Mammalian Lipidomic Network

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The research story

Total lipid profiling is being used to find biomarkers for a growing number of disease and mammalian physiological states. However, a more pertinent question is which enzymes have changes in their activity to cause the spectrum of observed lipid changes, because this reveals aspects of the underlying mechanism and could lead to points for therapeutic intervention. This is not straightforward as enzymes of lipid metabolism usually catalyse irreversible reactions of a very large number of potential substrates. To address this question a python script has been written that generates a tripartite graph of 127 enzymes linked to 13934 reactions linked to 7561 lipids. The resulting network underpins a web tool for discovering potential regulators causing lipidome perturbations [1].

The image

This art work shows the entire graph as laid out using Cytoscape. This has been visually enhanced by using a black background and colour-coding nodes by their lipid class, with enzymes and reactions respectively depicted as purple ellipses and light-bordered triangles. Most metabolic networks appear to be a “hairy ball”, but this is not the case here, because aspects of lipid metabolism have clustered into particular zones. Orange nodes are diglycerides which go on to produce triglycerides (red), sphingolipids (green) and phospholipids (pink), which are respectively energy sources, nerve-specific cell membrane components and general molecules of lipid-bilayers The pale green nodes on paths leading from the main graph represent synthesis of signalling molecules, including arachinodic acid (involved in inflammation) and cholesterol (the precursor of steroid hormones).

Reference

[1] Casbas-Pinto F, Ravipati S, Barrett DA, Hodgman TC, A methodology for elucidating regulatory mechanisms leading to changes in lipid profiles, Metabolomics 13: 81, 2017.

F. Matthäus et al. (eds.), *The Art of Theoretical Biology*, https://doi.org/10.1007/978-3-030-33471-0_17