General notes about proteomics in evolutionary and ecological research

Baer & Millar, J. Proteomics 2016 – ‘Proteomics in evolutionary ecology’

General introduction to the proteome as an active agent in evolution (which has not yet been fully recognised by molecular biologists).

Nice figure updating central dogma to add feedbacks from proteome to nucleic acid stages.

Protein networks (can be represented as n-dimensional matrix where n = number of proteins) as information processing and information storage mechanism.

They use some of their own research on social insects as an example to highlight the role of the proteome in ecology / evolution.

“We point out that the origins of cellular function are related to the properties of polypeptide and RNA and their interactions with the environment, rather than DNA descent, and that the critical role of horizontal gene transfer in evolution is more about coopting new proteins to impact cellular processes than it is about modifying gene function. Furthermore, post-transcriptional and post-translational processes generate a remarkable diversity of mature proteins from a single gene, and the properties of these mature proteins can also influence inheritance through genetic and perhaps epigenetic mechanisms. The influence of post-transcriptional diversification on evolutionary processes could provide a novel mechanistic underpinning for elements of rapid, directed evolutionary changes and adaptations as observed for a variety of evolutionary processes.”

Alvarez et al., Molecular Ecology 2015 – ‘Ten years of transcriptomics in wild populations: what have we learned about their ecology and evolution?’

Some comments and a few refs to follow up looking at variation in transcriptomics in response to environmental conditions.