

Nutrient-Limited Operational Strategies for Microbial Production of Biochemicals

Subjects: **Biotechnology & Applied Microbiology**

Contributor: Hemshikha Rajpurohit , Mark A. Eiteman

Limiting an essential nutrient has a profound impact on microbial growth. The notion of growth under limited conditions was first described using simple Monod kinetics proposed in the 1940s. Different operational modes (chemostat, fed-batch processes) were soon developed to address questions related to microbial physiology and cell maintenance and to enhance product formation. With more recent developments of metabolic engineering and systems biology, as well as high-throughput approaches, the focus of current engineers and applied microbiologists has shifted from these fundamental biochemical processes.

chemostat

Escherichia coli

fed-batch

metabolic engineering

1. Introduction

Biochemical processes use enzymes or microorganisms as catalysts to convert a substrate to a product, and are analogous to chemical processes in terms of basic design parameters including stoichiometry, energy relationships, kinetics, and equilibria [1]. Design and implementation of microbial bioprocesses additionally require an understanding of metabolic activity and its effect on growth and product formation as well as factors which influence organisms and these cellular reactions.

Operationally, microbial bioprocesses are often classified by the strategies used for substrate addition and product removal (**Figure 1**). In a *batch* process, the carbon-substrate/energy source as well as other nutrients are at the onset charged into the reactor, and product is harvested at the conclusion of the process, typically when the carbon source is depleted. Although material can be introduced into the reactor for oxygenation, pH control, foaming, and other minor reasons, a batch process is considered a closed system. Other operations in contrast are implemented as distinctly open systems. A *chemostat* occurs when the flowrates of a nutrient-containing feed and an effluent of products and residual nutrients are equal [2]. The dilution rate (D) normalizes that feed rate F by the constant volume of the system V ($D = F/V$). In addition, any of several semi-continuous *fed-batch* processes involve the feeding of nutrients often without product withdrawal [3][4]. Variations on these basic operational modes include a *turbidostat* [5][6], wherein the feed rate is controlled to maintain a constant cell density, and an *accelerostat* [7], wherein the dilution rate is changed progressively and slowly to maintain prolonged pseudo-steady-state conditions over a range of growth rates. A two-reactor cascade in which biomass formation and product formation are spatially distinct is another novel continuous operational mode which increases volumetric productivity of intracellular products [8]. Several of the methods for continuous cultivation have been critically compared for their utility in high-resolution characterization of metabolism [9].

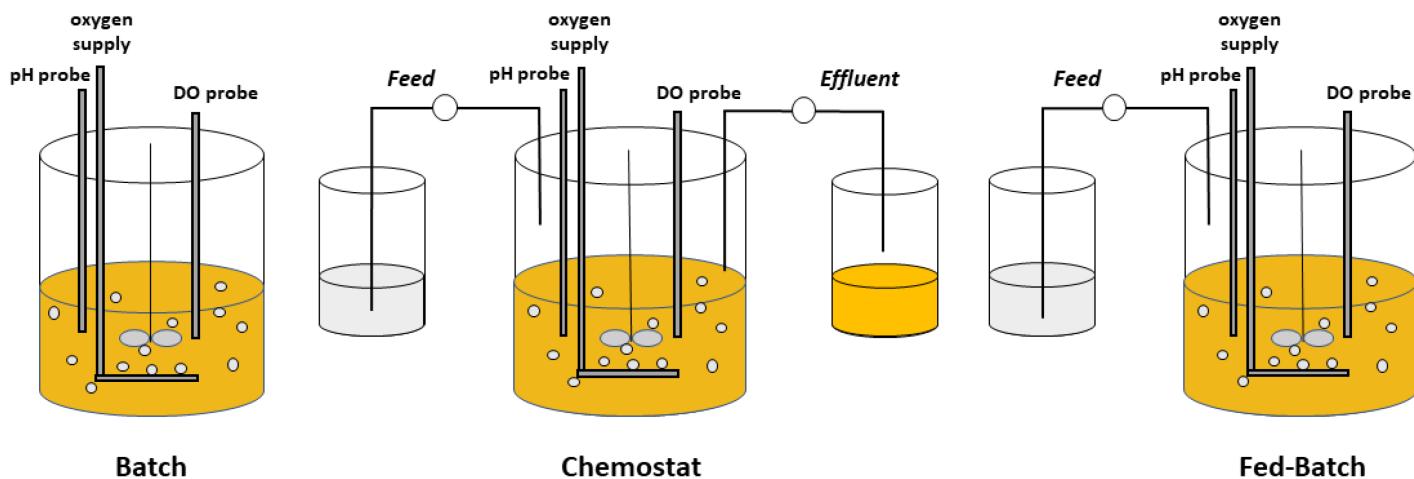


Figure 1. The three general modes of fermentation operation: batch, continuous, and fed-batch processes.

2. Chemostat Processes

Originally developed to study bacterial cultures for a long duration [10], the chemostat maintains the cell growth rate lower than the maximum specific growth rate (μ_{max}). The chemostat is an indispensable tool to investigate how growth rate affects cellular processes and how cells or consortia of cells evolve in response to nutrient limitation as a selective pressure [11], though it is particularly difficult to operate for microbes which grow on walls or aggregate such as filamentous fungi [12]. One can dictate which nutrient limits cell growth (e.g., C, N, P, etc.) merely by adjusting the medium composition [13]. Mean residence time in the chemostat is equal to the inverse of the dilution rate $1/D$ [14]. If the selected dilution rate is lower than the maximum specific growth rate (μ_{max}) at the given environmental conditions, then a steady-state is normally achieved: the growth rate the microbes experience (μ) becomes equal to D , and the limiting nutrient attains a low, constant concentration (e.g., Equation (2)). If the dilution rate approaches or exceeds the maximum specific growth rate, then the cells cannot grow as quickly as the medium is withdrawn, leading to net loss of cells and culture washout. Because chemostat processes maintain a high biomass concentration compared to batch processes, a chemostat achieves a fairly high product and biomass volumetric productivity or space-time yield. Unfortunately, a continuous operation has an increased prospect of contamination or genetic drift during a prolonged biological process because of competition for the limiting nutrients [15][16][17]. Indeed, given the likelihood for mutations, a chemostat does not strictly reach a physiological “steady-state” [18]. In fact, at a long time-scale, the chemostat is an invaluable tool to evolve strains with greater substrate affinity [19][20][21][22], with relieved auxotrophy [23] or with a gain of substrate utilization [24]. Different limiting nutrients (e.g., N-limited versus Fe-limited) change the profile of mutations that occur, and the rate of mutations [25]. Nutrient-limited conditions also encourage phenotypic heterogeneity [26].

