Casual Friday Presents

Type 1.5 Diabetes

and support considerations pt III

A BIOGENETIX CLINICAL PRESENTATION

biogenetix.com

Biogenetix

How type 1.5 differs differs

Feature	Type 1	Type 2	LADA (Type 1.5)
Cause	Autoimmune	Insulin resistance	Autoimmune
Onset	Rapid (often childhood)	Gradual	Gradual (adult)
*Insulin needed	Immediately	Sometimes later	*Eventually required
Body type	Often lean	Often overweight	*Often lean or average

Biogenetix

Testing:

If a patient is on insulin, just run the tests.

Autoantibodies

- GAD-65 ab
- Insulin ab
- Antipancreatic Islet cell antibodes
- Zn Transporter 8 Ab (targets beta cells)

- **C-peptide levels** (to measure insulin production)

Biogenetix

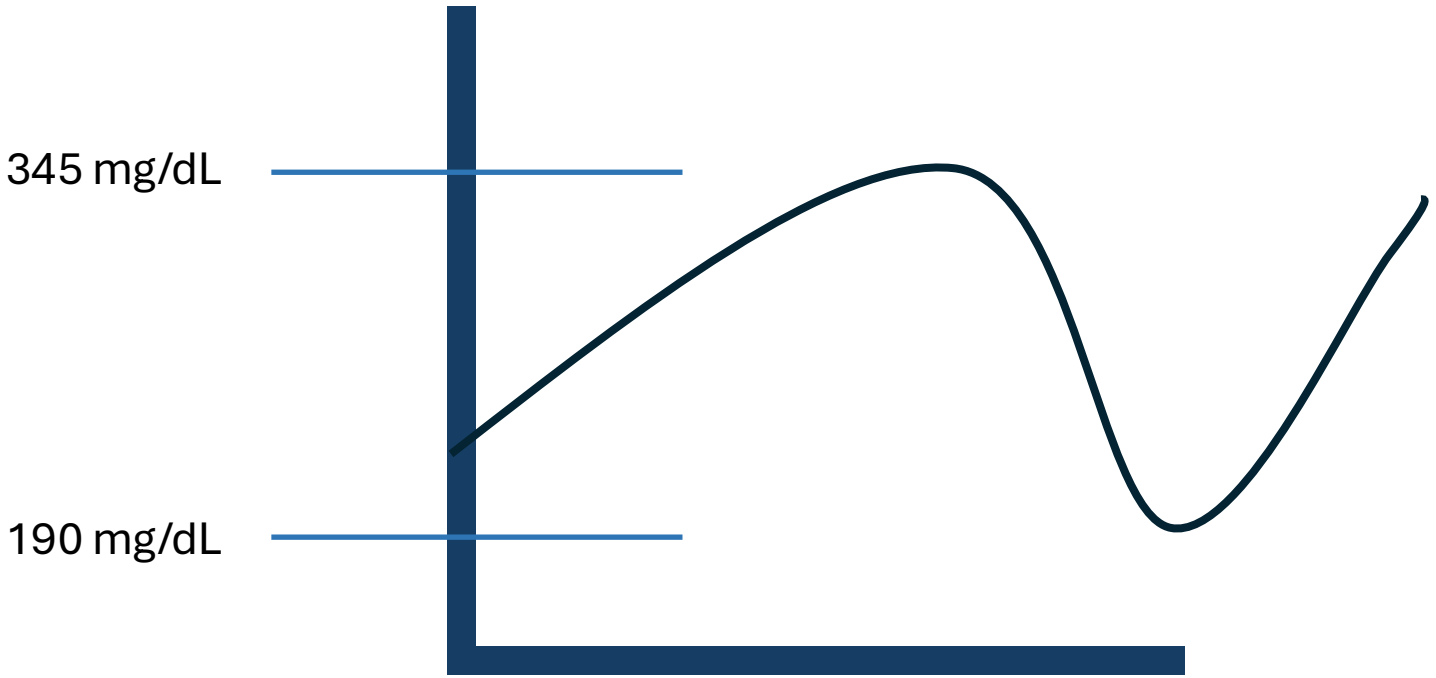
A1C Chart based on ADAG formula

A1C-Derived Average Glucose (ADAG) Study;
eAG in mg/dl = (28.7* hba1c)-46.7 or
eAG in mmol/l = (1.59 x HbA1c)-2.59

