Sajjad Toghiani (PhD)

Quantitative geneticist

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# Profile

Sajjad is an Animal Scientist at USDA in [Animal Genomics and Improvement Laboratory](https://www.ars.usda.gov/northeast-area/beltsville-md-barc/beltsville-agricultural-research-center/agil/) with a background in animal breeding and genetics. His main interests and strengths in the fields are focused on the application of the quantitative and molecular genetic approach to optimize the health and productivity of livestock and promote the development of sustainable and profitable farms.

# Education

**PhD** University of Georgia (Athens, GA, USA) 2015-2018

College of Agricultural and Environmental Sciences

Department of Animal and Dairy Science

Majored in Animal Breeding and Genetics

**MS** University of Georgia (Athens, GA, USA) 2013-2015

College of Agricultural and Environmental Sciences

Department of Animal and Dairy Science

Majored in Animal Breeding and Genetics

**MS** Guilan University (Rasht, IRAN) 2005-2007

College of Agricultural Sciences

Department of Animal Science

Majored in Animal Breeding and Genetics

**BS** Shiraz University (Shiraz, IRAN) 2001-2005

College of Agricultural Sciences

Department of Animal Science

Majored in Animal Science

# Professional experience

**Animal Scientist (USDA-ARS-AGIL) -** Beltsville, MD, USA 03/2020 – Present

Collaborate with AGIL scientists to revise the lifetime net merit ($NM) index

Evaluate the actual and expected use of foreign dairy bulls using global selection indices

Examine the impact of milk components and body weight composite on feed intake

Assess the maintenance cost and feed cost of milk components on feed intake

Provide the feed efficiency dataset in dairy cattle for research institutions

Support scientists for processing sequence analysis run8 from 1000 Genomes bull project

**Research Geneticist (USDA-ARS-LRRL) -** Miles City, MT, USA 10/2018 – 03/2020

Implement a novel approach to deal with genomic selection in beef cattle

Estimate the impact of cold stress on growth-related traits in beef cattle

Evaluate genomic and genetic inbreeding depression on growth traits in beef cattle

Study genomic breed composition and selection signatures of a composite beef cattle

# Research Experience

**Graduate Research Assistant** (**PhD**) 2015-2018

University of Georgia, Athens, GA, USA

Advisor: Dr. Romdhane Rekaya

Dissertation: Implementing genomic selection method based on using Fst prioritized SNPs

* Proposing the use of fixation index (FST) as screening tool to prioritize SNPs in genomic selection studies and reduce the dimensionality of high-density panels and to prioritize the relevant markers.
* Incorporating prioritized SNPs based on FST for developing genomic selection model and using its effectiveness for the genetic evaluation.

**Graduate Research Assistant** (**M.S.**) 2013-2015

University of Georgia, Athens, GA, USA

Advisor: Dr. Romdhane Rekaya

Thesis: Multi-generational imputation of SNP genotypes and accuracy of genomic selection

* Imputing low-density (3K) to medium density (42K) in simulated study and comparing the accuracy of imputed and original 42K genotype over multi-generation.
* Upgrading reference population to investigate the influence of the accuracy of genomic breeding value in imputed and original 42K genotype.

**Laboratory Research Assistant** 2009-2010

Iowa State University, Ames, IA, USA

Advisor: Dr. Diane Moody Spurlock

* Extracting DNA from dairy cattle blood to build genotype dataset for evaluating feed efficiency in dairy cattle.

**Graduate Research Assistant** (**M.S.**) 2005-2007

University of Guilan, Rasht, IRAN

Advisor: Dr. Abdol Ahad Shadparvar

Thesis: Estimation of genetic parameters for yield, fertility, and type traits in Iranian Holstein

# Publications

## Journal Publications

**Toghiani, S.**, & VanRaden, P. (2021). National Index Correlations and Actual vs. Expected Use of Foreign Sires. Interbull Bulletin, (56), 52-59.

