Type 2 Diabetes as a Stuck Program Mode of the Candida albicans Biochemical Computer

Glucose Harvesting Without Phase Transition

J. Craddock
Redacted Science Research Initiative
April 2026

Abstract

Type 2 diabetes mellitus (T2D) is characterized by progressive insulin resistance and beta cell failure, resulting in chronic hyperglycemia. The standard model attributes this deterioration to adiposity, sedentary behavior, and genetic predisposition, but does not fully explain why the deterioration is progressive and self-sustaining in patients who maintain adequate insulin production, or why certain interventions (bariatric surgery, extreme caloric restriction) produce remission in timeframes too short to reflect the structural changes the model invokes. This paper applies the biochemical computer framework (Craddock, 2026a; 2026b) to propose that T2D represents a stuck program mode in which the glucose harvesting capability of the commensal fungal symbiont Candida albicans runs continuously without phase transition. The organism possesses Hgt4, a membrane glucose sensor calibrated to approximately 5 mM human blood glucose. Its colonization measurably alters GLP-1, GIP, and insulin levels (Peroumal et al., 2022). The framework proposes that the modern dietary environment, providing effectively unlimited glucose, prevents the substrate shift signal that would normally advance the organism's program to the next phase. The resulting continuous glucose draw produces the progressive insulin resistance and eventual beta cell failure observed clinically. Five testable predictions are presented, including proposed studies correlating organism density with insulin resistance severity and differential therapeutic response.

Keywords: Candida albicans, type 2 diabetes, glucose sensing, Hgt4, insulin resistance, GLP-1, stuck program mode, biochemical computer, colonization density, quorum sensing, dietary antifungal, bariatric surgery, semaglutide, Homo Candidus

I. Introduction

The central pathology of type 2 diabetes is progressive insulin resistance followed by beta cell failure, resulting in chronic hyperglycemia. The standard model describes a metabolic deterioration driven by adiposity, sedentary behavior, and genetic predisposition. What the standard model does not explain is why the deterioration is progressive and self-sustaining in patients who maintain adequate insulin production, or why the condition responds to interventions such as bariatric surgery and extreme caloric restriction in timeframes too short to reflect the structural changes the model invokes.

The biochemical computer framework (Craddock, 2026a; 2026b) describes Candida albicans as a coevolved symbiont operating a phased program within the mammalian host. This universal commensal program was refined over tens of thousands of generations within the

Homo candidus phenotype (Craddock, 2026b): a symbiont-managed host with different cardiac architecture, active pituitary governance, a social infrastructure providing dietary protocol enforcement and communal transition cues, and a physiology calibrated to the organism's operational requirements. Each phase employs specific organism capabilities to manage host physiology for purposes that serve the symbiotic relationship. When the program functions correctly, phases cycle: the organism runs a capability, achieves the metabolic or physiological condition that phase requires, receives or generates the transition signal, and advances. Modern Homo sapiens carries the organism and its program but lacks the physiological and social architecture within which the program was designed to operate. When the transition signal fails, whether through the absence of Homo candidus social infrastructure, modern dietary conditions that prevent substrate depletion, or loss of the managed physiology the program expects, the capability continues running indefinitely. The host phenotype of that indefinite operation is what conventional medicine classifies as chronic disease.

This paper identifies a candidate driver of T2D that no current model accounts for: a resident organism with a glucose sensor calibrated to human blood glucose, consuming glucose directly and continuously from the host's circulating supply, and modulating the hormonal systems that govern glucose regulation.

II. The Mechanism

C. albicans possesses Hgt4, a membrane glucose sensor calibrated to approximately 5 mM, the concentration maintained in healthy human serum (Brown et al., 2006). This is not a passive transporter. It is a sensing instrument whose calibration point matches the host's glucose homeostatic target with precision that is difficult to attribute to coincidence and straightforward to attribute to coevolutionary tuning. When glucose is present at or above this threshold, the organism feeds. The glucose draw is invisible within normal metabolic noise because the volume consumed by a commensal-density population is small relative to total circulating glucose. The host does not notice the tax.

Hgt4 feeds into the cAMP-PKA signaling cascade that governs the organism's primary morphogenetic decisions (Maidan et al., 2005). Glucose availability is not merely a fuel input for C. albicans. It is an environmental signal governing tissue engagement. The organism reads glucose concentration as an instruction set: above threshold, remain in yeast form and feed quietly; below threshold, evaluate whether conditions warrant transition to the next operational mode. The glucose channel described in the companion paper (Craddock, 2026b, Section 5.10) is the organism's metabolic baseline, the commensal configuration in which the organism feeds from the same table as the host.

