

A four-way cross mapping population for QTL discovery in durum wheat

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Introduction

The identification and exploitation in the breeding activities of genetic factors underlying the basis of horizontal resistances to crop diseases is considered as one of the major goals to achieve for modern crop genetics: in fact, adult-plant resistances, even if partial, are often associated to durable resistance. In durum wheat, different sources of reliable resistances to the main wheat fungal diseases have been identified in the elite germplasm but most of them have not been characterized yet. Mapping of major QTLs requires the development of specific mapping populations.

Biparental mapping populations are not effective for (i) a thorough characterization of the functionally different alleles present at a target locus and (ii) the identification of epistatic interactions. To partially overcome these limitations, we have started to assemble a durum wheat linkage map utilizing a four-parental population developed by DiSTA (University of Bologna) and Produttori Sementi Bologna from the cross between Neodur, Claudio, Colosseo and Rascon, four cultivars characterized by different quality parameters and resistance genes to powdery mildew, leaf rust and *Fusarium* head blight (Tab. 1; Fig. 1).

Parental line	Characteristics
Neodur	- Good Fusarium head blight tolerance
Claudio	- Resistant to powdery mildew - High and stable test weight
Colosseo	- Carrying durable resistance to leaf rust (<i>P. recondita</i>)
Rascon	- High yield potential

Tab. 1 Parental lines main characteristics.

Multiparental genetic map development

As part of the European project “BioExploit Food CT 2005-513959”, an immortal Recombinant inbred populations will be obtained following the scheme attached (Figure 1). A “four-way F₁” segregating populations (ca. 400 segregating individuals) was obtained by manual crossing a balanced number of plants of bi-parental F₁ (Fig. 1). A genetic map is being generated for the F₁-NCCR progeny with AFLP® markers (Keygene N.V.) and anchoring SSR markers (DiSTA). After a prescreening of the four parental lines with more than 150 AFLP primer combinations (*Pst*I+3/*Taq*I+3), and 250 SSR markers, the most informative ones were used to generate the preliminary genetic F₁-NCCR map using CRIMAP software [Green P., Fall K. and Crooks S. (1989) Documentation for CRIMAP, V.2.4. Washington University School of Medicine, St. Louis, MO]. A total of 189 AFLP markers (*Pst*I+3/*Taq*I+3) and 70 SSRs were grouped on 23 main linkage groups, spanning a total of 1080 cM (Fig. 2).

The QTL analysis on quality and resistance traits will be performed on RIL-NCCR progenies at the F₇ stage.

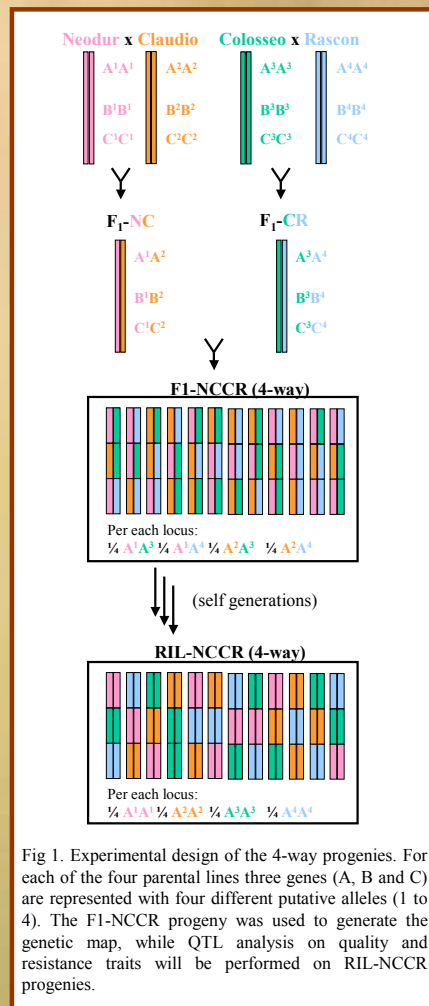


Fig 1. Experimental design of the 4-way progenies. For each of the four parental lines three genes (A, B and C) are represented with four different putative alleles (1 to 4). The F₁-NCCR progeny was used to generate the genetic map, while QTL analysis on quality and resistance traits will be performed on RIL-NCCR progenies.

Conclusions

To overcome the limits of traditional bi-parental mapping populations, we established a four-way cross population in durum wheat. The known resistance to major fungal pathogens of durum wheat of some of the parents of the mapping population will let us to map with good resolution resistance QTLs to fungal diseases. Moreover, the favorable major QTLs/QTL identified will be already available in a valuable elite genetic background.

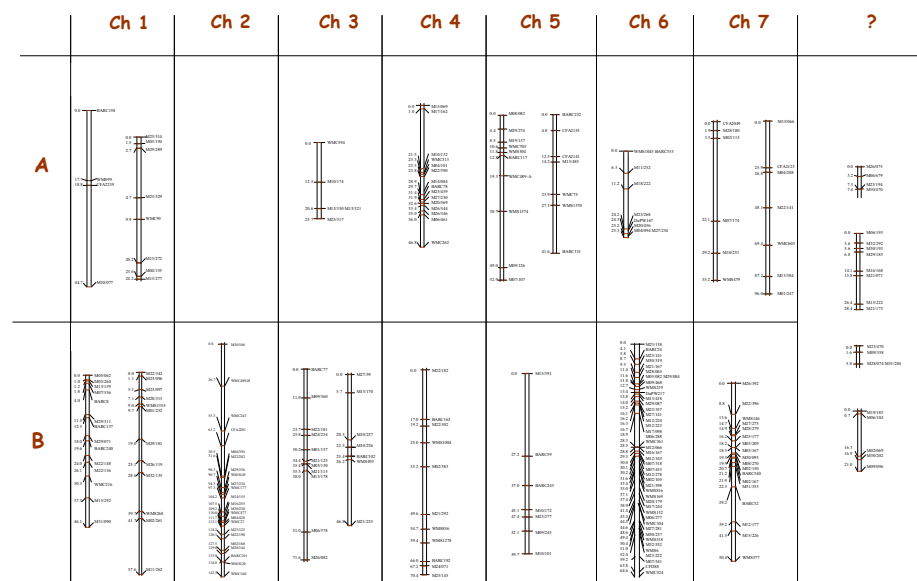


Fig 2 F₁-NCCR preliminary genetic map. The multiparental genetic map was generated by Keygene N.V. using CRIMAP software [Green P., Fall K. and Crooks S. (1989) Documentation for CRIMAP, V.2.4. Washington University School of Medicine, St. Louis, MO].