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The Art of Successful Translation Arabidopsis Seed Germination

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Abstract

I'm happy to share the first papers in our recently launched journal, Translational Proteomics, as we welcome in the New Year. Elsevier's strong backing and the passionate involvement of the Journal's Associate Editors and Editorial Board members have made this possible. Proteomics researchers and clinicians in academia and industry have grown increasingly frustrated with the challenges of translating fundamental proteomics discoveries to therapeutic applications over the years. The lack of communication between fundamental scientists and physicians who received their training using conceptions that are at odds with one another is one of the causes of this barrier. The latter demand quick actions on patients rather than total certainty, whilst the former desire to control and comprehend all aspects.

Keywords: Translational proteomics; Biological research cardiovascular disorders

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Introduction

Translational research is frequently seen as a two-way street that runs from bench to bedside and back again [1]. The patient and his disease should be the centre of a roundabout where fundamental, translational, and clinical scientists from the public and private sectors are constantly interacting with one another [2]. Proteomics research requires more than just a bridge to connect discoveries with treatments [3]. To fill all the gaps and enable cross-fertilization and synergies, networks of road connectors are needed. More than merely intriguing ideas and trending phrases, translational research and translational proteomics aim to enhance people's quality of life [4]. We hope to support the scientific and medical communities with the launch of Translational Proteomics [5]. The Journal will offer a venue for manuscripts describing proteome studies, from early discovery to validation and the bedside, by concentrating on connecting fundamental proteomics research to its final clinical applications [6]. The distinguishing feature of Translational Proteomics is its intention to publish multidisciplinary studies as single papers, without information loss studies that today would probably be split into two or three different pieces [7]. The Journal examines every facet of human proteome while utilising multidisciplinary strategies to clarify intricate disease processes [8]. Linking basic science and clinical research is obviously stressed in order to spread new discoveries quickly [9]. The discovery, development, and validation of biomarkers linked to complex human illnesses will be favoured with special emphasis [10]. This will help with early disease diagnosis, disease stratification, disease prognosis, disease monitoring, and treatment response prediction [11].

Discussion

Because of the enormous obstacles that scientists have had to overcome, such as wide genetic polymorphism, a huge heterogeneity of diseases, such as diabetes, cancer, and infections, as well as stringent societal constraints regarding ethics, finances, and time, their understanding of human diseases is still very limited. Why do two people with the same condition and the same clinical and laboratory data respond to the same treatment differently? Why do people encounter various adverse effects? Due to this intricacy, many scientists now employ animal models to simulate human diseases as closely as possible in order to predict the effects of drugs. This will facilitate the earliest possible disease diagnosis, stratification, prognosis, monitoring, and treatment efficacy prediction [12]. In comparison to actual humans, we currently know a lot more about effective human disease treatments in mouse models [13]. This emphasises the unique characteristics of each species and the extreme diversity of biological systems. Basic scientists nowadays would prefer

