CURRICULUM VITA

PERSONAL INFORMATION

First Name: Seyed Mohammad Farhad
Last Name: Vahidi
Date of Birth: 21 September 1974
Place of Birth: Zahedan, Iran
Nationality: Iranian
Marital status: married
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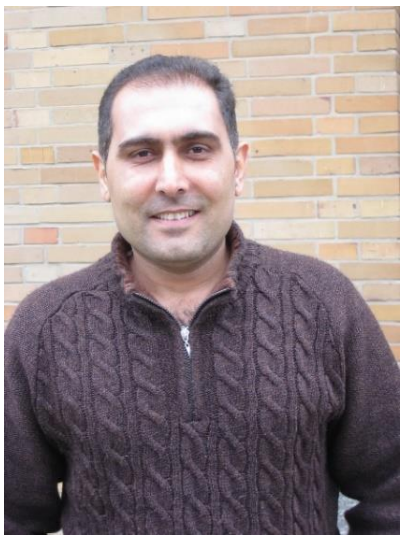

EDUCATION AND QUALIFICATIONS

2018. **PhD. In Molecular genetics,** Department of Genetics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, Iran.

Thesis Topic: Identification of sheep rumen microbiome to isolate hydrolyse enzymes of degradation of lignocellulosic wastes using metagenomics method.

2003. **MSc. in Animal Genetics and Breeding,** Department of Animal Sciences, Faculty of Agriculture, University of Guilan, Rasht, Iran.

Thesis Topic: Studying of DNA polymorphism in Iranian native cattle and buffalo populations using microsatellite markers.

1999. **BSc. in Animal Science,** Department of Animal Sciences, Faculty of Agriculture, University of Sistan & Baluchistan, Zabol, Iran.

PROFESSIONAL EXPERIENCE

- 09-14 August 2014. Three Workshops on NGS and Epigenetics. Mashhad, **Iran**
- 08-15 August 2011. Next-generation sequence analysis: practice and departure to new frontiers. Munich, **Germany.**
- 20-24 June 2011. Genomic selection in livestock. Davos, **Switzerland**.
- 09-19 August 2010. Linear Models and estimations. Munich, **Germany**.
- 19th October 2007-10th January 2008. Molecular Characterization using Microsatellite DNA markers. CAAS (Chinese Academy of Agricultural Science)-ILRI joint Laboratory, Beijing, **China**.
- 1st October- 30th November 2005. Molecular Characterization using Microsatellite DNA markers. ILRI, Nairobi, **Kenya**.
- 15-18 November 2005. Introduction to Bioinformatics; nucleic acid Sequence analysis, protein sequence analysis, accessing complete genomes, alignments and homology searching phylogenetic trees. International Livestock Research Institute (ILRI), Nairobi, **Kenya**.

SKILLS AND WORK EXPERIENCES

- I have been working as an academic researcher in the systems biology division of the Agriculture Biotechnology Research Institute of Iran (ABRII) from **November 2005 up to March 2021**.
- From April 2021 up to now I am working Research and Education Center for Agriculture and Natural Resources Qom, IRAN
- I worked as a visiting scientist at the University of Gottingen from **2010 to September 30, 2012** (with the permission of ABRII).

HONORS AND AWARDS

- Top researcher in Agricultural Biotechnology Research Institute of Iran, 2021.
- Top researcher in Agricultural Biotechnology Research Institute of Iran, 2017.
- Top researcher in Agricultural Biotechnology Research Institute of Iran, 2008.
- Awarded a research grant from The Food and Agriculture Organization and the International Atomic Energy Agency IAEA / FAO (2007-2011).

PUBLICATIONS

1. **Vahidi, F**., Gharechahi, J., Behmanesh, M., Ding, X-Z., Han, J.,Hosseini Salekdeh, GH. **2021**. Diversity of microbes colonizing forages of varying lignocellulose properties in the sheep rumen. ***PeerJ,*** 9, p.e10463.

2. Gharechahi, J., **Vahidi, S.M.F.,** Bahram, M., Ding, X-Z., Han, J., Salekdeh, Gh. **2021**. Genome sequencing of 538 microbes reveals a wealth of lignocellulose degradation potential in the cattle rumen. ***The ISME Journal,*** 15(4), pp.1108-1120.

3. Rafiepour, M., Ebrahimie, E., **Vahidi, S.M.F**., Salekdeh, G.H., Niazi, A., Dadpasand, M., Liang, D., Si, J., Ding, X., Han, J. and Zhang, Y., **2021**. Whole genome re-sequencing reveals adaptation prior to the divergence of buffalo subspecies. ***Genome Biology and Evolution,*** 13(1), p.evaa231.