Care must be made in medium design for nutrient-limited processes because cells use a portion of the carbon/energy source for maintenance and also often to accumulate storage products. Therefore, the proportion of nutrients needed for a growth limitation itself depends on the growth rate, and dual-nutrient-limited regions are possible [27][28][29][30]. One fixed medium composition can lead to C-limited growth at a low dilution rate, dual C/N-

limited growth at an intermediate dilution rate, and N-limited growth at a high dilution rate [28]. Nevertheless, operation of a chemostat is useful to identify optimal conditions for fed-batch operations for biochemical generation (e.g., [31]), and therefore, the chemostat is an indispensable tool for bioprocess development.

3. Fed-Batch Processes

Fed-batch is a semi-continuous process in which one or more nutrients are supplied to the growing microbial culture with or without periodic withdrawal [32]. A fed-batch process can be implemented so that nutrients are intermittently added to the reactor and are always in excess from the perspective of the cells (i.e., relative to K_S), resulting in a process physiologically similar to a batch process. Such a culture allows prolonged growth at μ_{max} and can be considered a non-limited-nutrient fed-batch or a *repeated fed-batch*, although the latter term is often applied to a fill-and-draw process in which a portion of culture is periodically withdrawn and fresh nutrients supplied [33]. This type of fed-batch process is particularly beneficial in cases for which a high concentration of a particular nutrient inhibits microbial growth, since that nutrient can be maintained below its inhibitory concentration while achieving a near maximal growth rate [34][35]. Alternatively, a *nutrient-starved fed-batch* is a common process which involves growing a culture first with ample nutrients, and then in a subsequent cycle, supplying the culture with a feed in which at least one essential nutrient is absent. In such a nutrient-starved process, often the carbon/energy source is supplied to satisfy the cultures' maintenance requirement, while the *absence* of another nutrient (e.g., N) prevents growth [36]. In this case, cells cannot continue growing without the missing essential nutrient(s), but they often remain able to metabolize the supplied carbon source and accumulate storage products or transform that carbon source into a desired product [37][38][39][40].

A fed-batch process can also be implemented as a *nutrient-limited fed-batch*, which like a chemostat necessitates that a nutrient feed is introduced at a rate lower than the growing culture can maximally metabolize. In contrast to a nutrient-starved process, though, the culture is growing continuously, and the rate of introducing the limiting nutrient controls the metabolic and growth rates [41]. Because no effluent typically exists, cells and products remain in the culture, enabling fed-batch processes to achieve high cell density and product concentration. A quasi-steady state is achieved in nutrient-limited fed-batch cultures [41].

Nutrient-limited fed-batch processes can be operated in several ways. For example, the growth-limiting nutrient can be introduced into the culture at a constant rate or at an exponential rate [32]. When a growth-limiting nutrient is fed at a fixed rate (F_c), the growth rate of the culture decreases with time [32][42]. In an exponential fed-batch process the nutrients are fed at an exponentially increasing rate to match the needs of the growing culture, to maintain a constant growth rate μ_c less than μ_{max} .

4. Nutrient Limitation Compared to Nutrient Starvation

From the cells' perspective, nutrient *limitation* is quite different from nutrient *starvation* [43], the latter which is often called a "resting cell" process. Nutrient limitation permits continued, possibly steady-state growth, whereas

starvation in one or more essential nutrient induces dynamic stress responses and ultimately prevents further growth [44][45][46]. Many researchers examine the effect of nutrient scarcity by *restricting* an essential nutrient in the medium to cause that nutrient to be depleted first, or by transferring washed and concentrated cells from a complete to a depleted medium (e.g., [47]). Similarly, batch processes are typically composed of a medium from which carbon is depleted first, leading many to refer to such a batch process as “carbon-limited”. The term “starved” would be preferred to describe a batch process: only after a period of maximal growth do the cells transition quickly to non-growth due to first deficiency then absence of that one (or more) nutrient. The distinction is more important when a nutrient other than the carbon source is the first to be depleted, because the remaining excess carbon/energy source often continues to be consumed and converted into an intracellular or extracellular product despite, or often because of, the lack of growth.

Because of these physiological differences, care should be taken when comparing results from nutrient *starvation* with nutrient *limitation*, wherein growth is maintained by the slow addition of one or more limiting nutrients. The literature is replete with studies describing “nutrient limitation”, when in fact the initial medium was merely adjusted so that the cells experience a short batch process until a specified nutrient is depleted, that is, the cells transition from a higher growth rate to being *starved* for that nutrient. Typically, these studies examine the culture for the metabolism of a remaining excess carbon source while the culture transitions from nutrient scarcity to nutrient exhaustion. *Nutrient limitation* implies a process in which the cells *continue to grow*.

To understand the physiological response of an organism to nutrient limitation, it is very important to have controlled conditions (pH, temperature, and oxygen) and a well-defined medium since common complex components such as yeast extract and peptone complicate the identification of the limiting nutrient and interpretation of the cellular response [14][48].

One important measurement associated with nutrient limitation and cell growth in general is the biomass yield, which expresses the quantity of cells on a dry basis generated per quantity of nutrient consumed (e.g., units of g cells/g nutrient).