A1C	4.0	4.1	4.2	4.3	4.4	4.5	4.6	4.7	4.8	4.9	5.0	5.1
mg/dl	68	71	74	77	80	82	85	88	91	94	97	100
mmol/l	3.8	3.9	4.1	4.3	4.4	4.6	4.7	4.9	5.1	5.2	5.4	5.6
A1C	5.2	5.3	5.4	5.5	5.6	5.7	5.8	5.9	6.0	6.1	6.2	6.3
mg/dl	103	105	108	111	114	117	120	123	125	128	131	134
mmol/l	5.7	5.8	6.0	6.2	6.3	6.5	6.7	6.8	6.9	7.1	7.3	7.4
A1C	6.4	6.5	6.6	6.7	6.8	6.9	7.0	7.1	7.2	7.3	7.4	7.5
mg/dl	137	140	143	146	148	151	154	157	160	163	166	169
mmol/l	7.6	7.8	7.9	8.1	8.2	8.4	8.5	8.7	8.9	9.0	9.2	9.4
A1C	7.6	7.7	7.8	7.9	8.0	8.5	9.0	9.5	10.0	11.0	12.0	13.0
mg/dl	171	174	177	180	183	197	212	226	240	269	298	326
mmol/l	9.5	9.7	9.8	10.0	10.2	10.9	11.8	12.5	13.3	14.9	16.5	18.1
Super Optimal		Optimal		Normal		Pre Diabetes		Diabetes		Dangerous		

