tion cycles and more rapid progress while not imposing yield or genetic diversity ceilings typical of backcrossing. The effectiveness of a recurrent selection program can furthermore be greatly enhanced by using genetic male sterility and by supplementing phenotypic selection with marker-aided selection strategies.

A highly diverse, prebreeding base population is being produced. It incorporates a wide range of native and exotic resistance and adaptation genes, most of which derive from either spring wheat or less cold-hardy winter wheats from the southern United States. These will be involved in a complex cross that will eventually combine genes from approximately 150 diverse genotypes contained within five parental populations. While making the cross, the *Ms3* (dominant male sterility) gene is simultaneously being established within the hybrid population such that the final F_1 will segregate 1:1 for male sterility/ fertility. This final F_1 will be randomly intercrossed for two further cycles to fully disperse the target genes before the onset of selection. The intermediate and final hybrid populations will furthermore be evaluated to confirm the genetic diversity that it contains by employing phenotypic and/or marker-based evaluations of disease resistance, adaptation and performance. Concurrent with the development of the program, a procedure for random, large-scale intercrossing of individual plants through the use of *Ms3* will be optimized.

Poster 18. Creation of a new resource for fine mapping in wheat: a nested association mapping population.

G. Charmet [1], M.R. Perretant [1], J.B. Beaufumé [2], and S. Praud [2].

[1] INRA–UBP, UMR GDEC, 234 av du Brezet 63100 Clermont-Ferrand, France, and [2] Biogemma, site de la garenne, Route d'Ennezat, CS 90126, F-63720 Chappes, France.

Linkage mapping using recombinant inbred lines usually achieves high power of QTL detection, but suffers from relatively poor accuracy of QTL location. Association or linkage disequilibrium (LD) mapping using panels of unrelated lines enables high mapping accuracy, depending on the range of LD, but is prone to several sources of false positive results if the panel is genetically structured. Nested association mapping (NAM) has been recently proposed as a method that combines the advantages of both linkage and LD mapping. It consists of developing a set of recombinant populations which are 'connected' by at least one common parent. The parental lines (founders) must be genotyped with a high marker density; the accuracy of QTL detection will rely on the short range LD among the founders. Then the recombinant progeny will be genotyped at low density. The small number of recombination events from founders to progeny enables large LD blocks to be conserved. The high density markers can therefore be imputed in the progeny from the information of low density markers thus keeping the high detection accuracy. On the other hand, recombination is sufficient to reshuffle the genetic background, thus limiting the source of spurious association with unlinked markers. Roughly, a NAM population achieves nearly the same accuracy as an unrelated association panel of similar size, while high-density genotyping or resequencing is only needed on a few dozen of founders. Simulations results suggest an optimal number of founders of 80-100 for a total sample size of 2,500–5,000.

In a cooperative program between Biogemma and INRA (ARN-08-GENM-005), we have developed a NAM population of RILs, and DHs, by producing recombinant progeny from a 'star' mating design. The pivot parental line was Altigo, a high-yielding, modern French cultivar. The other founders were taken either in the elite European cultivars or in a worldwide core collection built up at INRA GDEC Clermont-Ferrand France (http://www4.clermont.inra.fr/umr1095_eng/Teams/Technical-and-Experimental-Platforms/Genetic-Resources-Centre). Seed increase of the 5,000 progenies is now in progress. This new resource will be available soon for collaborative programs.