Nitric oxide (NO) and hydrogen sulfide (H₂S) are two major gaseous signaling molecules that regulate diverse physiological functions. Recent publications indicate the regulatory role of H₂S on NO metabolism. In this chapter, we discuss the latest findings on H₂S–NO interactions through formation of novel chemical derivatives and experimental approaches to study these adducts. This chapter also addresses potential H₂S interference on various NO detection techniques, along with precautions for analyzing biological samples from various sources. This information will facilitate critical evaluation and clearer insight into H₂S regulation of NO signaling and its influence on various physiological functions.
Familial prion protein (PrP) mutants undergo conversion from soluble and protease-sensitive to insoluble and partially protease-resistant proteins. Cyclin-dependent kinase 5 (Cdk5) phosphorylation of wild type PrP (pPrP) at serine 43 induces a conversion of PrP into aggregates and fibrils. Here, we investigated whether familial PrP mutants are predisposed to Cdk5 phosphorylation and whether phosphorylation of familial PrP mutants increases conversion. PrP mutants representing three major familial PrP diseases and different PrP structural domains were studied. We developed a novel in vitro kinase reaction coupled with Thioflavin T binding to amyloid structure assay to monitor phosphorylation-dependent amyloid conversion. Although non-phosphorylated full-length wild type or PrP mutants did not convert into amyloid, Cdk5 phosphorylation rapidly converted these into Thioflavin T-positive structures following first order kinetics. Dephosphorylation partially reversed conversion. Phosphorylation-dependent conversion of PrP from α-helical structures into β-sheet structures was confirmed by circular dichroism. Relative to wild type pPrP, most PrP mutants showed increased rate constants of conversion. In contrast, non-phosphorylated truncated PrP Y145X (where X represents a stop codon) and Q160X mutants converted spontaneously into Thioflavin T-positive fibrils after a lag phase of over 20 h, indicating nucleation-dependent polymerization. Phosphorylation reduced the lag phase by over 50% and thus accelerated the formation of the nucleating event. Consistently, phosphorylated Y145X and phosphorylated Q160X exacerbated conversion in a homologous seeding reaction, whereas WT pPrP could not seed WT PrP. These results demonstrate an influence of both the N terminus and the C terminus of PrP on conversion. We conclude that post-translational modifications of the flexible N terminus of PrP can cause or exacerbate PrP mutant conversion.
Stephanie:

Plant Molecular Biology

**TaRAR1 and TaSGT1 associate with TaHsp90 to function in bread wheat (Triticum aestivum L.) seedling growth and stripe rust resistance.**

Plant Mol. Biol.


Guan-Feng Wang, Renchun Fan, Xianping Wang, Daowen Wang, Xiangqi Zhang

RAR1 and SGT1 are important co-chaperones of Hsp90. We previously showed that TaHsp90.1 is required for wheat seedling growth, and that TaHsp90.2 and TaHsp90.3 are essential for resistance (R) gene mediated resistance to stripe rust fungus. Here, we report the characterization of TaRAR1 and TaSGT1 genes in bread wheat. TaRAR1 and TaSGT1 each had three homoeologs, which were located on wheat groups 2 and 3 chromosomes, respectively. Strong inhibition of seedling growth was observed after silencing TaSGT1 but not TaRAR1. In contrast, decreasing the expression of TaRAR1 or TaSGT1 could all compromise R gene mediated resistance to stripe rust fungus infection. Protein-protein interactions were found among TaRAR1, TaSGT1 and TaHsp90. The N-terminus of TaHsp90, the CHORD-I and CHORD-II domains of TaRAR1 and the CS domain of TaSGT1 may be instrumental for the interactions among the three proteins. Based on this work and our previous study on TaHsp90, we speculate that the TaSGT1-TaHsp90.1 interaction is important for maintaining bread wheat seedling growth. The TaRAR1-TaSGT1-TaHsp90.2 and TaRAR1-TaSGT1-TaHsp90.3 interactions are involved in controlling the resistance to stripe rust disease. The new information obtained here should aid further functional investigations of TaRAR1-TaSGT1-TaHsp90 complexes in regulating bread wheat growth and disease resistance.

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Nature Plants:

1) **Gates Foundation backs high-risk science for big wins!** Natasha Gilbert

2) **Protein turnover in plant biology** Clark J. Nelson & A. Harvey Millar

The protein content of plant cells is constantly being updated. This process is driven by the opposing actions of protein degradation, which defines the half-life of each polypeptide, and protein synthesis. Our understanding of the processes that regulate protein synthesis and degradation in plants has advanced significantly over the past decade. Post-transcriptional modifications that influence features of the mRNA populations, such as poly(A) tail length and secondary structure, contribute to the regulation of protein
synthesis. Post-translational modifications such as phosphorylation, ubiquitination and non-enzymatic processes such as nitrosylation and carbonylation, govern the rate of degradation. Regulators such as the plant TOR kinase, and effectors such as the E3 ligases, allow plants to balance protein synthesis and degradation under developmental and environmental change. Establishing an integrated understanding of the processes that underpin changes in protein abundance under various physiological and developmental scenarios will accelerate our ability to model and rationally engineer plants.

Nathen:

Genomic analysis of parallel-evolved cyanobacterium Synechocystis sp. PCC 6803 under acid stress.


Author information

Abstract

Experimental evolution is a powerful tool for clarifying phenotypic and genotypic changes responsible for adaptive evolution. In this study, we isolated acid-adapted Synechocystis sp. PCC 6803 (Synechocystis 6803) strains to identify genes involved in acid tolerance. Synechocystis 6803 is rarely found in habitats with pH < 5.75. The parent (P) strain was cultured in BG-11 at pH 6.0. We gradually lowered the pH of the medium from pH 6.0 to pH 5.5 over 3 months. Our adapted cells could grow in acid stress conditions at pH 5.5, whereas the parent cells could not. We performed whole-genome sequencing and compared the acid-adapted and P strains, thereby identifying 11 SNPs in the acid-adapted strains, including in Fo F1-ATPase. To determine whether the SNP genes responded to acid stress, we examined gene expression in the adapted strains using quantitative reverse-transcription polymerase chain reaction. sll0914, sll1496, sll0528, and sll1144 expressions increased under acid stress in the P strain, whereas sll0162, sll0163, slr0623, and slr0529 expressions decreased. There were no differences in the SNP genes expression levels between the P strain and two adapted strains, except for sll0528. These results suggest that SNPs in certain genes are involved in acid stress tolerance in Synechocystis 6803.