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HOST AND PARASITE GENE EXPRESSION PROFILING THROUGH TIME FROM INFECTION TO LATER STAGES OF DISEASE TO ALLOW RATIONAL DESIGN OF TRADITIONAL VACCINES, LATER-STAGE VACCINES AND THERAPIES TO TREAT SYMPTOMS

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It would be informative for rational design of vaccines and symptom management-therapies to do disease-progression from infection stage gene expression profiling microarray studies for parasitic infections. This would be the study of host cells infected or other cells affected by the parasitic disease but not infected, at different stages of the infection to see what is the progression of parasite genes turned on/off up/down-regulated and the same for the host genes. This would give valuable data from infection of cell to cell death programme of say an HIV-infected T-cell. This could also be done for non-virus parasites such as bacterial infections, and nematode infections as well as say malaria. This could give information about how to rationally design post-infection vaccines if epitopes are created by the parasite due to particular gene expression patterns at any stage from initial infection to later stages. Later-stage vaccines could be designed to stimulate the host immune system against later stages of parasitic epitopes allowing later-stage vaccine intervention, where vaccination has not been possible before infection and yet a strong vaccine-stimulated immune response could cause later-stage elimination of the parasitic infection or at least amelioration by bringing down the levels of infectious agents. Vaccines can be rationally designed also for immune system elimination of infectious agent to fend off attempted infection. Thorough studies of gene expression profiles of host and parasite at all stages of the infection process and infection progression could allow rational design of drugs to counter symptoms. Annotation of all the studies described with gene/protein function data could allow valuable insights.

Recent Publications

1. Shi Z, Derow C K and Zhang B (2010) Co-expression module analysis reveals biological processes, genomic gain, and regulatory mechanisms associated with breast cancer progression. BMC Systems Biology 4:74.
2. Aranda B, Achuthan P, Alam-Faruque Y, Armean I, Bridge A, Derow C, Feuermann M, Ghanbarian A T, Kerrien S, Khadake J, Kerssemakers J, Leroy C, Menden M, Michaut M, Montecchi-Palazzi L, Neuhauser SN, Orchard S, Perreau V, Roechert B, van Eijk K and Hermjakob H (2009) The IntAct molecular interaction database in 2010. Nucleic Acids Research 38(1):D525–D531
3. Chatr-aryamontri A, Kerrien S, Khadake J, Orchard S, Ceol A, Licata L, Castagnoli L, Costa S, Derow C and Huntley R (2008) MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. Genome Biology doi: 10.1186/gb-2008-9-s2-s5.
4. Kerrien S, Alam-Faruque Y, Aranda B, Bancarz I, Bridge A, Derow C, Dimmer E, Feuermann M, Friedrichsen A, Huntley R, Kohler C, Khadake J, Leroy C, Liban A, Lieftink C, Montecchi-Palazzi L, Orchard S, Risse J, Robbe K, Roechert B, Thorneycroft D, Zhang Y, Apweiler R and Hermjakob H (2007) IntAct--open source resource for molecular interaction data. Nucleic Acids Research 35:D561-5.
5. Chassagnole C, Jackson R C, Hussain N, Bashir L, Derow C, Savin J and Fell D A (2006) Using a mammalian cell cycle simulation to interpret differential kinase inhibition in anti-tumour pharmaceutical development. Biosystems 83(2-3):91-7.

Biography

Catherine K Derow research is focused on applying Systems Biology to Genomics and Proteomics as a means of solving health problems and answering important questions in the field of the Life Sciences. She currently works as an Associate for Biopharma Vantage, a competitive intelligence provider for Life Sciences companies. She has worked for Physiomics plc. on *in silico* anti-cancer therapeutics development, as well as at the European Bioinformatics Institute on the database IntAct, a molecular interactions resource, in the Proteomics section. She has also served as an expert invited by the European Union to evaluate research proposals as part of a panel to aid in the selection of projects for fellowship funding.

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