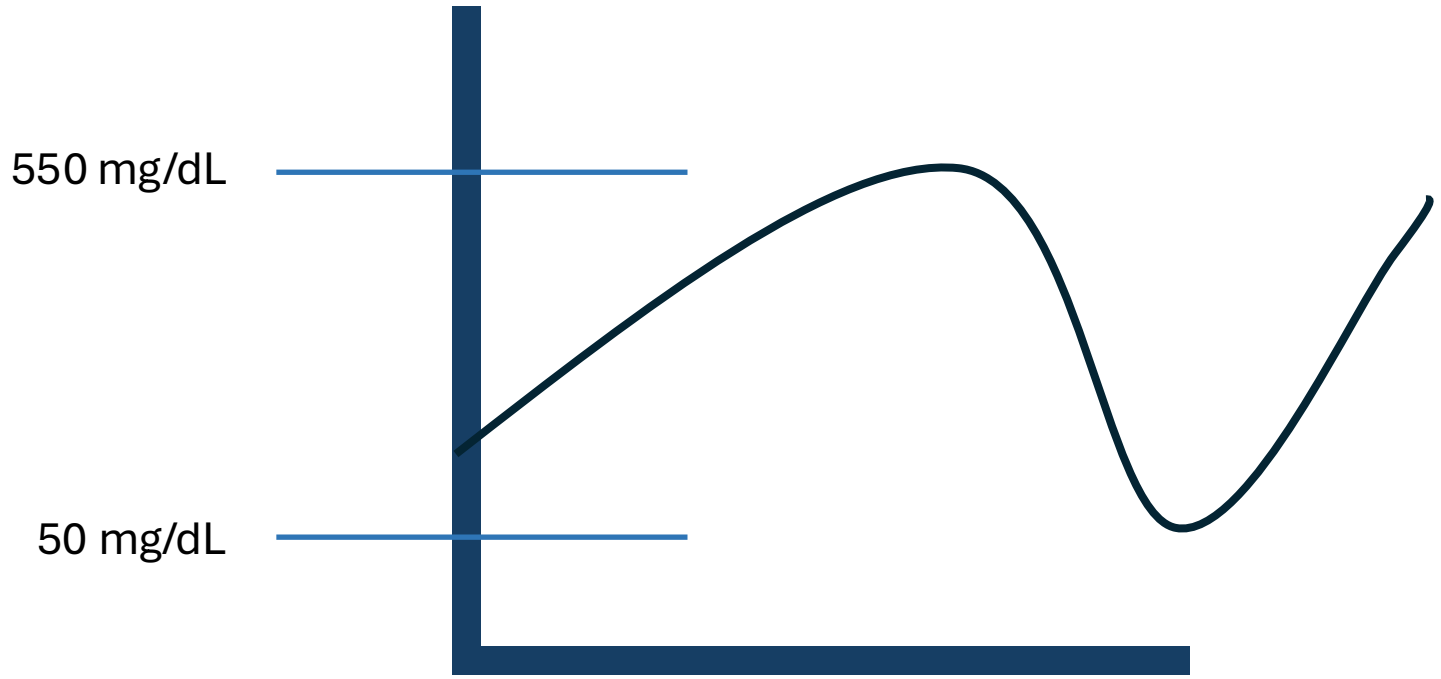
Biogenetix

Glucose Window

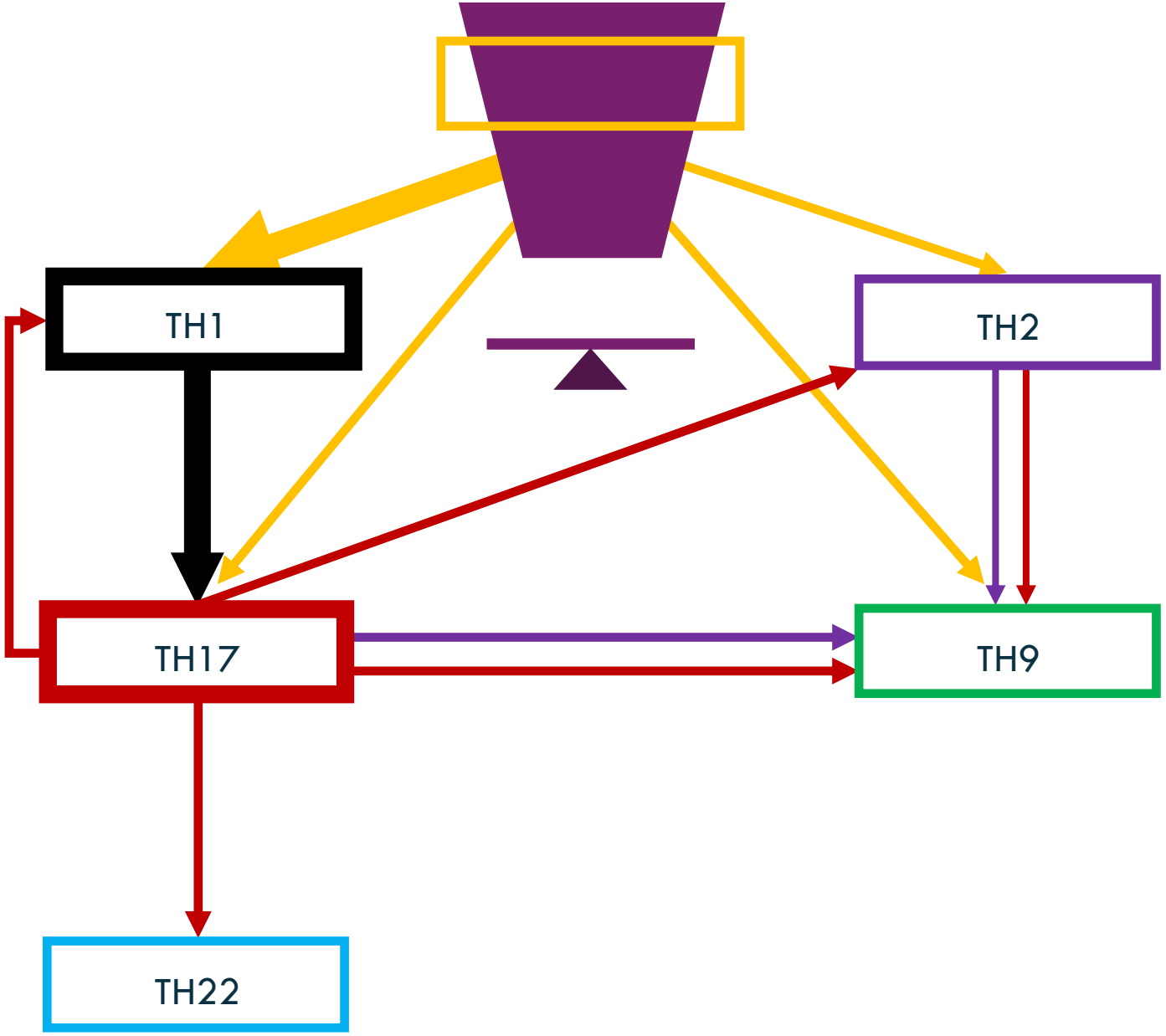


Biogenetix

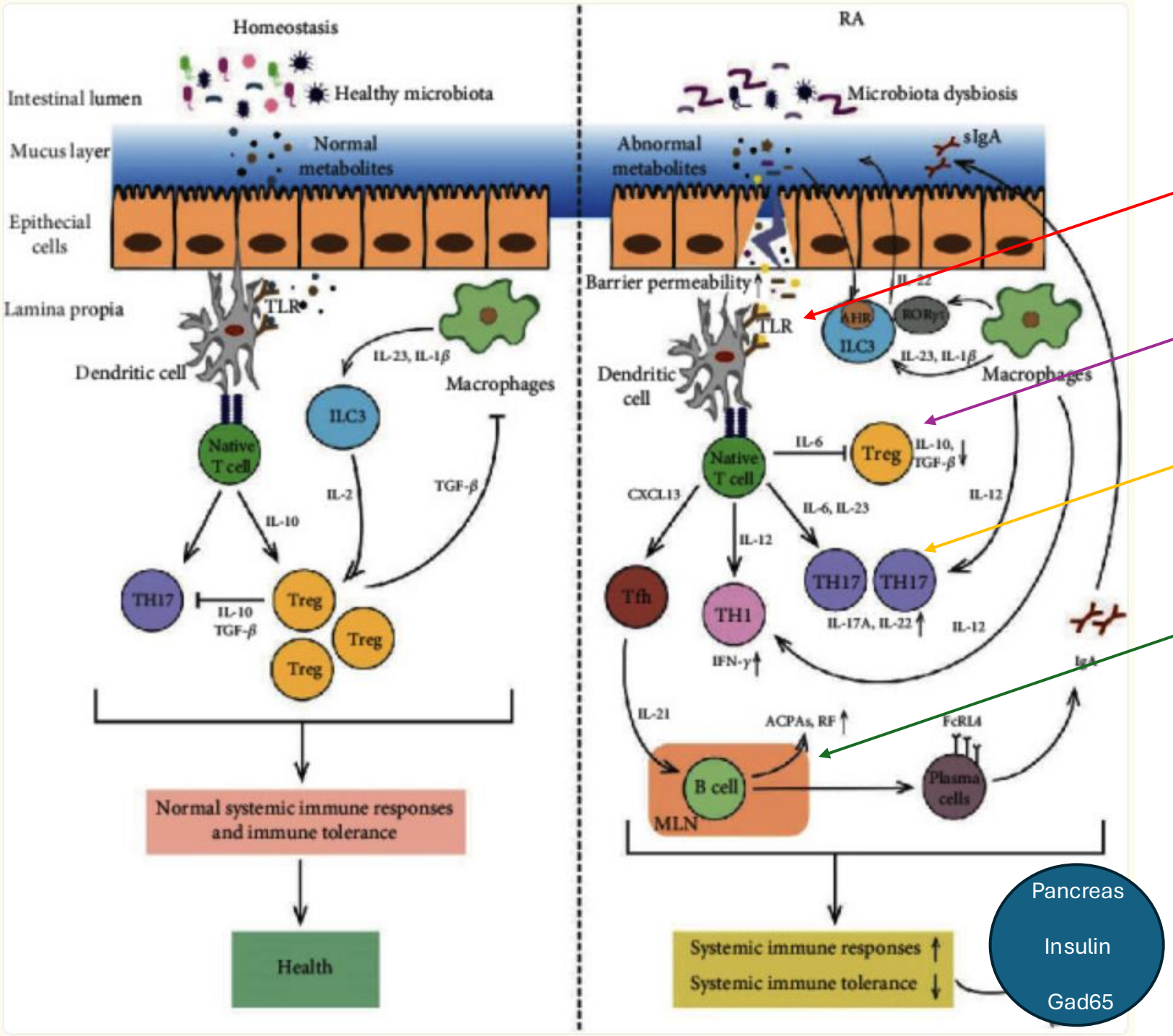
Glucose Window



Biogenetix



Biogenetix


Homeostasis
Intestinal lumen
Healthy microbiota
Mucus layer
Normal metabolites
Epithecial cells
Lamina propia
TLR
Dendritic cell
IL-23, IL-1β
Macrophages
ILC3
Native T cell
IL-2
TGF-β
IL-10
TH17
IL-10 TGF-β
Treg
Treg
Treg
Normal systemic immune responses and immune tolerance
Health
RA
Microbiota dysbiosis
Abnormal metabolites
sIgA
Barrier permeability
IL-22
AHR
RORγt
ILC3
TLR
Dendritic cell
IL-23, IL-1β
Macrophages
Native T cell
IL-6
Treg
IL-10, TGF-β
CXCL13
IL-6, IL-23
IL-12
IL-12
Tfh
TH1
IFN-γ
TH17
TH17
IL-17A, IL-22
IL-12
IgA
IL-21
ACPAs, RF
FcRL4
B cell
MLN
Plasma cells
Systemic immune responses
Systemic immune tolerance
Pancreas
Insulin
Gad65

Biogenetix

Diabetes Care. 2021 Oct 7;44(12):2738–2746. doi: 10.2337/dc20-2975

Characteristics of the Gut Microbiota and Metabolism in Patients With Latent Autoimmune Diabetes in Adults: A Case-Control Study

Yuanyuan Fang [1], Chenhong Zhang [2], Hongcai Shi [3], Wei Wei [1], Jing Shang [1], Ruizhi Zheng [1], Lu Yu [1], Pingping Wang [1], Junpeng Yang [1], Xinru Deng [1], Yun Zhang [1], Shasha Tang [1], Xiaoyang Shi [1], Yalei Liu [1], Huihui Yang [1], Qian Yuan [1], Rui Zhai [4], Huijuan Yuan [1,✉]

Author information Article notes Copyright and License information

PMCID: PMC8669532 PMID: 34620611

Patients with LADA had a significantly different structure and composition of the gut microbiota and their metabolites as well as a severe deficiency of short-chain fatty acid–producing bacteria. The gut microbiota structure of the patients with LADA was more similar to that of patients with type 1 diabetes who were positive for GAD antibody. We identified seven serum metabolite modules and eight fecal metabolite modules that differed between the LADA group and the other groups.

