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3 December 1989
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My research focuses on genetics and genomics applied to both livestock and wild species, including pigs, cattle, rabbits, sea cucumbers, sea bass, and bees. I am particularly interested in the application of genomics within the animal production sector, with an emphasis on food characterization, authentication, traceability, and environmental adaptation.

My work involves a range of molecular biology techniques, including DNA/RNA extraction, PCR-RFLP, Sanger sequencing, and next-generation sequencing (NGS) using the Ion S5 platform. In addition to laboratory methods, I have experience in managing biological databases and using bioinformatics tools such as NCBI, BLAST, and ENSEMBL. I am also proficient in DNA sequence analysis and alignment software, including Galaxy, CodonCode, MEGA, and ClustalW.

22 peer-reviewed publications (h index = 8, 21/07/2025).

Scopus: 57217963404

ORCID: 0000-0001-5349-1606

Work experience:
11/2023- Current PostDoc of the Animal and Food Genomics Group – Department of Agricultural and Food Sciences – University of Bologna
11/2020 –11/2023
PhD Student in Agricultural, Environmental, Food Science and Technology
Department of Agricultural and Food Sciences (DISTAL) - University of Bologna
City: Bologna
Country: Italy
Title of project: Applied genomics to monitor the genetic diversity and integrity of honey bee (*Apis mellifera*) populations and define sustainable strategies to benefit the beekeeping sector

Name and address of employer:
University of Bologna–School of Agriculture and Veterinary Medicine
DISTAL (Department of Science and Agricultural Technologies)
Viale Fanin 48, 40127 Bologna

Supervisor: Prof. Luca Fontanesi

Research Experiences and Technical skills:

Wet-lab: DNA/RNA extraction and purification from different biological tissues; DNA amplification with PCR; PCR-RFLP; Sanger sequencing; preparation of libraries and running of a NSG experiment(S5), qPCR, dPCR.

Bioinfomatic skills: Biological databases and bioinformatic tools (NCBI, BLAST, ENSEMBL, SwissProt, UniProt, MitoZoa, Plink). DNA sequence analysis and alignment softwares (CodonCode, MEGA, SeaView, CLC Sequence Viewer, IGV, DNA Alignment, ClustalW, MAFFT, T-Coffee, bwa). SNP calling software for NGS (SAMtools). RNA-seq data analysis softwares (TopHat, Clufflinks). Phylogeny softwares (Haploview, ModelTest, PAUP, MrBayes, Past,Arlequin) knowledge of R and python.

Education and training:
2014 – 2019 *Master Degree in Biodiversity and Evolution - Adress: Zoology*
Alma Mater Studiorum - University of Bologna
Address: Bologna, Italy
2008 – 2014 *Bachelor Degree in Biology - Address: Bioecology*
Alma Mater Studiorum - University of Bologna
Address: Bologna, Italy
13/09/2021 – 17/09/2021 *Short course: Principles of data science applied to livestock*
University of Padova
Address: Padova, Italy
20/06/2022 – 24/06/2022 Corso di analisi statistica avanzata per le scienze zootecniche.
University of Pisa
June 2023-September 2023 Research period spent at University of Maribor, Faculty of Agriculture and Life sciences
29-30/01/2025 Crash course of quantitative genetics, Population simulation, Dissemination – Training School organized by Improved Knowledge Transfer for Sustainable Insect Breeding (Insect-IMP) Cost Action CA22140 Athens, Greece
14-18/07/2025 From Data to Discovery: Measuring and Analysing Livestock Phenotypes - Second Training School – European Network on Livestock Phenomics (EU-LI-PHE) Cost Action CA22112, KU Leuven, Leuven, Belgium

Paper:

1. Taurisano V., Ribani A., Utzeri V.J., Sami D., Johnson K.E.N., Formato G., Milito M., Schiavo G., Bovo S., Bertolini F., Fontanesi L.Comparing Morphometric and Mitochondrial DNA Data from Honeybees and Honey Samples for Identifying *Apis mellifera ligustica* Subspecies at the Colony Level (2025), 15 (12), art. no. 1743
   DOI: 10.3390/ani15121743

