System wide cofactor turnovers can propagate metabolic stability between pathways

Yang, Y.; Guan, Y.H.; Villadsen, John

Published in:
Metabolic Engineering Communications

Link to article, DOI:
10.1016/j.meteno.2016.06.002

Publication date:
2016

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
Yang, Y., Guan, Y. H., & Villadsen, J. (2016). System wide cofactor turnovers can propagate metabolic stability between pathways. Metabolic Engineering Communications, 3, 196-204. DOI: 10.1016/j.meteno.2016.06.002

DTU Library
Technical Information Center of Denmark

General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.
System wide cofactor turnovers can propagate metabolic stability between pathways

Y. Yang, Y.H. Guan, J. Villadsen

Abstract

Metabolic homeostasis, or low-level metabolic steady state, has long been taken for granted in metabolic engineering, and research priority has always been given to understand metabolic flux control and regulation of the reaction network. In the past, this has not caused concerns because the metabolic networks studied were invariably associated with living cells. Nowadays, there are needs to reconstruct metabolic networks, and so metabolic homeostasis cannot be taken for granted. For metabolic steady state, enzyme feedback control has been known to explain why metabolites in metabolic pathways can be kept at nearly constant concentration (or internal metabolites) are kept at metabolic steady states, enzyme feedback control has been known to explain why metabolites in metabolic pathways can be kept at nearly constant concentration (or internal metabolites) are kept at

Keywords:
Metabolic stability
Metabolic steady state
Cofactor balance
Cofactor turnover
Enzyme feedback control
Emergent property of metabolic network

1. Introduction

Metabolic reaction networks entail thousands of enzymes and connect to a myriad of metabolites, with intermediate number being of the order of 10<sup>3</sup> and average concentration 32 μM for a prokaryote (Atkinson, 1968; Palsson, 2011). A remarkable feature of such networked reaction system is that all the intracellular metabolic intermediates (or internal metabolites) are kept at metabolic homeostasis (in a physiological term) or low level steady state (in an engineering-orientated term). Such networks have been observed to be inherently robust (Stephanopoulos and Vallino, 1991; Ishii et al., 2007; De la Fuente et al., 2014), predominantly operated at thermodynamic non-equilibrium (Prigogine, 1955; Fell, 1997), and are able to accommodate a widely varied metabolic fluxes (Stephanopoulos, 1998; Villadsen, 2016).

Metabolic control and regulation take place notably at metabolic and gene-expression levels (Reich and Sel’kov, 1981; Palsson, 2015). The time constant (or time scale) can be used to differentiate study regimes (Palsson, 2011; Reich and Sel’kov, 1981). Control and regulation at metabolic level is a spontaneous, dynamic reaction process. Representative time constants at this level are in the range of 0.1–10 s (Reich and Sel’kov, 1981; Wiechert, 2002). In contrast, gene-expression and transcriptional control and regulation regimes for remapping metabolic fluxes involve biosynthesis/biodegradation of large molecules (e.g. enzymes), and their typical time constants are ~1 h (Wiechert, 2002; Palsson, 2011). The present work concerns with the control and regulation at the metabolic level with small time constants. An important milestone in understanding metabolic regulation at metabolic level came from the discovery of enzyme negative feedback control by inhibition (Umbarger, 1956; Yates and Pardee, 1956; Gerhart and Pardee, 1962). Supported by mechanism explorations, such feedback control mechanism largely avoids metabolite build-up (Monod et al., 1963; Savageau, 1969, 1974; Chandra et al., 2011; He et al., 2013). The most efficient feedback
control for a linear pathway at metabolic level is end-product inhibition, which may be termed as the optimal design of feedback inhibition control (Savageau, 1974). It is optimal because such feedback control requires only one inhibition for a linear carbon backbone pathway (Fig. 1(A)), and at least 3 feedback inhibition loops for a bifurcated pathway system (Fig. 1(B)) (Savageau, 1974, 1976). Even in the case that this mechanism is not functioning, the cell can still use a contingency mechanism to enzymatically hydrolyse the end-product to avoid its build-up (Reaves et al., 2013).

Nevertheless, spontaneous establishment of metabolic homeostasis does not rely only on allosteric enzyme regulation mechanisms. Morowitz et al. were probably the first in reporting the very nature of such autonomous homeostasis – in their wording “passive stability in a metabolic network” (Morowitz et al., 1964). These authors attributed a number of factors to the occurrence of metabolic homeostasis. Among their claims, the role of carbon backbone topology has been well substantiated (Morowitz et al., 2000; Smith and Morowitz, 2004), but the role of the cofactor topology, superimposed onto the carbon backbone topology, has never been evidenced.

