Opinion

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Powerhouse of Secondary Metabolites

Andrzej Joachimiak *

Department of Biochemistry and Molecular Biology, University of Chicago, Chicago, Illinois, USA
*Corresponding author: Andrzej Joachimiak, Department of Biochemistry and Molecular Biology, University of Chicago, Chicago, Illinois, USA, E-mail: miakandrzejj@anl.gov

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Description

Microbial laccases, also known as blue copper-containing oxidases, are resistant to inhibitors like sodium azide and sodium fluoride and can function under extreme conditions like high temperature and broad pH. Lac cases of microbial origin are being investigated in various industrial sectors for the treatment of textile industry effluents, lignin degradation in biofuels, dye degradation, bio printing, and a number of other applications. With its filamentous morphology and high G+C content in its genome, the genus Streptomyces is a wealth of commercially valuable secondary metabolites and enzymes. Small lac cases from Streptomyces have a low redox potential, but their ability to function across a wide pH range, their substrate specificity, and their unusual resistance to inhibitors open up new commercial applications. However, there are no in-depth reviews of lac Streptomyces cases in the literature. The lac cases of Streptomyces origin are small and structurally composed of only two domains organized homotrimerically. Streptomyces' genome contains the genes for multi copper oxidase and multi copper polyphenol oxidase, also known as lac case like polyphenol oxidase. An attempt has been made to comprehend the genomic distribution, complex homotrimeric structural organization, and genetic manipulations to engineer lac cases with high redox potential, which can be used for a variety of commercial applications, keeping in mind the advantages of Streptomyces lac cases.

Factors Influence Dementia

A growing public health concern is the increasing incidence of Alzheimer's disease. However, recent birth cohorts in several high-income nations are estimated to have a lower age-specific dementia incidence. The adoption of healthy lifestyle practices like increased physical activity, a decrease in the incidence of cardiovascular disease, and improved access to education are all responsible for this shift. In an effort to delay or prevent the onset of dementia, there is growing interest in focusing on dementia risk factors. In its most recent report on dementia prevention, intervention, and care, the Lancet Commission identified 12 potentially modifiable risk factors and estimated that eliminating these factors at key life stages could prevent up to 40% of all cases of dementia. However, only a partial understanding exists of the mechanisms by which these factors influence dementia risk and whether or not they are truly causal. Sleep problems, depression, social isolation, and difficulty hearing may, at least partially, act as prodromal risk markers rather than causal risk factors. In addition, the proposed modifiable risk factors frequently coexist with one another and have a strong correlation. Despite this, the majority of current research focuses on bivariate relationships or select subsets of risk factors. As a result, potential networks of shared etiological pathways that could influence dementia risk in an additive manner have not been extensively measured. It is urgently necessary to gain a better understanding of the causal pathways that lead to the development of clinical dementia in order to prioritize targets for intervention studies and support prevention efforts. Global pleiotropy and the shared genetic architecture of complex traits have been revealed thanks to advancements in large, powerful genome-wide association studies. Many behavioral and disease traits have been shown to have significant bivariate genetic correlations measured by Linkage Disequilibrium (LD) score regression. This suggests that there is a lot of overlap in genetic pathways between phenotypes that seem to be different. Genomic Structural Equation Modeling (SEM) studies in the field of psychiatric genetics have revealed patterns of shared genetic architecture among a number of psychiatric disorders. This suggests that, in addition to disease-specific mechanisms, these disorders share pathophysiological mechanisms that are driven by common pleiotropic risk variants. We wanted to use these methods on AD and the main risk factors for it in this study. We hypothesized that AD and its risk factors would share complex genetic architecture, and that a factor analysis approach would suggest distinct an etiological pathways between various traits. Future research to better comprehend the potential causal biological mechanisms that link modifiable risk factors to AD will benefit from this novel application, which may aid in the discovery of shared or moderating risk factor pathways.

Focuses of Structural Genomics

Projects in structural and functional genomics aim to reduce the typical costs of structure and function assurance while simultaneously expanding our understanding of natural macromolecules. The sequencing and mapping of genomes are the primary focuses of structural genomics. Its efforts to determine each protein structure are encoded by the genome,

which also provides the location of the entire set of genes in the genome through sequencing. On the other hand, functional genomics focuses on how genes are expressed as well as the properties and functions of those genes. It tries to figure out how genes and their products interact with each other. As a result, the use of structural and functional genomics in nutrition research is outlined in this chapter. However, the best primary science labs are significantly more efficient than the average lab and, like SG fixate, are also working on testing structures. Additionally, functional genomics methods are ideal for elucidating the effects of novel beneficial foods, dietary enhancements, and nutraceuticals on global quality articulation and cell function without assuming what hazards to look for. The evaluation of the safety of foods that are hereditarily controlled makes use of methods that are straightforwardly comparable to one another. Biology research has been transformed by the emergence of the omics disciplines following large-scale sequencing projects. The availability of sequence data for entire genomes has provided structural biology with new opportunities to formulate scientific questions. In the past, structural biologists have typically concentrated on the structural characterization of systems that have already been thoroughly characterized from a cell and molecular biology, biochemical, and biological perspective. As a result, the selection of research projects has been heavily influenced by previous research conducted by scientists in other fields. The abundance of newly discovered protein sequences has now made it possible to select research projects with less bias. This, in addition to the development of mature technologies for the effective production of recombinant proteins, has resulted in a rapid expansion of the number of potential research systems. There have been two major research themes: Can the fundamental shapes of all proteins be predicted from the structures of uncharacterized or novel protein sequences? To enable a deeper comprehension of fundamental molecular mechanisms and to lay the groundwork for applied biomedical research, is it possible to methodically identify the structures of a large number of proteins from important organisms? Several academic researchers started pilot projects to answer these questions, and companies like SGX, Integrative Proteomics and Syrrx started using high-throughput methods to find the structures of potential drug target proteins. This was the beginning of structural genomics, which has grown to play a significant role in structural biology since its inception more than ten years ago. The main themes of structural genomics and how it affects biomedicine and drug discovery will be discussed in this review.