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GENETIC STRATEGIES TO IMPROVE AND CONTROL THE QUALITY OF ANIMAL PRODUCTS

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Quality of animal products is one of the most important objectives of the breeding strategies in farm animal species. With the use of quantitative genetics, efficient selection plans, that made it possible to have important improvements in meat, milk and egg quality, have been developed. However, the recent developments and achievements of the molecular genetics and genomics technologies, the large amount of data that comes from the sequencing of the pig, cattle and chicken genomes, have opened new opportunities in the identification of genes affecting quality traits and in the use of this information for the improvement of the quality of animal products. Moreover, these new tools and information have paved the way to new approaches and strategies in the control of the quality by tracing the products using DNA technologies.

This review will illustrate the actual applications and the future prospects of the genetics and genomics for the improvement and control of the quality of animal products.

Different approaches, like the genome scan and the candidate gene approaches or the integration of both, combined with different experimental designs (i.e: F2 and half sib populations; selective DNA pooling; etc.), have been used to find genes or genomic regions responsible for the variation of quality traits. Recently, new strategies that are based on the transcriptome analysis have been proposed and applied in order to obtain additional information on the role of the genes in the investigated traits.

In pig, two major genes, *RYR1* (*HAL* locus) and *PRKAG3* (*RN* locus), responsible for defects of the meat known has PSE (pale, soft, exudative) meat and "acid meat", respectively, have been identified and the analysis of their mutations is currently in use in marker assisted selection (MAS) plans in order to eliminate the carriers of the negative alleles. Other genes and chromosome regions have been indicated to be associated to meat quality traits in pigs. Moreover, other studies are in progress to identify genes affecting the activity of lysosomal proteinases that is related to the defect of excessive softness of dry cured hams. Some examples can be mentioned also in beef cattle: mutations in the myostatin (*MSTN*) gene have indicated to affect meat quality traits and the tyroglobulin (*TG*) gene has been associated to marbling. In dairy cattle, two quantitative trait genes affecting milk quality traits have been identified: the *DGAT1* gene that affects mainly milk fat content and the growth hormone receptor (*GHR*) gene that affects milk protein percentage. Furthermore, several studies have identified quantitative trait loci (QTL) for milk production and quality traits. A tremendous amount of data has been produced by the BovMAS project that involves several dairy and dual purpose cattle breeds including the Italian Holstein-Friesian and Italian Brown breeds. Using the results of this project application of MAS will be possible in the near future for these two Italian breeds.

Besides quality, the knowledge of the origin of the products represents an important issue for the consumers. The traceability of foods of animal origin should be guaranteed during the entire food chain,

from the farm to the market. DNA technologies can once more provide powerful tools to meet this requirement through the realisation of a sort of genetic identity card of the individual animal. Moreover, application of breed traceability is also possible and can be used as a protection of some mono–breed animal products.