

AN INTEGRATED GENETIC AND PHYSICAL MAP OF *GAMETOPHYTE FACTOR 1 (Gal)* GENE IN MAIZE

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Gal (*Gametophyte Factor 1*) is a gametophyte mutant involved in the phenomenon of cross-sterility. Such mutant is widely present in many popcorn inbred lines. The presence of the dominant allele *Gals* in the sporophyte prevents fertilization by pollen carrying the recessive allele *gal*. The gene was discovered in 1923 and roughly mapped on maize chromosome 4, exploiting its loose linkage with another mutant, *sugary 1 (Su1)* (House and Nelson, 1958). However, its position was never determined in greater detail, and up to now this gene has never been precisely mapped on public genetic maps.

Our present aim is the isolation of *Gal* through a positional cloning approach.

First, we generated a large segregating population of around 3000 individuals, phenotypically and molecularly characterized.

Various approaches to identify molecular markers in the region of interest have been adopted; search on public maize databases has been performed, followed by the exploitation of rice-maize synteny.

We then integrated data from physical and genetic maps. We placed additional molecular markers obtained from maize ESTs, genomic and BAC-ends sequences derived from clones sequencing in order to further reduce the region containing *Gal*.

Analysis of the public physical map (<http://www.genome.arizona.edu>) has led to the identification of a single BAC contig.

We subsequently created a high-resolution map of the chromosomal region of interest, delimiting a genetic region of 1.8 cM encompassing *Gal*, and we could thus link our genetic map to the physical one.

The exploitation of rice-maize synteny has been pursued to identify a region on rice chromosome 11, syntenous to the maize interval flanking *Gal* (www.gramene.org).

At the present stage we can search for new sequences in this delimited rice region, orthologous to the maize region surrounding *Gal*. Furthermore, we will attempt to restrict the physical region to few clones in order to sequence them and search for potential candidate genes.

In any case, we will need a genomic library of the line *Gal/Gal* in the final steps of positional cloning, as the public physical map was obtained from inbred line *gal/gal* (B73). Indeed, it is well known that genetic diversity among inbred lines in maize could be surprisingly wide.