

MOHAMMAD HOSSEIN BANABAZI


Institutionen för Husdjurens Biovetenskaper (HBIO)

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 [ORCID](#): 0000-0002-7873-8123

| **Researcher** |

| **Computational Biologist** |

| **Bioinformatician** |

Professional Summary

A **Ph.D.** in Animal Genetics with extensive expertise in computational biology, focusing on analyzing large-scale datasets and developing scalable bioinformatics pipelines. Proven expertise in various omics analyses, including genomics, transcriptomics, proteomics, epigenetics, and data integration to support biological research.

A researcher at the Swedish University of Agricultural Sciences (SLU) and the key bioinformatician to WP10 of the EU-funded [DEFEND](#) project (Horizon 2020), leading bioinformatics efforts to uncover host transcriptomic signatures associated with resilience mechanisms against two emerging viral infections.

Proficient in high-performance computing (HPC) environments, with expertise in developing reproducible workflows using Python, R, and Bash scripting; an applicable computational skillset that broadly translates across diverse domains, including human, animal, and plant research.

Skilled in statistical inference, including Bayesian modeling, and downstream analyses such as gene ontology (GO) enrichment and KEGG pathway analysis to extract meaningful insights from large datasets.

An experienced molecular geneticist with hands-on knowledge of wet-lab protocols, including DNA/RNA extraction, PCR/qPCR, and sequencing, and the ability to bridge laboratory insights with computational analyses.

Demonstrated ability to decode biological complexity through [Publications](#) in high-impact journals, with a strong commitment to innovative, collaborative, and interdisciplinary research. Eager to apply my computational biology expertise in human health settings where it drives translational impact.

Education

Ph.D. in Animal Genetics | University of Tehran, IRAN | August 2016

Dissertation: Computational strategies for integration of transcriptomic data (RNA-Seq) into genomic-enabled predictions

M.Sc. in Animal Genetics | University of Tehran, IRAN | June 2002

Focus on the molecular phylogenetics of local animal populations

Careers

Postdoctoral Fellow (Remote) | North Dakota State University (NDSU), USA | Jun 2024 – Sep 2024

USDA-ARS-funded Project: "Multi-Omics Data and Non-Coding Genomic Variants to Improve Crop Climate Resilience"

- Navigating Transposable Elements (TEs) flanking each syntenic gene across pan-genomes as the potential regulatory elements.
- Developing a large-scale software library for TE mapping across pan-genomes with over 47,000 gene cards, and calculated LTR Assembly Index (LAI) to evaluate genome assembly quality.

Researcher | Swedish University of Agricultural Sciences (SLU), Sweden | Jan 2022 – Dec 2023

- Led transcriptomics and genomic analyses within the EU-H2020 DEFEND project.

Assistant Professor | Animal Science Research Institute of Iran (ASRI), Iran | Aug 2016 - Jan 2022

- Led research in genomics, transcriptomics, and multi-omics data integration.
- National Coordinator for Animal Genetic Resources at FAO/DAD-IS (2019–2022).

Visiting Researcher | Swedish University of Agricultural Sciences (SLU), Sweden | Mar - Sep 2015

- Variant calling, Allele-Specific Expression (ASE), parent-of-origin effects, and personalizing the genome.

Research Associate | Animal Science Research Institute of Iran (ASRI), Iran | 2006 – 2016

- Contributed to research projects, data collection, and statistical analyses.

Laboratory Engineer | Animal Science Research Institute of Iran (ASRI), Iran | 2004 – 2006

- Supported molecular genetics laboratory work.

Analytical and Laboratory Skills

Genomics: Genome-Wide Association Studies (GWAS), haplotyping, genome-enabled prediction, selection signature, transposable element annotation, pan-genomics, and comparative genomics across taxa.

Transcriptomics: Bulk and Single-cell RNA-Seq analysis, differential gene expression (DGE), transcriptome-wide association studies (TWAS), eQTL mapping, allele-specific expression (ASE), and variant calling.

Epigenomics: DNA methylation analysis and epigenome-wide association studies (EWAS).

Statistical Modeling: Generalized linear models (GLM), Bayesian hierarchical modeling (JAGS), descriptive and inferential statistics, PCA, and temporal/spatial models.

Bioinformatics: Development of scalable, reproducible pipelines using Snakemake and Nextflow; version control via GitHub; cloud computing, high-performance computing (HPC); multi-omics data integration, data visualization, and simulation.

Programming: R, Python, Bash/Shell scripting under Linux/Unix-based environments.

Downstream Analysis: Gene annotation, gene ontology (GO), pathway analysis, gene set enrichment, and multi-layer networking.

Molecular Genetics: DNA/RNA extraction, conventional PCR and real-time PCR (qPCR), Sanger and NGS-based sequencing.

Collaborative Research: Experience in international, interdisciplinary collaborations; mentoring of graduate students; and active contribution to open and reproducible science.

Training & Teaching

Courses, recently completed: AI in Biomedical Science (IGS, Online, 2025) | DNA Methylation Profiling (SLU, 2024) | Bayesian Ecological Models (SLU, 2023) | RNA-Seq Data Analysis (SLU, 2022) | Reproducible Genomics Workflows (CRG, 2020) | Disease to Sequence & Protein Structure (SLU, 2015) | Parasite Resistance (Embrapa, 2011) | Lentiviral Gene Transfer to Stem Cells (NIGEB, 2010) |

Teaching: Bioinformatics | Genome-enabled predictions | Transcriptomics | Genetic resistance |

Awards and Recognition

Best Young Researcher Award, AREEO, Tehran, Iran – 2010 | Best Researcher Award, ASRI, Karaj, Iran – 2007 | Full Scholarship, Parasite Resistance Research Training, Embrapa, Brazil – 2011 | Full Scholarship, Molecular Characterization of Genetic Resources, ICARDA, Syria – 2007 | Research Grant, "Transcriptomic Signatures on the Pituitary-Immune System Axis", INSF, Iran – 2020

Languages & Memberships


Languages: English: Fluent | Persian (Farsi): Native | Swedish: Basic

Memberships: Board Member, Animal Genetics Branch, Iranian Genetics Society (IGS), 2014-2016 | Member, Swedish Association of University Teachers and Researchers (SULF), 2022-2024 | Board Member, Artificial Intelligence (AI) Genetics Branch, Iranian Genetics Society (IGS), July 2025-Now

Selected Publications (the Persian papers and presentations have not been included)

| [Scopus](#) | [Web of Science](#) | [SLUpub \(2022 - 2025\)](#) | [Google Scholar](#) |

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