As a broad objective, this work is aimed to shed light for understanding why a metabolic network is stable and why all metabolite concentrations are kept at low levels. With low level steady state being taken for granted, up to now the metabolic control and regulation community has given priorities to understanding how metabolic fluxes are amenable to changes in magnitude and distribution (Hofmeyr and Cornish-Bowden, 1991). Such convention had been directed to curate genome-based metabolic reaction networks without involving metabolite concentrations (Palsson, 2015). Understanding of metabolic homeostasis observed for living cells (Savageau, 1976) has long been separated from research on metabolic flux control and regulation (Kacser and Burns, 1973; Heinrich and Rapoport, 1974). In the past, this arbitrary separation had not caused concerns because the metabolic networks investigated were invariably associated with living cells where metabolic homeostasis is out of question. Nowadays, there are challenging needs for reconstructing metabolic networks in synthetic biology or metabolic engineering. In contrast, metabolic homeostasis for multi-enzyme reaction systems under investigation can no longer be taken for granted (Rollin et al., 2015; Keller et al., 2016). In detail, the present work will describe an emergent property resulted from interactions between cofactor intermediate (CIs) turnovers and enzyme feedback inhibition. This property may play a pivotal role to the emergence of metabolic homeostasis.

2. Theoretical framework

In order to unfold this research, we first separated CIs from non-cofactor intermediates (NCIs) to reveal the important role of the CIs, and then conceptually connect the systems used to various multi-enzyme reaction systems. We quantitatively illustrated how the metabolic homeostasis of in vivo systems is robust against an environmental perturbation (i.e. substrate concentration variation). This outcome then guided us in validating a suitable type of working open systems.

2.1. CIs versus NCIs

The metabolic network entails 2 types of internal metabolites: (i) a limited number of paired or grouped CIs and (ii) a vast number of standalone NCIs. Enzymes utilise NCIs for stepwise chemical conversion from substrate(s) to desired end products. CIs are usually paired and each paired CI pool size is fixed for global uses at the metabolic level. Common CI pairs/groups include ATP/ADP/AMP (for energy transduction), NAD+/NADH, NADP+/NADPH, Q/QH2 (for redox transfer), and CoA-SH/acyetyl-CoA/malonyl-CoA/succinyl-CoA (for carbon chain translocation). The energy CI pool should be referred to as ATP+ADP+AMP+Pi at the metabolic reaction time scale (Wiechert, 2002). The catabolic and anabolic redox CIs pool sizes are NAD+/NADH and NADP+/NADPH respectively. The CoA-related CI pool size is the sum of CoASH in free form and covalently bound to certain carbon backbone chains (e.g. acetyl-CoA). Hence, the CoA-bound metabolites are both CIs and NCIs. Besides, metabolism contains further unique reaction topologies comparable to CI turnovers. For instance, cyclic-like reactions for transferring nitrogen-containing groups are different in that there is a net consumption of e.g. NH2 groups.

Each CI pool size is inherently small (e.g. ATP + ADP + AMP pool typically at 2 mM) (Atkinson, 1977; Palsson, 2011). To simultaneously sustain so many reactions in a homogeneous space, ATP (ADP) has no options but to turn around at globally balanced rates through numerous ATP (ADP)-consuming and generating reactions. Usually, an NCI conversion reaction is realised by utilising a CI as the second reactant. In such network topologies, each CI [e.g. B (Q) out of the B + Q pool, Fig. 2(A)–(C)] can only stay either in steady or oscillating status (Chassagnole, 2002; De la Fuente et al., 2014). At such metabolic homeostasis, the net B-to-Q or Q-to-B flux can be termed as CI turnover flux or CI flux. To make a distinction, the well-understood carbon backbone flux (Stephanopoulos et al., 1998; Villadsen, 2016) can thus be termed as NCI flux. Each reaction stoichiometry connects a CI flux to relevant NCI flux (es). Without metabolic homeostasis, any discussions on fluxes will become groundless and meaningless. This work underpins how metabolic homeostasis may be constructed from scratch, and metabolic flux regulation is not the focus.

