Innovative tools for phenotypic characterization and genetic improvement of meat quality in the *Piemontese* breed

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Outline

- Meat quality meaning and limitations connected to its improvement
- The “Qualipiém” project
- Main results of the research
- Conclusions
Introduction

- Interest in enhancing meat quality traits has increased in the last few years because of consumer demands for a tender, lean and healthy product.

- The term “meat quality” includes high number of desirable characteristics in the final product, linked to technological, sensory and nutritional aspects.

- Conventional traits used to investigate meat quality are related to physical characteristics of meat: color parameters, pH, water losses and tenderness.
Introduction

Large number of traits involved, high costs for sample collection and analytical procedures, time consuming lab methods.

Few breeding programmes oriented to meat quality improvement.

Great interest in the development and study of innovative tools for an economic and feasible phenotypes detection of meat quality traits.

Visible and Near Infrared Spectroscopy (Vis-NIRS) and genomics are the most promising applications.
The “QualiPiem” project

Investigating potential use of genomic tools for enhancing meat quality.

Investigating potential application of Vis-NIRS spectroscopy to predict meat quality traits.

Investigating phenotypic and genetic variations of carcass and meat quality traits.

Explore the possibility of selecting meat quality traits in the Piemontese breed.
Phenotypes collection

- The project involved 1,327 slaughtered *Piemontese* young bulls.
- Young bulls were progeny of 204 A.I. purebred sires all registered in the Italian Piemontese Herd Book.
- **Vis-NIRS spectra** were collected at slaughterhouse with two portable spectrometers after the division of carcasses in two quarters on the exposed *Longissimus Thoracis* muscle.
- **Sample** of exposed *L.T.* muscle was collected for meat quality analysis.
- At day 8th of ageing, **meat quality** was assessed by measurements of: lightness (*L*), redness (*a*), yellowness (*b*), *pH*, purge loss (*PL*), cooking loss (*CL*) and tenderness (*WBSF*).
- All young bulls were **genotyped** with GGP Bovine LD array (30,111 SNPs).
## Vis-NIRS, spectrometers

<table>
<thead>
<tr>
<th>Spectrometer</th>
<th>Weight (g)</th>
<th>Wave range (nm)</th>
<th>Data point (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td>“top” portable Vis-NIRS</td>
<td>5,600</td>
<td>350-1,830</td>
<td>1,481</td>
</tr>
<tr>
<td>hand-held Micro-NIRS</td>
<td>60</td>
<td>905-1,649</td>
<td>125</td>
</tr>
</tbody>
</table>

Average spectra absorbance by Vis-NIRS (blue-color) and Micro-NIRS (red-color) on L.T. samples.
**Vis-NIRS, predictions**

- Bayesian approach (Bayes B - BGLR library of R-software) used to develop calibration equations for each meat quality trait.
- External validation performed to assess the accuracy of predictions.

<table>
<thead>
<tr>
<th></th>
<th>L*</th>
<th>a*</th>
<th>b*</th>
<th>pH</th>
<th>PL</th>
<th>CL</th>
<th>WBSF</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>General mean</strong></td>
<td>39.9</td>
<td>28.6</td>
<td>9.7</td>
<td>5.5</td>
<td>4.51</td>
<td>16.8</td>
<td>27.2</td>
</tr>
<tr>
<td><strong>Vis-NIRS</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$R^2$ cal</td>
<td>0.88</td>
<td>0.62</td>
<td>0.70</td>
<td>0.57</td>
<td>0.29</td>
<td>0.26</td>
<td>0.34</td>
</tr>
<tr>
<td>$R^2$ ext-val</td>
<td>0.78</td>
<td>0.55</td>
<td>0.63</td>
<td>0.30</td>
<td>0.31</td>
<td>0.16</td>
<td>0.16</td>
</tr>
<tr>
<td><strong>Micro-NIRS</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$R^2$ cal</td>
<td>0.81</td>
<td>0.51</td>
<td>0.63</td>
<td>0.30</td>
<td>0.20</td>
<td>0.10</td>
<td>0.16</td>
</tr>
<tr>
<td>$R^2$ ext-val</td>
<td>0.80</td>
<td>0.52</td>
<td>0.61</td>
<td>0.22</td>
<td>0.27</td>
<td>0.19</td>
<td>0.19</td>
</tr>
</tbody>
</table>

For selection purposes, besides calibration parameters, $h^2$ of predictions and their genetic correlations with reference analyses must be investigated.
Except for CL and WBSF, Vis-NIRS and Micro-NIRS predictions showed genetic variability and $h^2$ exploitable for selection.
Considering $h^2$ and genetic correlations, for L*, a*, b*, pH and PL NIRS predictions could be used for selection purposes. For CL and WBSF: alternative strategies are to be investigated.
Meat quality phenotypes were pre-corrected for all non-genetic effects prior to estimation of variance components and SNPs effects.

For each trait, the entire data-set was split into training population (80%) and validation population (20%) for 15 times.

The estimation of variance components and SNP effects was performed simultaneously on each training population data using SNP-BLUP model, Bayesian approach and Markov-chain Monte Carlo (MCMC) with the GS3 software (Legarra et al., 2016), fitting a polygenic effect.

The prediction accuracy of DGV was evaluated as $r/h$ (Pryce et al., 2012).
Accuracy of genomic breeding values:

Considering the low-accuracy of the variables used for the training population, the low-density of the array used and the absence of sires and progeny relationships in the training and validation populations, the results are satisfactory.

Young candidates for selection could be evaluated for meat quality traits using their genotype information.
Conclusions

- Thanks to their $h^2$ meat quality traits could be theoretically improved by selection.

- Vis-NIRS predictions of color, PL and pH were satisfactory, with both instruments.

- Considering $h^2$ and genetic correlations, all the predicted traits, except CL and WBSF, were exploitable for selection purposes.

- The study showed that Vis-NIRS spectra collection at the abattoir could be easily implemented.

- The prediction accuracy of genomic breeding values was large enough to suggest that young candidates could be selected using their genotype information.
Thank you for your attention
Genomics, $h^2$

$h^2$, reference analyses vs genomic and polygenic effects.

Linkage disequilibrium between SNPs and QTLs is incomplete, taking into account pedigree information is needed in the prediction of genomic breeding values.