Metabolic reprogramming of immune cells

Also known: IMMUNOMETABOLISM

Immunometabolism across the immune system



Variety of cell types

- multiple phenotypes
- local microenvironments
- different functions

Common denominators

- actionable
- highly plastic
- interactive
- migrate and adapt



Immunometabolism or metabolic immunology

- Pathogenic defense is necessary for survival
- The body's immune response involves key changes to metabolic processes
- Immune mediators, such as cytokines, also dictate changes in metabolism



Early observations that inflammatory cytokines are induced in obese adipose tissue and that these cytokines contribute to metabolic disease

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Impact of Childhood Malnutrition on Host Defense and Infection

Marwa K. Ibrahim,^a Mara Zambruni,^{b,c} Christopher L. Melby,^d Peter C. Melby^{b,c,e,f,g,h}



Increased Adipose Tissue Expression of Tumor Necrosis Factor- α in Human Obesity and Insulin Resistance

Gökhan S. Hotamisligil, * Peter Amer, * José F. Caro, [§] Richard L. Atkinson, ^{||} and Bruce M. Spiegelman

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In addition to metabolic tissues regulating immune cells, the metabolism of immune cells themselves is highly regulated. Signaling pathways are activated to promote aerobic glycolysis in stimulated immune cells and play key roles to reprogram metabolism from catabolic oxidative pathways to anabolic pathways.



Activation stimulates proliferation

Immune cell activation



During an immune response, activated cells of the immune system, such as T lymphocytes, undergo rapid expansion in order to fight infection or disease. Many interactions also occur between activated immune cells (e.g., T cell interactions with antigen-presenting cells and interactions between T cells themselves).

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Activation stimulates glycolysis



Increased glycolysis can be considered a hallmark metabolic change in most immune cells undergoing rapid activation, for instance, in response to stimulation of PRRs, cytokine receptors or antigen receptors. Enhanced glycolysis enables the immune cell to generate sufficient ATP and biosynthetic intermediates to proliferate.

There is abundant evidence that metabolic pathways are closely tied to cell signaling and differentiation which leads different subsets of immune cells to adopt unique metabolic programs specific to their state and environment. In this way, metabolic signaling drives cell fate.

It is also apparent that microenvironment greatly influences cell metabolism. Immune cells adopt programs specific for the tissues where they infiltrate and reside. In this way, nutrient availability impacts effector function.

Metabolism in macrophage function

Enhanced glycolysis enables macrophages to generate sufficient ATP and biosynthetic intermediates to carry out its particular effector functions. For macrophages this includes phagocytosis and inflammatory cytokine production.



Metabolism in macrophage function

The NLRP3 inflammasome is a crucial regulator of caspase 1, which generates mature IL-1 β , as well as active IL-18, and induces a type of cell death called pyroptosis. The inflammasome is activated in response to mitochondrial (and glycolytic) activity.



Macrophages adapt their redox status in response to infection

NADPH has multiple functions in immune cells.

It is used by the NADPH oxidase to generate reactive oxygen species (ROS) during the respiratory burst, but as a counter-balance it is also used to generate glutathione and other antioxidants.

During an infection, macrophages and neutrophils probably require both of these NADPH-dependent functions — rapid ROS production to clear the infectious agent followed by induction of antioxidants to prevent excessive tissue damage.





Macrophages adapt their redox status in response to infection

LPS-activated macrophages induce PPP to elevate NADPH availability



Hypercholesterolemia impairs macrophage redox status



Hypercholesterolemia Attenuates Inflammatory Macrophage Responses without Major Changes in Glycolysis or the TCA Cycle



Hypercholesterolemia Reduces LPS-Mediated Induction of the PPP in Macrophages

Hypercholesterolemia impairs macrophage redox status Cell S

NFD

HFD

+ LPS





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M1: Glycolytic, broken TCA, elevated PPP

M2: Oxidative metabolism, including FAO



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PKM switch dictates macrophage polarization

PKM2 promotes M2 skewing



Highlights

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- Tetramerization of PKM2 reverses the LPS-induced Warburg effect
- PKM2 plays a key role in stabilizing Hif-1α and regulates Hif-1α-dependent genes
- Tetramerization of PKM2 attenuates LPS-induced M1 macrophage traits
- PKM2 is a critical determinant of glycolytic reprogramming in macrophages

TCA intermediates in macrophage polarization



In M2 macrophages, there is an intact TCA cycle that is coupled to oxidative phosphorylation. This allows the generation of UDP-GlcNAc intermediates that are necessary for the glycosylation of M2-associated receptors, such as the mannose receptor.

