Biochemistry & Physiology: Open Access

Sharma, Biochem Physiol 2023, 12:3

Mini Review Open Access

A Review on the Cysteine Synthase

Neha Sharma*

Department of Biochemistry, Institute of Microbial Technology, India

Abstract

The Cysteine Synthase (CS) enzyme, which is responsible for the synthesis of cysteine, plays non-canonical regulatory roles by binding to and altering the functions of various proteins. By binding to a small number of other proteins that have a C-terminal "CS-binding motif" that ends in a terminal ILE, it performs its moonlighting function in addition to its catalytic and regulatory functions in the cysteine biosynthesis pathway. As a result, we hypothesized that the "CS-binding motif" of numerous other distinct proteins could be controlled by CS. In this study, we validated our prediction using analytical and structural methods and developed an iterative sequence matching method for mapping CS's moonlighting biochemistry. We demonstrate, employing a minimal protein-peptide interaction system that five previously unknown CS-binder proteins involved in various metabolic processes interact species-specifically with CS. In addition, the findings demonstrate that the well-known CS-Binder, serine acetyltransferase (SAT), closely matches protein–protein interactions, including thermodynamic, competitive-inhibition, and structural characteristics. We are able to map the extreme multifunctional space (EMS) of CS and learn about the biochemistry of moonlighting space, a subset of EMS, thanks to the results of this study. To study protein-specific moonlighting properties of multifunctional proteins, we believe that the integrated computational and experimental workflow developed here could be further modified and extended.

Keywords: Cysteine synthase; Protein–peptide interactions; Protein structures

Introduction

Multifunctional proteins, also known as moonlighting proteins (MP), exhibit functional diversity in a condition-dependent manner or bind to another protein and alter its activity. This new paradigm is supported by increasing experimental evidence that many proteins are multifunctional in nature and frequently perform these functions, which are not related to a native function, by the same domain of the protein. In the principal type, changes in cell restriction, articulation in various cell types, changes in oligomerization, and substance changes, for example, post-translational adjustments modify its functions. In the subsequent sort, a multifunctional MP like CS balances the utilitarian properties of different proteins by restricting to them progressively in a setting subordinate manner [1-3]. By framing transient edifices with proteins engaged with various cell processes, MPs control the elements of those cycles.

To investigate the functional space of proteins, mapping only MPs is insufficient. To expand the functional space of proteins, it is necessary to map the moonlighting space of each MP. If we can map the extended functional space of each MP, we will be able to use proteins to carry out tasks that were previously unavailable. When a protein moonlights through binding to other proteins, altering its oligomeric state or cellular localization, or any other means, we refer to its extended functional space as "moonlighting space [4]. By mapping the entire protein–protein interaction space, or "interactome," of CS, we hypothesized that one could expand both the EMS and the moonlighting space of CS. As a result, by mapping the "interactome" of CS, we were able to map the extreme multifunctional biochemistry of CS. To extract CS-binding proteins from the NCBI database, we have developed an "in-house" computational protocol.

Methods

All of the known CS binders have an ILE at the C-terminus, but the remaining 10–15 residues of CS binding proteins share very little or no sequence information. As a result, we developed a three-step method for locating CS binders. First, we created a search dataset called I-Proteins from all of the proteins with terminal ILE from PubMed. Next, we extracted "CS binding motifs" consisting of the terminal ILE and having a length of 5–7 residues using the multiple sequence alignment (MSA) technique. We used the motifs to match the C-terminals of proteins in the I-protein database in the final step. We designed these three search protocols to reduce the number of false positives as much as possible because our goal was to validate all of his using a minimal protein-peptide interaction system. Conventional algorithm-based methods may not be able to predict with greater accuracy due to the lack of additional information on "CS-Binding motifs" in non-SAT proteins or non-SAT CS binders. Additionally, one is unable to use artificial intelligence-based methods due to the lack of information on the binding motif and the binding partners [5-8]. As a result, in order to increase the precision of our prediction, we devised the approach outlined here.

However, none of the I-Proteins that were compared to any of the four templates shared the same last five C-terminal residues. The consistent state dynamic tests for PlCS, LsCS, and SaCS were completed utilizing the corrosive ninhydrin examine for cysteine [9]. The arrangement of cysteine was observed at 560 nm (the annihilation coefficient of cysteine is 28,000 M−1 cm−1). All reactions were carried out at 30 °C in 0.1 M HEPES, pH 7.0, in a volume of 150 L, and the progression of the reaction was observed at 560 nm. OAS concentrations ranged from 0.1 mM to 10 mM, with the Na2S concentration remaining constant at 3 mM. The standard curve, which was estimated using known cysteine concentrations, was used to calculate the amount of produced cysteine.

