Relationships between immune gene expression and circulating cytokine levels in wild house mice

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May 22, 2020

Abstract

1. Quantitative PCR (qPCR) has been commonly used to measure gene expression in a number of research contexts, but the measured RNA concentrations do not always represent the concentrations of active proteins which they encode. This can be due to transcriptional regulation or post-translational modifications, or localisation of immune environments, as can occur during infection. However, in studies using free-living non-model species, such as in ecoimmunological research, qPCR may be the only available option to measure a parameter of interest, and so understanding the quantitative link between gene expression and associated effector protein levels is vital. 2. Here we use qPCR to measure concentrations of RNA from mesenteric lymph node (MLN) and spleen tissue, and multiplex ELISA of blood serum to measure circulating cytokine concentrations in a wild population of a model species, Mus musculus domesticus. 3. Few significant correlations were found between gene expression levels and circulating cytokines of the same immune genes or proteins, or related functional groups. Where significant correlations were observed, these were most frequently within the measured tissue (i.e. the expression levels of genes measured from spleen tissue were more likely to correlate with each other rather than with genes measured from MLN tissue, or with cytokine concentrations measured from blood). 4. Potential reasons for discrepancies between measures, including differences in decay rates and transcriptional regulation networks are discussed. We highlight the relative usefulness of different measures under different research questions, and consider what might be inferred from immune assays.

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