



**Mehdi Momen**  
*Statistical and Quantitative Geneticist*  
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CONTACT  
INFORMATION

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RESEARCH  
INTERESTS

I am a statistical and quantitative geneticist interested in applying statistical learning methods to multi-layer omic data. My research interests span a broad range of topics including animal breeding, plant breeding, and human quantitative genetics.

EDUCATION

**Shahid Bahonar University Of Kerman (SBUK), Kerman, IRAN**

**Ph.D., Animal Breeding and Genetics, April 2017**

- Dissertation: "Predictive ability and sensitivity of Whole Genome Prediction (WGP) statistical Models for Genomic Selection in complex Traits with Additive, Dominance and Epistatic Genetic Architecture."
- Advisors: Ahmad Ayatollahi Mehrgardi & Ali Esmailizadeh

**University of Wisconsin-Madison, Madison, Wisconsin, USA**

**Visiting Ph.D. Student., Animal Breeding and Genetics, October 2015 - Jun 2016**

- Project: "Development and predictive assessment of whole-genome prediction machines in Genomic selection and Genome-wide association studies."
- Advisor: Daniel Gianola

**Tehran University, Aboureihan Campus, Tehran, IRAN**

**M.S., Genetic and Animal Breeding, May 2010**

- Dissertation: "Genetic Analysis of Reproductive and Growth traits In Purebred and Crossbred Lambs from three Iranian Sheep Breeds."
- Advisor: Nasser Emam-Jomea Kashan

**Zabol University, Agricultural College, Sistan Province, IRAN**

**B.S., Animal Science, May 2007**

- Advisor: Nasser Emam-Jomea Kashan

EMPLOYMENT

**Virginia Polytechnic Institute and State University, Blacksburg, Virginia, USA**

**Post-doctoral Researcher in Statistical and Quantitative Genetics, November 2018 - Present**

- Advisor: Gota Morota

**Shahid Bahonar University of Kerman (SBUK), Kerman, Iran.**

**Researcher in Statistical Genetics and Genomics**, November 2017 - November 2018

- Advisor: Ahmad Ayatollahi Mehrgardi & Ali Esmailizadeh

PUBLICATIONS

**Preprints**

1. **Momen M**, Campbell MT, Walia H, Morota G. Predicting longitudinal traits derived from high-throughput phenomics in contrasting environments using genomic Legendre polynomials and B-splines. *bioRxiv*. doi: 10.1101/632117
2. **Momen M**, Campbell MT, Walia H, Morota G. Harnessing phenotypic networks and structural equation models to improve genome-wide association analysis. *bioRxiv*. doi: 10.1101/553008

**Journal papers**

1. Campbell M T, **Momen M**, Harkamal H, Morota G. 2019. Leveraging breeding values obtained from random regression models for genetic inference of longitudinal traits. *The Plant Genome*. doi: 10.1101/435685
2. Fazel Y, Esmailizadeh K A, **Momen M**, Assadi Foozi M. 2018. Importance of genotype by environment interaction on genetic analysis of milk yield in Iranian Holstein cows using random regression model. *Animal Production Science*. doi: 10.1071/AN17714
3. **Momen M**, Ayatollahi Mehrgardi A, Amiri Roudbar M, Kranis A, Mercuri Pinto R, Valente B D, Morota G, Rosa G J M, Gianola D. 2018. Including phenotypic causal networks in genome-wide association studies using mixed effects structural equation model. *Frontiers in Genetics*. **9**:455. doi: 10.3389/fgene.2018.00455
4. **Momen M**, Gota M. 2018. Quantifying genomic connectedness and prediction accuracy from additive and non-additive gene actions. *Genetics Selection Evolution*. **50**:45. doi: 10.1186/s12711-018-0415-9
5. **Momen M**, Ayatollahi Mehrgardi A, Sheikhy A, Kranis A, Tusell L, Morota G, Rosa G J M, Gianola D. 2018. Predictive ability of genome-assisted prediction machines under various statistical genetic architectures. *Scientific Reports*. **8**:12309. doi: 10.1038/s41598-018-30089-2
6. **Momen M**, Ayatollahi Mehrgardi A, Sheikhy A, Esmailizadeh Koshkoieh A, Assadi Foozi M, Kranis A, Valente B D, Rosa G J M, Gianola D. 2017. A genome-enabled predictive assessment of genetic correlations between traits in chickens. *Genetics Selection Evolution*. **49**: 16 . doi: 10.1186/s12711-017-0290-9

