% of the seed sample. Only the highest and the lowest protein fraction was grown. In 2014, each sample was again sorted in the same way, but only the highest fraction were sown from the high protein fraction seed, and the low fraction of the low fraction seed. All seed from each fraction were sown increasing plot size to 3-15m².

Results and discussion

Bunt in winter wheat

Infection level of bunt in the populations seems to be stable from year to year in both the narrow population with 40 crosses, and the broader CCP with 220 crosses. It did increase the last three years, but whether this is a trend or a case of climatic fluctuation is unclear. In the wheat populations, the pathogen population was propagated within the wheat population allowed it to adapt to the genetic composition of the wheat. Compared with the pure lines grown in the same way, the bunt infection level was much lower, comparable with pure lines grown with new spores each year. I think this means that despite a stable infection level, resistance may increases in the populations from year to year, but in the same time, the virulence of the pathogen increases and eliminate this effect.

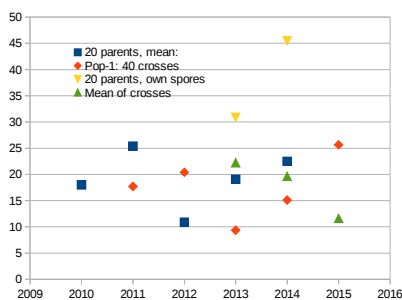


Figure 1: Common bunt in CCPs, single cross populations and in pure lines

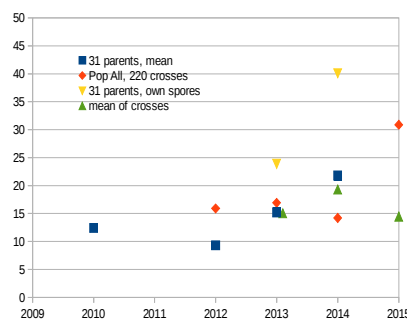


Figure 2: Common bunt in CCPs, single cross populations and in pure lines

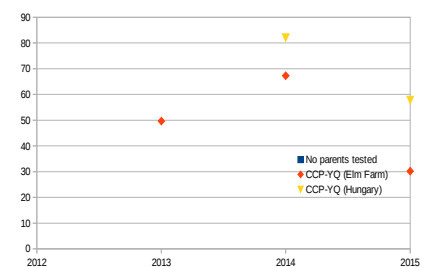


Figure 3: Common bunt in ORC Wakelyns CCP

The ORC Wakelyns CCP had a much higher infection level as my own CCP, and the CCP grown in Hungary was even higher. This can be explained by the fact that the parents of the ORC Wakelyns CCP were not selected for their resistance to bunt, leading to a more susceptible CCP.

Most of the parents were resistant to some virulence races of bunt, but susceptible to others (Borgen 2015). Crosses with parents with resistance to all tested virulence races had a stable low infection level over the three years (<10%), while crosses where parents were susceptible to some virulence races had higher and in many cases increasing infection level over the years. This indicates that virulence had build up within the individual populations. The average infection level between the individual crossings was comparable with the the infection level in the CCP of the same parents indicating that no synergistic effect was achieved by the higher diversity of the CCPs.

Protein content in spring wheat

After two generations of seed sorting, the protein content of the high protein fraction was higher than the content in the low protein fraction (Borgen *et al* 2014). Growing the same fraction without further seed sorting maintained the differences in protein content, meaning that the achieved differences was indeed heritable traits as shown in Figure 4. The protein content was in average 11.5% in the samples grown from the low protein fraction seed, and 12.3% in the high protein fraction. The yield on the other hand decreased from 5674 to 5252 kg/ha respectably.

The experiment shows that it is possible with automatic single seed sorting to increase the protein content in populations, but that this (like it is known from pure line varieties) is on the expense of a yield loss of about 10% for each protein content increase.

Acknowledgement

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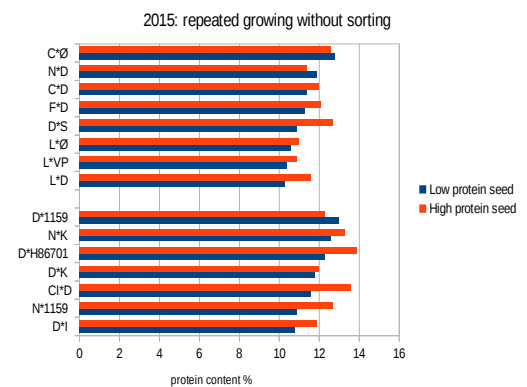


Figure 4: Protein content in cross populations of spring wheat

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