Biogenetix

Diabetes Care. 2021 Oct 7;44(12):2738–2746. doi: 10.2337/dc20-2975

Characteristics of the Gut Microbiota and Metabolism in Patients With Latent Autoimmune Diabetes in Adults: A Case-Control Study

Yuanyuan Fang [1], Chenhong Zhang [2], Hongcai Shi [3], Wei Wei [1], Jing Shang [1], Ruizhi Zheng [1], Lu Yu [1], Pingping

Remarkably, the gut microbiota of patients with LADA showed distinctive characteristics (e.g., significantly decreased abundance of *Faecalibacterium* spp., *Roseburia* spp., and *Blautia* spp.) compared with the other groups. These are short-chain fatty acid (SCFA)–producing bacteria. SCFA-producing bacteria are known to positively affect glucose metabolism; they strengthen the gut barrier function, reduce chronic inflammation, and modulate intestinal hormones to improve insulin sensitivity and reduce pancreatic autoimmunity (27–29). The structure and composition of the gut microbiota in patients with T1D and T2D are different from that in healthy subjects, with a decrease in the abundance of SCFA-producing bacteria (9,30). Our study found that patients with LADA show a severe deficiency in SCFA-producing bacteria compared not only with healthy subjects but also with patients with classic T1D and T2D. Accordingly, the severe SCFA-producing bacterial deficiency in the guts of patients with LADA may contribute to the occurrence and progression of the disease. However, further studies are needed to identify the key microbiota players and investigate their disease-linked mechanisms of action.

Biogenetix

Diabetes Care. 2021 Oct 7;44(12):2738–2746. doi: 10.2337/dc20-2975

Characteristics of the Gut Microbiota and Metabolism in Patients With Latent Autoimmune Diabetes in Adults: A Case-Control Study

Additionally, we found that the autoantibody GADA strongly associates with the structure and composition of the microbiome but negatively correlates with SCFA-producing bacteria. GADA is one of the most potent autoantigens involved in β-cell–specific autoimmunity. LADA is defined as a heterogeneous disease with respect to susceptibility genes, effects on autoimmunity, and phenotype. The potential causes of LADA involve heterogeneous pathways in the initiation of islet autoimmunity and heterogeneity in cellular responses (31). Interestingly, animal studies found that the SCFAs acetate and butyrate produced by gut microbes protected nonobese diabetic mice from insulitis and slowed the progression of diabetes, whereas butyrate in the diet improved regulatory T cell count and enhanced regulatory T cell function (32). Additionally, several cross-sectional studies have shown that the GADA titer correlates with the phenotypic heterogeneity of autoimmune diabetes, particularly in patients with LADA (33,34). Importantly, in the current study, the findings were similar. Therefore, we hypothesized that the gut microbiota may significantly affect the clinical classification and therapy of autoimmune diabetes. Our understanding of these diseases is insufficient and needs further exploration, and the gut microbiota may provide new insights.

Biogenetix

Notes:

Less Faecalibacterium:
↓ butyrate
↓ Treg signaling
↑ intestinal permeability
↑ immune activation

Biogenetix

Notes:

Usually decline alongside Faecalibacterium:

- **Roseburia**

Butyrate producer

Anti-inflammatory

Often ↓ in diabetes

- **Eubacterium rectale**

Major butyrate producer

Supporting gut barrier

Biogenetix

Notes:

Too many…

Bacteroides species:

- Increase lipopolysaccharide (LPS) exposure
- LPS → activates innate immune system (TLR4 signaling)
- TLR signaling is directly implicated in β-cell autoimmunity pathways (seen in LADA models)

Biogenetix

Notes:

Proteobacteria (typically ↑)
Ex.
•Escherichia
•Enterobacter

Often increased in dysbiosis

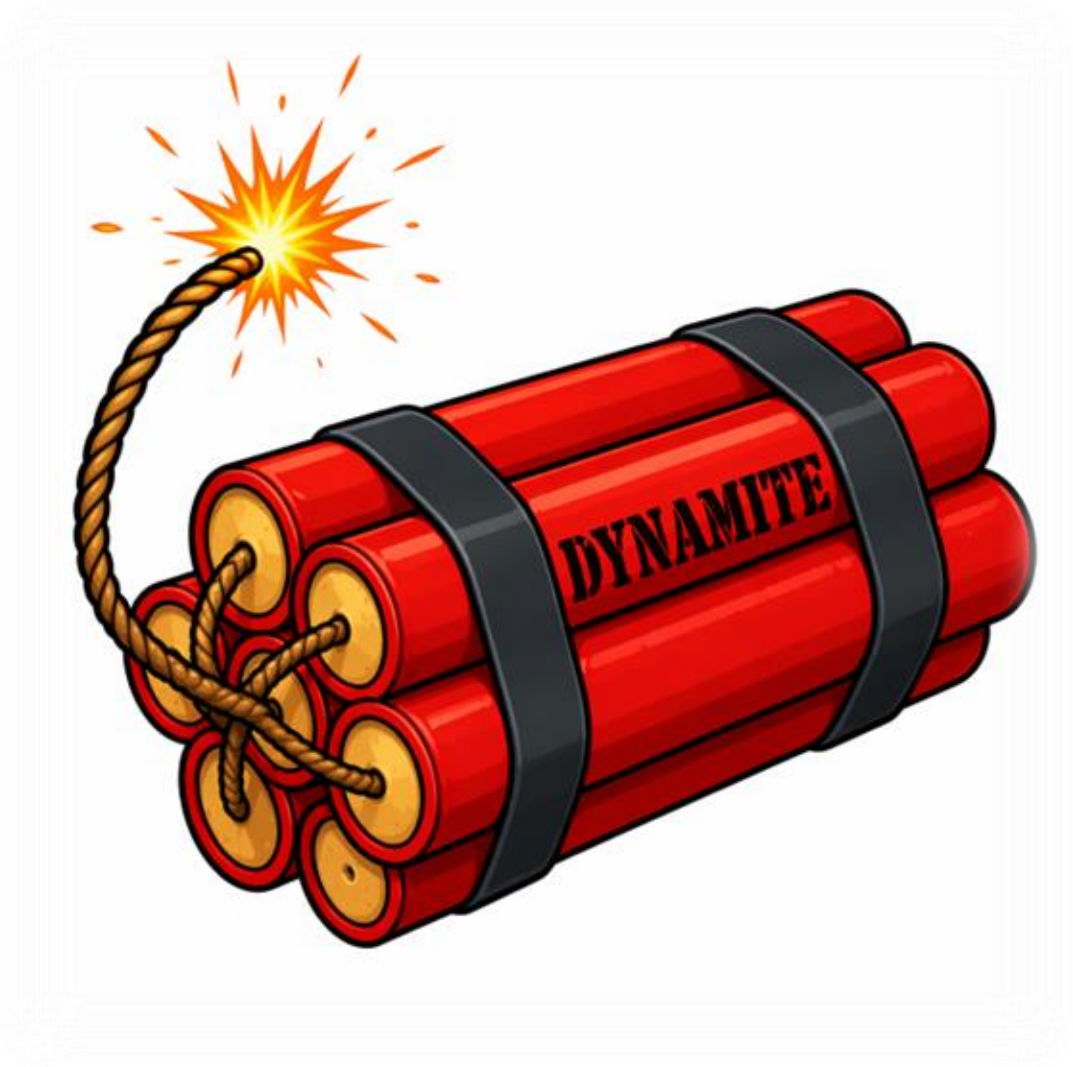
Many produce:
- endotoxins
- pro-inflammatory signals

Clinically:
•chronic inflammation
•autoimmune activation

Biogenetix

Drivers:

- SAD.
- Low fermentable fiber intake.
- C Section birth.
- Lack of breast feeding.
- Antibiotic use.
- Circadian rhythm distortion.
- Chronic stress.
- Sedentary lifestyle.
- Medications (ex: PPI’s).
- Toxic burden



Biogenetix

Influence of bisphenol A and its analogues on human gut microbiota composition and metabolic activity: Insights from an *in vitro* mod

Paulina Śr
Dominik P

Food contamination is a primary route of human exposure to bisphenols (BPs), which are known to affect gut microbiota (GM) and intestinal health. This study comprehensively assessed the impact of bisphenol A (BPA) and three of its substitutes—bisphenol S (BPS), bisphenol F (BPF), and tetramethyl bisphenol F (TMBPF, the monomer of valPure V70) — on the taxonomic and functional profile of human GM using an *in vitro* model. Human GM was acutely exposed to 1 mM concentrations of these BPs during a 48 h anaerobic cultivation. We first examined the effects of BPA, BPS, BPF, and TMBPF on GM taxonomic and metabolic profiles, mainly focusing on short-chain fatty acids (SCFAs) production. We then evaluated the degradation potential of these BPs by GM and its influence on their estrogenic activity. Finally, we assessed the impact of GM metabolites from BPs-exposed cultures on the viability of intestinal epithelial cells (Caco-2). BPA, BPS, and BPF severely disrupted GM taxonomic composition and metabolite profiles, significantly reducing SCFAs production. In contrast, TMBPF exhibited the least disruptive effects, suggesting it may be a safer alternative. Although the GM did not biotransform the BPs, bioadsorption occurred, with affinity correlating to hydrophobicity in the order of TMBPF > BPA>BPF>BPS. GM reduced the estrogenic activity of BPs primarily through bioadsorption. However, exposure of gut epithelial cells to Post-Culture Supernatants of BPA, BPF, and TMBPF significantly reduced Caco-2 cell viability, indicating the potential formation of harmful GM-derived metabolites and/or a depletion of beneficial GM metabolites.

