Scientists advance cutting edge of immunology through study of macrophages

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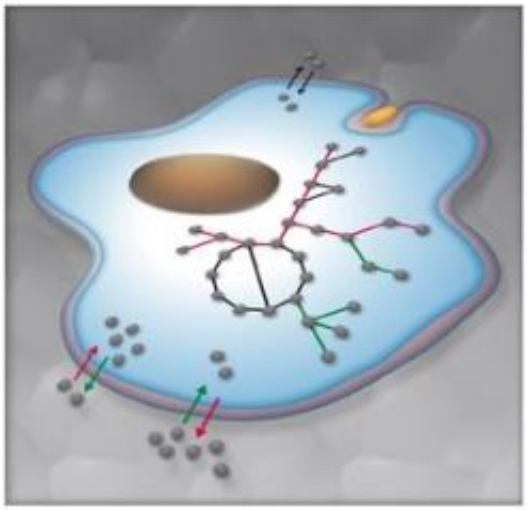

(Phys.org)—Macrophages are heavy hitters of the immune system. Their name literally means "to eat large objects." They are critical members of the body's defense team, such as in the lungs where they ingest invading microorganisms and at wound sites where they rush in and secrete coagulation factors that help form scabs. Macrophages also scavenge the body to find, digest, and recycle cell debris such as worn out red blood cells.

Researchers recently gained new knowledge about how macrophages are

activated by studying a leukemic line of macrophages called RAW 264.7 that were treated with endotoxin from Salmonella. The team used high-throughput mass spectrometers and custom software tools at EMSL to identify proteins (using proteomics analyses) and metabolites (using metabolomics analyses) that the cells produced under different conditions, as well as the RNAs (using transcriptomics analyses) that led to the proteins being expressed. They then built a computational model of all of the known metabolic pathways for RAW 264.7. The proteomic, metabolomic, and transcriptomic data were incorporated into the metabolic model, which improved the effectiveness of the model to predict new functions for metabolites in macrophages. Researchers found that the simple sugar, glucose, and the amino acid, arginine, played activating roles in macrophage defense mechanisms, while the amino acid, tryptophan, and vitamin D had an immune suppressive effect.

This study and its methodology significantly advance the cutting edge of immunology and disease prevention. For example, traditional therapies target invading bacteria. The research team's novel work may, however, lead to new therapy options such as using metabolic approaches to activate macrophages in response to an invader and to suppress macrophages when the threat is neutralized. In addition, novel immunotherapeutic drugs could be designed to mimic the activation or inhibition of specific metabolic pathways.

More information: Bordbar A, ML Mo, ES Nakayasu, AC Schrimpe-Rutledge, YM Kim, TO Metz, MB Jones, BC Frank, RD Smith, SN Peterson, DE Hyduke, JN Adkins, BO Palsson. 2012. "Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation." *Molecular Systems Biology* 8:558. DOI:10.1038/msb.2012.21

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