2. Bovo S., Carneiro M., Ribani A., Bolner M., Taurisano V., Schiavo G., Schiavitto M., Bertolini F., Fontanesi L.Signatures of selection detected from whole-genome sequencing indicate that the small body size in dwarf rabbit breeds is caused by polygenic effects with a few major loci (2025), 56 (4), art. no. e70025
   DOI: 10.1111/age.70025

3. Bovo S., Ribani A., Schiavo G., Taurisano V., Bolner M., Bertolini F., Fontanesi L.
   Mining Porcine Blood Whole-DNA Sequencing Datasets to Uncover Pig Viromes: An Exploratory Application to Identify Potential Infecting Agents of an Undefined Disease Outbreak (2025), 12 (6), art. no. 513

DOI: 10.3390/vetsci12060513

4. Bovo S., Ribani A., Fanelli F., Galimberti G., Martelli P.L., Trevisi P., Bertolini F., Bolner M., Casadio R., Dall'Olio S., Gallo M., Luise D., Mazzoni G., Schiavo G., Taurisano V., Zambonelli P., Bosi P., Pagotto U., Fontanesi L.
   Merging metabolomics and genomics provides a catalog of genetic factors that influence molecular phenotypes in pigs linking relevant metabolic pathways (2025), 57 (1), art. no. 11

   DOI: 10.1186/s12711-025-00960-8

5. Ribani A., Taurisano V., Rakaj A., Fianchini A., Grosso L., Pensa D., Pulcini D., Buttazzoni L., Schiavo G., Bovo S., Bertolini F., Utzeri V.J., Tinti F., Capoccioni F., Fontanesi L.

   Monitoring the genetic diversity in holothurian populations from the Italian coasts with mitochondrial DNA sequences (2024), 14 (1), art. no. 24592
   DOI: 10.1038/s41598-024-76087-5

6. Bolner M., Bovo S., Ballan M., Schiavo G., Taurisano V., Ribani A., Bertolini F., Fontanesi L.
   A comprehensive atlas of nuclear sequences of mitochondrial origin (NUMT) inserted into the pig genome (2024), 56 (1), art. no. 64

   DOI: 10.1186/s12711-024-00930-6

7. Bovo S., Ribani A., Schiavo G., Taurisano V., Bertolini F., Fornasini D., Frabetti A., Fontanesi L.
   Genome-wide association studies for diarrhoea outcomes identified genomic regions affecting resistance to a severe enteropathy in suckling rabbits (2024), 141 (3), pp. 328 - 342

   DOI: 10.1111/jbg.12844

8. Taurisano V., Ribani A., Sami D., Nelson Johnson K.E., Schiavo G., Utzeri V.J., Bovo S., Fontanesi L.
   Distribution of honey bee mitochondrial DNA haplotypes in an Italian region where a legislative act is protecting the *Apis mellifera ligustica* subspecies (2024), 14 (1), art. no. 20583

   DOI: 10.1038/s41598-024-71233-5

9. Bovo S., Ribani A., Utzeri V.J., Taurisano V., Bertarini G., Fontanesi L.
   Whole genome sequencing identifies candidate genes and mutations that can explain diluted and other colour varieties of domestic canaries (*Serinus canaria*) (2023), 54 (4), pp. 510 - 525

   DOI: 10.1111/age.13331

10. Ribani A., Taurisano V., Karatosidi D., Schiavo G., Bovo S., Bertolini F., Fontanesi L.
    Signatures of Admixture and Genetic Uniqueness in the Autochthonous Greek Black Pig Breed Deduced from Gene Polymorphisms Affecting Domestication-Derived Traits (2023), 13 (11), art. no. 1763

    DOI: 10.3390/ani13111763

11. Fontanesi L., Taurisano V., Ribani A., Utzeri V.J.
    A reply to the Letter to the Editor of Moškrič et al. entitled "A comment on the paper from Utzeri et al. (2022) "Entomological authentication of honey based on a DNA method that distinguishes *Apis mellifera* mitochondrial C mitotypes: Application to honey produced by *A. m. ligustica* and *A. m. carnica*, Food control, Volume 121, March 2021, 107626". (2023), 147, art. no. 109570

    DOI: 10.1016/j.foodcont.2022.109570

12. Utzeri V.J., Ribani A., Taurisano V., Fontanesi L.
    Entomological authentication of honey based on a DNA method that distinguishes *Apis mellifera* mitochondrial C mitotypes: Application to honey produced by *A. m. ligustica* and *A. m. carnica* (2022), 134, art. no. 108713

