Utilisation de données d'expression génique pour prédire la qualité de viande chez le porc

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Using gene expression data to predict pork quality

Availability of biomarkers for pork quality is essential to control its variability and predict meat quality. In this study, two pure pig breeds, Large White (conventional, n=20) and Basque (local breed, high sensory pork quality, n=30) reared in different production systems, were investigated for eight meat quality traits: colour (lightness: L*, redness: a*), ultimate pH, drip loss, intramuscular fat content, shear force, sensory tenderness and juiciness. Not only should a biomarker for meat quality be correlated with a meat quality trait but it should also be useful in predicting it; accordingly, we developed predictive models for each of these eight traits. Two linear statistical methods (regression and sparse PLS) and a nonparametric method (random forest) were applied on gene expression data obtained on 50 *Longissimus* muscle samples. Within each statistical model, the number of factors (or predictors) chosen was the one that minimized the predicted residual error. Afterward, for each trait, the model with the minimum error between the three statistical methods was selected as the best predictive model. Lists of four to eleven predictors, which explained between 36% and 86% of the variability observed, were found for seven of the eight meat quality traits considered. The choice of predictors for the eighth trait, meat juiciness, was not successful. These models remain to be validated on meat samples from other pork chains before they can be considered for use in the development of actual tools for predicting pork quality.