

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 “**Qualipiem**” 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

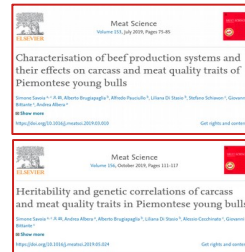


Explore the possibility of **selecting meat quality traits** in the *Piemontese* breed

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

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

Investigating **potential use of genomic tools** for enhancing meat quality.





Phenotypes collection

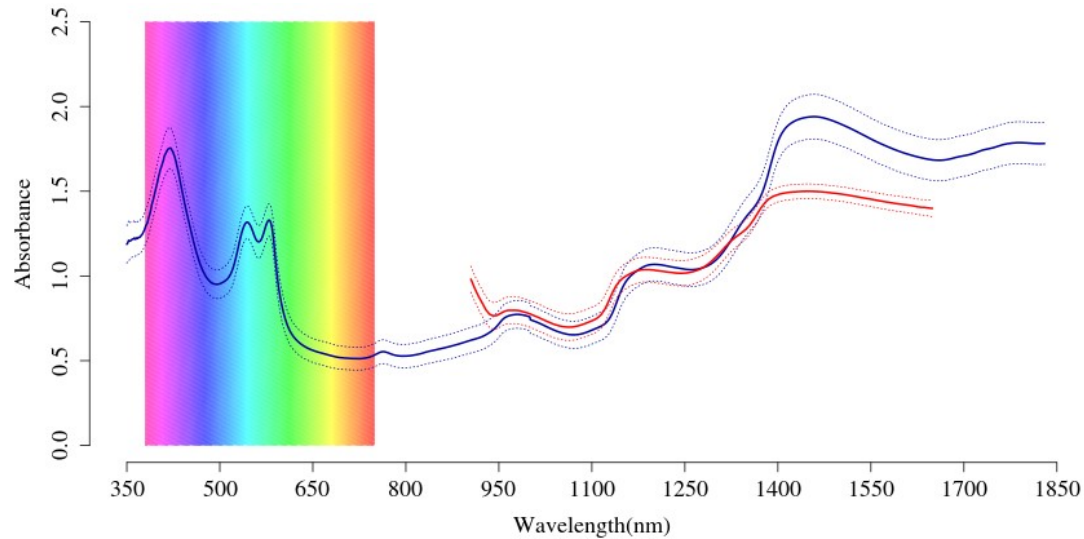
- The project involved **1,327 slaughtered *Piemontese* young bulls**.
- Young bulls were progeny of 204 **A.I. purebred sires** all registered in the Italian Piemontese Herd Book.
- **Vis-NIRS spectra** were collected at slaughterhouse with two portable spectrometers after the division of carcasses 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

| Spectrometer | Weight (g) | Wave range (nm) | Data point (n) |
|---|------------|-----------------|----------------|
|  | 5,600 | 350-1,830 | 1,481 |
|  | 60 | 905-1,649 | 125 |

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



Vis-NIRS, predictions

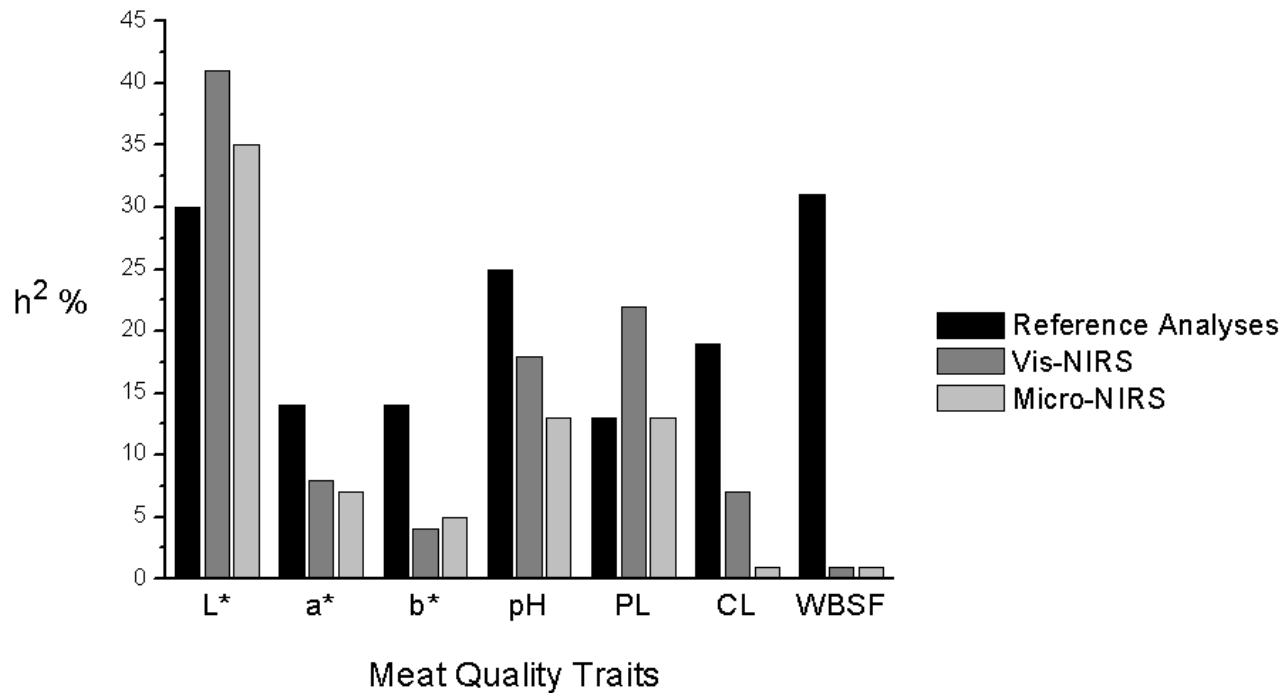
- Bayesian approach (Bayes B - BGLR library of R-software) used to develop calibration equations for each meat quality trait.
- External validation performed to assess the accuracy of predictions.