4. Gharechahi, J., **Vahidi, S.M.F.,** Ding, X.Z., Han, J.L. and Salekdeh, G.H., **2020**. Temporal changes in microbial communities attached to forages with different lignocellulosic compositions in cattle rumen. ***FEMS Microbiology Ecology***, 96(6), p.fiaa069.

5. Liu, S., Liu, Y., Jelen, E., Alibadian, M., Yao, C.T., Li, X., Kayvanfar, N., Wang, Y., **Vahidi, S.M.F.,** Han, J.L. and Sundev, G., **2020**. Regional drivers of diversification in the late Quaternary in a widely distributed generalist species, the common pheasant Phasianus colchicus. ***Journal of Biogeography,*** 47(12), pp.2714-2727.

6. Xier Luo, Yu Zhou, Bing Zhang, Yi Zhang, Xiaobo Wang, Tong Feng, Zhipeng Li, Kuiqing Cui, Zhiqiang Wang, Chan Luo, Hui Li, Yanfei Deng, Fenghua Lu, Jianlin Han, Yongwang Miao, Huaming Mao, Xiaoyan Yi, Cheng Ai, Shigang Wu, Alun Li, Zhichao Wu, Zijun Zhuo, Do Da Giang, Bikash Mitra, **Mohammad Farhad Vahidi,** Shahid Mansoor, Sahar Ahmed Al-Bayatti, Eka Meutia Sari, Neena Amatya Gorkhali, Sigit Prastowo, Laiba Shafique, Guoyou Ye, Qian Qian, Baoshan Chen, Deshun Shi, Jue Ruan, Qingyou Liu. **2020**. Understanding divergent domestication traits from the whole-genome sequencing of swamp- and river-buffalo populations. ***National Science Review***, 7(3), pp.686-701.

7. Potki, P., Mirhoseini, S.Z., Afraz, F. and **Vahidi, S.M.F. 2020**. A Profile of Single Nucleotide Polymorphisms in Fecundity Genes Among Iranian Sheep Breeds by Using Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) Method. ***Iranian Journal of Applied Animal Science***, 10(2), pp.265-285.

8. Marta Pereira Verdugo, Victoria E Mullin, Amelie Scheu, Valeria Mattiangeli, Kevin G Daly, Pierpaolo Maisano Delser, Andrew J Hare, Joachim Burger, Matthew J Collins, Ron Kehati, Paula Hesse, Deirdre Fulton, Eberhard W Sauer, Fatemeh A Mohaseb, Hossein Davoudi, Roya Khazaeli, Johanna Lhuillier, Claude Rapin, Saeed Ebrahimi, Mutalib Khasanov, **SM Farhad Vahidi**, David E MacHugh, Okan Ertuğrul, Chaido Koukouli-Chrysanthaki, Adamantios Sampson, George Kazantzis, Ioannis Kontopoulos, Jelena Bulatovic, Ivana Stojanović, Abdesalam Mikdad, Norbert Benecke, Jörg Linstädter, Mikhail Sablin, Robin Bendrey, Lionel Gourichon, Benjamin S Arbuckle, Marjan Mashkour, David Orton, Liora Kolska Horwitz, Matthew D Teasdale, Daniel G Bradley., **2019**. Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. ***Science***, 365(6449), pp.173-176.

9. Royan, M., KORDGHASHLAGHI, H.A., Afraz, F., Hashemi, M., **Vahidi, S.M.F**. and Seighalani, R., **2018**. Screening Lactobacilli Isolates from Northern Iran Backyard Chickens

as Bio-control Strategy Against Salmonella Enteritidis and Salmonella Typhimurium. ***Kafkas Üniversitesi Veteriner Fakültesi Dergisi***, 24(3).

10. Periasamy, K., **Vahidi, S.M.F.,** Silva, P., Faruque, M.O., Naqvi, A.N., Basar, M., Cao, J., Zhao, S., Pichler, R., Podesta, M.G. and Shamsuddin, M., **2017**. Mapping molecular diversity of indigenous goat genetic resources of Asia. ***Small Ruminant Research***, 148, pp.2-10.

11. Naqvi, A.N., Bukhari, J.F., **Vahidi, S.M.F.**, Utsunomiya, Y.T., Garcia, J.F., Babar, M.E., Han, J.L., Pichler, R. and Periasamy, K., **2017**. Microsatellite based genetic diversity and mitochondrial DNA D-Loop variation in economically important goat breeds of Pakistan. ***Small Ruminant Research***, 148, pp.62-71.