5. Physiological Effects of Non-Carbon Nutrient Limitation

5.1. Nitrogen

Nitrogen occurs throughout cells, in proteins, nucleotides, and many metabolites. Nitrogen as ammonium is assimilated in *E. coli* and most bacteria and yeast into glutamine and glutamate [49], which are the primary intracellular nitrogen donors. In bacteria, 88% of the cellular nitrogen is derived from glutamate, while 12% is derived from glutamine [50]. Glutamate is the most abundant metabolite in *E. coli*, accounting for about 40% of the total metabolite concentration [51]. In many bacteria such as *E. coli*, two ammonium-assimilating pathways are available, a NADPH-dependent glutamate dehydrogenase and a high-affinity glutamate synthase (glutamine oxoglutarate aminotransferase, GOGAT)/glutamine synthase. Glutamate dehydrogenases generally have high values of K_M for ammonium, so that during N-limited growth, glutamine synthase expression is elevated to maintain

sufficient glutamate [52]. Dynamic N starvation in *E. coli* and *S. cerevisiae* growing on glucose depletes glutamine and to a lesser extent glutamate while α -ketoglutarate increases markedly and can even be excreted [47][53]. Accumulation of α -ketoglutarate occurs in cyanobacteria also, a signal which upregulates nitrogen assimilation via the global regulator NtcA and other regulators [54][55]. In yeast, the concentration of tryptophan, which relies on glutamine for its synthesis, decreases, while phenylalanine and tyrosine, which rely on glutamate for nitrogen, do not change, resulting in an accumulation of phenylpyruvate and phenylethanol, a quorum-sensing signal [56]. Accumulated α -ketoglutarate in *E. coli* noncompetitively and cooperatively inhibits EI of the PTS [57], citrate synthase [58], and PEP synthetase [59]. Furthermore, sudden nitrogen availability in N-starved wild-type *E. coli* induces a decrease in α -ketoglutarate and rapid increase in glucose uptake rate, while in a PTS-deficient strain with elevated galactose permease, glucose uptake is insensitive to N-availability [57]. In general, *S. cerevisiae* N-limitation leads to depletion of intracellular amino acids, particularly at low dilution rates [53]. Because intracellular glutamine and arginine concentration correlates strongly with dilution rate, these compounds likely control growth in N-limited *S. cerevisiae* [53]. *Synechocystis* also accumulate α -ketoglutarate [60] under N-starvation as well as glycogen, which is associated with the induction of the *glgX* gene [61][62][63]. *E. coli* has a high protein turnover under N-limited conditions compared to C-limited or P-limited conditions [64].

5.2. Phosphorus

Phosphorus occurs in cells as phosphorylated organic compounds such as general sugar-phosphates, phospholipids, phosphorylated proteins, RNA, DNA, and ATP. The response to a P-deficiency is typically mediated by a two-component signal transduction system. The sensor kinase component, PhoR, phosphorylates a response regulator that amplifies its own response, increases expression of proteins which scavenge phosphate such as a high-affinity phosphate transporter [65]. Thus, P-limitation has multiple physiological consequences. For example, P-limitation causes a shift in the structure of the cell wall of Gram-positive microbes such as *B. subtilis* from P-containing teichoic acid to teichuronic acid which lacks phosphorus [66][67]. As a result, P-limited *B. subtilis* contain less than half as much cellular phosphate as bacteria grown in excess P, and phages which bind to teichoic acid bind less effectively under P-limited conditions [68][69]. In this case, phosphorylated PhoPR represses *tagAB* operon to restrict teichoic acid synthesis and activates the *tua* operon to stimulate teichuronic acid synthesis [65]. P-limitation triggers the synthesis of phosphate-mobilizing hydrolases such as alkaline phosphatases and ribonucleases [70]. In *S. cerevisiae*, genes responsible for uptake of inorganic phosphates and inositol phosphates are upregulated under steady-state P-limitation at 0.1 h^{-1} , and surprisingly, polyphosphates accumulate in this yeast's vacuoles [71]. Cells appear to use ribosomes for protein synthesis at higher efficiency under phosphate limitation [72], and the RNA content is 6–8-fold greater than expected to be necessary for maintenance of the growth rate, though this RNA is immediately usable when P-limitation is relieved [73].

5.3. Sulfur

Sulfur is present in the amino acids methionine and cysteine, and important metabolites such as S-adenosylmethionine, Coenzyme A (CoA), and lipoic acid. In most media, S is supplied as the sulfate ion, and thus, S-limitation is often studied specifically as sulfate-limitation.

Unsurprisingly, S-limited growth leads to increased transcription of proteins encoding for the uptake of sulfur, such as in *S. cerevisiae* [71], *E. coli* [74]. Under S-limitation or S-starvation, several organisms preferentially express proteins having a low sulfur content [71][75][76][77]. For example, under S-limitation, *S. cerevisiae* upregulates by as great as 50-fold the PDC6 transcript expressing a protein with only 6 sulfur-containing amino acids [71], while *K. aerogenes* maintains lower protein content in the cell wall under S-limitation compared to other nutrient-limited conditions, and this remaining protein contains a low sulfur content [78]. The ABC transporter sulfate-binding proteins of *Salmonella typhimurium* and *E. coli* responsible for sulfate uptake in a low S environment themselves contain no sulfur [79]. When *Pseudomonas putida* encounters S-depletion, it replaces proteins having high S content with proteins having lower amounts of cysteine and methionine [80]. *K. aerogenes* also excretes proteins lacking S when grown under S-limited conditions on glucose [81]. This phenomenon has been observed in many microbes, including cyanobacteria [77]. In transitioning between S-limitation and S-enrichment, cells must synthesize new RNA, whereas under C-limitation, the cells use previously synthesized translation machinery, including inactive ribosomes [72][82].

In *E. coli*, S-starvation resulted in a 2.8-fold greater glucose uptake rate than N-starvation, and 40% greater glucose uptake rate than P-starvation, but about 70% less than the glucose uptake rate observed during Mg-starvation [83]. In *B. subtilis*, S-starvation resulted in identical glucose uptake rates as observed during N-, P-starved conditions [83]. S-limitation in *E. coli* led to secretion of pyruvate (yield of 0.33 g/g), succinate (0.11 g/g), and acetate (0.10 g/g) despite the aerobic conditions [83]. S-limited chemostat cultures of *K. aerogenes* also secreted more pyruvate than N-, P- or C-limited growth on glucose [81], while S-limited chemostat cultures of *K. aerogenes* (formerly *Aerobacter aerogenes*) at high growth rate (0.42 h^{-1}) showed pyruvate and 2-oxoglutarate accumulation [84]. These observations may be explained by comparing a typical protein (~3% S content by mass) to the sulfur-containing cofactors CoA-SH (4.2% S), lipoic acid (31.1% S), and thiamine pyrophosphate (7.5% S). Each one of these cofactors is a component of the subsequent pyruvate/2-oxoglutarate dehydrogenase step, and the limitation of these cofactors would likely limit metabolic conversion of pyruvate under S-limited conditions [84]. Further evidence identifies lipoic acid as the predominant limiting factor [85]. Interestingly, in contrast to growth on glucose which generated pyruvate and acetate, acetate was the only significant product when *K. aerogenes* was grown on glycerol, mannitol or lactate under S-limited conditions [81].