| | L* | a* | b* | pH | PL | CL | WBSF |
|------------------------|------|------|------|------|------|------|------|
| General mean | 39.9 | 28.6 | 9.7 | 5.5 | 4.51 | 16.8 | 27.2 |
| Vis-NIRS | | | | | | | |
| R ² cal | 0.88 | 0.62 | 0.70 | 0.57 | 0.29 | 0.26 | 0.34 |
| R ² ext-val | 0.78 | 0.55 | 0.63 | 0.30 | 0.31 | 0.16 | 0.16 |
| Micro-NIRS | | | | | | | |
| R ² cal | 0.81 | 0.51 | 0.63 | 0.30 | 0.20 | 0.10 | 0.16 |
| R ² ext-val | 0.80 | 0.52 | 0.61 | 0.22 | 0.27 | 0.19 | 0.19 |

For selection purposes, besides calibration parameters, h² of predictions and their genetic correlations with reference analyses must be investigated.

Vis-NIRS, predictions' h^2

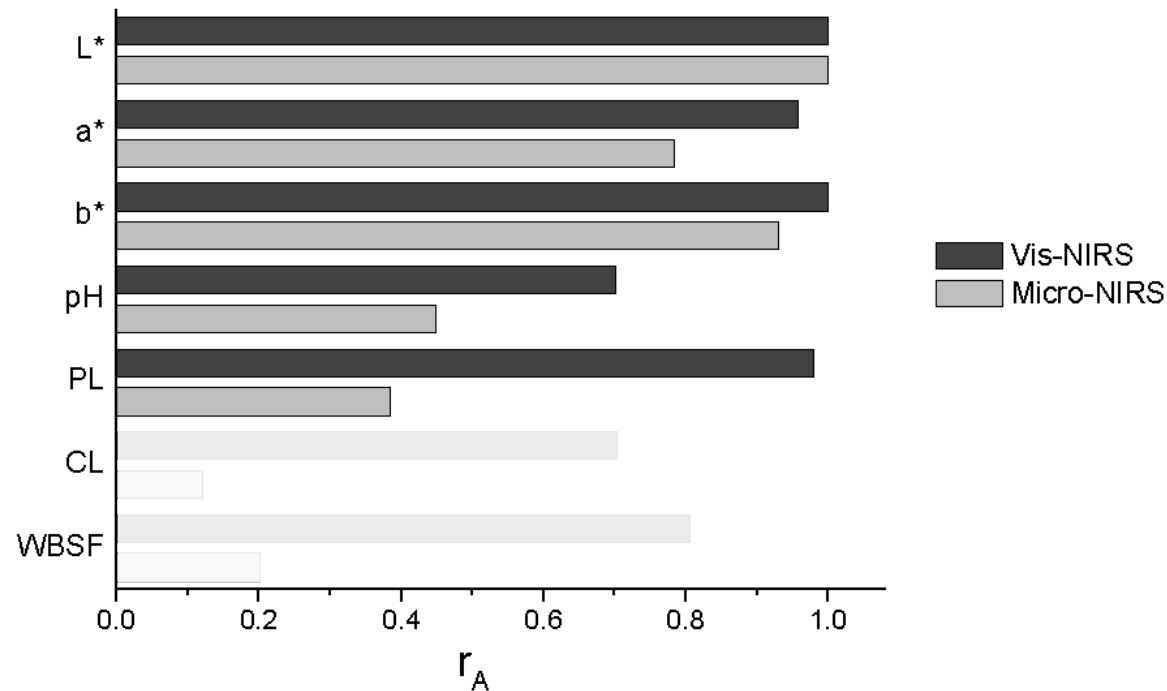
h^2 , reference analyses vs Vis-NIRS predictions



Except for CL and WBSF, Vis-NIRS and Micro-NIRS predictions showed genetic variability and h^2 exploitable for selection.