7. **Momen M**, Ayatollahi Mehrgardi A, Sheikhy A, Esmailizadeh A K, Assadi Foozi M. 2016. Predictive Ability of Statistical Genomic Prediction Methods When Underlying Genetic Architecture of Trait Is Purely Additive. *Iranian Journal of Applied Animal Science (IJAS)*. Volume 6 (Issue 1): **6(4)**:815-822, Volume 6 (Issue 4).doi:
8. **Momen M**, Emam Jomea Kashan N, Sharifi S D, Amiri Roudbar M, Ayatollahi Mehrgardi A. 2015. Fatty acid composition of fat-tail and visceral fat depots from Chaal and Zandi pure lambs and their crosses with Zel (Three Iranian breeds). *Iranian Journal of Applied Animal Science (IJAS)*. **6(1)**: 107-112.

**Posters:**

1. Pegolo S., **Momen M**., Morota G., Rosa Guilherme J. M., Gianola D., Bittante G., Alessio C. 2019. Genome-based discovery of trait networks in dairy cattle. The EAAP Annual Meeting, Ghent, Belgium.
2. **Momen M**, Ayatollahi Mehrgardi A, Brito Lopez F, Rosa GJ M, Gianola D. 2016. Combining marker and pedigree information may enhance multiple-trait genome-enabled prediction. 5th International Conference on Quantitative Genetics Madison, Wisconsin, USA.
3. Jabari M, Sharifi F, **Momen M**. 2012. Application of Fuzzy Linear Regression (FLR) in agricultural economic studies. 2012. 1th International conference on Econometrics, Methods and Applications, Azad university of sanandaj, Iran, on 25-27 august 2012.
4. **Momen M**, Kashan NEJ, Sanjari H. 2011. Study of Gut morphological traits in pure and crossbreeds lambs of Zandi with Zel. The 1th national conference on new technologies in agriculture science. Zanzan University, Zanzan province, Iran.
5. Kashan NEJ, **Momen M**, Nasiri Kh. 2011. Simulation experiments for detection of quantitative trait loci (QTLs) in Animal Populations. The 1th national conference on new technologies in agriculture science. Zanzan University, Zanzan province, Iran.
6. Sanjari H, **Momen M**, Kashan NEJ. 2011. Evaluation of the number and homozygosity of sex alleles in honey bee colonies. 2011. The 1th national conference on rearing management of livestock in tropical region. Kerman University, Kerman province, Iran.
7. **Momen M**, Nasiri Kh. 2011. Genetic algorithm simulations for detection of quantitative traits loci effects. The 5th national conference on new ideas in agriculture. Khorasgan azad university unit, Esfahan province, Iran.
8. Vesi A, **Momen M**. 2011. Application of Fuzzy logic in economic improvement of animal production units. 2011. the 5th national conference on new ideas in agriculture. Khorasgan azad university unit, Esfahan province, Iran.
9. **Momen M**, Kashan NEJ, Sharifi SD. 2010. Investigation of fatty acids profile on fat-tail and visceral fats of Zandi pure lambs and their crosses with Zel rams.

The 4th national conference in animal science. Tehran University, karaj campus, Iran.

10. **Momen M**, Kashan NEJ, Sharifi SD. 2010. Study of relationship between blood-biochemical traits with carcass traits in pure lambs of Chal and Zandi and their cross with Zel rams. The 4th national conference in animal science. Tehran University, karaj campus, Iran.
11. **Momen M**, Kashan NEJ, Sharifi SD. 2009. Study of growth performance on crossbred lambs of fat-tailed and tailed sheep breeds, proceeding of The British Society of Animal Science Association conference, Queen's University, Belfast, April, UK
12. Mohseni M, Kashan NEJ, **Momen M**, 2009. Study seasonal and liver/lung condemnation in sheep, cattle and buffalo in khoy abattoir in northwest, Iran, Proceeding of The British Society of Animal Science Association conference, Queen's University, Belfast, April, UK.
13. Mohseni M, Kashan NEJ, **Momen M**, 2009. An abattoir survey of the incidence of liver fluke disease and Hydatidosis in sheep in Khoy abattoir, West Azarbyjan, Iran, Proceeding of the British Society of Animal Science Association conference, Queen's University, Belfast, April, UK.