Sumreddee, P., Hay, E. H., **Toghiani, S.**, Roberts, A., Aggrey, S. E., & Rekaya, R. (2021). Grid search approach to discriminate between old and recent inbreeding using phenotypic, pedigree and genomic information. BMC genomics, 22(1), 1-17.

Sumreddee, P., **Toghiani, S.**, Hay, E. H., Roberts, A., Aggrey, S. E., and Rekaya, R. (2020). Runs of homozygosity and analysis of inbreeding depression. Journal of Animal Science, 98(12), skaa361.

**Toghiani, S**., Hay, E., Roberts, A., and Rekaya, R. (2020). Impact of cold stress on birth and weaning weight in a composite beef cattle breed. Livestock Science, 104053.

**Toghiani, S**., Hay, E., Fragomeni, B., Rekaya, R., and Roberts, A. J. (2020). Genotype by environment interaction in response to cold stress in a composite beef cattle breed. Animal-The International Journal of Animal Biosciences, 1-12.

Aggrey, S. E., **Toghiani, S**., Chang, L. Y., and Rekaya, R. (2020). Improving accuracy of genomic prediction using a selected small set of prioritized SNP markers. Proceedings, 68th Annual Poultry Breeders’ Round Table Conference.

Chang, L. Y., **Toghiani, S**., Hay, E. H., Aggrey, S. E., and Rekaya, R. (2019). A Weighted Genomic Relationship Matrix Based on Fixation Index (FST) Prioritized SNPs for Genomic Selection. Genes, 10(11), 922.

Chang, L. Y., **Toghiani, S**., Aggrey, S. E., and Rekaya, R. (2019). Increasing accuracy of genomic selection in presence of high-density marker panels through the prioritization of relevant polymorphisms. BMC genetics, 20(1), 21.

Sumreddee, P., **Toghiani, S**., Hay, E. H., Roberts, A., Aggrey, S. E., and Rekaya, R. (2018). Inbreeding depression in Line1 Hereford cattle population using pedigree and genomic information. Journal of Animal Science, 97(1), 1-18.

Rekaya, R., **Toghiani, S**., Sumreddee, P., Ling, A., and Aggrey, S. (2018). Multivariate genome wide association for continuous and discrete responses using multivariate Bernoulli prior. Journal of Animal Science, 96(suppl\_3), 126-126.

Chang, L. Y., **Toghiani, S.**, Ling, A., Aggrey, S. E., and Rekaya, R. (2018). High density marker panels, SNPs prioritizing and accuracy of genomic selection. BMC genetics, 19(1), 4.

**Toghiani, S.**, Hay, E., Sumreddee, P., Geary, T. W., Rekaya, R., and Roberts, A. J. (2017). Genomic prediction of continuous and binary fertility traits of females in a composite beef cattle breed. Journal of animal science, 95(11), 4787-4795.

**Toghiani, S.**, Chang, L. Y., Ling, A., Aggrey, S. E., and Rekaya, R. (2017). Genomic differentiation as a tool for single nucleotide polymorphism prioritization for Genome wide association and phenotype prediction in livestock. Livestock Science, 205, 24-30.

Chang, L. Y., **Toghiani, S.**, Ling, A., Hay, E. H., Aggrey, S. E., and Rekaya, R. (2017). Analysis of multiple binary responses using a threshold model. Journal of Agricultural, Biological and Environmental Statistics, 22(4), 640-651.

Sumreddee, P., **Toghiani, S.**, Aggrey, S. E., and Rekaya, R. (2017). Joint genome-wide association analysis of continuous and discrete traits. Journal of Animal Science, 95(suppl\_4), 104-105.

Chang, L. Y., **Toghiani, S.**, Aggrey, S. E., and Rekaya, R. (2017). Increasing accuracy of genomic selection in presence of high-density marker panels through the prioritization of relevant polymorphisms. Journal of Animal Science, 95(suppl\_4), 91-92.