However, in M1 macrophages the TCA cycle has been shown to be broken in two places — after citrate (owing to a decrease expression of isocitrate lyase) and after succinate.

Different acetyl-CoA utilization in M1 vs M2

The citrate that accumulates in M1 macrophages has been shown to be exported from the mitochondria via the citrate transporter. It is then utilized for the production of fatty acids, which in turn are used for membrane biogenesis.

Excess citrate can also feed into pathways that generate nitric oxide and prostaglandins, which are key effector molecules made by macrophages.



Different acetyl-CoA utilization in M1 vs M2





A third metabolite generated from citrate is <u>itaconic acid</u>, which has been shown to have direct bactericidal effects on species such as *Salmonella enterica* and *Mycobacterium tuberculosis*. This particular example shows how a metabolic rewiring event can generate metabolites with direct antimicrobial activity.



Itaconate is a competitive inhibitor (endogenous)



Inhibiting SDH, Itaconate promotes reverse electron flow along the ETC and ROS generation (to support phagocytosis)



Complex II is the site of reverse electron transport (RET) in inflammatory macrophages (ROS, hence NRF2 activation) and is also responsible for regulating fumarate levels linking to epigenetic changes.

In trained immunity, fumarate-induced epigenetic changes (i.e., H3K27Ac and H3K4me3) can restore the inflammatory response to LPS, rescuing immune paralysis.







Succeinate that accumulates in M1 macrophages as a consequence of a broken TCA cycle has a direct impact on macrophage cytokine production. One mechanism involved is inhibition of prolyl-hydroxylases by succinate, leading to the stabilization of HIF1 α and the sustained production of IL-1 β . This pathway will operate under normoxia as well as in hypoxia, and is therefore a mechanism for HIF1 α activation under aerobic conditions.



aKG supports hypoxic response

Succinate inhibits PDHs, leading to HIF stabilization

Itaconate prevents abdominal aortic aneurysm formation through inhibiting inflammation via activation of Nrf2

Haoyu Song^{a,b}, Tong Xu^a, Xiaofei Feng^a, Yanxian Lai^a, Yang Yang^a, Hao Zheng^a, Xiang He^a, Guoquan Wei^a, Wangjun Liao^d, Yulin Liao^a, Lintao Zhong^{a,c,*}, Jianping Bin^{a,b,*}

Abdominal aortic aneurysm (AAA) is a chronic inflammatory disease.

An AAA is a swelling in the aorta, the artery that carries blood from the heart to the tummy (abdomen). Most aneurysms do not cause any problems, but they can be serious because there's a risk they could burst (rupture).



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Exogenous addition of the itaconate analogue 4-octyl itaconate (OI) attenuates Ang II-induced AAA formation in ApoE-/- mice.
β-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance

Boris Novakovic,^{1,7} Ehsan Habibi,^{1,7} Shuang-Yin Wang,^{1,7} Rob J.W. Arts,² Robab Davar,¹ Wout Megchelenbrink,¹ Bowon Kim,¹ Tatyana Kuznetsova,¹ Matthijs Kox,³ Jelle Zwaag,³ Filomena Matarese,¹ Simon J. van Heeringen,⁴ Eva M. Janssen-Megens,¹ Nilofar Sharifi,¹ Cheng Wang,¹ Farid Keramati,¹ Vivien Schoonenberg,¹ Paul Flicek,⁵ Laura Clarke,⁵ Peter Pickkers,³ Simon Heath,⁶ Ivo Gut,⁶ Mihai G. Netea,² Joost H.A. Martens,¹ Colin Logie,¹ and Hendrik G. Stunnenberg^{1,8,*}





Amino acid (AA) metabolism supports macrophage functions



Arginine metabolism for M1 and M2

Arginine metabolism has been found to have a key role in the inflammatory function of macrophages. Macrophages use arginine in two distinct metabolic pathways, the nitric oxide synthesis pathway and the arginase pathway.



The pathway used for arginine metabolism in macrophages has profound effects on the immune function of the cell.

Arginine metabolism for M1 and M2

Macrophage flux of arginine into the nitric oxide synthesis pathway is associated with an inflammatory M1 phenotype. When macrophages direct arginine into this pathway, arginine (via citrulline) is converted into nitric oxide, a process mediated by inducible nitric oxide synthase (iNOS). It has been known for some time that iNOS expression is itself required for inflammatory macrophage function.

In contrast to the inflammatory involvement of arginine metabolism in the nitric oxide synthesis pathway, arginine flux through the arginase pathway is associated with a more tolerant immune response, often associated with wound healing.