2.2. The in-vivo-like system

In the synthetic biology era, the boundary separating an in vivo and an in vitro systems is becoming more and more blurred. In order to discuss this subject systematically, it is useful to define a new concept termed the in-vivo-like system. In the present context, it refers to a multi-enzyme reaction system which possesses CI turnover and metabolic homeostasis. Such a system can be either completely man-made, or derived from native cells. Indeed,
new frontiers of metabolic engineering such as cofactor engineering have been researched for years (San et al., 2002; Rollin et al., 2015). In this work, we developed a new theory to tell if a multi-enzyme reaction is an in-vivo-like system or not.

To reveal system wide properties of CIs in a multi-enzyme reaction system, the 1st network type for this work is composed of 2 parallel linear carbon backbone pathways (Fig. 2(A)–(C)), and the 2nd branched pathways (Fig. 2(D)). In the living cell, all the carbon...
backbone pathways are ultimately connected. A pair of linear pathways can thus be viewed to represent those scenarios where the only link between 2 pathways is via CI turnover. Consequently, focus in Fig. 2(A)–(C) has been given to the CI-related reaction network topologies. To avoid concentrations of the 2 substrates becoming disparate (Fig. 2(A)–(C)), kinetic parameters and enzyme loadings have been arranged symmetrically for the 2 pathways.

Fig. 2(A) is configured so that product of the 1st pathway exerts inhibition on its 1st enzyme whilst the 2nd pathway is free from inhibition. In addition to the end-product inhibition on the same pathway (Fig. 2(A)), it is common that product of another seemingly unrelated pathway (i.e. the 2nd pathway) can also exert inhibition over that pathway (i.e. the 1st pathway). This scenario is presented by the Fig. 2(B) reaction topology. Fig. 2(C) is configured so that substrate of the 1st pathway exerts inhibition on its own enzyme whilst the 2nd pathway is free from enzyme inhibition. Using these 3 separate enzyme inhibition topologies, we investigated possible roles that CI turnover plays in maintaining metabolic homeostasis. The Fig. 2(D) reaction topology resembles that of glycolysis, but is an intact in-vivo-like system.

2.3. The open system

Metabolism can take place only in open system. As will be shown in the subsequent section, the Fig. 2(A) reaction topology can be classified as an in-vivo-like system (see Section 4). With this pre-knowledge, the effects of substrate feeding on the metabolite Y1 are illustrated (Fig. 3). This “dry” experiment was designated so that the combined amount of substrate fed has been kept the same over the total time duration regardless of the feeding regime. When the substrate is fed at a fixed rate, a low-concentration quasi-steady state for Y1 is observed (Fig. 3(A)). When 3 discrete feedings are made, each feeding causes a disturbance, but the Y1 level reverts back to its quasi-steady state (Fig. 3(B)). When all of the substrate is fed at the very outset, the Y1 level again reverts back to its quasi-steady state (Fig. 3(C)). Over this time duration, the Fig. 3(C) operation appears to be a batch reaction system. As batch reaction is much easy to operate in practice, in the following we will stick to this reaction modality.

Continuous stirred-tank reactor (CSTR) at steady state is an open system, and has often been used for conducting in vivo reactions (Palsson, 2011; Villadsen et al., 2011, 2016). On one hand, even though the reaction system does not have homeostasis property, use of CSTR may lead to steady states for each intermediate. Consequently, CSTR is inappropriate in our quest on the emergence of metabolic homeostasis. On the other hand, if one is using an in vivo system (i.e. cellular reaction system), use of CSTR allows selecting different metabolic states by adjusting dilution rate (another environmental factor). Unlike CSTR, the working open system portrayed above can only reach quasi-steady state owing to the fact that the product is not been removed.

3. Methods

Reaction mechanisms for a two-substrate enzyme reaction are: (i) compulsory-order mechanism, (ii) random-order mechanism, and (iii) double-displacement mechanism (Cornish-Bowden, 2012; Fell, 1997). The mechanism adopted in this work is based on the compulsory-order mechanism. To simplify the calculation, we regard only one three-body enzyme complex, rather than two, for each concerned enzyme. Therefore, each 2-substrate reaction entails 4 elemental reaction steps. Although arbitrariness is involved in reaction mechanism selection, it is nevertheless so that the outcome kinetic expression formality is expected to be the same or similar regardless of the above mechanisms (Cornish-Bowden, 2012).