#### PRESENTATIONS

1. Gain obtained by enriching whole genome prediction machines using genotypic data and bioinformatics initiative tools, Department of Animal Sciences, University of Tehran. (March 6, 2018)
2. The Bayesian controversy in genome-enabled prediction in animal breeding, Department of Animal Sciences, Shahid Bahonar University of Kerman (SBUK). (May 10, 2017)

#### TEACHING

##### Graduate courses

- Biostatistics, Quantitative Genetics, and Genomics in Animal Breeding, Statistical Analysis of Large Genomic data, Advance Genetic Prediction, Department of Animal Science, Shahid Bahonar University of University of Kerman, Kerman, Iran (2017-2018).

##### Undegraduate courses

- Biostatistics and Statistical in Agricultural Research, Department of Animal Science, University of Kerman, Kerman, Iran (2012-2018).
- General Biochemistry, department of agriculture improvement, Payam Noor University, Darab city, Fars province, Iran (2012).
- The basic of plant and animal genetic, department of agriculture improvement, Payam Noor University, Darab city, Fars province, Iran (2011).
- The basic of biotechnology in agricultural sciences, department of agriculture improvement, Payam Noor University, Darab city, Fars province, Iran (2011).
- Biostatistics and Statistical Designs in Agricultural Research as a teacher assistant, Department of Animal Science, University of Tehran, Tehran, Iran (2008).

OSS  
CONTRIBUTIONS

R packages

- "Connectedness": <https://haipengu.github.io/Rmd/Vignette.html>

SKILLS

**Statistical and Genetic Software:** ASReml, Wombat, BLUPF90, Plink, GCTA, GenSel, MCMCglimm, QTL Cartographer, Grid QTL, GenAlEx, SNPEVG, GVCBLUP, MEGA, and POPGENE

**Programming Language:** R, SAS, SPSS, C++, and L<sup>A</sup>T<sub>E</sub>X

ADDITIONAL  
TRAINING

**Short courses**

- Genomic Selection in Animal and plant breeding. 2016. Instructor: Prof. Mike Goddard. A.B chapman lecture, February 6-8, Madison, Wisconsin, USA
- Genomic Selection in the Era of Genome Sequencing. 2016. Instructor: Ben Hayes. The 5th International Conference on Quantitative Genetics, January 6-8, Madison, Wisconsin, USA.
- Statistical Genetics of Quantitative Traits and Complex Disease. 2016. Instructor: Matt Robinson. The 5th International Conference on Quantitative Genetics, January 8-10, Madison, Wisconsin, USA.
- Genomic selection methods and analysis of huge genomic data in animal breeding programs and genomics. 2013. Instructor: Rostam Abdolahi-Arpanahi. August 26, Shahid Bahonar University of Kerman, Faculty of Agriculture (SBUK), Kerman, IRAN.
- Programming and advance data analysis with R software. 2013. Instructor: Rostam Abdolahi-Arpanahi. August 27-28, Shahid Bahonar University of Kerman(SBUK), Faculty of Agriculture, Kerman, IRAN.

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REFERENCES

**Prof. Gota Morota,**  
*Assistant Professor, Theoretical Quantitative Genetics*  
*Department of Animal and Poultry Sciences*  
*Virginia Polytechnic Institute and State University*  
[morota@vt.edu](mailto:morota@vt.edu)  
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**Prof. Daniel Gianola,**  
*Sewall Wright Professor of Animal Breeding and Genetics*  
*Department of Animal Sciences*

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Department of Dairy Science  
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<https://www.biostat.wisc.edu/content/gianola-daniel>  
<http://qbi.wisc.edu/gianola-daniel.htm>*

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*Professor in Quantitative Genetic and Genomics  
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