Arginine metabolism for M1 and M2



Note: forcing one pathway (ex: NOS2 KO) dictates macrophage polarization (*Palmieri et al, Nat Comm, 2020*)

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Lymphocytes face major metabolic challenges upon activation. They must meet the bioenergetic and biosynthetic demands of increased cell proliferation and also adapt to changing environmental conditions, in which nutrients and oxygen may be limiting.

Why T cells adopt specific metabolic programs and the impact that these programs have on T cell function and, ultimately, immunological outcome remain unclear.

- Improve response to infections (lower morbidity)
- Tune subtype differentiation
- Improve efficiency of vaccination
- Ameliorate (cure or prevent) auto-immune diseases
- Curtail exhaustion (*i.e.: immune evasion by cancer*)
- Improve immunotherapy (*adaptive: CAR T cells*)

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...hinge on the ability to activate immunogenic programs (gene expression) and generate effector/memory cells (epigenetic rearrangements).

Metabolic rewiring of activated T cells



Bioenergetic profiling of T cells has revealed that T cell metabolism changes dynamically with activation state. Upon antigen encounter, T cells become activated, undergo extensive proliferation, and differentiate into effector T cells (T_{EFF}); upon pathogen clearance, most T_{EFF} cells die, leaving behind a small population of long-lived antigen-specific memory T cells (T_M). Resting naïve T cells maintain low rates of glycolysis and predominantly oxidize glucose-derived pyruvate. Upon activation, T cells switch to a program of anabolic growth and biomass accumulation to generate daughter cells, which by definition dictates increased demand for ATP and metabolic resources. In this state, T cells are considered to be metabolically activated. T cell receptor (TCR) signaling directs the metabolic reprogramming of naïve T cells.

Entry of glucose- and glutamine-derived carbons into the citric acid cycle supports early steps of HIV-1 infection in CD4 T cells

Isabelle Clerc^{1,6}, Daouda Abba Moussa^{1,6}, Zoi Vahlas^{1,6}, Saverio Tardito^{2,3}, Leal Oburoglu¹, Thomas J. Hope⁴, Marc Sitbon¹, Valérie Dardalhon¹, Cédric Mongellaz^{1,7*} and Naomi Taylor^{1,5,7*}





Mitochondria Are Required for Antigen-Specific T Cell Activation through Reactive Oxygen Species Signaling

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Metabolic rewiring of activated T cells



As a quiescent T cell population, T_M cells adopt a metabolic profile similar to that of naïve T cells — a catabolic metabolism characterized by increased reliance on OXPHOS and lower rates of nutrient uptake and biosynthesis relative to T_{EFF} cells. However, T_M cells also display a characteristic increase in mitochondrial mass, which translates into greater mitochondrial spare respiratory capacity (SRC) relative to naïve or TEFF populations. SRC can be viewed as the maximal respiratory capacity available to a cell, much like the maximum speed that can be achieved by a car engine. Under increased workload, stress, or nutrient limitation, cells en- gage this reserve capacity to generate more energy and promote cell viability

CD8 memory T cells have a bioenergetic advantage that underlies their rapid recall ability

Gerritje J. W. van der Windt^a, David O'Sullivan^a, Bart Everts^a, Stanley Ching-Cheng Huang^a, Michael D. Buck^a, Jonathan D. Curtis^a, Chih-Hao Chang^a, Amber M. Smith^a, Teresa Ai^a, Brandon Faubert^b, Russell G. Jones^b, Edward J. Pearce^a, and Erika L. Pearce^{a,1}



Mechanism??

Aerobic glycolysis promotes T helper 1 cell differentiation through an epigenetic mechanism

Min Peng,¹* Na Yin,¹* Sagar Chhangawala,^{2,3} Ke Xu,^{1,4} Christina S. Leslie,² Ming O. Li¹†



-LDHA promotes INFg expression through acetyl-CoA dependent histone acetylation.



Distinct modes of mitochondrial metabolism uncouple T cell differentiation and function

Will Bailis^{1,2,12}, Justin A. Shyer^{1,12}, Jun Zhao^{1,3,4}, Juan Carlos Garcia Canaveras^{5,6,7}, Fatimah J. Al Khazal⁸, Rihao Qu^{1,3,4}, Holly R. Steach¹, Piotr Bielecki¹, Omair Khan¹, Ruaidhri Jackson¹, Yuval Kluger^{3,4,9}, Louis J. Maher III⁸, Joshua Rabinowitz^{5,6,7}, Joe Craft^{1,10}* & Richard A. Flavell^{1,11}*



Mitochondria promote both cell proliferation and INFg expression



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L. monocytogenes

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Balmer et al, **Immunity**, 2016 Qiu et al, **Cell Rep**, 2019



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Balmer et al, **Immunity**, 2016 Qiu et al, **Cell Rep**, 2019







Balmer et al, **Immunity**, 2016 Qiu et al, **Cell Rep**, 2019





T cells need acetyl-CoA to mature

Anabolic substrate for macromolecule synthesis (proliferation) Histone acetylation substrate for gene expression (effector function)

How is this impaired in disease??





