

Evolutionary breeding of healthy wheat: from plot to farm

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Summary

Genetically diverse Composite Cross Populations (CCPs) may be useful in environmentally variable low-input systems as an alternative to pure line varieties. They are formed by hybridising lines with diverse evolutionary origins, bulking the F_1 progeny, and allowing natural selection of the progeny in successive crop environments. CCPs derived from 10 high yielding parents (YCCPs), 12 high quality parents (QCCPs), or all 22 parents (YQCCPs), were grown at four sites (2 organic, 2 conventional) in the UK; they are currently (2006) in F5. The YCCPs out yielded the QCCPs, which had better quality characteristics. Although the CCPs performed within the range of the parents, the values obtained were often better than the mean of the parents. Some population samples are now being grown on farms and other sites in England, France, Germany and Hungary.

Keywords: Composite cross population, wheat, *Triticum aestivum*, male sterility, yield, quality

Introduction

Crop health may be defined as the ability to be productive under a wide range of environments without need for external inputs. This requires appropriate varieties that are largely lacking for wheat in both organic and conventional agriculture (Jones & Wolfe, 2005). Without agrochemical inputs, productivity of modern varieties bred for conventional production falls heavily, for a range of reasons, as the crop plants are exposed to wide diversity and variability in production environments. Breeding pedigree lines able to cope with such environmental variation would be difficult, time-consuming and expensive. One potential solution is to use genetically variable populations that are able to buffer against variation including diseases, pests and weeds (Suneson, 1956; Phillips & Wolfe, 2005). Evidence suggests that composite cross populations may be an efficient way of providing heterogeneous crops (Clay & Allard, 1969), which can be allowed to evolve on-farm. In addition, generation of novel genotypes should allow selection of pure lines adapted to low inputs (Soliman & Allard, 1991).

Composite cross populations (CCPs) are formed from parent lines with diverse evolutionary origins that are recombined by hybridisation. The F_1 progeny is bulked to allow subsequent natural selection of the mass progeny in successive crop environments (Suneson, 1956). Continued production of hybrids can be encouraged by introducing male sterility genes into the populations (Suneson, 1951). The success of such populations depends upon recombination and segregation over many generations, and the correlation between natural selection and agricultural desirability

(Allard & Hansche, 1964), although this correlation may be manipulated by directed mass selection (Phillips & Wolfe 2005). One successful example (Thomas *et al.*, 1991) was a composite population of wheat that yielded 15% more than the mean of the parents in pure stands.

This paper reports on the early performance of six CCPs relative to their parents and to physical mixtures of the parent components. The results refer to two organic and two conventional farm sites, although population samples are now under selection on other organic farms in England (farm-scale adaptation) and on sites in France, Germany and Hungary (regional adaptation).

Materials and Methods

Replicated plot trials

Elm Farm Research Centre, with the John Innes Centre, developed six CCPs based on successful wheat varieties. They were derived from all possible combinations of 10 high yielding parents (45 crosses), or 12 high quality parents (66 crosses), or of all 22 parents (231 crosses). Each of the three bulk populations was split into those that did, or did not, contain a range of male sterile crosses (33) developed from naturally occurring male sterile parents crossed with the other varieties.

The first field exposure of the populations was in 2003/04 in the F₃ generation. The populations, their parents and mixtures of the high yield, high quality and all parents were sown at 2 organic (Sheepdrove Organic Farm, Berkshire and Wakelyns Agroforestry, Suffolk) and 2 conventional sites (Metfield Hall Farm, Suffolk and Morley Research Centre, Norfolk). In 2004/05 randomised block trials were established at the same four sites, with all populations, parents and mixtures.

Participatory farm trials

For harvest year 2006 (F5), population samples are being grown by farmers on larger plots on six farms to allow potential adaptation to the farm sites. Differentiation among these populations will be investigated later; as this is the first year of selection, there are no data yet available. In a similar way, population samples are being selected in France, Germany and Hungary to try to estimate the potential for regional adaptation.

Results

Yield

For 2005, there were significant ($P < 0.001$) differences in grain yield among parent varieties, mixtures and CCPs with and without male sterility (CCP(ms)) at both conventional sites and at one organic site (Sheepdrove). The Yield CCP(ms)s also had significantly ($P < 0.01$) higher yields than the Quality CCP(ms)s at these sites (Table 1). The Yield/Quality CCP(ms)s generally yielded between the Yield and Quality CCP(ms)s at the conventional sites (Table 1), whereas at the organic sites the Yield/Quality CCP(ms)s yielded at the same level as Yield CCP(ms).