Vis-NIRS, genetic correlations

Additive genetic correlations (r_A) between reference analyses and their predictions, Vis-NIRS vs Micro-NIRS.



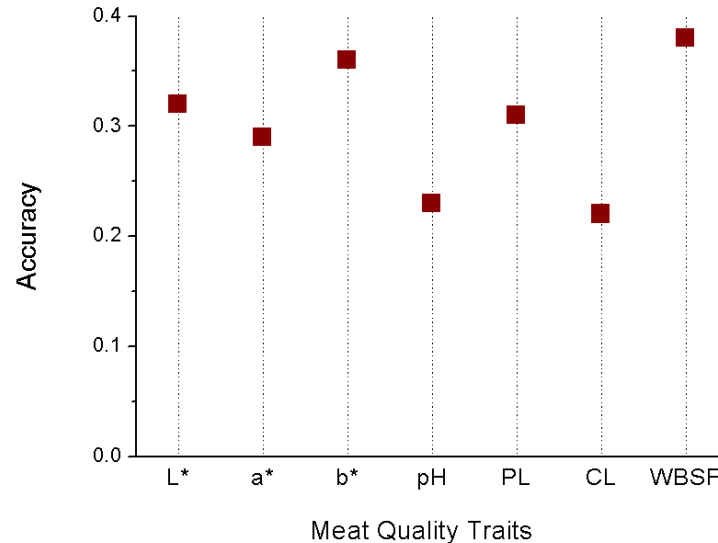
Considering h^2 and genetic correlations, for L*, a*, b*, pH and PL NIRS predictions could be used for selection purposes. For CL and WBSF: alternative strategies are to be investigated.

Genomic breeding values prediction

- 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).

Genomics, DGV's accuracy

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.

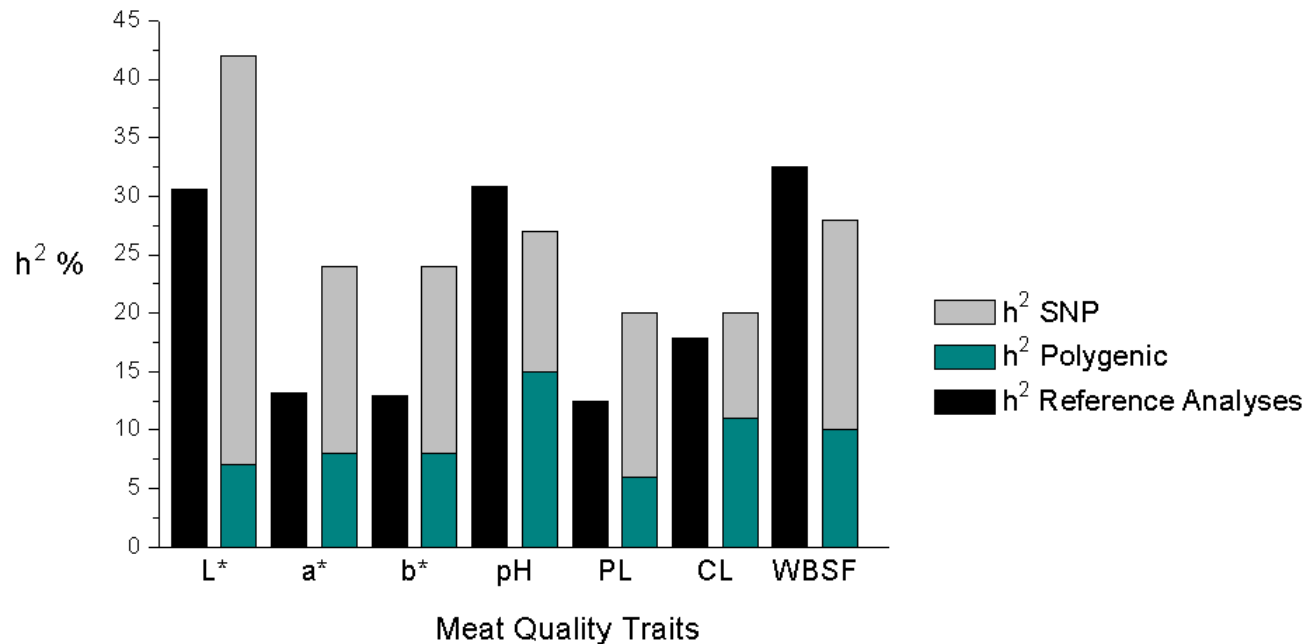
Young candidates for selection could be evaluated for meat quality traits using their genotype information.

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.**

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.