**Toghiani, S.**, Chang, L. Y., Aggrey, S. E., and Rekaya, R. (2017). A hybrid of prioritized SNP and polygenetic effect method for implementation of genomic selection. Journal of Animal Science, 95(supplement4), 92-92.

Chang, L. Y., **Toghiani, S**., Aggrey, S. E., and Rekaya, R. (2016). High density marker panels, SNPs prioritizing and accuracy of genomic selection. Journal of Animal Science, 94(suppl\_5), 141-142.

**Toghiani, S**., Chang, L. Y., Aggrey, S. E., and Rekaya, R. (2016). SNP filtering using Fst and implications for genome wide association and phenotype prediction. Journal of Animal Science, 94(suppl\_5), 143-143.

**Toghiani, S**., Aggrey, S. E., and Rekaya, R. (2016). Multi-generational imputation of single nucleotide polymorphism marker genotypes and accuracy of genomic selection. Animal-The International Journal of Animal Biosciences, 10(7), 1077-1085.

Foroughi, M., Najafi, P., **Toghiani, S**., and Honarjoo, N. (2014). Using Ceratophyllum demersum for Treatment of Saline Municipal Wastewater. Journal of Residuals Science & Technology, 11(2).

Foroughi, M., Najafi, P., **Toghiani, S**., Toghiani, A., and Honarjoo, N. (2013). Nitrogen Removals by Ceratophyllum Demersum from Wastewater. Journal of Residuals Science & Technology, 10(2).

**Toghiani, S**. (2012). Genetic relationships between production traits and reproductive performance in Holstein dairy cows. Archives Animal Breeding, 55(5), 458-468.

Foroughi, M., and **Toghiani, S**. (2012). Phosphorus removal from aquaculture wastewater and latex by Ceratophyllum demersum. African Journal of Biotechnology, 11(7), 1639-1643.

Foroughi, M., Najafi, P., and **Toghiani, S**. (2011). Trace elements removal from wastewater by Ceratophyllum demersum. Journal of Applied Sciences and Environmental Management, 15(1).

**Toghiani, S**. (2011). Genetic parameters and correlations among linear type traits in the first lactation of Holstein Dairy cows. African Journal of Biotechnology, 10(9), 1507-1510.

**Toghiani Pozveh, S**., Shadparvar, A. A., Shahrbabak, M. M., and Taromsari, M. D. (2009). Genetic analysis of reproduction traits and their relationship with conformation traits in Holstein cows. Livestock Science, 125(1), 84-87.

## Conference Proceedings (Poster)

Sumreddee, P., **Toghiani, S.**, Hay, E., Aggrey, S. E., and Rekaya, R. PSXII-29 Partitioning of Inbreeding Depression using Pedigree and Genomic Approaches, Journal of Animal Science, Volume 98, Issue Supplement\_4, November 2020, Pages 247–248.

**Toghiani, S**., Hay, E., Fragomeni, B., Rekaya, R., and Roberts, A. J. Genotype by environment interaction in response to cold stress in a composite beef cattle breed. Plant and Animal Genome XXVIII Conference, San Diego, CA, January 11 - 15, 2020.

Sumreddee, P., **Toghiani, S**., Hay, E., Roberts, A., Aggrey, S. E., and Rekaya, R. Runs of homozygosity and analysis of inbreeding depression. Plant and Animal Genome XXVIII Conference, San Diego, CA, January 11 - 15, 2020.

Chang, LY., **S. Toghiani**, S. Aggrey, and R. Rekaya. A weighted genomic relationship matrix based on FST prioritized SNPs for genomic selection. American Society of Animal Science meeting, 2019, Austin, Texas.

Sumreddee, P., **S. Toghiani**, S. Aggrey, and R. Rekaya. Joint genome-wide association analysis of continuous and discrete traits. American Society of Animal Science meeting, 2017, Baltimore, Maryland.