Biogenetix

Major heavy metals and human gut microbiota composition: a systematic review with nutritional approach

Mahsa Rezazadegan[1], Bita Forootani[2], Yeganeh Hoveyda[3], Niloufar Rezazadegan[4] and Reza Amani[3*]

HMs exposure in different ways induces alterations that can lead to microbial dysbiosis. Changes in the microbiota composition and production of related metabolites may have a major impact on human health. There is a need to conduct future review studies with enough included studies on each HMs and more homogenous information. Our findings elucidate the necessity to support limiting environmental HMs contamination and the implementation of nutritional plans including more access to probiotics, prebiotics, antioxidant-rich foods, healthy and low-fat products, and treatment of micronutrients deficiency through national and international policies.

Biogenetix

Front Nutr. 2026 Feb 25;13:1783295. doi: 10.3389/fnut.2026.1783295

Microbiome–mycotoxin interactions and probiotic strategies: implications for gut health and cancer

Alice N Mafe

Author inf

PMCID: PMC

This structured, hypothesis-driven narrative review examines how mycotoxins, pervasive food contaminants, disrupt intestinal microbial balance, epithelial barrier integrity, xenobiotic metabolism, and carcinogenic signaling. Emerging evidence indicates that bidirectional interactions between the gut microbiome and mycotoxins modulate these effects, with microbial detoxification enzymes influencing toxin metabolism, immune responses, and epithelial resilience. However, the mechanistic understanding of microbiome–mycotoxin interplay remains incomplete, particularly regarding enzymatic pathways, microbial metabolites, and cancer-associated signaling. This review synthesizes recent (2016–2025) mechanistic studies on gut microbiota–mediated mycotoxin biotransformation, enzymatic detoxification, and probiotic interventions as strategies to mitigate mycotoxin-induced gut and cancer-related damage, focusing on key dietary toxins such as aflatoxin B_1, deoxynivalenol, zearalenone, ochratoxin A, fumonisins, and patulin. Evidence indicates that microbial enzymes, including de-epoxidases, lactonases, and reductases, contribute to mycotoxin biotransformation, while probiotics can enhance epithelial barrier function, restore microbial ecosystem balance, and modulate immune responses through toxin binding, competitive exclusion, and anti-inflammatory actions. The review further highlights the strain-specific nature of detoxification, the impact of mycotoxin-induced dysbiosis on short-chain fatty acid production and inflammation, and the modulation of cancer-related pathways including NF-κB, STAT3, and IL-6. Finally, it provides an integrated framework linking microbial mechanisms, bioactive microorganisms, and regulatory considerations, identifies critical knowledge gaps, and outlines mechanistically informed probiotic strategies for mitigating mycotoxin exposure and its associated health risks.

Biogenetix

From Exposure to Dysfunction: The Intestinal Toxicity of Per- and Polyfluoroalkyl Substances

by **Kashi Brunetti** [1], **Giulia Serena Galletti** [2], **Elisabetta Catalani** [3], **Davide Cervia** [2,*] and **Simona Del Quondam** [2,*]