The composition of the microenvironment affects acetyl-CoA availability and global levels of histone acetylation/methylation







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T cells exposed to increased [K⁺]e recycle nutrients via autophagy during functional caloric restriction.



Eil et al, Nature, 2016 Vodnala et al, Science, 2019










Eil et al, **Nature**, 2016 Vodnala et al, **Science**, 2019

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B cell maturation and Germinal Center (GC) reaction



Calciolari et al, Open Biol, 2022

B cell maturation and Germinal Center (GC) reaction



B cell maturation and Germinal Center (GC) reaction







In vitro-activated B cells enhance acetyl-CoA metabolism



In vitro-activated B cells enhance acetyl-CoA metabolism



In vitro-activated B cells show increased histone acetylation



In vitro-activated B cells show increased histone acetylation



In vitro-activated B cells show increased histone acetylation



Murine GCs are hyperacetylated

i.p. challenged (immunized)



**also seen in FACS sorted cells

Bromodomain inhibition suppresses GC maturation in vitro



ACLY ablation suppresses GC maturation in vitro



ACLY ablation hampers GC histone hyperacetylation in vitro



Working model:

B cell maturation is promoted by metabolic-dependent histone acetylation



Diet and immune function Is cell metabolism involved??

Adequate and appropriate nutrition is required for all cells to function optimally and this includes the cells in the immune system.





Diet and immune function Is cell metabolism involved??

Adequate and appropriate nutrition is required for all cells to function optimally and this includes the cells in the immune system.



Energetically expensive vital functions such as immunological responses might have thus evolved to respond accordingly to dietary surplus and deficit of macronutrient intake.



An "activated" immune system further increases the demand for energy during periods of infection, with greater basal energy expenditure during fever for example. Thus, optimal nutrition for the best immunological outcomes would be nutrition, which supports the functions of immune cells allowing them to initiate effective responses against pathogens but also to resolve the response rapidly when necessary and to avoid any underlying chronic inflammation.

The immune system's demands for energy and nutrients can be met from exogenous sources i.e., the diet, or if dietary sources are inadequate, from endogenous sources such as body stores. Some micronutrients and dietary components have very specific roles in the development and maintenance of an effective immune system throughout the life course or in reducing chronic inflammation.

For example, the amino acid arginine is essential for the generation of nitric oxide by macrophages, and the micronutrients vitamin A and zinc regulate cell division and so are essential for a successful proliferative response within the immune system.





As well as nutrition having the potential to effectively treat immune deficiencies related to poor intake, there is a great deal of research interest in whether specific nutrient interventions can further enhance immune function in sub-clinical situations, and so prevent the onset of infections or chronic inflammatory diseases.



Humans evolved with larger and intensive energetic demands for brain function. Host survival thus required mechanisms that balance the energetic costs of essential functions such as successful immune response against infections and tissue repair. Accordingly, humans have developed an integrated immunometabolic response (IIMR) that involves sensing of nutrient balance by neuronal (sympathetic and sensory innervation) and humoral signals (e.g., hormones like insulin, FGF21, GDF15, ghrelin...) between the hypothalamus and peripheral tissues to allow the host to prioritize storage and/or utilize substrates for tissue growth, maintenance, and immune responses.

Hence, severe reduction in nutrient and energy intake might cause tradeoffs in non-essential functions.



In an event of low glucose availability, such as food restriction, the limited glycogen reserves in the liver and muscle cannot sustain non-essential metabolic demand. Instead, triglycerides undergo fatty acid oxidation, ketogenesis, and ketolysis to support ATP production.

Calorie restriction (CR) has typically beneficial effects on the immune system (and longevity)



Modern diets are rich in saturated fats and processed carbohydrates, such as high fructose corn syrup, and are deficient in fiber, vitamins, and minerals, while containing high levels of salt. These diets are a leading cause of the emergence of obesity-associated chronic diseases, the majority of which are linked to chronic inflammation.

