Title:	Evolution of the metabolome in response to selection for increased immunity in populations of Drosophila melanogaster
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Abstract:	We used NMR-based metabolomics to test two hypotheses-(i) there will be evolved differences in the metabolome of selected and control populations even under un-infected conditions and (ii) post infection, the metabolomes of the selected and control populations will respond differently. We selected replicate populations of Drosophila melanogaster for increased survivorship (I) against a gram-negative pathogen. We subjected the selected (I) and their control populations (S) to three different treatments: (1) infected with heat-killed bacteria (i), (2) sham infected (s), and (3) untreated (u). We performed 1D and 2D NMR experiments to identify the metabolic differences. Multivariate analysis of the metabolic profiles of the untreated (Iu and Su) flies yielded higher concentrations of lipids, organic acids, sugars, amino acids, NAD and AMP in the Iu treatment as compared to the Su treatment, showing that even in the absence of infection, the metabolome of the I and S regimes was different. In the S and I regimes, post infection/injury, concentration of metabolites directly or indirectly associated with energy related pathways (lipids, organic acids, sugars) declined while the concentration of metabolites that are probably associated with immune response (amino acids) increased. However, in most cases, the I regime flies had a higher concentration of such metabolites even under un-infected conditions. The change in the metabolite concentration upon infection/injury was not always comparable between I and S regimes (in case of lactate, alanine, leucine, lysine, threonine) indicating that the I and S regimes had evolved to respond differentially to infection and to injury.
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