Experimentally measured cofactor intermediates (i.e. CI) concentrations vary to some extents. On average and typically for E. coli cells, Palsson (Palsson, 2011) listed the following figures: ATP 1.6 mM, ADP 0.29 mM, AMP 0.087 mM, NAD+ 0.06 mM, NADH 0.03 mM. Specifically, for E. coli cells, Bennett et al. (2009) documented the following experimental results: ATP 9.6 mM, ADP 0.56 mM, AMP 0.28 mM, NAD+ 0.083 mM, NADH 2.6 mM, NADP+ 0.0028 mM, and NADPH 0.12 mM. For yeast S. cerevisiae, Teusink et al. (2000) reported experimental data: ATP 2.5–2.54 mM, ADP 1.31–1.33 mM, AMP 0.18–0.32 mM, NAD+ 1.07–1.33 mM, and NADH 0.3–0.48 mM. These data have been used as guidance for considering CI pool size in this work.

![Fig. 3. Effects of substrate feeding regimes on the Y1 (Fig. 2A reaction topology).](image-url)

Three feeding regime are shown, where 500 mM of substrate is added over 342.5 h: (A) continuous feeding at a fixed rate of 0.902 mM/h, (B) initial substrate at 250 mM, followed by 3 discrete feedings (100 mM, 100 mM and 50 mM respectively), and (C) all 500 mM substrate starts at the beginning.
For the systems presented in Fig. 2, a set of ordinary differentiation equations (ODEs) is established based on mass action law and mass conservation on every metabolite, enzyme and enzyme complex. These equations are simultaneously solved using Matlab with ODE 15 s as the solver. The kinetic parameters, initial conditions, and enzyme loadings used for simulation are given in Tables S1, S2 and S3 of the Supplementary Material.

4. Results and discussion

The central theme of the present work is to testify the presence of a property in the living cell, which emerges by interacting enzyme feedback inhibition with CI turnover. As the starting point, one needs to exclude those systems where the metabolic stability has already been achieved even though the enzyme inhibition and CI turnover are artificially made absent. As a further point, one needs also to exclude those systems where enzyme inhibition alone is sufficient in causing metabolic stability. To the basal system meeting these 2 criteria, the following 3 additional situations were then constructed: (i) the enzyme inhibition is incorporated, (ii) the CI turnover is incorporated, and (iii) both the enzyme inhibition and the CI turnover are incorporated. To introduce CI turnover effects, pertinent in-vivo-like systems were constructed. To remove CI turnover effects, 2 approaches were designed: (i) if present, to turn each pathway into an independent reaction (i.e. an in vitro reference reaction), (ii) to make the CI pool size extraordinarily large. Metabolic stability results (if any) out of these situations were then compared.

4.1. The Fig. 2(A) reaction topology: single end-product inhibition, on its own pathway

Realisation of the optimal end-product inhibition control (i.e. the 1st pathway in Fig. 2(A)) was made decades ago (Umbarger, 1956; Umbarger and Brown, 1957; Monod, 1963). This type of inhibition limits accumulation of metabolic intermediates on the 1st pathway (Savageau, 1976), but we do not have knowledge whether low level steady state can also be established for the 2nd pathway intermediates in Fig. 2(A).

When the only feedback inhibition is taken out, the deficient in-vivo-like system (Row 2 of Fig. 4) and its in vitro reference reactions (Row 4 of Fig. 4) have the same NCI and substrate/product profiles, where the internal metabolites except Y3 and Y6 are at steady states. Clearly, in the absence of enzyme inhibition, CI turnover alone cannot lead to metabolic homeostasis.

When enzyme end-product inhibition is brought back, for the in vitro reactions (Row 3 of Fig. 4), low level steady states are attained only for the 1st pathway (i.e. for Y1, Y2 and Y3) but not for the 2nd pathway (i.e. Y6 accumulates and Y4 is stabilized at elevated level). However, when the CI turnover is incorporated with end-product inhibition to make the in-vivo-like system, all metabolic intermediates in both pathways are confined at low levels (Row 1 of Fig. 4). Indicatively, interactions between the CI turnover and the end-product inhibition lead to metabolic homeostasis. These interactive effects consequently constitute an emergent property mentioned above. For this in-vivo-like system, NCI stabilized levels increase with either decreasing inhibition strength or increasing the CI pool size, or both (Fig. S1, Supplementary material). Overall, these NCI concentrations are very low. In terms of

![Fig. 4](image-url)
the present experimental technologies, measured results may well reject a significant change even though the effect per se is numerically significant.

