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## Research Direction

Plant RNA biology

## Research Unit

National Key Laboratory of Plant Molecular Genetics

# Xiaofei Yang

## Personal Profile

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2015.03- 2022.02, Postdoctoral fellow, John Innes Centre, UK

2008.09-2015.02, Ph.D., Institute of Plant Physiology and Ecology, SIBS, CAS

2004.09-2008.07, B.S., Nanchang University, Jiangxi, China

## Research Work

The environmental signals caused by global climate change have a significant impact on the growth and development of plant and agricultural industry. Plants sense the external environment signals through a various of ways and regulate gene expression to respond to environmental changes. The intermediate molecule of gene expression, the vivo folding of RNA, depends on the cellular environment. Alteration of RNA structure by environmental changes can turn "on" or "off" the expression of downstream genes, thus functioning as the "molecular switch". However, the knowledge of plant RNA switching is still very limited. The main research projects include:

1) Identification and functional analysis of plant RNA switches

2) Agronomic trait design and gene editing breeding based on RNA switch

## Main Achievements

### (1) RNA G-quadruplex structure regulates protein translation and plant growth and development

The plasticity of gene expression is regulated by a variety of functional RNA structural elements and is closely related to specific biological processes. For example, a complex RNA structure called the G4-quadruplex (RG4) has been related to cancer and neurodegenerative diseases in mammals. Studies on RG4 in plants are initiated recently and limited, while some studies have shown that RG4 is associated with development of sieve tube in plants. However, due to the lack of quantitative methods to detect RG4 structure in living cells, there is a lack of direct evidence that RG4 regulates the expression of key genes, which limits the in-depth study on the biological functions of RG4.

In order to overcome the shortcomings of this technique, we designed a brand-new method, SHALiPE-seq, to quantitatively measure RG4 folding in vivo. SHALiPE-seq detected hundreds of RG4s in rice and Arabidopsis, providing the first direct evidence that RG4 is present and plays an important regulatory role in eukaryotic cells.

### (2) RNA G-quadruplex structure modulates plant cold-responsive

Using SHALiPE-seq method, we quantitatively measured the RG4 folding of Arabidopsis thaliana with and without cold treatment. The folding score of RG4 significantly increased in response to cold treatment, indicating that low temperature can promote the RG4 folding in plants. Further analysis showed cold induced RG4 folding contributes to repressing RNA decay. Genetic and physiological analysis demonstrated that the mutation on an individual cold-responsive RG4 structure attenuated the cold induced growth inhibition on Arabidopsis. This study demonstrated that RNA G-quadruplex structure acts as “cold sensor” in plants.

### (3) RNA structure modulates translational subgenome expression asymmetry

Polyploidy is one of the major routes to speciation in plants. Many important crops, such as wheat and rape are allopolyploidy species. Huge number of mutations in orthologous genes lead to subfunctionalization and asymmetric expression of genes, which may play a potential role in polyploid dominance. However, the molecular mechanisms that how the mutations across orthologous genes contribute to the subfunctionalization of orthologous genes remain illusive.

Sequence variation is one of the important factors of the changes in RNA structure, which can greatly alter the gene functionality. Our group developed a robust method, SHAPE-Structure-seq, for RNA structure determination. SHAPE-Structure-seq can determine the RNA structure at single nucleotide resolution and at transcriptome-wide, therefore can effectively distinguish the RNA structure differences between homologous genes. We mapped the RNA structurome and translatome of more than 13000 pairs of homologous genes in tetraploid wheat. We found the differences in RNA structure between homologous genes lead to the translation asymmetry and gene expression plasticity. Interestingly, the mutations that change the RNA structure of homologous genes had a higher fixed index than those do not change the RNA structure, suggesting RNA structure plays a role in SNV selection in wheat domestication. This study provides the first evidence of translational asymmetry in polyploidy plants, and revealed RNA structure provides important driving force of wheat domestication.

## Publications

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2. Yu H*#, Qi Y*, Yang B, **Yang X**, Ding Y#. G4Atlas: a comprehensive transcriptome-wide G-quadruplex database. ***Nucleic Acids Res.*** 2022 Oct 16, gkac896
3. Liu H, Chu Z#, **Yang X#**. A Key Molecular Regulator, RNA G-Quadruplex and its function in plants. ***Front Plant Sci.*** 2022 Jun 15, 926953
4. **Yang X***, Yu H*, Sun W, Ding L, Li J, Cheema J, Ramirez-Gonzalez R, Zhao X, Martin A, Lu F, Liu B, Uauy C, Ding Y, Zhang H. Wheat in vivo RNA structure landscape reveals a prevalent role of RNA structure in modulating translational subgenome expression asymmetry. ***Genome Biol.*** 2021 Nov 30,22:326.
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10. Deng H, Cheema J, Zhang H, Woolfenden H, Norris M, Liu Z, Liu Q, **Yang X**, Yang M, Deng X, Cao X, Ding Y. Rice In Vivo RNA Structurome Reveals RNA Secondary Structure Conservation and Divergence in Plants. ***Mol Plant.*** 2018 Apr 2;11(4):607-622.

11. **Yang X***, Yang M*, Deng H*, Ding Y. New Era of Studying RNA

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12. **Yang X**, Wang Y, Chen S, Li J, Shen H, Guo F. PBR1 selectively controls biogenesis of photosynthetic complexes by modulating translation of the large chloroplast gene Ycf1 in Arabidopsis. ***Cell Discov.*** 2016; 2:16003