Grain yields of CCP(ms)s were always within the range of yields attained by the parents but, at both conventional sites, CCP(ms)s had higher yields than the means of their parents. This also occurred in the Yield and Yield/Quality categories at the organic sites (Table 1).

An increase in grain yield of CCP(ms)s relative to the mean of the parents was also found in the first year of field exposure (2003/04; F3) at the conventional sites. However, the differences were smaller, and there was no evidence of such an effect at the organic sites.

Table 1. Mean grain yields ($t\ ha^{-1}$ @ 15% moisture content) of Yield (Y), Quality (Q) and Yield and Quality (YQ) composite cross populations with or without male sterility (CCP(ms)) and their parental means. Data for 2005(F5)

System	Y	Q	YQ	P	LSD	SED (df)
Conventional (mean, 2 sites)						
CCP(ms)	10.9	9.8	10.1	0.023	0.83	0.412 (42)
Parental mean	10.4	9.5	9.3			
Organic (mean, 2 sites)						
CCP(ms)	6.3	5.5	6.4	<0.001	0.54	0.269 (55)
Parental mean	6.0	6.0	5.9			

The Yield CCP(ms)s had significantly ($P < 0.001$) shorter straw than the Quality CCP(ms)s at the conventional sites; similar differences at the organic sites were not significant. There were, however, significant ($P < 0.05$) differences in harvest index (HI) among categories of CCP(ms) at both organic sites with the HIs of the Yield CCP(ms)s higher than those of the Quality CCP(ms)s. This was also the case at one of the conventional sites (Morley) but not significantly so at Metfield, the other conventional site. These latter effects may have been influenced by differing applications (timing and active ingredient) of growth regulator at the two conventional sites.

Grain quality

There were significant differences in the grain quality parameters of protein concentration and Hagberg falling number (HFN) among varieties, mixtures and CCP(ms)s at all sites. Protein concentrations differed significantly ($P < 0.01$) among Yield, Quality and Yield/Quality CCP(ms)s at conventional sites: Quality and Yield/Quality CCP(ms)s had higher protein concentrations than Yield CCP(ms)s (Table 2). A similar effect at the organic sites was not significant.

Table 2. Mean protein concentrations (%) of Yield (Y), Quality (Q) and Yield and Quality (YQ) composite cross populations

System	Y	Q	YQ	P	LSD	SED (df)
Conventional (mean, 2 sites)	12.1	13.1	12.7	0.002	0.57	0.28 (43)
Organic (mean, 2 sites)	11.1	12.1	11.9	0.318	1.50	0.747 (52)

The same trends occurred in the HFN results, which were significant at both the organic ($P < 0.05$) and conventional ($P < 0.01$) sites. Similar differences among CCP categories (Y, Q or YQ) were also seen in the first year of field exposure of the CCPs.

Discussion

The composite cross populations have performed as expected according to their categories; the Yield composites had higher yields and Harvest Indices, and the Quality composites had higher protein concentrations and Hagberg Falling Numbers. More importantly, although the populations performed within the range of the parents, they often yielded more than the mean of the parents. This shift in the performance of the CCPs relative to the mean of their parents would suggest that the winter wheat populations over two seasons in the field have started to evolve in response to field conditions of the two alternative agricultural systems. The literature suggests (Phillips

& Wolfe, 2005) that further beneficial shifts in yield and quality will occur in later generations. However, under organic conditions, it seems likely that adaptation of the populations to improved nutrient extraction and use, whether general or local, is likely to be slow. It is also clear that, to encourage adaptation to a wide range of environments, the populations will need to be exposed to many environments, which may take many cycles. For these reasons we aim to extend the current project.

For practical exploitation in the field, the direction and scale of population changes may be improved by mass selection. We therefore intend to select for large grain which may simultaneously shift the populations towards better resistance to seed-borne diseases and improved weed competition (see Weiner *et al.*, 2001). Performance of the populations may also be improved by introducing appropriate new varieties either as parents in crosses with existing parents or lines, or simply as physical mixtures. The populations may also be exploited indirectly by selection of desirable lines to develop as pure line or synthetic varieties. These varied approaches should be helpful in ensuring healthy wheat crops under organic conditions and in providing material to improve the sustainability of conventional production.

To better understand the directions of selection for performance under low input conditions, a set of molecular markers that can identify each of the parents will be used to assess the relative contributions of the parents in each of the six populations.

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