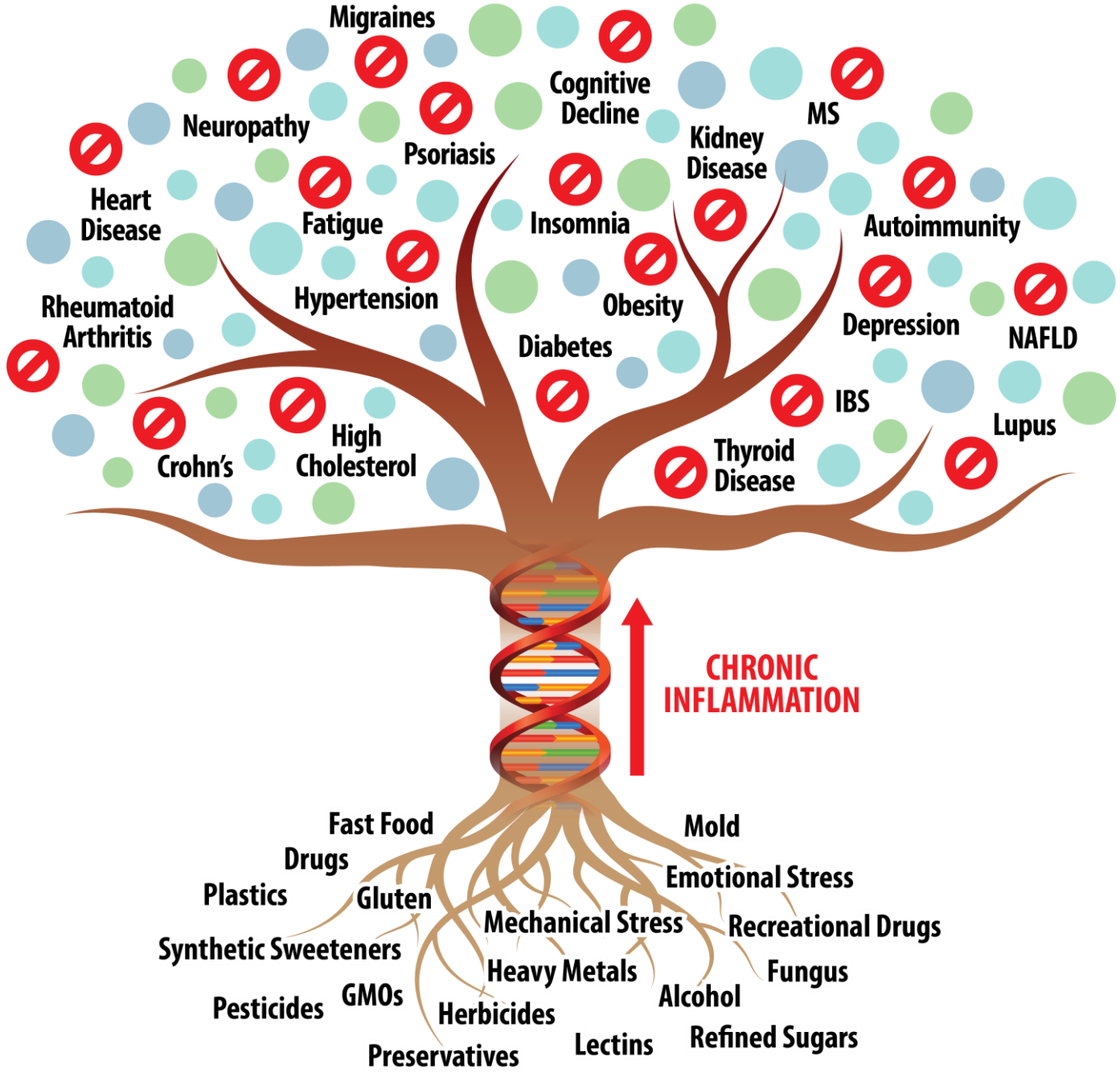
[1] ASST Fatebenefratelli Sacco Hospital, 20157 Milano, Italy

[2] Department for Innovation in Biological, Agro-Food and Forest Systems (DIBAF), University of Tuscia, 01100 Viterbo, Italy

[3] Department of Life Science, Health, and Health Professions, Link Campus University, 00165 Roma, Italy

Per- and Polyfluoroalkyl substances (PFAS) are highly persistent synthetic chemicals increasingly associated with adverse health outcomes. The gastrointestinal tract represents both a major route of exposure and a key target of PFAS toxicity. This review integrates updated evidence on how PFAS compromise intestinal homeostasis through interrelated structural, metabolic, and immunological mechanisms. PFAS disrupt epithelial integrity by down-regulating tight-junction proteins, inducing oxidative stress, and activating inflammasome signaling. Concurrently, metabolic reprogramming and PFAS-driven microbial dysbiosis contribute to barrier dysfunction and altered production of signal/metabolic molecules. These alterations may link environmental exposure to chronic intestinal inflammation and increase susceptibility to inflammatory bowel disease and related metabolic disorders. By synthesizing recent findings, key mechanistic gaps were highlighted also emphasizing the need for integrative experimental and translational studies to refine risk assessment in humans and develop preventive and therapeutic strategies.

Biogenetix


Migraines
Neuropathy
Psoriasis
Cognitive Decline
MS
Kidney Disease
Heart Disease
Fatigue
Insomnia
Autoimmunity
Rheumatoid Arthritis
Hypertension
Obesity
Depression
NAFLD
Diabetes
IBS
Lupus
Crohn's
High Cholesterol
Thyroid Disease
CHRONIC INFLAMMATION
Fast Food
Drugs
Plastics
Gluten
Synthetic Sweeteners
Pesticides
GMOs
Herbicides
Preservatives
Lectins
Refined Sugars
Heavy Metals
Mechanical Stress
Alcohol
Mold
Emotional Stress
Recreational Drugs
Fungus

Biogenetix