12. Naqvi, A.N., Mahmood, S., **Vahidi, S.M.F.,** Abbas, S.M., Utsunomiya, Y.T., Garcia, J.F. and Periasamy, K., **2017**. Assessment of genetic diversity and structure of major sheep breeds from Pakistan. ***Small Ruminant Research,*** 148, pp.72-79.

13. Ahmadi, A., Afraz, F., Talebi, R., Farahavar, A. and **Vahidi, S.M.F., 2016**. Investigation of GDF9 and BMP15 polymorphisms in Mehraban sheep to find the missenses as impact on protein. ***Iranian Journal of Applied Animal Science***, 6(4), pp.863-872.

14. **Vahidi, S.M.F.,** Faruque, M.O., Falahati Anbaran, M., Afraz, F., Mousavi, S.M., Boettcher, P., Joost, S., Han, J.L., Colli, L., Periasamy, K. and Negrini, R., **2016**. Multilocus genotypic data reveal high genetic diversity and low population genetic structure of Iranian indigenous sheep. ***Animal genetics***, 47(4), pp.463-470.

15. Colli, L., Lancioni, H., Cardinali, I., Olivieri, A., Capodiferro, M.R., Pellecchia, M., Rzepus, M., Zamani, W., Naderi, S., Gandini, F. and **Vahidi, S.M.F.**, **2015**. Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. ***BMC genomics***, 16(1), p.1115.

16. Feng-Hua Lv, Wei-Feng Peng, Ji Yang, Yong-Xin Zhao, Wen-Rong Li, Ming-Jun Liu, Yue-Hui Ma, Qian-Jun Zhao, Guang-Li Yang, Feng Wang, Jin-Quan Li, Yong-Gang Liu, Zhi-Qiang Shen, Sheng-Guo Zhao, EEr Hehua, Neena A Gorkhali, **SM Farhad Vahidi**, Muhammad Muladno, Arifa N Naqvi, Jonna Tabell, Terhi Iso-Touru, Michael W Bruford, Juha Kantanen, Jian-Lin Han, Meng-Hua Li., **2015**. Mitogenomic meta-analysis identifies two phases of migration in the history of eastern Eurasian sheep. ***Molecular Biology and Evolution***, 32(10), pp.2515-2533.

17. Arbani, R.S., Tarang, A., Rafeie, F., Potki, P., Seighalani, R., Baniyaghoub, S., **Vahidi, M.F.** and Ajamian, F., **2015**. Genetic Monitoring for Severe Combined Immunodefici ency Disease (SCID) Carriers in Arabian Horses of Iran. ***Journal of Agricultural Science and Technology***, 17: 3.

18. **Vahidi, S.M.F.,** Tarang, A.R., Anbaran, M.F., Boettcher, P., Joost, S., Colli, L., Garcia, J.F. and Ajmone-Marsan, P., **2014**. Investigation of the genetic diversity of domestic Capra hircus breeds reared within an early goat domestication area in Iran. ***Genetics Selection Evolution***, 46(1), pp.1-12.

19. Zhang, G., **Vahidi, S.M.F.,** Ma, Y.H. and Han, J.L., **2012**. Limited polymorphisms of two Y- chromosomal SNPs in Chinese and Iranian sheep. ***Animal genetics***, 43(4), pp.479-480.

20. Di, R., **Farhad Vahidi, S.M**., Ma, Y.H., He, X.H., Zhao, Q.J., Han, J.L., Guan, W.J., Chu, M.X., Sun, W. and Pu, Y.P., **2011**. Microsatellite analysis revealed genetic diversity and population structure among Chinese cashmere goats. ***Animal genetics***, 42(4), pp.428-431.

21. Finlay, E.K., Gaillard, C., **Vahidi, S.M.F.,** Mirhoseini, S.Z., Jianlin, H., Qi, X.B., El-Barody, M.A.A., Baird, J.F., Healy, B.C. and Bradley, D.G., **2007**. Bayesian inference of population expansions in domestic bovines. ***Biology Letters,*** 3(4), pp.449-452.

22. Mirhoseini, S. Z., **Vahidi, S. M. F.,** Gharehyazie B., **2005**. Survey of efficiency of six microsatellite loci in Iranian indigenous cattle and buffalo populations. ***Iranian Journal of Biotechnology***. Vol.3, 1:41-47.