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Mapping Economic Trait

Loci in Cattle : towards

positional cloning of the

« Polled » locus and dairy QTLs

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Over the past 10 years, considerable efforts have been done into the establishment of genome maps for several species. In cattle, international collaboration, european supported projects and national initiatives were the basis for the construction of genetic and physical maps of the bovine genome : more than 600 genes and 1500 microsatellite markers are mapped (BOVMAP : <http://locus.jouy.inra.fr>). Therefore the selection of a panel of 200-300 well distributed informative markers is no more a challenge. Using these markers, several economic trait loci have been localized and Marker Assisted Selection (MAS) can now be applied in breeding programs. However, the use of MAS is limited due to the risk of recombination between the markers and the gene and to their within family validity. Identification of the gene of interest and the causal mutation would represent a great benefit : the genotyping would be restricted to a single genetic test, the procedure could be transfered to other populations and such a test could serve as basis to start understanding the genetic determinism of the trait.

In human genetics, four general strategies have been described for identifying genes of interest : these strategies are also widely used in animal genetics : 1) **Functional cloning**, 2) **Position-independent candidate gene approaches**, 3) **Positional candidate gene approaches** and 4) **Positional cloning**.

Positional cloning of the Polled locus :

In *Bos taurus*, the presence or absence of horns is under the genetic control of the autosomal « polled » locus, characterized by two alleles and causing the dominant polled or hornless phenotype. However, in most population in which *polled* is segregating, a third phenotype, *scurred*, is present, most probably under the control of a second locus. George et al. mapped the *polled* locus to bovine chromosome 1, between the 2 microsatellites AGLA17 and TGLA49 (Georges et al., 1993). The position of the *polled* locus was confirmed in several different breeds (Brenneman et al., 1995 ; Harzilius et al., 1996 ; Eggen et al., 1996). In commercial beef production, horns present management problem and hazards to animal handlers as well as to other cattle : therefore, many breeders dehorn their cows and most calves are routinely dehorned. Breeding programs have been designed to select for the polled allele but these programs are limited and

expensive as they require the production of several offspring in order to discriminate between homozygotes and heterozygotes. In France, as Charolais breeders were interested in the implementation of MAS for the polled locus and the identification of the gene, a large pedigree was collected in order to first confirm the localization of the polled locus in the breed and to start the positional cloning of the gene of interest (*Figure 1*). The critical interval containing the polled locus was reduced to 5 cM before starting the construction of a genomic contig of the region. YAC and BAC libraries (*INRA*, Jouy-en-Josas, France and *Infigen Inc.*, DeForest, USA) were screened by PCR followed by a chromosome walking approach in order to complete the entire interval (*Figure 2*). New microsatellite markers were developed and are currently used in MAS for the Charolais breed (*Figure 3*). Coding sequences of the region were identified using comparative mapping and a YAC differential display procedure. Similar efforts are currently under way for several region containing Quantitative Trait Loci.

Figure 2 : YAC contig of the polled region

**Figure 3 : Marker Assisted
Selection for the Polled locus**

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