



Dr. Francisco Peñagaricano

Assistant Professor

Department of Animal Sciences, University of Florida

Francisco Peñagaricano is Assistant Professor of Quantitative Genetics and Genomics in the Department of Animal Sciences at the University of Florida. Francisco is originally from Uruguay where he received two B.S degrees, one in Biology and another in Biochemistry, and also a M.S. degree in Animal Quantitative Genetics, all from Universidad de la República. He continued his graduate studies at the University of Wisconsin-Madison where he gained a M.S. in Statistics and a Ph.D. in Animal Science in 2014.

Francisco's research interests are in quantitative genomics and computational biology. His research program focuses on development and application of methods to dissect the genetic architecture of economically relevant traits in livestock. He typically combines large, nationwide phenotypic datasets or field experiments, with high throughput genomic technologies, and advanced theoretical, statistical and computational methods in order to elucidate the connection between (epi)genome and phenotype. His research involves gene mapping, gene-set analysis, genomic prediction, network modelling, methylome and transcriptome analysis, and multi-omics data integration.

Some related publications:

JD Leal Gutierrez et al. (2018) Structural equation modeling and whole-genome scans uncover chromosome regions and enriched pathways for carcass and meat quality in beef. *Front Genet* 9: 532.

GJM Rosa, VPS Felipe, and F Peñagaricano (2016) Applications of Graphical Models in Quantitative Genetics and Genomics. In: *Systems Biology in Animal Production and Health*, Vol. 1. pp 95-116. Springer International Publishing.

F Peñagaricano et al. (2015) Exploring causal networks underlying fat deposition and muscularity in pigs through the integration of phenotypic, genotypic and transcriptomic data. *BMC Syst Biol* 9: 58.

BD Valente et al. (2015) The causal meaning of genomic predictors and how it affects construction and comparison of genome-enabled selection models. *Genetics* 200: 483-494.

F Peñagaricano et al. (2015) Searching for causal networks involving latent variables in complex traits: application to growth, carcass, and meat quality traits in pigs. *J Anim Sci* 93: 4617-4623.

More info, including a full list of publications:

<http://fpenagaricano-lab.org>