S-limitation appears to favor plasmid stability compared to C-, N- or P-limitation, particularly at high growth rate [86]. This observation was attributed to the fact that among these four nutrients, only S is not a constituent of nucleic acids. S-starvation resulted in the greatest mevalonate yield from glucose (0.6 mol/mol) compared to Mg-, P- or N-starvation [87][88]. S-starvation (referred to as MgSO_4 limitation) increased limonene formation by *E. coli* [89]. Similarly, lipid formation elevated when the oleaginous yeast *Rhodosporidium toruloides* became starved for S [90]. The fluxes through the TCA cycle and toward acetate formation were suppressed by S-starvation, and the pentose phosphate pathway appears to be the principal route for NADPH generation [87].

5.4. Magnesium

Magnesium is an integral component of ribosomes [91], and stabilizes the outer membrane in Gram-negative prokaryotes through the creation of ionic bridges [92]. The element as Mg^{2+} is also involved in DNA stability and repair [93], and it plays an important role as an enzyme cofactor. Many complex medium formulations supplemented with carbon source (such as “Lysogeny Broth” medium) become starved for Mg, and can lead to protein acetylation at lysine residues [94]. There have been a few reports on cellular Mg composition, and the yield coefficient is highly dependent on cell growth rate.

Mg-starvation causes *E. coli* cells to restructure the outer membrane and redistribute Mg [95][96]. Although the yield coefficient decreased with increasing dilution rate, Mg-limited *K. aerogenes* cultures do not synthesize intracellular polysaccharides, which is attributed to an impaired ability to synthesize these materials when Mg is limiting [97]. Mg-limitation results in larger and filamentous *E. coli* cells [98][99]. Within 400 steady-state Mg-limited generations, mutations arise in genes involved in the cell-membrane in *E. coli* [95]. Under Mg-limited conditions, both yeast [100] and bacteria [95] reduce the surface hydrophobicity of the lipopolysaccharide (LPS) component of the outer membrane, likely by increasing the proportion of polar sugar residues in the LPS, such that lower amounts of Mg are needed for stabilization of the LPS.

5.5. Iron

Consistent with the theme of cells conserving limited resources, Fe-limitation causes cells to reduce their reliance on pathways which contain significant Fe, such as the tricarboxylic acid cycle (aconitase, fumarate hydratase, succinate dehydrogenase) and the proton-pumping components of the electron transport chain [101][102][103]. This realignment of metabolism has physiological consequences. For example, under Fe-limiting aerobic conditions, *E. coli* generates acetate at a yield of 0.25 g/g at a dilution rate of 0.4 h^{-1} , but accumulates predominantly lactate (yield of 0.60 g/g) at 0.1 h^{-1} [101]. Elevated lactate under the most severe steady-state Fe-limitation provides cells a means to oxidize NADH when the Fe-requiring Nuo complex is curtailed, while an increased glucose uptake rate serves to meet ATP demand [101]. Lactate formation is also observed for *Staphylococcus aureus* exposed to Fe-starvation [104]. The reduction in activity of TCA cycle enzymes and accumulation of NADH encourages the formation of ethyl acetate by *Kluyveromyces marxianus* [105] and *Candida utilis* [106]. Because of the restricted capacity of the electron transport chain subject to Fe-limited conditions, cells essentially behave like they are encountering anaerobic conditions. For example, *E. coli* accumulates acetate and formate under Fe-limited steady-state conditions, attains a 60% greater glycolytic flux, and reduces by a factor of 5 the fraction of glucose entering the TCA cycle [107]. More generally, Fe-limitation impacts oxygenation and redox state because numerous electron-carrying enzymes contain Fe-S clusters, and many Fe-containing enzymes or pathways are constrained under Fe-limitation. For example, the nitrogenase enzyme system contains significant Fe [108], and Fe-limitation thus severely reduces nitrogen fixation by *Azotobacter vinelandii* [109]. Notably, lactic acid bacteria, which lack cytochrome and show generally high tolerance to peroxide, do not require iron for growth at all [110][111].

References

1. Gaden, E.L., Jr. Bioengineering and fermentation. *Appl. Microbiol.* 1960, 8, 123–131.
2. Maxon, W.D. Continuous fermentation: A discussion of its principles and applications. *Appl. Microbiol.* 1955, 3, 110–120.
3. Yoshida, F.; Yamane, T.; Nakamoto, K.-I. Fed-batch hydrocarbon fermentation with colloidal emulsion feed. *Biotechnol. Bioeng.* 1973, 15, 257–270.
4. Pirt, S.J. The theory of fed batch culture with reference to the penicillin fermentation. *J. Appl. Chem. Biotechnol.* 1974, 24, 415–424.
5. Fox, M.S. A device for growing bacterial populations under steady state conditions. *J. Gen. Physiol.* 1955, 39, 261–266.
6. Maxon, W.D. Continuous fermentation. *Ind. Eng. Chem.* 1960, 52, 64–65.
7. Paalme, T.; Kahru, A.; Elken, R.; Vanatalu, K.; Tiisma, K.; Vilu, R. The computer-controlled continuous culture of *Escherichia coli* with a smooth change in dilution rate (A-stat). *J. Microbiol. Meth.* 1995, 24, 145–153.
8. Schmideder, A.; Weuster-Botz, D. High-performance recombinant protein production with *Escherichia coli* in continuously operated cascades of stirred-tank reactors. *J. Ind. Microbiol. Biotechnol.* 2017, 44, 1021–1029.
9. Adamberg, K.; Valgepea, K.; Vilu, R. Advanced continuous cultivation methods for systems microbiology. *Microbiology* 2015, 161, 1707–1719.
10. Novick, A.; Szilard, L. Experiments with the chemostat on spontaneous mutations on bacteria. *Proc. Natl. Acad. Sci. USA* 1950, 36, 708–719.
11. Ziv, N.; Brandt, N.J.; Gresham, D. The Use of Chemostats in Microbial Systems Biology. *J. Vis. Exp.* 2013, 80, e50168.
12. Lameiras, F.; Heijnen, J.J.; van Gulik, W.M. Development of tools for quantitative intracellular metabolomics of *Aspergillus niger* chemostat cultures. *Metabolomics* 2015, 11, 1253–1264.
13. Egli, T. Microbial growth and physiology: A call for better craftsmanship. *Front. Microbiol.* 2015, 6, 287.
14. Herbert, D.; Elsworth, R.; Telling, R.C. The continuous culture of bacteria; a theoretical and experimental study. *J. Gen. Microbiol.* 1956, 14, 601–622.
15. Powell, E.O. Criteria for the growth of contaminants and mutants in continuous culture. *J. Gen. Microbiol.* 1958, 18, 259–268.
16. Rosenzweig, R.F.; Sharp, R.R.; Treves, D.S.; Adams, J. Microbial evolution in a simple unstructured environment: Genetic differentiation in *Escherichia coli*. *Genetics* 1994, 137, 903–917.