In the majority of cases, it is not possible to obtain the in vitro reference reactions out of an in vivo-like system (e.g. the Fig. 2(B) and (D) reaction topologies). In such cases, use of an extra-large CI pool size (e.g. B + Q = 1000 mM) is the only alternative for damping or even removing the CI turnover effect. Validity of this approach is confirmed by comparing Row 2 with Row 6 (Fig. 4), and Row 3 with Row 5 (Fig. 4). The difference between Row 1 and Row 5 (Fig. 4) indicates that metabolic homeostasis is more likely to be associated with small CI pool size.

4.2. The Fig. 2(B) reaction topology: single end-product inhibition, cross pathways

In the absence of enzyme inhibition, all the displayed metabolites behave identically between the deficient in vivo-like system (Row 2 in Fig. 5) and that with extra-large CI pool size (Row 4 in Fig. 5). Y1 and Y4 are stabilized but at an unacceptably high level (i.e. 30 mM), Y2 and Y5 stabilized at a low level (i.e. 0.02 mM), and Y3 and Y6 simply accumulate almost in a linear fashion. This outcome confirms that metabolic homeostasis cannot be achieved without the enzyme inhibition. For the in vivo-like system where both the enzyme inhibition and the CI turnover are present, metabolic homeostasis is satisfactorily reached (Row 1 of Fig. 5). Quantitatively, NCI steady state concentrations for this in vivo-like system can be increased by reducing inhibition strength (Fig. S2A in Supplementary material) or increasing the CI pool size (Fig. S2B, Supplementary material), or a combination of both. In the presence of the enzyme inhibition and with the extra-large CI pool size (Row 3 of Fig. 5), NCI concentrations on the 1st pathway (i.e. Y1, Y2 and Y3) can be stabilized to low levels, but those on the 2nd pathway (i.e. Y4, Y5 and Y6) cannot. In detail, Y4 is stabilized yet its level is too high, Y5 is stabilized to a low level, and Y6 simply keeps accumulating. Indicatively, low-level CI steady states for the 1st pathway are independent of the CI turnover when the CI pool size becomes extra-large. Note that the 1st pathway has inhibition whereas the 2nd pathway does not have. Again, the enzyme inhibition is essential for metabolic homeostasis, which can be propagated to another inhibition free pathway with the aid of small size CI turnover.

4.3. The Fig. 2(C) reaction topology: single substrate inhibition, on its own pathway

Substrate inhibition is also important for enzyme regulation at both gene and metabolic levels (Cornish-Bowden, 2012; Yoshino and Murakami, 2015; Reed et al., 2010). It is therefore worth providing evidences at the metabolic level that the emergent property out of the CI turnover and the enzyme inhibition is also present for this in vivo-like system (Fig. 2(C)).

When the enzyme inhibition is absent, the corresponding NCI profiles are identical between the deficient in vivo-like system, the in vitro reference reactions, and the deficient in vivo-like system with extra-large CI pool size (Row 2, Row 4 and Row 6 of Fig. 6). When the substrate inhibition is introduced, (i) the in vivo-like system instantaneously reaches metabolic homeostasis (Row 1 of Fig. 6), (ii) for the in vitro reference reactions (Row 3 of Fig. 6), all NCIs on the 1st pathway (Y1, Y2 and Y3) and 2 NCIs on the 2nd pathway (Y4 and Y5) reach low-level steady states whereas Y6 keeps accumulating, (iii) the NCI profiles between the (deficient) in vivo-like system with extra-large CI pool size and the in vitro reference reactions (Row 5 and Row 3 of Fig. 6) are very similar. These observations corroborate with conclusions made on the 2 previous in vivo-like systems that an emergent property is exhibited following interactions between the enzyme inhibition and small pool size CI turnover. Initial substrate concentration in Fig. 6 is reduced to 5 mM (rather than 500 mM) due to the substrate inhibition nature. This alteration however is avoided for the 2nd in vitro reference reaction and for the 2nd pathway of the (deficient) in vivo-like system with extra-large CI pool size (Row 3 and Row 5 of Fig. 6).

To separate the effects of enzyme inhibition and CI pool size for the in vivo-like system, it is observed that (i) high enzyme inhibition strength does not noticeably reduce steady state NCI concentrations (Fig. S3A, Supplementary material), (ii) alteration of CI pool size does not noticeably affect NCIs levels on the 1st pathway whereas a reduction in CI pool size can result in a further decrease of NCI levels on the 2nd pathway (Fig. S3B, Supplementary material). These properties for this in vivo-like system (Fig. 2(C)) are different to those for the other 2 in vivo-like systems (i.e.,
Fig. 2(A) and (B), in Supplementary material). As the NCI levels in these 3 in-vivo-like systems are unanimously low, effects of enzyme inhibition and CI pool size on NCI concentrations are likely to be practically insignificant in response to environmental changes. These results might underpin the well-observed metabolic robustness (Kitano, 2007; Stephanopoulos and Vallino, 1991).