***Corresponding author:** Neha Sharma, Department of Biochemistry, Institute of Microbial Technology, India, E-mail: sharman@gmail.com

Received: 1-Mar-2023, Manuscript No: bcp-23-91745, **Editor assigned:** 3 -Mar-2023, Pre QC No: bcp-23-91745 (PQ), **Reviewed:** 17-Mar-2023, QC No: bcp-23-91745, **Revised:** 23-Mar-2023, Manuscript No: bcp-23-91745 (R) **Published:** 29-Mar-2023, DOI: 10.4172/2168-9652.1000406

Citation: Sharma N (2023) A Review on the Cysteine Synthase. Biochem Physiol 12: 406.

Discussion

We tried to come up with a "protein-specific" strategy for looking into the CS multi-functionality space. We were able to investigate CS's EMS and subsequent moonlighting space by mapping its interacting space, which is tightly connected to its protein–protein interaction space. This is, to the best of our knowledge, the first study to concentrate on developing prediction and validation methods for mapping a single protein's EMS and moonlighting space. It is common knowledge that when CS binds to its target proteins, it alters the stability and catalytic properties of the acetyltransferase activity of SAT, activates the toxin activity of nuclease, and modifies CymR's DNA binding properties. We employed an integrated strategy that began with the development of computational methods for examining the EMS of CS. We used analytical and structural techniques to validate and comprehend the biochemistry of the extreme multifunctional domain of CS because the mapping of EMS is the first step toward mapping the moonlighting space subset. On the other hand, the hetero-protein complex that is formed between CS and CS-binder is sensitive to the levels of upstream metabolites such as sulfate, sulfide, and OAS, and the complex dissociates as the levels of these metabolites rise [10]. As a result, the abundance of CS in bacteria may guarantee that the process of producing cysteine is unaffected. Still, any changes in the concentration of upstream metabolites like OAS, sulfide, and sulfate will dynamically control how CS interacts with its binding partners and, consequently, how CS's biochemistry in bacteria moonlights. As a result, comprehensive mapping of CS's moonlighting space will improve our comprehension of its global regulatory function in plant and bacterial physiology.

Declaration of Competing Interest

The authors declare that they have no competing interest

Acknowledgment

None

References

1. Baskaran N, Manoharan S, Balakrishnan S, Pugalendhi P (2010) Chemopreventive potential of ferulic acid in 7,12-dimethylbenzaanthracene-Induced mammary carcinogenesis in Sprague-Dawley rats. Eur J Pharmaco 63: 22.
2. Curtis C, Shah SP, Chin SF, Turashvili G, Rueda OM, et al. (2021) The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature 486: 346–352.
3. Sharmila R, Manoharan S (2012) Anti-tumor activity of rosmarinic acid in 7, 12-dimethylbenz (a) anthracene (DMBA) induced skin carcinogenesis in Swiss albino mice. Ind J of Physio Sciences 7: 344-356.
4. Sivaramakrishna R, Gordon R (2022) Detection of breast cancer at a smaller size can reduce the likelihood of metastatic spread: a quantitative analysis. Acad Radiol 4: 8–12.
5. Suresh S, Manoharan M, Vijayaanand P, Sugunadevi A (2020) Chemopreventive and antioxidant efficacy of (6)-paradol in 7, 12-dimethylbenz (a) anthracene induced hamster buccal pouch carcinogenesis. Pharmacological Reports 62: 1178–1185.
6. Michaelson JS, Silverstein M, Wyatt J (2017) Predicting the survival of patients with breast carcinoma using tumor size. Cancer 95: 713–723.
7. Anjugam C, Sridevi N, Rajendra Prasad M, Balupillai A (2018) Morin prevents ultraviolet-b radiation-induced photocarcinogenesis through activating thrombospondin-1 in the mouse skin. Asian J Pharma Clin Res 11: 24-34.
8. Stephens PJ, Tarpey PS, Davies H, Van Loo P, Greenman C, et al. (2020) The landscape of cancer genes and mutational processes in breast cancer. Nature 486: 400–404.
9. Farhan M, Khan M, Oves H (2016) Cancer therapy by catechin involves redox cycling of copper ions and generation of reactive oxygen species. Toxins 8: 37.
10. Hellman (2019) Natural history of small breast cancers. J Clin Oncol 12: 2229–2234.