17. Weikert, C.; Sauer, U.; Bailey, J.E. Use of a glycerol-limited, long-term chemostat for isolation of *Escherichia coli* mutants with improved physiological properties. *Microbiology* 1997, 143, 1567–1574.
18. Bull, A.T. The renaissance of continuous culture in the post-genomics age. *J. Ind. Microbiol. Biotechnol.* 2010, 37, 993–1021.
19. Wick, L.M.; Weilenmann, H.; Egli, T. The apparent clock-like evolution of *Escherichia coli* in glucose-limited chemostats is reproducible at large but not at small population sizes and can be explained with Monod kinetics. *Microbiology* 2002, 148, 2889–2902.
20. Jansen, M.L.A.; Diderich, J.A.; Mashego, M.; Hassane, A.; de Winde, J.H.; Pascale, D.-L.; Pronk, J.T. Prolonged selection in aerobic, glucose-limited chemostat cultures of *Saccharomyces cerevisiae* causes a partial loss of glycolytic capacity. *Microbiology* 2005, 151, 1657–1669.
21. Gresham, D.; Hong, J. The functional basis of adaptive evolution in chemostats. *FEMS Microbiol. Rev.* 2015, 39, 2–16.
22. Brickwedde, A.; van den Broek, M.; Geertman, J.-M.A.; Magalhães, F.; Kuijpers, N.G.A.; Gibson, B.; Pronk, J.T.; Daran, J.-M.G. Evolutional engineering in chemostat cultures for improved maltotriose fermentation kinetics in *Saccharomyces pastorianus* lager brewing yeast. *Front. Microbiol.* 2017, 8, 1690.
23. van Maris, A.J.A.; Geertman, J.-M.A.; Vermeulen, A.; Groothuizen, M.K.; Winkler, A.A.; Piper, M.D.W.; van Dijken, J.P.; Pronk, J.T. Directed evolution of pyruvate decarboxylase-negative *Saccharomyces cerevisiae*, yielding a C2-independent, glucose-tolerant, and pyruvate-hyperproducing yeast. *Appl. Environ. Microbiol.* 2004, 70, 159–166.
24. Arensdorf, J.J.; Loomis, A.K.; DiGarazia, P.M.; Monticello, D.J.; Piendos, P.T. Chemostat approach for the directed evolution of biodesulfurization gain-of-function mutants. *Appl. Environ. Microbiol.* 2002, 68, 691–698.
25. Maharjan, R.P.; Ferenci, T.A. shifting mutational landscape in 6 nutritional states: Stress-induced mutagenesis as a series of distinct stress input-mutation output relationships. *PLoS Biol.* 2017, 15, e2001477.
26. Schreiber, F.; Littmann, S.; Lavik, G.; Escrig, S.; Meibom, A.; Kuypers, M.M.M.; Ackermann, M. Phenotypic heterogeneity driven by nutrient limitation promotes growth in fluctuating environments. *Nat. Microbiol.* 2016, 1, 16055.
27. Cooney, C.L.; Wang, D.I. Transient response of *Enterobacter aerogenes* under a dual nutrient limitation in a chemostat. *Biotechnol. Bioeng.* 1978, 18, 189–198.
28. Egli, T. On multiple-nutrient-limited growth of microorganisms, with special reference to dual limitation by carbon and nitrogen substrates. *Antonie Van Leeuwenhoek* 1991, 60, 225–234.

29. Egli, T.; Zinn, M. The concept of multiple-nutrient-limited growth of microorganisms and its application in biotechnological processes. *Biotechnol. Adv.* 2003, 22, 35–43.

30. Zinn, M.; Witholt, B.; Egli, T. Dual nutrient limited growth: Models, experimental observations and applications. *J. Biotechnol.* 2004, 113, 263–279.

31. Lis, A.V.; Schneider, K.; Weber, J.; Keasling, J.D.; Jensen, M.K.; Klein, T. Exploring small-scale chemostats to scale up microbial processes: 3-hydroxypropionic acid production in *S. cerevisiae*. *Microb. Cell Factories* 2019, 18, 50.

32. Yamanè, T.; Shimizu, S. Fed-batch techniques in microbial processes. In *Bioprocess Parameter Control Advances in Biochemical Engineering/Biotechnology*; Springer: Berlin/Heidelberg, Germany, 1984; Volume 30, pp. 147–194.

33. Trilli, A.; Michelini, V.; Mantovani, V.; Pirt, S.J. Estimation of productivities in repeated fed-batch cephalosporin fermentation. *J. Appl. Chem. Biotechnol.* 1977, 27, 219–224.

34. Yano, T.; Kurokawa, M.; Nishizawa, Y. Optimum substrate feed rate in fed-batch culture with the DO-stat method. *J. Fermentation Bioeng.* 1991, 71, 345–349.

35. Hu, Z.-C.; Zheng, Y.-G.; Shen, Y.-C. Dissolved-oxygen-stat fed-batch fermentation of 1,3-dihydroxyacetone from glycerol by *Gluconobacter oxydans* ZJB09112. *Biotechnol. Bioprocess Eng.* 2010, 15, 651–656.

