

Genetic tests for food quality

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During the last decades there has been increasing interest in rapid and effective methods for evaluation of food quality and food safety. One of the promising approaches is the development of genetic tests and genetic markers for selective breeding towards genotypes with desirable food quality characteristics. This presentation will give an overview of research on the development of genetic markers for meat quality in pigs and cattle.

There are two major directions in the development of genetic markers: (i) DNA sequencing and identification of trait-related polymorphisms and (ii) identification of quantitative trait loci (QTL). The latest investigates the association between a trait and a particular region of a chromosome which includes a number of genes.

Single nucleotide polymorphisms (SNPs) have been detected in a number of porcine and bovine genes and have been linked to carcass composition, meat palatability, fat content and other meat quality traits. For example polymorphisms in the coding region and the promoter of bovine leptin gene have been shown to be associated with carcass fatness and intramuscular fat content (Buchanan et al., 2002; Nkrumah et al., 2005). SNPs in cattle myostatin gene have been associated with fat depth, total carcass fat weight and intramuscular fat content (Esmailzadeh et al., 2008). There is association between SNPs in calpain/calpastatin genes and meat tenderness (Barendse et al., 2008). It has to be taken into account that majority of the SNPs have been identified and tested only in one or two breeds. The challenge now is to validate the SNPs on various breeds and to evaluate them on large pig or cattle populations.

In parallel with SNPs identification QTL have been detected for almost every important pork or beef quality traits. This includes QTL for carcass composition, meat palatability, pH, marbling, boar taint and many other (Lee et al., 2005; Demeure et al., 2005; Rohrer et al., 2005; Barendse et al., 2008; Davis et al., 2008;). However only a few QTL have been transferred to the industry, which is partially related to a high cost of the assays. Moreover, some of the QTLs are breed-specific and further evaluation on various breeds is required. In addition some of the QTLs cover quite large areas of chromosome and this need to be narrowed down prior giving recommendations for their application for selective breeding.

Although a large number of genes controlling meat quality traits have been discovered, there is a lack of information on multigene interactions. Research towards understanding of the impact of the selective breeding on other aspects of animal performance and health are required.

References:

- Barendse W., Harrison, B.E., Bunch, R.J., Thomas, M.B. (2008) *BMC Genet.* 9, 41.
- Buchanan F.C., Fitzsimmons C. J., Van Kessel A.G., Thue C., Winkelman-Sim C, Schmutz S. M. (2002) *Genet.Sel.Evol.* 34: 105-116.
- Davis G.P, Moore, S.S., Drinkwater R.D., Shorhose W.R., Loxton I.D., Barendse W. Hetzel, D.J. (2008) *Animal Genet.* 39, 40-45.
- Demeure O., Sanchez M.P., Roquet J., Iannuccelli N., Demars, K at al. (2005) *J.Anim.Sci.*, 83, 1979-1987.
- Esmailzadeh A.K., Bottema, C.D.K., Sellick, G.S., Verbyla, A.P., Morris, C.A., Cullen, N.G., Pitchford, W.S. (2008) *J.Anim.Sci.*, 86, 1038-1046.
- Lee G.J., Archibald A.L., Law A.S., Lloyd S., Wood J., Haley C.S. (2005) *Anim.Genet.* 36, 14-22.
- Nkrumah J.D., Li C., Yu, J., Hansen C., Keisler D.H., Moore S.S. (2005), *J.Anim.Sci.*83, 20-28.
- Rohrer G.A., Thallman, R.M., Shackelford, S., Wheeler T and Koohmaraie M. (2005) *Animal genet.* 37, 17-27.