    DOI: 10.1016/j.foodcont.2021.108713

13. Ribani A., Taurisano V., Utzeri V.J., Fontanesi L.
    Honey Environmental DNA Can Be Used to Detect and Monitor Honey Bee Pests: Development of Methods Useful to Identify *Aethina tumida* and *Galleria mellonella* Infestations (2022), 9 (5), art. no. 213

    DOI: 10.3390/vetsci9050213

14. Bovo S., Utzeri V.J., Ribani A., Taurisano V., Schiavo G., Fontanesi L.
    A genotyping by sequencing approach can disclose *Apis mellifera* population genomic information contained in honey environmental DNA (2022), 12 (1), art. no. 19541

    DOI: 10.1038/s41598-022-24101-z

15. Bovo S., Ribani A., Utzeri V.J., Taurisano V., Schiavo G., Bolner M., Fontanesi L.
    Application of next generation semiconductor-based sequencing for the identification of *Apis mellifera* complementary sex determiner (CSD) alleles from honey DNA (2021), 12 (10), art. no. 868

    DOI: 10.3390/insects12100868

16. Bovo S., Schiavo G., Ribani A., Utzeri V.J., Taurisano V., Ballan M., Muñoz M., Alves E., Araujo J.P., Bozzi R., Charneca R., Di Palma F., Djurkin Kušec I., Etherington G., Fernandez A.I., García F., García-Casco J., Karolyi D., Gallo M., Martins J.M., Mercat M.-J., Núñez Y., Quintanilla R., Radović Č., Razmaite V., Riquet J., Savić R., Škrlep M., Usai G., Zimmer C., Ovilo C., Fontanesi L.
    Describing variability in pig genes involved in coronavirus infections for a One Health perspective in conservation of animal genetic resources (2021), 11 (1), art. no. 3359

    DOI: 10.1038/s41598-021-82956-0

17. Utzeri V.J., Ribani A., Taurisano V., Banqué C.H.I., Fontanesi L.
    Distribution of the main *Apis mellifera* mitochondrial DNA lineages in Italy assessed using an environmental DNA approach (2021), 12 (7), art. no. 620

    DOI: 10.3390/insects12070620

18. Ribani A., Utzeri V.J., Taurisano V., Galuppi R., Fontanesi L.
    Analysis of honey environmental DNA indicates that the honey bee (*Apis mellifera* L.) trypanosome parasite *Lotmaria passim* is widespread in the apiaries of the North of Italy (2021), 184, art. no. 107628

    DOI: 10.1016/j.jip.2021.107628

19. Tinarelli S., Ribani A., Utzeri V.J., Taurisano V., Bovo C., Dall'olio S., Nen F., Bovo S., Schiavo G., Gallo M., Fontanesi L.
    Redefinition of the mora romagnola pig breed herd book standard based on DNA markers useful to authenticate its "mono-breed" products: An example of sustainable conservation of a livestock genetic resource (2021), 11 (2), art. no. 526, pp. 1 - 16

    DOI: 10.3390/ani11020526

20. Ribani A., Utzeri V.J., Taurisano V., Fontanesi L.
    Honey as a source of environmental DNA for the detection and monitoring of honey bee pathogens and parasites (2020), 7 (3), art. no. 113

    DOI: 10.3390/VETSCI7030113

21. Utzeri V.J., Ribani A., Bovo S., Taurisano V., Calassanzio M., Baldo D., Fontanesi L.
    Microscopic ossicle analyses and the complete mitochondrial genome sequence of *Holothuria* (Roweothuria) *polii* (Echinodermata; Holothuroidea) provide new information to support the phylogenetic positioning of this sea cucumber species (2020), 51, art. no. 100735

    DOI: 10.1016/j.margen.2019.100735

22. Grilz-Seger G., Utzeri V.J., Ribani A., Taurisano V., Fontanesi L., Brem G.
    Known loci in the KIT and TYR genes do not explain the depigmented white coat colour of Austro-Hungarian Baroque donkey (2020), 19 (1), pp. 739 - 743

    DOI: 10.1080/1828051X.2020.1790997

Poster:
A list of congress participations, including poster and oral presentations, is available at:
https://scholar.google.com/citations?user=l5RDjKAAAAAJ&hl=it