36. Jørgensen, H.; Olsson, L.; Rønnow, B.; Palmqvist, E.A. Fed-batch cultivation of baker's yeast followed by nitrogen or carbon starvation: Effects on fermentative capacity and content of trehalose and glycogen. *Appl. Microbiol. Biotechnol.* 2002, 59, 310–317.

37. Shang, L.; Jiang, M.; Chang, H.N. Poly(3-hydroxybutyrate) synthesis in fed-batch culture of *Ralstonia eutropha* with phosphate limitation under different glucose concentrations. *Biotechnol. Lett.* 2003, 25, 1415–1419.

38. Shen, X.-F.; Liu, J.-J.; Chauhan, A.S.; Hu, H.; Ma, L.-L.; Lam, P.K.S.; Zeng, R.J. Combining nitrogen starvation with sufficient phosphorus supply for enhanced biodiesel productivity of *Chlorella vulgaris* fed on acetate. *Algal Res.* 2016, 17, 261–267.

39. Kim, H.M.; Chae, T.U.; Choi, S.Y.; Kim, W.J.; Lee, S.Y. Engineering of an oleaginous bacterium for the production of fatty acids and fuels. *Nat. Chem. Biol.* 2019, 15, 721–729.

40. Nayak, M.; Suh, W.I.; Chang, Y.K.; Lee, B. Exploration of two-stage cultivation strategies using nitrogen starvation to maximize the lipid productivity in *Chlorella* sp. HS2. *Bioresour. Technol.* 2019, 276, 110–118.

41. Pirt, S.J. Fed-batch culture of microbes. *Ann. N. Y. Acad. Sci.* 1979, 326, 119–125.

42. Dunn, I.J.; Mor, J.-R. Variable-volume continuous cultivation. *Biotechnol. Bioeng.* 1975, 17, 1805–1822.

43. Förberg, C.; Häggström, L. Effects of cultural conditions on the production of phenylalanine from a plasmid-harboring *E. coli* strain. *Appl. Microbiol. Biotechnol.* 1987, 26, 136–140.

44. Werner-Washburne, M.; Braun, E.L.; Crawford, M.E.; Peck, V.M. Stationary phase in *Saccharomyces cerevisiae*. *Mol. Microbiol.* 1996, 19, 1159–1166.

45. Gasch, A.P.; Werner-Washburne, M. The genomics of yeast responses to environmental stress and starvation. *Funct. Integr. Genom.* 2002, 2, 181–192.

46. Peterson, C.N.; Mandel, M.J.; Silhavy, T.J. *Escherichia coli* starvation diets: Essential nutrients weigh in distinctly. *J. Bacteriol.* 2005, 187, 7549–7553.

47. Brauner, M.J.; Yuan, J.; Bennett, B.D.; Lu, W.; Kimball, E.; Botstein, D.; Rabinowitz, J.D. Conservation of the metabolomic response to starvation across two divergent microbes. *Proc. Natl. Acad. Sci. USA* 2006, 103, 19302–19307.

48. Minihane, B.J.; Brown, D.E. Fed-batch culture technology. *Biotechnol. Adv.* 1986, 4, 207–218.

49. Reitzer, L. Nitrogen assimilation and global regulation in *Escherichia coli*. *Annu. Rev. Microbiol.* 2003, 57, 155–176.

50. Hu, P.; Leighton, T.; Ishkhanova, G.; Kustu, S. Sensing of nitrogen limitation by *Bacillus subtilis*: Comparison to enteric bacteria. *J. Bacteriol.* 1999, 181, 5042–5050.

51. Bennett, B.D.; Kimball, E.H.; Gao, M.; Osterhout, R.; van Dien, S.J.; Rabinowitz, J.D. Absolute metabolite concentrations and implied enzyme active site occupancy in *Escherichia coli*. *Nat. Chem. Biol.* 2009, 5, 593–599.

52. Reitzer, L.J. Ammonia assimilation and the biosynthesis of glutamine, glutamate, aspartate, asparagine, L-alanine, and D-alanine. In *Escherichia coli and Salmonella: Cellular and Molecular Biology*; Neidhardt, F.C., Curtiss, R., III, Ingraham, J.L., Lin, E.C.C., Low, K.B., Magasanik, B., Eds.; American Society for Microbiology Press: Washington, DC, USA, 1996; pp. 391–407.

53. Boer, V.M.; Crutchfield, C.A.; Bradley, P.H.; Botstein, D.; Rabinowitz, J.D. Growth-limiting intracellular metabolites in yeast growing under diverse nutrient limitations. *Mol. Biol. Cell.* 2010, 21, 198–211.

54. Muro-Pastor, M.I.; Reyes, J.C.; Florencio, F.J. Ammonium assimilation in cyanobacteria. *Photosynth. Res.* 2005, 83, 135–150.

55. Espinosa, J.; Rodriguez-Mateos, F.; Salinas, P.; Lanza, V.F.; Dixon, R.; de la Cruz, F.; Contreras, A. PipX, the coactivator of NtcA, is a global regulator in cyanobacteria. *Proc. Natl. Acad. Sci. USA* 2014, 111, e2423–e2430.

56. Chen, H.; Fink, G.R. Feedback control of morphogenesis in fungi by aromatic alcohols. *Genes Dev.* 2006, 20, 1150–1161.

57. Doucette, C.D.; Schwab, D.J.; Wingreen, N.S.; Rabinowitz, J.D. α -ketoglutarate coordinates carbon and nitrogen utilization via enzyme I inhibition. *Nat. Chem. Biol.* 2011, 7, 894–901.

58. Pereira, D.S.; Donald, L.J.; Hosfield, D.J.; Duckworth, H.W. Active site mutants of *Escherichia coli* citrate synthase. *J. Biol. Chem.* 1994, 269, 412–417.

59. Chulavatnatol, M.; Atkinson, D.E. Phosphoenolpyruvate synthetase from *Escherichia coli*: Effects of adenylate energy charge and modifier concentrations. *J. Biol. Chem.* 1973, 248, 2712–2715.

60. Muro-Pastor, M.I.; Reyes, J.C.; Florencio, F.J. Cyanobacteria perceive nitrogen status by sensing intracellular 2-oxoglutarate levels. *J. Biol. Chem.* 2001, 276, 38320–38328.

61. De Marsac, N.T.; Castets, A.-M.; Cohen-Bazire, G. Wavelength modulation of phycoerythrin synthesis in *Synechocystis* sp. 6701. *J. Bacteriol.* 1980, 142, 310–314.