4.4. Fig. 2(A)–(C): metabolic stability propagation from one pathway to the other

When the difference is only on inhibition topology (Fig. 2: A, B and C), the 3 in-vivo-like systems achieve metabolic homeostasis all based on the interaction between enzyme inhibition and CI turnover. When the enzyme inhibition is taken away, NCIs on both pathways of any system lose low-level steady states. When one significantly dampens the CI turnover effect, only NCIs on the 1st pathway of any system remain to have low-level steady states. This specific outcome is consistent with the existing knowledge that enzyme feedback control can avoid metabolite build-up (see Section 1).

4.5. The Fig. 2(D) reaction topology: branched network

When considering in-vivo-like systems containing branched backbone pathways, the Fig. 2(D) reaction topology has been used to explain establishment of spontaneous metabolic homeostasis. This example entails B1/Q1 and B2/Q2 to resemble ATP/ADP and NAD⁺/NADH in glycolysis. To globally balance the CI turnovers, an overall biomass (X) production “pathway” is introduced. This in-vivo-like system does not have reference in vitro reactions, and so extra-large CI pool size is used to remove the CI turnover effects. Without enzyme inhibition, most NCIs (i.e. Y3, Y4, Y7, Y8, Y10, Y11 and Y12) cannot be stabilized to low levels in this deficient in-vivo-like system, and so the system is unable to reach metabolic homeostasis (Fig. 7(B)). In contrast, the in-vivo-like system with the end-product inhibition acquires instantaneous metabolic homeostasis (Fig. 7(A)). When the B1 + Q1 pool size for the in-vivo-like system is increased to extra-large, the NCI profiles show decent similarities to the deficient in-vivo-like system where the enzyme inhibition is absent (Fig. 7(B) vs (C)). As before, the in-vivo-like system with extra-large CI pool size (Fig. 7(C)) cannot spontaneously reach metabolic homeostasis. However, metabolic homeostasis for the in-vivo-like system is not affected when the
B₂ + Q₂ pool size is increased to extra-large (Fig. 7(D) vs (A)). On one hand, it is the B₁/Q₁ turnover with the end-product inhibition that contributes to homeostasis establishment. On the other hand, this homeostasis-forming property does not emerge from those CI turnover topologies in which the concerned NCI flux(es) has(have) no influence on the overall CI balance. For instance, B₂/Q₂ in the Fig. 2(D) topology has been shown to balance their turnover unconditionally. Except linear pathways, it can be difficult to visually identify such CI turnover topologies.

With regards to the influence on NCIs in this in-vivo-like system, an increase of the end-product inhibition strength (Fig. S4A, Supporting material) or a decrease of the B₁ + Q₁ pool size (Fig. S4B, Supporting material) slightly suppresses their steady-state concentrations. However, a change in the B₂ + Q₂ pool size has little effects on their steady-state concentrations (Fig. S4C, Supporting material). This is consistent with the above analysis that no emergent property is present between the end-product inhibition and the B₂/Q₂ turnover.

4.6. Comments on in vivo, in-vivo-like, and in vitro systems

A clear intention of the present work is to uncover reaction topologies used by living cells to maintain their intracellular metabolic reactions at homeostasis. Understanding of such mechanisms would allow us to construct perhaps simplified multi-enzyme reaction systems that are more readily understood and manipulated. Indeed, most of the experimentally explored remain to be in vitro systems rather than in-vivo-like systems (e.g. Rollin et al., 2015). We will compare both pros and cons of in vitro and in-vivo-like systems in the forthcoming publications.

A foundation in reasoning in-vivo-like systems is based upon the spontaneous robustness of any such systems in response to drastic environmental changes. The results we used for illustration (Fig. 3) may seem to be specific, but it is obvious to us that such property is generic for any in vivo and thus in-vivo-like systems. Further work is under way in our group to provide evidence in a more systematic fashion.

5. Conclusion

Based on simple but characteristic metabolic reaction systems, this work has identified a fundamental mechanism that contributes to the establishment of metabolic stability at metabolic level (i.e. typical time scale of 0.1–1 s). This mechanism has been phrased as follows: located rather evenly in the metabolic network, CIs are present in most reactions and turnover globally using a fixed and small pool size. Working with enzyme feedback inhibition for the in vivo metabolic reaction topology, omnipresence of CIs and their balanced turnovers contribute to establish metabolic homeostasis.

