In silico large scale discovery of SNPs to fine map meat quality QTL regions in porcine genome

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ABSTRACT

The pH of pig meat is an important parameter involved in the assessment of the quality of fresh and seasoned meat products. This trait is under genetic control and is also strongly influenced by environmental factors, mainly the pre-slaughter events. Nevertheless, the genetic effects are very important; only two major genes affecting this parameter, *RYR1* and *PRKAG3*, have been identified so far. Several researches have reported QTL regions in at least 10 porcine chromosomes influencing meat pH and some of them have been confirmed by more authors. With the aim to contribute to the fine mapping of these regions and to locate the genes responsible of the effect of the QTLs we chose three of the most relevant QTL regions so far detected, in order to find SNPs *in silico* in transcribed sequences. The selected QTL regions were: SSC1 (60-80 cM), SSC2 (55-66 cM), SSC3 (42-60 cM). We then localised more than 2,000 porcine UniGene clusters of genes/ESTs in the selected regions comparing the homologous part of pig and human chromosomes using the NCBI map viewer tool. We filtered the identified clusters selecting only those with a minimum of eight ESTs or mRNAs, then discarding the clusters without at least one mRNA. On the whole, we considered 634 clusters and the sequences corresponding to each one were aligned using BLAST in order to find polymorphisms. We marked as putative SNP a mutation detected in at least three sequences to avoid considering sequencing errors and also to exclude SNPs with a very low frequency of the rarest allele. A first use of this strategy carried out on 264 clusters located in the three analysed chromosomes, allowed us to find 159 putative SNPs with a detection efficiency of 60.2% relative to the 264 initial clusters. For some of the SNPs detected *in silico*, primer pairs were designed in order to confirm the presence of the polymorphisms. The proposed approach will be applied to detect several hundred SNPs in large regions spanning 10-20 cM each, where QTLs for meat pH were reported. Moreover, the detection of SNPs within transcribed sequences (including the 5'-UTR, the coding region, and the 3'-UTR) will be useful for further researches aimed to fine map the considered QTLs in order to narrow the regions where the genes responsible to the QTL effect are located.