The organism's interaction with the host glucose economy extends beyond direct consumption. Peroumal et al. (2022) demonstrated that C. albicans colonization of the murine gut measurably alters levels of GLP-1, GIP, insulin, and other metabolic hormones. The organism is not simply eating glucose. It is modulating the hormonal systems that govern glucose regulation. The incretin system, the target of semaglutide and tirzepatide, is confirmed to be within the organism's signaling reach. [*It's a symbiont with cross-kingdom sensing and signaling*]

Hgt4 calibration at approximately 5 mM represents the organism's commensal sensing threshold, not a fixed operational ceiling. At elevated colonization densities and advanced

program states, the organism's metabolic demands increase with population size and tissue engagement. The framework predicts that the organism can shift its effective glucose operating range upward, not by recalibrating the sensor itself but by modulating host hepatic glucose output, incretin signaling, and insulin sensitivity to maintain a higher circulating glucose concentration that serves expanded operational requirements. The T2D patient with a fasting glucose of 200 mg/dL is not experiencing a failure of the organism to maintain its setpoint. The setpoint has moved.

The Randle cycle provides an additional mechanism. The organism's lipid metabolism via CYP52 fatty acid processing can simultaneously inhibit cellular glucose uptake at the metabolic level (Randle et al., 1963). When this channel is active, the host cell faces a dual block: glucose is both consumed by the organism in the extracellular environment and excluded from the cell interior by fatty acid oxidation products competing for mitochondrial substrate priority. The glucose is present in circulation. The insulin is present. The doors are locked from both sides. [*This condition recurs throughout the Homo Candidus timeline, likely composing more than half of the overall program. The difference is that Homo Candidus is built for it*]

III. The Stuck State

Within the phased program model, glucose harvesting represents an early or intermediate program stage. The organism draws host glucose to fuel its own activity during a phase whose metabolic requirements are primarily carbohydrate-driven. In a functioning program, this phase is temporary. Glucose conditions shift, either through dietary change, seasonal variation, fasting, or the organism's own metabolic activity drawing glucose below the Hgt4 threshold, and the program advances to the next substrate priority: lipids, amino acids, ketones, or the tissue-level engagement described in the substrate multiplexing architecture (Craddock, 2026b, Section 5.10).

The stuck state occurs when the transition signal never arrives. In the modern North American dietary environment, glucose is not just available. It is inescapable. High-fructose corn syrup is in bread, ketchup, salad dressing, and yogurt. A single fast food meal can deliver more glycemic load than an ancestral human encountered in a day. The average American consumes over 60 pounds of added sugar per year, on top of the refined carbohydrates that convert to glucose before they reach the ileum. Processed food does not just deliver continuous high-glycemic substrate. It delivers it in forms the organism's Hgt4 sensor was never calibrated for: rapid, massive, unrelenting. The host never enters the sustained glucose scarcity that would trigger the organism's substrate shift. The transition signal is not delayed. It is buried under a permanent flood. The glucose harvesting phase runs indefinitely because the environment that would end it no longer exists in the standard American grocery cart.

The low-fat dietary movement that dominated American nutritional guidance from the 1980s through the 2000s accelerated this precisely. When manufacturers removed fat from processed foods, they replaced it with sugar and refined carbohydrates to preserve palatability. The result was a generation taught that fat was the enemy while consuming unprecedented quantities of the exact substrate the organism's glucose harvesting program requires to maintain itself. Dietary guidance designed to prevent heart disease may have optimized the conditions for a stuck metabolic program that drives both diabetes and obesity. The organism did not need to evolve a strategy for the modern diet. The modern diet was engineered to feed it.

The host consequences are progressive. The organism's continuous glucose draw creates a sustained, unrecognized demand on circulating glucose. The host's pancreatic beta cells compensate by increasing insulin output. Peripheral tissues, receiving insulin signals that do not correspond to their own glucose utilization patterns, because a portion of circulating glucose is being consumed by an organism no one is measuring, develop insulin resistance. The resistance is not a malfunction. It is an appropriate cellular response to a signaling mismatch: the insulin says "take up glucose," but the glucose that should be available after uptake is partially absent, consumed by the organism before the cell can use it.

Over years, beta cells fail from sustained overwork [*overclock anything and you are reducing its lifetime*]. The progression from insulin resistance to beta cell exhaustion to frank diabetes is the host's metabolic system degrading under a demand it was never designed to sustain indefinitely. The organism is not causing diabetes. It is running a glucose management program that was designed to be temporary, and the modern dietary environment prevents the transition signal from firing.