Adipose is an immunologic tissue



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Obesity promotes hyperglycemia and hyperlipidemia



Dietary components can affect immunity



Some metabolite bypass homeostatic control at the systemic (or tissue) level and can impact immune cell differentiation and/or effector function

Mechanisms:

- Lack of feedback regulation
- Feedforward regulation
- Microbiome processing

Hypercholesterolaemia



Excessive lipid intake leads to hypercholesterolemia (including elevated ox-LDL)

Hypercholesterolaemia



Exogenous cholesterol promotes immunosuppression (highly heterogeneous effects)





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,¹ Lintao Liu,¹ Qiang Wang,¹ Maojie Yang,¹ Dale J. Hamilton,⁴ Chengyun Zheng,⁵ and Qing Yi^{1,7,*}



Cholesterol supports signaling


Cholesterol supports signaling





Cholesterol and metabolite regulate T cell receptor clustering. Cholesterol can directly bind to the transmembrane domain of TCR- β chain to mediate TCR clustering on T cell surface, which can increase the avidity of TCR to foreign antigens and therefore augment TCR signaling.

Intake of carbohydrates is elevated in WD



Novel nutritional concepts promote a restriction of carbohydrates in favor of fat to ameliorate detrimental low-grade inflammation (*Paoli et al, 2015; Bosco et al, 2018; Myette-Coté et al, 2018*)



Hirschberger et al, EMBO Mol Med, 2021

Very-low-carbohydrate diet enhances human T-cell immunity through immunometabolic reprogramming

Simon Hirschberger^{1,2,†}, Gabriele Strauß^{1,2,†}, David Effinger^{1,2}, Xaver Marstaller¹, Alicia Ferstl¹, Martin B Müller^{1,2}, Tingting Wu¹, Max Hübner^{1,2}, Tim Rahmel³, Hannah Mascolo¹, Nicole Exner⁴, Julia Heß^{5,6}, Friedrich W Kreth¹, Kristian Unger^{5,6} & Simone Kreth^{1,2,*}



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Differential peripheral immune signatures elicited by vegan versus ketogenic diets in humans

Article





https://doi.org/10.1038/s41591-023-02761-2

Differential peripheral immune signatures elicited by vegan versus ketogenic diets in humans

Article



A ketogenic diet was associated with a significant upregulation of pathways and enrichment in cells associated with the adaptive immune system.

In contrast, a vegan diet had a significant impact on the innate immune system, including upregulation of pathways associated with antiviral immunity.

Fructose utilization has increased dramatically





Contributes to obesity pandemic

Source: USDA reports

Fructose metabolism alters nucleotide, UA and lipid abundance



Note: only in cells that express SLC25A2 (GLUT5) and KHK-C (hepatocytes and colonocytes)

UA release impacts pro-inflammatory phenotypes in macrophages



Fructose is sensed by mTORC1 in adipocytes



Excessive fructose is converted into acetate



An acetate-yielding diet imprints an immune and anti-microbial programme against enteric infection

Yu Anne Yap^{1†} , Keiran H McLeod^{1†}, Craig I McKenzie^{1†}, Patrick G Gavin², Mercedes Davalos-Salas¹, James L Richards¹, Robert J Moore^{3,4}, Trevor J Lockett⁵, Julie M Clarke⁶, Vik Ven Eng^{3,7}, Jaclyn S Pearson^{3,7,8}, Emma E Hamilton-Williams² , Charles R Mackay³ & Eliana Mariño¹









Restored concentrations of SCFA acetate by HAMSA diet is associated with reduced susceptibility to *C. rodentium* infection (colitis).

Increased regulatory intraepithelial lymphocytes (IELs) induced by HAMSA are associated with protection against *C. rodentium*.

Calorie restriction is beneficial for health



Calorie restriction is beneficial for health

Although the mechanisms of <u>CR</u> are not completely understood, protein quality and <u>amino acid composition</u> of diet have been more strongly associated with metabolic and age-associated health.



One of the pathways that are induced with protein and amino acid restriction, is the <u>transsulfuration</u> <u>pathway</u> (TSP). The TSP involves the catabolism of methionine to generate intermediates such as the methyl donor S-adenosylmethionine (SAM), S-adenosylhomocysteine (SAH), <u>homocysteine</u>, and <u>cystathionine</u>. The TSP also allows for the generation of cysteine through the action of cystathionine- γ lyase (CSE), which can further provide important metabolites and byproducts such as <u>glutathione</u>, <u>pyruvate</u>, and <u>hydrogen</u> <u>sulfide</u> (H2S).

Some TSP metabolites such as SAM and homocysteine are increased with obesity and aging and have been implicated with inflammation and disease risk.