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Genetic Bases of Host Response to Infections and Chronic Diseases

Position

Associate Professor, Sackler Faculty of Medicine

Research

The research in my laboratory is focused on understanding the genetic bases of host response to infections and chronic diseases, which are important for human health. My team uses mouse model for speeding up the process of identifying such genes, which may involve making some people resistant to a disease while others are not. After finding the genes in mouse, it will be possible to identify the homologous genes in human. The product of our research can be used in developing new prevention and treatment tools for these diseases.

The main ongoing research projects at his lab are:

Identifying and characterizing genes involved in host response to bacterial infection by *Klebsiella Pneumoniae*.

Identifying and characterizing genes involved in host response to fungal infection by *Aspergillus Fumigatus* (Aspergillosis)

Identifying and characterizing genes involved in host response to bacterial that causes dental infection (periodontitis)

Identifying and characterizing genes involved in development of type-2 diabetes (T2D) in humans as a result of obesity and high fat-diet.

Identifying and characterizing genes involved in host immune response to infectious and chronic diseases.

Identifying and characterizing genes involved in development of colon cancer.

Publications

Behnke, J.M., Menge, D., Nagda, S., Noyes, H.A., **Iraqi, F.A.**, Kemp, S.J., Mugambi, J.M., Baker, L.R., Wakelin, D. and Gibson, J.P. (2010) Quantitative trait loci for resistance to worm infections and associated immunological and pathological traits in mice: Comparison of loci on chromosomes 5, 8 and 11 in F₂ and F_{6/7} intercross lines of mice. *Parasitol.* 137:311-32.

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Aylor, D.L., Valdar, W., Foulds-Mathes, W., Buus, R.J., Ricardo, A., Verdugo, R.A., Ralph, S., Baric, R.S., Ferris, M.T., Frelinger, F.A., Heise, M., Frieman,

M.B., Gralinski, L.E., Bell, T.A., Didion, J.P., Hua, K., Nehrenberg, D.L., Powell, C.L., Steigerwalt, J., Xie, Y., Kelada, S.N.P., Collins, F.S., Yang, I.V., Schwartz, D.A., Branstetter, L.A., Chesler, E.J., Miller, D.R., Spence, J., Liu, E.Y., McMillan, L., Sarkar, A., Wang, J., Wang, W., Zhang, Q., Broman, K.W., Korstanje, R., Durrant, C., Mott, R., **Iraqi, F.A.**, Pomp, D., Threadgill, D., Pardo-Manuel de Villena, F. and Churchill, G.A. (2011) Genetic analysis of complex traits in the emerging collaborative cross. *Gen Res* 21:1213-1222.

Durrant, C., Tayem, H., Yalcin, B., Cleak, J., Goodstadt, L., Pardo-Manuel de Villena, F., Mott, R. and **Iraqi, F.A.** (2011) Mapping QTL associated with host susceptibility to *Aspergillus fumigatus* infection in the Collaborative Cross mouse resource population. *Gen Res* 21:1239-1248.

Silva, M.V.B., Sonstegard, T., Hanotte, O., Mugambi, J., Garcia, J.F., Nagda, S., Gibson, J., **Iraqi, F.A.**, McClintock, S., Kemp, S., Boettcher, P., Malek, M., Van Tassell, C.P. and Baker, L.R. (2012) Identification of quantitative trait loci affecting resistance to gastro-intestinal parasites in a double backcross population of Red Maasai and Dorper sheep. *Anim Genet* 43:63-71.

Shusterman A, Durrant C, Mott R, Schaefer A, Weiss EI, **Iraqi FA*** and Houri-Haddad Y* (2013) Host susceptibility to periodontitis: Mapping murine genomic regions. *J Dent Res* 92: 438-443.

Shusterman A, Salaymeh Y, Nashef A, Soller M, Wilensky A, Mott R, Weiss EI, Houri-Haddad Y and. **Iraqi FA** (2013) Genotype is an important determinant factor of host susceptibility to periodontitis in the Collaborative Cross and inbred mouse populations. *BMC Genet* 14: 68-79.

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Mott R, Soller M. (2014) Heritability and coefficient of genetic variation analyses of phenotypic traits provide strong basis for high-resolution QTL mapping in the Collaborative Cross mouse genetic reference population. *Mamm Genome*. 25:109-19.

Review and editorials

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Hernandez-Valladares M, Rihet P, Iraqi FA (2014) Host susceptibility to malaria in human and mice: compatible approaches to identify potential resistant genes. *Physiol Genomics* 46:1-16.

Grants

2012-2015	European Sequence and Genotyping Institutes (ESGI), Understanding genetic susceptibility to fungal infection using naïve collaborative cross mice (Collaborators: Ron Shamir and Irit Gat-Viks (TAU), Richard Mott (University of Oxford)
2013-2016	EU-FP7-Infrafrontier, European Mouse Mutant and Archiving (EMMA) (co-PI*, collaborators: 23 Members from European countries)
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