The quorum sensing dimension reinforces the stuck state at the population level. The organism's density-dependent coordination through farnesol and tyrosol (Hornby et al., 2001) maintains program coherence above a population threshold. As glucose abundance supports organism expansion, colonization density increases, strengthening the quorum-mediated maintenance of the glucose harvesting mode. The stuck state is self-reinforcing: more glucose availability produces more organism, which consumes more glucose, which signals the host to produce more insulin, which fails to address the actual draw. [*In process controls, we call that a runaway process*]

IV. The Persistence Problem Resolved

The standard clinical puzzle in T2D is why insulin resistance develops progressively in patients with adequate, even elevated, insulin production. The pancreas is working. The insulin is present. Why does it not work?

The framework provides the missing variable: a consumer of glucose that operates outside the insulin signaling system entirely. Hgt4 does not respond to insulin. It reads glucose directly. The organism's draw continues regardless of how much insulin the host produces. Every compensatory increase in insulin output addresses the wrong problem. The host is trying to force glucose into cells while the organism is removing glucose from circulation through a channel insulin cannot regulate. The mismatch is invisible to every standard metabolic assay because no one is measuring organism density or metabolic activity as a variable in glucose homeostasis.

This resolves the progressive nature of the disease. The organism does not reduce its glucose draw as the host deteriorates. If anything, increased colonization density over time, driven by the very glucose abundance that prevents phase transition, increases the draw. The disease is progressive because the driver is progressive: more organism, more consumption, more compensatory demand on beta cells, more resistance, more failure.

It also resolves a secondary puzzle: why fasting glucose in many pre-diabetic and early T2D patients trends toward but rarely drops significantly below approximately 90-100 mg/dL (5.0-5.6 mM). This range corresponds to the Hgt4 calibration point. The organism's own glucose consumption establishes a metabolic floor at its sensor's operating threshold. The host's fasting

glucose reflects not just hepatic glucose output and peripheral uptake, but the organism's draw stabilizing circulating glucose at the level its sensor is tuned to detect.

V. Clustering Evidence

T2D prevalence shows demographic patterns that resist complete explanation through diet, lifestyle, and known genetic risk factors. Indigenous, African American, Pacific Islander, and South Asian populations carry substantially elevated risk that persists after controlling for socioeconomic and dietary variables. Within the framework, these populations represent evolutionary lineages with different organism-host equilibria, shaped by different dietary histories, different environmental exposures, and different coevolutionary trajectories through the saline oscillation period described in the companion paper (Craddock, 2026b). Colonization density, organism programming variation (phenotypic switching states, epigenetic memory, and bet hedging strategies shaped by different coevolutionary histories with different host populations), and host-side genetic variation in the receptor systems the organism exploits (endocannabinoid, incretin, HPA axis) would all contribute to population-level prevalence differences that current models attribute to incompletely characterized genetic risk.

The post-1970s acceleration of T2D prevalence globally is consistent with antibiotic-era disruption of the gut mycobiome altering organism population dynamics. Broad-spectrum antibiotics eliminate bacterial competitors that constrain C. albicans density in the gut (Noverr et al., 2004).

The numbers: In 2024, the overall antibiotic prescribing rate was 752 prescriptions per 1,000 population (Centers for Disease Control and Prevention, 2026). With a U.S. population of roughly 335 million, that's approximately 252 million outpatient antibiotic prescriptions per year. The ratio of broad- to narrow-spectrum antibiotics was 1.49 in 2016 (Barlam, T. F., et al., 2021) meaning broad-spectrum prescriptions outnumber narrow-spectrum. That ratio puts broad-spectrum at roughly 60% of total prescriptions, or about 150 million broad-spectrum antibiotic courses per year in the U.S. alone.

A quarter billion antibiotic prescriptions a year. 150 million of them broad-spectrum. Every single one eliminating bacterial competitors that constrain C. albicans density in the gut. Quite simply put, a population-level mycobiome disruption event running continuously since the 1950s.

Reduced bacterial competition allows organism expansion. Expanded organism populations consume more glucose. The population-level result is increased T2D incidence in the decades following mass antibiotic adoption, a timeline that matches the observed epidemiology.

Familial clustering of T2D beyond genetic heritability is consistent with vertical transmission of organism populations from parent to child, establishing colonization patterns in early life that persist into adulthood and carry their associated metabolic burden forward.

