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A Gaspé flint × B73 introgression library suitable for the genetic dissection of flowering time and other agronomic traits

--Salvi, S; Corneti, S; Giuliani, S; Sanguinati, MC; Talamè, V; Tuberosa, R

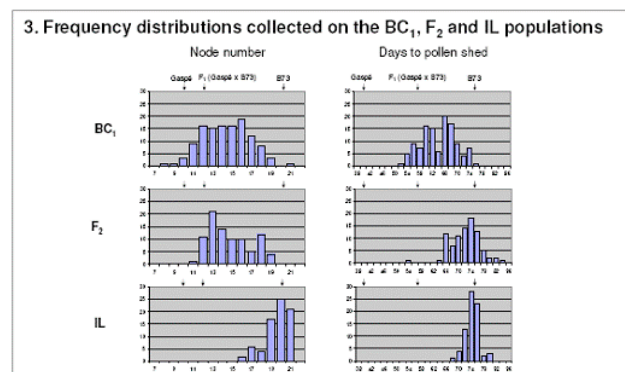
An introgression library (IL) is a collection of lines each carrying a well-defined chromosome segment introgressed from a donor accession into the genetic background of a common line (Zamir, Nat. Rev. Genet. 2:983-989, 2001). Introgression libraries are ideal for mapping and cloning QTLs (Zamir, 2001; Salvi and Tuberosa, TIPS 10:297-304, 2005), two increasingly important goals in maize breeding in view of the importance of quantitative traits for the improvement and sustainability of yield. We are interested in identifying major QTLs influencing flowering time and root architecture, two important features for the adaptation of maize to different environments and to counteract the negative consequences of global climate change (e.g. increase in temperature, drought, flooding, etc.). B73 and Gaspé flint differ greatly in flowering time (25-30 days in our environment) and in a number of other architectural features, including root architecture, an important trait in improving maize performance under lower-input agriculture (e.g., less irrigation and fertilizer application). Additionally, B73 was chosen because of its importance in maize breeding and the vast amount of genetic and genomics information that is available for this line.

Materials. The [(B73 × Gaspé flint) × B73] BC₁ to BC₅ generations were grown from 2002 to 2005. In each generation, plants heterozygous for a given chromosome interval were identified based on SSR analysis and backcrossed to B73. At BC₅, one plant homozygous for the Gaspé flint introgression for each one of the 70 BC families was chosen to assemble the IL. On average, outside the introgressed regions ca. 98% of the B73 genome should have been recovered for each line. The following materials were evaluated: the 88 BC₁ plants and 126 B73 × Gaspé flint F₂ plants, along with the 70 IL lines.

Molecular markers. 165 SSRs (maizeGDB at www.maizeGDB.org) were used, 86 (52%) of which were polymorphic between B73 and Gaspé flint. Among the polymorphic SSRs, 72 were utilized to produce a linkage map based on the BC₁ population.

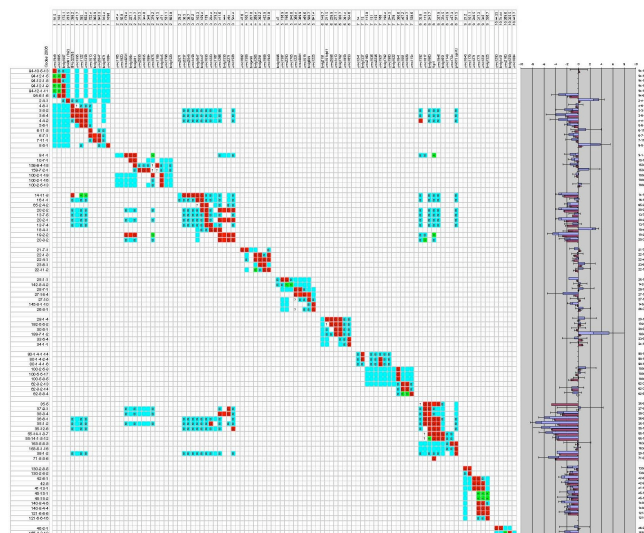
Traits analyzed. Days to pollen shed (DPS), node number (ND) and other traits were measured in the BC₁, F₂ and IL populations. The BC₁ population was grown in 2002, and the F₂ and IL lines in 2006. The 70 IL lines were grown in four reps with 10 plants per plot. The figure below presents the frequency

distribution of flowering time of the BC₁, F₂ and IL populations.



Root traits were evaluated at the seedling stage and in pots. Preliminary observations indicate the presence of extensive variability for root features (Salvi et al., unpublished). The data are being analyzed.

Structure and phenotyping of the Gaspé flint × B73 introgression library. In the figure below, rows represent the IL lines while columns indicate the SSR markers. Red, blue and green squares with/without letters indicate homozygosity for Gaspé, homozygosity for B73 and heterozygosity, respectively, as per SSR analysis. White squares indicate homozygosity for B73 ($P > 0.98$). The blue dashed lines indicate the approximate position for newly identified QTLs for flowering time, herein named *Vgt* (*Vegetative to generative transition*) 3 to *Vgt*6, after the previously described *Vgt*1 and *Vgt*2 (Vladutu et al., Genetics 153:993–1007, 1999, Salvi et al., Plant Mol. Biol. 48:601-603, 2002). Recently, *Vgt*1 has been positionally cloned (Salvi et al., PNAS 104:11376-11381, 2007). (NOTE: the figure below has viewable detail if zoomed, online.)



Conclusions and perspectives. We produced a Gaspé flint x B73 introgression library through five marker-assisted backcrosses. The 70 introgression lines cover ca. 70% of the Gaspé flint genome in a B73 genetic background. The evaluation of the IL lines confirmed the important role of *Vgt1* and *Vgt2*, and revealed the presence of four additional QTLs for flowering time. The fine mapping of *Vgt3* is underway. Extensive phenotyping, both as lines per se and testcrosses, is in progress to identify additional QTLs for the genetic control of yield and other agronomically important traits. The IL lines are available for collaborative studies.

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