By separating global turnover of the paired CIs from the carbon backbone metabolic flux for each reaction topology, we have identified that low-concentration steady states for NCIs are able to propagate from one pathway to the other. By contrast, metabolic flux analysis and the likes have always been based on the prior assumption that metabolic homeostasis had already been there. In our view, this is the reason why this unique property concerning CI turnover had not been discovered before. Broadly speaking, this work offers a new perspective for understanding the role of cofactor intermediates (e.g. the energy metabolism (Atkinson, 1968)].

Fig. 7. Reaction time profile comparison for the Fig. 2D network topology. B₁ and Q₁ are paired and each starts at 0.75 mM for their normal pool size. B₂ and Q₂ are paired and each starts at 0.4 mM for their normal pool size. B₁ + Q₁ pool of 1500 mM, and B₂ + Q₂ pool of 8000 mM, are regarded as extra-large. Inhibition strength applied is high (Kᵢ = 3.8 × 10⁻⁴).
and the presence of metabolic homeostasis in the living cell. Specifically, this work might provide clues for constructing non-natural metabolic networks either using multi-enzyme reactions or by degenerating metabolic reaction networks from the living cell.

Author contributions

Y.H.G. designed the research, Y.Y. and Y.H.G. worked together for all the work, and J.V. gave advice throughout this work and ensured the paper quality.

Acknowledgments

The authors are particularly indebted to contributions from Limei Zhang (Bioengineering College), and also to Baiji Cai (Bioengineering), Xiaoming Gao and Lingyi Tang (Applied Mathematics Department). Encouragement and support from our ECUST colleagues Professors Yingping Zhung, Siliang Zhang, and Jianhe Xu is much appreciated. The authors are grateful for financial support of State Key Laboratory of Bioreactor Engineering (China). YHG and YY are grateful to Dr. Gerold Baier (University College London) for introducing Matlab applications via a BBSRC sponsored Systems Biology course at www.sysmic.ac.uk.

Appendix A. Supplementary material

Supplemental data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.meteno.2016.06.002.