The geographic clustering of T2D also presents a pattern consistent with the framework. Populations with traditional diets high in natural antifungal compounds, including coconut-based cuisines (lauric acid, caprylic acid), garlic-heavy Mediterranean and Asian diets (allicin), and cinnamon-utilizing food traditions (cinnamaldehyde), may historically have maintained organism density below the threshold at which the glucose harvesting program becomes metabolically significant. The transition to processed Western diets eliminates these dietary antifungal inputs

while simultaneously providing unlimited glucose substrate, a dual shift that the framework predicts would accelerate T2D emergence.

VI. Unfreezing: Therapeutic Implications

If the stuck state is maintained by continuous glucose availability preventing the organism's phase transition, then the most direct intervention is providing the transition signal: sustained glucose reduction sufficient for Hgt4 to register a substrate shift.

Dietary Carbohydrate Restriction

The clinical literature on low-carbohydrate and ketogenic diets in T2D shows consistent improvement in glycemic control, insulin sensitivity, and in some cases complete remission (Hallberg et al., 2018). The framework interprets this as providing the transition signal the organism has been waiting for. Glucose drops. Hgt4 registers the shift. The program can advance to the next substrate priority, and the glucose harvesting mode releases. The relapse that commonly follows dietary relaxation is the organism reverting to glucose harvesting mode when glucose abundance returns.

Bariatric Surgery

Bariatric surgery provides the strongest evidence for the stuck-program interpretation. T2D remission frequently occurs within days of surgery, well before significant weight loss (Rubino et al., 2006). This is not a caloric effect. It is an acute, massive disruption of the organism's primary habitat. The gut environment changes overnight. Anatomical rearrangement alters transit time, nutrient absorption patterns, bile acid circulation, and the physical environment in which the organism's gut population resides. The organism's operating context shifts so dramatically that the glucose harvesting program cannot maintain itself. The remission precedes the weight loss because the driver was never the weight. It was the organism's program state.

GLP-1 Receptor Agonists

Semaglutide and tirzepatide produce dramatic improvements in glycemic control and body weight by acting on a receptor that Peroumal et al. (2022) demonstrated is within the organism's signaling reach. The framework interprets their efficacy as pharmacological jamming of the sensing channel the organism uses for metabolic state assessment. The organism reads GLP-1 signaling as part of its evaluation of whether the host is in a fed or fasting state. Sustained GLP-1 agonism provides a continuous signal that overrides the organism's own assessment, disrupting the stuck state through the sensing layer rather than through substrate change.

Antifungal Pressure

The framework predicts that reducing organism density below the quorum sensing threshold maintaining the glucose harvesting mode should allow the program to release independently of dietary change. Pharmaceutical antifungals (fluconazole, azoles) or dietary

antifungals (coconut oil, garlic, cinnamon) provide this pressure. Dietary antifungals are of particular interest because they are accessible without prescription, carry no significant risk at dietary doses, and have been present in human food traditions for millennia. Their inconsistent effects across individuals is itself predicted by the framework: variable organism density and morphological state produces variable response to unmeasured antifungal pressure.

Combined Intervention

The strongest therapeutic prediction: combined substrate change (carbohydrate restriction) plus antifungal pressure (pharmaceutical or dietary) plus sustained duration should outperform any single intervention. Substrate change provides the transition signal. Antifungal pressure reduces the organism's capacity to resist the transition. Duration allows the organism time to register new conditions, lose quorum coordination, and release the stuck program. No current clinical trial tests this combination because no one is measuring organism density as a variable in T2D management.

VII. Testable Predictions

Prediction D1: Oral and fecal C. albicans colonization density correlates positively with insulin resistance severity (HOMA-IR) in pre-diabetic and T2D populations, after controlling for BMI and dietary variables.

Prediction D2: Antifungal intervention (pharmaceutical or dietary) combined with carbohydrate restriction produces faster and more durable T2D remission than carbohydrate restriction alone. The magnitude of additional benefit correlates with baseline organism density.

Prediction D3: Post-bariatric patients who maintain T2D remission long-term show different fecal mycobiome trajectories (specifically, sustained reduction in C. albicans density) compared to those who relapse. Mycobiome shift precedes and predicts metabolic improvement timing.

Prediction D4: The fasting glucose floor in T2D patients with documented C. albicans colonization trends toward the Hgt4 calibration point (approximately 5 mM / 90 mg/dL) rather than toward hypoglycemic ranges, reflecting the organism's own glucose consumption establishing a metabolic floor. This pattern should be distinguishable from the glucose floor in T2D patients on insulin therapy, where iatrogenic hypoglycemia can drive glucose below the organism's operating threshold.

