

Novel Insights into Infection and Immunity

Gholamreza Nikbakht Brujeni 

Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Received: 2022-01-05

Accepted: 2022-01-26

Email: nikbakht@ut.ac.ir

Copyright © 2022. This is an open-access article distributed under the terms of the Creative Commons Attribution- 4.0 International License which permits Share, copy and redistribution of the material in any medium or format or adapt, remix, transform, and build upon the material for any purpose, even commercially.

Dear Editor

Understanding host and pathogens interactions necessitate comprehensive knowledge concerning highly complex biological systems. In a simplified pathway, pathogen flags (PAMPs) or virulence factors interact or stimulate the host receivers, including many pattern recognition receptors. These interactions happen or don't happen in an environment with hundreds of spatiotemporal as well as epidemiological variables. Furthermore, the coevolution of host and pathogen brings the interactions into a more complex and dynamic system. Health or disease status systematically could be changed based on our idea about combat or coexistence between host and pathogens.

On the other hand, it depends on whether we would like to change our objectives of fighting against infections or favor a homeostatic balance in response to stimuli. Balance is the key to life, what we can learn from the immune organ system. Based on the novel insight, the sense of interaction could be changed from "fighting" to "fitting". Despite a traditional idea of fighting against infections by means of drugs or vaccines, the balance or coexistence with lower injury or energy consumption would be ideal and cost-benefit. A life-history strategy, our pattern of survival and reproduction, evolves by natural selection based on the characteristics that affect our fitness. Also, pathogens do not necessarily evolve to enhance or diminish virulence beyond the details concerning the cellular or molecular basis. Coevolution of host and pathogen, in its own manner, develops an exclusive "trade of" and/or "balance" with remarkable reduction of pathogenicity and host immune responses.

Disease control or altering the situation to a norm, standard, or desired status quo can be reached in several ways: management and rearing measures, immunization, and decision for improved disease resistance. Although ideal decision-making needs intuition, experimentation and field trials often involve expensive and unethical procedures. Mathematical modeling and simulations have become essential experimental and analytical tools for complex and dynamic systems. Interestingly, due to the disciplines and principles in its behaviors and responses, the immune system provides precious designs for these kinds of approaches.

Mathematical modeling helped us analyze the spread and control of newly emerging or reemerging infectious diseases and led to novel insights into infection and immunity. Mathematical models brought explicit concepts such as "herd immunity" for vaccination policies in veterinary science (Smith, 2019). Nevertheless, choosing a model for host-pathogen interactions is complicated and needs some considerations. As a criterion for model selection, the goodness of fit describes how well the host immunity "fits" with the pathogens in its environment. In this context, mathematical models are faced with dissipation or "fitness flux" related to population genetics (Altan-Bonnet *et al.*, 2020). Accordingly, parameters associated with immunogenetics and pathogenic coevolution should be incorporated into the model. In several experiments, using mathematical models helped us to predict the effect of genetic and epidemiological changes on disease incidence (Nikbakht *et al.*, 2015; Ali *et al.*, 2019; Vahedi *et al.*, 2019). Results also show the benefits of mathematical modeling for breeding disease resistance animals

that is now practiced in cattle, sheep, chicken and fish farming (Stear *et al.*, 2012).

Traditional selection for phenotypic values has significantly improved the growth rate during the past half-century. Still, now, high selection intensity for growth and production rate predisposed animals to physiological disorders as well as a reduction in overall immunocompetence. In this situation, marker-assisted selection (MAS) is expected to be a more effective breeding approach. The combination of traditional genetic selection and modern molecular methods may be preferred for breeding in the future. To simultaneously improve production and fitness traits, molecular markers associated with one or both sets of traits may be useful. The important role of major histocompatibility complex (MHC) in disease resistance and production traits have made it a precious marker in selection programs (Emam *et*

al., 2014; Nikbakht & Esmailnejad, 2015; Nikbakht *et al.*, 2016; Ali *et al.*, 2019).

Decision-making for sustainable development must be reviewed based on the new insights into Infection and immunity and the impacts of mathematical modeling on vaccination and disease control. Regarding the important role of immune genes in disease resistance and controlling production traits, immunogenetic parameters should be considered in modeling for disease control. Investigating the polymorphism as well as associations and linkages to traits in native animals, as a genetic resource of our country, would be worthwhile and can be used in future native breeding programs.

Conflict of Interest

The authors declared no conflict of interest.

References

- Ali, A. O., Murphy, L., Stear, A., Fairlie-Clarke, K., Nikbakht Brujeni, G., Donskow-Lysoniewska, K., ... & Stear, M. J. (2019). Association of MHC class II haplotypes with reduced faecal nematode egg count and IgA activity in British Texel sheep. *Parasite Immunology*, 41(7), e12626. [DOI:10.1111/pim.12626] [PMID]
- Altan-Bonnet, G., Mora, T., & Walczak, A. M. (2020). Quantitative immunology for physicists. *Physics Reports*, 849, 1-83. [DOI:10.1016/j.physrep.2020.01.001]
- Emam, M., Mehrabani-Yeganeh, H., Barjesteh, N., Nikbakht, G., Thompson-Crispi, K., Charkhkar, S., & Mallard, B. (2014). The influence of genetic background versus commercial breeding programs on chicken immunocompetence. *Poultry Science*, 93(1), 77-84. [DOI:10.3382/ps.2013-03475] [PMID]
- Brujeni, G. N., Ghorbanpour, R., & Esmailnejad, A. (2016). Association of BoLA-DRB3. 2 alleles with BLV infection profiles (persistent lymphocytosis/lymphosarcoma) and lymphocyte subsets in Iranian Holstein cattle. *Biochemical Genetics*, 54(2), 194-207. [DOI:10.1007/s10528-016-9712-6] [PMID]
- Brujeni, G. N., Esmailnejad, A., & Oskoui, N. K. (2015). Study of the association of major histocompatibility complex with antibody response to vaccines in Khorasan native chickens. *Journal of Veterinary Research*, 70(2). [DOI:10.22059/jvr.2015.53733]
- Nikbakht, G., & Esmailnejad, A. (2015). Chicken major histocompatibility complex polymorphism and its association with production traits. *Immuno-genetics*, 67(4), 247-252. [DOI:10.1007/s00251-015-0832-7] [PMID]
- Smith, D. R. (2019). Herd immunity. *Veterinary Clinics: Food Animal Practice*, 35(3), 593-604. [DOI:10.1016/j.cvfa.2019.07.001] [PMID]
- Stear, M., Nikbakht, G., Matthews, L., & Jonsson, N. (2012). Breeding for disease resistance in livestock and fish. *Animal Science Review*, 7, 1-10. [DOI:10.1079/PAVSNNR20127007]
- Vahedi, S. M., Nikbakht, G., Jamshidi, S., Lankarani, L., Alimi, N., & Esmailnejad, A. (2019). Association between DLA-DRB1. 2 allelic diversity and development of mammary gland tumors in dogs. *Acta Veterinaria Scandinavica*, 61(1), 1-8. [DOI:10.1186/s13028-019-0491-z] [PMID] [PMCID]