**Toghiani, S**., L. Chang, and R. Rekaya. Genome wide association in presence of high-density marker panels and genotyped causal variants. The Allied Genetics Conference, 2016, Orlando, Florida.

**Toghiani, S**., and R. Rekaya. [Multi-generational imputation of SNP genotypes and accuracy of genomic selection.](https://www.researchgate.net/publication/310329835_Multi-generational_imputation_of_SNP_genotypes_and_accuracy_of_genomic_selection?_iepl%5BviewId%5D=JXrvI8WEvQe5PgaOhuksiu8F&_iepl%5BprofilePublicationItemVariant%5D=default&_iepl%5Bcontexts%5D%5B0%5D=prfpi&_iepl%5BtargetEntityId%5D=PB%3A310329835&_iepl%5BinteractionType%5D=publicationTitle) Joint Annual Meeting 2015, Orlando, Florida.

## Conference Proceedings (Oral)

**Toghiani, S.,** P. VanRaden. National Index Correlations and Expected vs. Actual Use of Foreign Sires. Interbull Virtual Conference, 2021, Leeuwarden, The Netherlands.

**Toghiani, S**., L. Chang, Hay, E. H., Roberts, S. Aggrey, and R. Rekaya. A hybrid model for genomic selection using prioritized SNPs based on FST scores in the presence of non-genotyped animals. American Society of Animal Science meeting, 2019, Austin, Texas.

**Toghiani, S**., L. Chang, S. Aggrey, and R. Rekaya. A hybrid of prioritized SNP and polygenetic effect method for implementation of genomic selection. American Society of Animal Science meeting, 2017, Baltimore, Maryland.

Chang, LY., **S. Toghiani**, S. Aggrey, and R. Rekaya. Increasing accuracy of genomic selection in presence of high-density marker panels through the prioritization of relevant polymorphisms. American Society of Animal Science meeting, 2017, Baltimore, Maryland.

**Toghiani, S**., L. Chang, S. Aggrey, R. Rekaya. SNP filtering using Fst and implications for genome wide association and phenotype prediction. Joint Annual Meeting 2016, Salt Lake City, Utah.

Chang, LY., **S. Toghiani**, S. Aggrey, and R. Rekaya. High density marker panels, SNPs prioritizing and accuracy of genomic selection. Joint Annual Meeting 2016, Salt Lake City, Utah.

## Book Chapters

**Toghiani, S**. (2012). Quantitative Genetic Application in the Selection Process for Livestock Production. In Livestock Production. InTech.

# Honors and Awards

**Graduate Assistantship (PhD)** 2016-2018

Supported from USDA-ARS Livestock and Range Research Laboratory, Miles city, MT

**Graduate Assistantship (M.S.)** 2013-2015

Supported from the Department of Animal and Dairy science (University of Georgia)

# Editorial Activities

Frontiers in Genetics – Section Livestock Genomics: [Reducing the Environmental Footprint of Livestock Through Genomic Selection](https://www.frontiersin.org/research-topics/24065/reducing-the-environmental-footprint-of-livestock-through-genomic-selection?utm_source=LOP&utm_medium=Profile&utm_campaign=editorialRolesBrick_FrontiersRTSubmissions_OpenSubmit).

# Computer Skills

**Programming**: Fortran, R, Python, Unix shell scripting

**Applications**: MS office (Word, Excel, PowerPoint, Outlook)

**Analysis Tools**: **Plink** (GWAS analysis software), **Gensel** (Bayesian method for GS/GWAS analysis), **Blupf90 family** (Genetic/Genomic evaluation), **QMsim** (QTL and marker simulator for livestock populations), **FImpute** (Genotype imputation tool), **Bioconductor** (Statistical and graphical methods for analyzing genomic data), **Admixture** (A tool to estimate individual ancestry from SNP genotype datasets)

# others

Citizenship: United State of America

Language: English, Farsi

# References

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Athens, GA 30602

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