Prediction D5: Population-level epidemiological data on dietary antifungal intake (coconut oil, garlic, cinnamon, lemon herb, etc consumption by region) shows an inverse correlation with T2D prevalence after controlling for total caloric intake and macronutrient composition. Populations with high traditional dietary antifungal intake carry lower T2D burden than predicted by their carbohydrate consumption alone.

VIII. Limitations

The framework does not propose that C. albicans is the sole driver of T2D. Genetic predisposition, adiposity, activity levels, and metabolic syndrome contribute through pathways

independent of organism activity. The claim is narrower: that organism-mediated glucose draw represents an unrecognized variable whose inclusion improves the explanatory power of existing models, particularly for the progressive and self-sustaining nature of insulin resistance.

The Hgt4 calibration to human blood glucose, while striking, has been demonstrated in vitro. Whether the in vivo glucose draw by commensal-density C. albicans populations is metabolically significant at the whole-organism level remains unquantified. The framework predicts that it is, but the magnitude of the effect relative to total glucose flux requires direct measurement. In its much more complex native habitat, *C. albicans* is multiplexing hundreds of inputs and outputs. This calibration point moves with colonization density.

The dietary antifungal dose-response relationship is entirely uncharacterized. The prediction that dietary antifungals reduce organism density sufficiently to affect T2D outcomes is logically derived from the framework but has no supporting clinical data [*because big pharma cannot profit from such things, not because it is not worthy of investigation]*. The gap between documented antifungal properties of these compounds and demonstrated clinical effect in T2D remains open.

This paper is part of a series applying the biochemical computer framework to chronic disease. The companion umbrella paper (Craddock, 20263) describes the stuck-program model and the selection methodology. The foundational framework is described in Craddock (2026a) and Craddock (2026b).

References

Barlam, T. F., et al. (2021). Changes in US Outpatient Antibiotic Prescriptions from 2011-2016. Clinical Infectious Diseases, 73(3), e682-e687. https://doi.org/10.1093/cid/ciaa1896 (PMC8078491)

Brown, A. J., et al. (2006). Oxygenation and nutrient status sensing by Candida albicans. Molecular Microbiology, 65(6), 1421-1434.

Centers for Disease Control and Prevention. (2026). Antibiotic Use and Stewardship in the United States, 2025 Update: Progress and Opportunities. https://www.cdc.gov/antibiotic-use/hcp/data-research/stewardship-report.html

Craddock, J. (2026a). Candida albicans as a Biochemical Computer. Zenodo. https://doi.org/10.5281/zenodo.19502218

Craddock, J. (2026b). The Saline Oscillation Hypothesis. Zenodo. https://doi.org/10.5281/zenodo.19557740

Craddock, J. (2026c). Chronic Disease as Stuck Program Modes of the Candida albicans Biochemical Computer, https://doi.org/10.5281/zenodo.19582792

Craddock, J. (2013). Personal case study documentation. Unpublished manuscript.

Hallberg, S. J., et al. (2018). Effectiveness and safety of a novel care model for the management of type 2 diabetes at 1 year. Diabetes Therapy, 9(2), 583-612.

Hornby, J. M., et al. (2001). Quorum sensing in the dimorphic fungus Candida albicans is mediated by farnesol. Applied and Environmental Microbiology, 67(7), 2982-2992.

Maidan, M. M., et al. (2005). The G protein-coupled receptor Gpr1 and the Galpha protein Gpa2 act through the cAMP-protein kinase A pathway to induce morphogenesis in Candida albicans. Molecular Biology of the Cell, 16(4), 1971-1986.

Noverr, M. C., et al. (2004). Development of an in vitro model of Candida albicans and bacterial interactions in the context of antibiotic-mediated dysbiosis. Infection and Immunity, 72(11), 6206-6210.

Peroumal, D., et al. (2022). Commensal fungus Candida albicans maintains a long-term mutualistic relationship with the host to modulate gut microbiota and metabolism. Microbiology Spectrum, 10(3), e01345-22.

Randle, P. J., et al. (1963). The glucose fatty-acid cycle. Its role in insulin sensitivity and the metabolic disturbances of diabetes mellitus. Lancet, 281(7285), 785-789.

Rubino, F., et al. (2006). The mechanism of diabetes control after gastrointestinal bypass surgery reveals a role of the proximal small intestine in the pathophysiology of type 2 diabetes. Annals of Surgery, 244(5), 741-749.