References

Atkinson, D.E., 1968. The energy charge of the acetylaldehyde pool as a regulatory parameter: interaction with feedback modifiers. Biochemistry 7, 4030–4034. Atkinson, D.E., 1977. Cellular Energy Metabolism and Its Regulation. Academic, London. Bennett, D.B., et al., 2009. Absolute metabolite concentrations and implied enzyme active site occupancy in Escherichia coli. Nat. Chem. Biol. 5, 593–599. Cornish-Bowden, A., 2012. Fundamentals of enzyme kinetics, 4th edition. Wiley-Blackwell, Weinheim. Chandra, F.A., Buzi, G., Doyle, J.C., 2011. Glycolytic oscillations and limits on robust efficiency. Science 333, 187–192. Chassagnole, C., Rizzi, N.N., Schmid, J.W., Mauch, K., Reuss, M., 2002. Dynamic modelling of the central carbon metabolism of Escherichia coli. Biotechnol. Bioeng. 1, 54–73. De la Fuente, L.M., Cortés, J.M., Valero, E., Desroches, M., Rodrigues, S., et al., 2014. On the dynamics of the adenyate energy system: homeorhesis vs homeostasis. PLoS One 9 (10), e108676. Fell, D., 1997. Understanding the Control of Metabolism. Portland, London. Gerhardt, J.C., Pardee, A.B., 1962. The enzymology of control by feedback inhibition. J. Biol. Chem. 237, 891–896. He, F., Fromon, V., Westerhoff, H.V., 2013. (In)Perfect robustness and adaptation of metabolic networks subject to metabolic and gene-expression regulation: marrying control engineering with metabolic control analysis. BMC Syst. Biol. 7, 131–152. Heinrich, R., Rapoport, T.A., 1974. A linear steady-state theory of enzymatic chains: general properties, control and effector strength. Eur. J. Biochem. 42, 89–95. Hofmeyr, J.S., Cornish-Bowden, A., 1991. Quantitative assessment of regulation in metabolic systems. Eur. J. Biochem. 200, 223–236. Ishii, N., Nakahigashi, K., Baba, T., Robert, M., Soga, T., Kanai, A., Hirasawa, T., Naba, M., Hirai, K., Hoque, A., Ho, P.Y., Kakazuy, S., Sugawara, K., Igarashi, S., Harada, S., Masuda, T., Sugiyama, N., Togashi, T., Hasegawa, M., Takai, Y., Yugi, K., Akaraka, K., Iwata, N., Toya, Y., Nakayama, Y., Nishioke, T., Shimizu, K., Mori, H., Tomita, M., 2007. Multiple high-throughput analyses monitor the response of E. coli to perturbations. Science 27, 593–597. Kacser, H., Burns, J.A., 1973. The control of flux. Symp. Soc. Exp. Biol. 27, 65–104. Keller, M.A., Zylstra, A., Castro, C., et al., 2016. Conditional iron and pH-dependent activity of a non-enzymatic glycolysis and pentose phosphate pathway. Sci. Adv. 2, e1501235. Kitano, H., 2007. Towards a theory of biological robustness. Mol. Syst. Biol. 3, 1–7. Monod, J., Changeux, J.-P., Jacob, F., 1963. Allosteric proteins and cellular control systems. J. Mol. Biol. 6, 306–329. Morowitz, H.J., Higginbotham, W.A., Matthysse, S.W., Quastler, H., 1964. Passive homeostasis is accomplished by directed over flow metabolism. Nature 500, 237–242. Reed, M.C., Lieb, A., Nihout, H.F., 2010. The biological significance of substrate inhibition: a mechanism with diverse functions. BioEssays 32, 422–429. Reich, J.G., Seifkov, E.E., 1981. Energy Metabolism of the Cell: a Theoretical Treatise. Academic, London. Rollin, J.A., del Campo, J.M., Myung, S., Sun, F., You, C., Bakovic, A., Castro, R., Chandrakany, S.K., Wu, C.-H., Adams, M.W.W., Senger, R.S., Zhang, Y.-H.P., 2015. High-yield hydrogen production from biomass by in vitro metabolic engineering: mixed sugars costabilization and kinetic modulation. PNAS 112, 4964–4969. San, K.-Y., Bennett, G.N., Berrios-Rivera, S.J., Vadali, R.V., Yang, Y.-T., Horton, E., Rudolph, F.B., Sariyar, B., Blackwood, K., 2002. Metabolic engineering through cofactor manipulation and its effects on metabolic flux redistribution in Escherichia coli. Metab. Eng. 4, 182–192. Savageau, M.A., 1974. Optimizing network of feedback control by inhibition: steady state considerations. J. Mol. Evol. 4, 139–156. Savageau, M.A., 1969. Biochemical systems analysis II. The steady state solutions for an n-pool system using a power-law approximation. J. Theor. Biol. 25, 370–379. Savageau, M.A., 1976. Biochemical Systems Analysis. Addison-Wesley, London. Smith, E., Morowitz, H.J., 2004. Universality in intermediary metabolism. PNAS 101, 11368–11373. Stephanopoulos, G.N., Artisidou, A.A., Nielsen, J., 1998. Metabolic Engineering: Principles and Methodologies. Academic, London. Stephanopoulos, G., Vallino, J.J., 1991. Network rigidity and metabolic engineering in metabolic overproduction. Science 252, 1675–1681. Teusink, B., et al., 2000. Can yeast glycolysis be understood in terms of in vitro kinetic of the constituent enzymes? Testing biochemistry. Eur. J. Biochem. 267, 5313–5329. Umbarger, H.E., 1956. Evidence for a negative-feedback mechanism in the biosynthesis of isocitric acid. Science 123, 848–849. Umbarger, H.E., Brown, B., 1957. Isocitric and isocitrate metabolism in Escherichia coli VII. A negative feedback mechanism controlling isocitric biosynthesis. J. Biol. Chem. 233, 415–420. Villadsen, J., Nielsen, J., Lindén, G., 2011. Bioreactor Engineering Principles, 3rd ed. Springer, New York. Villadsen, J., 2016. Fundamental Bioengineering (Advanced Biotechnology). Wiley, Weinheim. Wiechert, W., 2002. Modeling and simulation: tools for metabolic engineering. J. Biotechnol. 94, 37–63. Yates, R.A., Pardee, A.B., 1956. Control of pyrimidine biosynthesis in Escherichia coli by a feedback mechanism. J. Biol. Chem. 221, 757–770. Yoshino, M., Murakami, K., 2015. Analysis of the substrate inhibition of complete and partial types. SpringPlus 4, 292–300.