to expand the reach of their biological discoveries to as many patients as possible, but their universities' or hospitals' capability frequently prevents them from doing so. By collaborating with pharmaceutical and biotechnology firms, translational researchers can more effectively get their discoveries to patients [14]. Pharmaceutical firms are prepared for the push toward greater translational research to both catalyse and participate in the medical applications of fundamental biological research as their drug development pipelines in treatments and diagnostics are running dry [15]. Being on the cusp of tradition and innovation So, in the disciplines of applied human proteomics, Translational Proteomics is meant for academic, industrial, and clinical researchers, medical professionals, pharmaceutical scientists, biochemists, clinical chemists, and disease molecular biologists. Oncology, neurology, immunology, cardiovascular disorders, viral diseases, and any internal medicine condition are a few examples of diseases. Additionally, a number of special sections, including Systems Biology and Integrative Bioinformatics, Clinical Proteomics and Personalised Medicine, Comparative Proteomics and Drug Development, Medical Bioinformatics and Biostatistics, and Food and Health, will be highlighted. An invitation to join the board as Associate Editors has been accepted by a group of highly esteemed professionals who cover most of the aforementioned fields as well as the basic and clinical elements of human sciences. An online-only, open access journal is called Translational Proteomics. Copyright will be retained by authors. To assure the quality of human research, the journal publishes original research submissions via an exhaustive peer review procedure. It additionally publishes reviews and thoughts. Finally, I would like to take this occasion to congratulate each and every one of the editorial board members who have recently joined our organisation. We are starting an exciting journey together to advance and promote translational proteomics. All the participants in our trip urgently need to think outside their own box of test tubes since the art of translation is growing more nuanced and intricate. The editorial board members all firmly feel that it is our societal obligation and responsibility to make translation a priority in the larger biomedical community. A significant worry for the management for plant propagation as well as for maximising agricultural yield, the switch during seed germination from a quiescent metabolic state in a dry mature seed to a proliferative metabolic state in a robust seedling is essential. This study explains in great detail how protein synthesis changes over the duration of germination, proving that mRNA translation is both sequential and selective at this period. Cycloheximide, a translation inhibitor, completely inhibited the germination process, demonstrating the importance of mRNA translation for Arabidopsis seed germination. However, there has been no discussion of the kinetics of protein turnover and the selectivity of protein synthesis (mRNA translation) during Arabidopsis seed germination. Using our comprehensive understanding of the Arabidopsis seed proteome the transition during seed germination from a quiescent metabolic state in a dry mature seed to a proliferative metabolic state in a vigorous seedling is crucial for plant proliferation as well as for increasing agricultural productivity. This study demonstrates that mRNA translation is sequential and selective during this time period by explaining in great detail how protein synthesis changes during the course of germination. The total inhibition of germination by the translation inhibitor Cycloheximide highlights the significance of mRNA translation for Arabidopsis seed germination. The kinetics of protein turnover and the selectivity of protein synthesis mRNA translation during Arabidopsis seed germination, however, have not been covered. By utilising our thorough comprehension of the Arabidopsis seed proteome following the recommendations outlined in the National Academy of Medicine's study on the creation of omics-based tests for clinical trials played a significant role in the design of both successful clinical tests. One of the main factors to take into account while creating an omics-based test is the potential for overfitting to the data, which can lead to tests performing dramatically worse than expected when they undergo independent validation in other test populations.

Conclusion

As a result, these risks must be minimised in the study design in order to prevent the problem of many candidate biomarkers failing to survive the arduous transition to clinical usage. Tests of the biomarkers during the discovery stage in numerous populations thus averaging the diverse genetic and LC-MRM-MS analyses are taken into account. Typically, diagnostic tests are created on platform A of technology before being released for clinical usage on platform B of the same technology. The rationale for this is that although technology platform B is appropriate for high throughput, low cost, and low complexity clinical testing, and technology platform A is appropriate for low throughput, higher cost, highly multiplexed discovery investigations. A platform based on capture agents, such as antibodies or modified) aptamers, with deployment is an example of discovery or verification employing an SRM-MS platform. In complex mixes like blood, these platforms might be constrained by cross-reactivities as a result, they often perform better clinically with panels containing a few number of proteins the expense of tuning each antibody pair for ELISA experiments is high. And important cross-reactivities might still exist even after optimization. Developing protein capture agents holds significant promise for addressing these issues and reducing cross-reactivities. The transition from technological platform A to platform B, however, is fraught with danger. First, analyses tested on platform A may perform analytically quite differently from those measured on platform B. Second, based on the correlation value utilising the empirical distribution of correlation scores for peptides from various proteins, there is no certainty that the analytes detected on technology platform A are the same analytes as measured by confidence. Figure 2 for the Preterm discovery assay shows this. For plant propagation as well as for maximising agricultural yield, the switch during seed germination from a quiescent metabolic state in a dry mature seed to a proliferative metabolic state in a robust seedling is essential. This study explains in great detail how protein synthesis changes over the duration of germination, proving that mRNA translation is both sequential and selective at this period. Cycloheximide, a translation inhibitor, completely inhibited the germination process, demonstrating the importance of mRNA translation for Arabidopsis seed germination. However, the kinetics of protein turnover and the selectivity of mRNA translation during the germination of Arabidopsis seeds have not

yet been discussed. Using our comprehensive understanding of the Arabidopsis seed proteome.

Acknowledgement

None

Conflict of Interest

None

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