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### **Education:**

- PhD student in Animal and Food Science (October 2021- present)
- Research fellowship: “STALLA 4.0 – the dairy farm sustainability of the future: economy, environment and social issues towards the emerging needs of the community” (May 2019 - September 2021)
- Research fellowship: “Alternative system for meat rabbit breeding: economic, health, welfare and consumer perception” (January - April 2019)
- Master student in Animal Science (2016-2018)
- Bachelor student in Animal Science (2013-2016)

### **Research areas:**

- Pigs
- Genomic selection
- Animal Breeding and Genetics

### **Brief description of Ph project:**

Improving feed efficiency and reducing the environmental footprint are major goals in the animal breeding programs that also affect the pig farming. In this project I will focus on the selective strategies of a purebred sire line (C21 Goland, Gorzagri, Fonzaso, Italy) selected for productive traits and dry-cured ham quality. In particular, I will study the variability of growth, feed efficiency, and nitrogen and phosphorous excretion and their relationships. This will allow to identify the optimal combination of genetic, feeding and husbandry techniques, while maintaining high product quality standards in line with the requirements of the PDO product specification.

The associations between the individual genetic profile of the animal, feed efficiency and behavior, excretion, body composition, and qualitative characteristics of the PDO raw and dry-cured ham will be investigated. The identification of these associations will allow to direct animal breeding strategies towards the improvement of feed efficiency and sustainability, through the development of genomic selection procedures for genetic evaluation of breeding candidates. Implementation of breeding programs based on genomic selection might facilitate the prediction of genetic merit and selection procedures in boar lines when traits measurable only after slaughter, as ham quality traits, and difficult to record, as traits related to the dry-cured ham making process, are in the breeding goal. With genomic selection, EBVs (Estimated Breeding Values) of candidates are predicted on the basis of a very large number of single nucleotide polymorphisms (SNPs) spread throughout the genome and by exploiting existing linkage disequilibrium between SNPs and genes that affect phenotypic variation in traits of concern.

**Supervisor:**

Professor Paolo Carnier

Publications: Google scholar link

[https://scholar.google.it/citations?view\\_op=list\\_works&hl=it&authuser=1&user=JaH9goIAAAAJ](https://scholar.google.it/citations?view_op=list_works&hl=it&authuser=1&user=JaH9goIAAAAJ)