62. Osanai, T.; Imamura, S.; Asayama, M.; Shirai, M.; Suzuki, I.; Murata, N.; Tanaka, K. Nitrogen induction of sugar catabolic gene expression in *Synechocystis* sp. PCC 6803. *DNA Res.* 2006, 13, 185–195.

63. Yoo, S.-H.; Keppel, C.; Spalding, M.; Jane, J.-L. Effects of growth condition on the structure of glycogen produced in cyanobacterium *Synechocystis* sp. PCC6803. *Intl. J. Biol. Mol.* 2007, 40, 498–504.

64. Gupta, M.; Johnson, A.; Cruz, E.; Costa, E.; Guest, R.; Li, S.H.-J.; Hart, E.M.; Nguyen, T.; Stadlmeier, M.; Bratton, B.P.; et al. Global protein-turnover quantification in *Escherichia coli* reveals cytoplasmic recycling under nitrogen-limitation. *bioRxiv* 2022.

65. Devine, K.M. Activation of the PhoPR-mediated response to phosphate limitation is regulated by wall teichoic acid metabolism in *Bacillus subtilis*. *Front. Microbiol.* 2018, 9, 2678.

66. Ellwood, D.C.; Tempest, D.W. Teichoic acid or teichuronic acid in the walls of *Bacillus subtilis* var. *niger*, grown in a chemostat. *Biochem. J.* 1967, 104, 69.

67. Ellwood, D.C.; Tempest, D.W. Control of teichoic acid and teichuronic acid biosynthesis in chemostat cultures of *Bacillus subtilis* var. *niger*. *Biochem. J.* 1969, 111, 1–5.

68. Anderson, A.J.; Green, R.S.; Archibald, A.R. Wall composition and phage-binding properties of *Bacillus subtilis* W23 grown in chemostat culture in media containing varied concentrations of phosphate. *FEMS Microbiol. Lett.* 1978, 4, 129–132.

69. Lang, W.K.; Glassey, K.; Archibald, A.R. Influence of phosphate supply on teichoic acid and teichuronic acid content of *Bacillus subtilis* cell walls. *J. Bacteriol.* 1982, 151, 367–375.

70. Wouters, J.T.M.; Buysman, P.J. Production of some exocellular enzymes by *Bacillus licheniformis* 749/C in chemostat cultures. *FEMS Microbiol. Lett.* 1977, 1, 109–112.

71. Boer, V.M.; de Winde, J.H.; Pronk, J.T.; Piper, M.D. The genome-wide transcriptional responses of *Saccharomyces cerevisiae* grown on glucose in aerobic chemostat cultures limited for carbon, nitrogen, phosphorous, or sulfur. *J. Biol. Chem.* 2003, 278, 3265–3274.

72. Li, S.H.-J.; Li, Z.; Park, J.O.; King, C.G.; Rabinowitz, J.D.; Wingreen, N.S.; Gitai, Z. *Escherichia coli* translation strategies differ across carbon, nitrogen and phosphorous limitation conditions. *Nat. Microbiol.* 2018, 3, 939–947.

73. Alton, T.H.; Koch, A.L. Unused protein synthetic capacity of *Escherichia coli* grown in phosphate-limited chemostats. *J. Mol. Biol.* 1974, 86, 1–9.

74. Gyaneshwar, P.; Paliy, O.; McAuliffe, J.; Popham, D.L.; Jordan, M.I.; Kustu, S. Sulfur and nitrogen limitation in *Escherichia coli* K-12: Specific homeostatic response. *J. Bacteriol.* 2005, 187, 1074–1090.

75. Merchant, S.S.; Helmann, J.D. Elemental economy: Microbial strategies for optimizing growth in the face of nutrient limitation. *Adv. Microb. Physiol.* 2012, 60, 91–210.

76. Cuhel, R.L.; Taylor, C.D.; Jannasch, H.W. Assimilatory sulfur metabolism in marine microorganisms: Sulfur metabolism, growth, and protein synthesis of *Pseudomonas halodurans* and *Alteromonas luteo-violaceus* during sulfate limitation. *Arch. Microbiol.* 1981, 130, 1–7.

77. Mazel, D.; Marlière, P. Adaptive eradication of methionine and cysteine from cyanobacterial light-harvesting proteins. *Nature* 1989, 341, 245–248.

78. Robinson, A.; Tempest, D.W. Phenotypic variability of the envelope proteins of *Klebsiella aerogenes*. *J. Gen. Microbiol.* 1973, 78, 361–370.

79. Pardee, A.B. Purification and properties of a sulfate-binding protein from *Salmonella typhimurium*. *J. Biol. Chem.* 1966, 241, 5886–5892.

80. Beil, S.; Kertesz, M.A.; Leisinger, T.; Cook, A.M. The assimilation of sulfur from multiple sources and its correlation with expression of the sulfate-starvation-induced stimulon in *Pseudomonas putida* S-313. *Microbiology* 1996, 142, 1989–1995.

81. Neijssel, O.M.; Tempest, D.W. The regulation of carbohydrate metabolism in *Klebsiella aerogenes* NCTC 418 organisms, growing in chemostat culture. *Arch. Microbiol.* 1975, 106, 251–258.

82. Koch, A.L.; Deppe, C.S. In vivo assay of protein synthesizing capacity of *Escherichia coli* from slowly growing chemostat cultures. *J. Mol. Biol.* 1971, 55, 549–562.

83. Chubukov, V.; Sauer, U. Environmental dependence of stationary-phase metabolism in *Bacillus subtilis* and *Escherichia coli*. *Appl. Environ. Microbiol.* 2014, 80, 2901–2909.

84. Stouthamer, A.H.; Bettenhaussen, C.W. Determination of the efficiency of oxidative phosphorylation in continuous cultures of *Aerobacter aerogenes*. *Arch. Microbiol.* 1975, 102, 187–192.

85. Zinebi, S.; Raval, G.; Petitdemange, H. Effect of oxygenation and sulfate concentrations on pyruvate and lactate formation in *Klebsiella oxytoca* ZS growing in chemostat culture. *Curr. Microbiol.* 1994, 29, 79–85.

86. Chew, L.C.K.; Tacon, W.C.A.; Cole, J.A. Effect of growth conditions on the rate of loss of the plasmid pAT153 from continuous cultures of *Escherichia coli* HB101. *FEMS Microbiol.* 1988, 56, 101–104.

87. Masuda, A.; Toya, Y.; Shimizu, H. Metabolic impact of nutrient starvation in mevalonate-producing *Escherichia coli*. *Bioresour. Technol.* 2017, 245, 1634–1640.

88. Li, S.; Jendresen, C.B.; Nielsen, A.T. Increasing production yield of tyrosine and mevalonate through inhibition of biomass formation. *Process Biochem.* 2016, 51, 1992–2000.

89. Willrodt, C.; Hoschek, A.; Bühler, B.; Schmid, A.; Julsing, M.K. Decoupling production from growth by magnesium sulphate limitation boosts de novo limonene production. *Biotechnol. Bioeng.* 2016, 113, 1305–1314.

90. Wu, S.; Zhao, X.; Shen, H.; Wang, Q.; Zhao, Z.K. Microbial lipid production by *Rhodosporidium toruloides* under sulfate-limited conditions. *Bioresour. Technol.* 2011, 102, 1803–1807.

91. Tissières, A.; Watson, J.D. Ribonucleoprotein particles from *Escherichia coli*. *Nature* 1958, 182, 778–780.

92. Nikaido, H. Molecular basis of bacterial outer membrane permeability revisited. *Microbiol. Mol. Biol. Rev.* 2003, 67, 593–656.

93. Hartwig, A. Role of magnesium in genomic stability. *Mutat. Res.* 2001, 475, 113–121.

94. Christensen, D.G.; Orr, J.G.; Rao, V.G.; Wolfe, A.L. Increasing growth yield and decreasing acetylation in *Escherichia coli* by optimizing the carbon to magnesium ratio in peptide-based medium. *Appl. Environ. Microbiol.* 2017, 83, e03034-16.

95. Warsi, O.M.; Andersson, D.I.; Dykhuizen, D.E. Different adaptive strategies in *E. coli* populations evolving under macronutrient limitation and metal ion limitation. *BMC Evol. Biol.* 2018, 18, 72.

96. Fiil, A.; Branton, D. Changes in the plasma membrane of *Escherichia coli* during magnesium starvation. *J. Bacteriol.* 1969, 98, 1320–1327.

97. Tempest, D.W.; Hunter, J.R.; Sykes, J. Magnesium-limited growth of *Aerobacter aerogenes* in a chemostat. *J. Gen. Microbiol.* 1965, 39, 355–366.

98. Brock, T.D. Effects of magnesium ion deficiency on *Escherichia coli* and possible relation to the mode of action of novobiocin. *J. Bacteriol.* 1962, 84, 679–682.

99. Dean, A.C.R.; Rogers, P.L. The cell size and macromolecular composition of *Aerobacter aerogenes* in various systems of continuous culture. *Biochim. Biophys. Acta* 1962, 148, 267–279.

100. Smit, G.; Straver, M.H.; Lugtenberg, B.J.; Kijne, J.W. Flocculence of *Saccharomyces cerevisiae* cells is induced by nutrient limitation, with cell surface hydrophobicity as a major determinant. *Appl. Environ. Microbiol.* 1992, 58, 3709–3714.

101. Folsom, J.P.; Parker, A.E.; Carlson, R.P. Physiological and proteomic analysis of *Escherichia coli* iron-limited chemostat growth. *J. Bacteriol.* 2014, 196, 2748–2761.

102. Parente, A.F.A.; Bailão, A.M.; Borges, C.L.; Parente, J.A.; Magalhães, A.D.; Ricart, C.A.O.; Soares, C.M.A. Proteomic Analysis Reveals That Iron Availability Alters the Metabolic Status of the Pathogenic Fungus *Paracoccidioides brasiliensis*. *PLoS ONE* 2011, 6, e22810.

103. McHugh, J.P.; Rodríguez-Quiñones, F.; Abdul-Tehrani, H.; Svistunenko, D.A.; Poole, R.K.; Cooper, C.E.; Andrews, S.C. Global iron-dependent gene regulation in *Escherichia coli*: A new mechanism for iron homeostasis. *J. Biol. Chem.* 2003, 278, 29478–29486.

104. Friedman, D.B.; Stauff, D.L.; Pishchany, G.; Whitwell, C.W.; Torres, V.J.; Skaar, E.P. *Staphylococcus aureus* redirects central metabolism to increase iron availability. *PLoS Path.* 2006, 2, 777–789.

105. Löser, C.; Urit, T.; Stukert, A.; Bley, T. Formation of ethyl acetate from whey by *Kluyveromyces marxianus* on a pilot scale. *J. Biotechnol.* 2013, 163, 17–23.

106. Armstrong, D.W.; Yamazaki, H. Effect of iron and EDTA on ethyl acetate accumulation in *Candida utilis*. *Biotechnol. Lett.* 1984, 6, 819–824.

107. Baez, A.; Sharma, A.K.; Bryukhanov, A.; Anderson, E.D.; Rudack, L.; Olivares-Hernandez, R.; Quan, D.; Shiloach, J. Iron availability enhances the cellular energetics of aerobic *Escherichia coli* cultures while upregulating anaerobic respiratory chains. *New Biotechnol.* 2022, 71, 11–20.

108. Georgiadis, M.M.; Komiya, H.; Chakrabarti, P.; Woo, D.; Kornuc, J.J.; Rees, D.C. Crystallographic structure of the nitrogenase iron protein from *Azotobacter vinelandii*. *Science* 1992, 257, 1653–1659.

109. Fekete, F.A.; Spence, J.T.; Emery, T. Siderophores produced by nitrogen-fixing *Azotobacter vinelandii* OP in iron-limited continuous culture. *Appl. Environ. Microbiol.* 1983, 46, 1297–1300.

110. MacLeod, R.A.; Snell, E.E. Some mineral requirements of the lactic acid bacteria. *J. Biol. Chem.* 1947, 170, 351–365.

111. Archibald, F. *Lactobacillus plantarum*, an organism not requiring iron. *FEMS Microbiol. Lett.* 1983, 19, 29–32.

Retrieved from <https://encyclopedia.pub/entry/history/show/80867>