

Xue Zhang, PhD

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SKILLS & PROFICIENCIES

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| • Science communication | • Command line proficiency: (Unix, bash, R) | Chinese <div><div></div></div> |
| • Data Analysis (NGS sequencing Analysis, Data Mining) | • Imaging analysis: Cell Profiler, Image-J, FISH-quant, Cellpose (limited proficiency) | English <div><div></div></div> |
| • Molecular biology, Cell biology, Chromatin biology | | Swedish <div><div></div></div> |

PROFESSIONAL EXPERIENCE

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| Since
Sep 2020 | ● Postdoctoral Researcher (plant biology department, Swedish University of Agricultural Sciences, Uppsala)
Project: transcription coordination at convergent overlapping sense/antisense gene pairs at single locus level in <i>Arabidopsis thaliana</i> (Stefanie Rosa's lab) <ul style="list-style-type: none">• Selected candidates for downstream experiments through customized bioinformatics analysis (analyzing bulk stranded RNA-seq, ChIP-seq and scRNA-seq datasets, and statistical analysis (Slurm, conda, R, python)• Pioneered the novel application of RNA detection in single cells by smFISH methodology in plant cryosections and established its workflow (automated RNA probe sequences design – smFISH experiments – microscopy imaging – imaging analysis)• Created and led a new project regarding the involvement in cytokinin biosynthesis of a long non-coding RNA• Wrote and applied for a research proposal that led to the award of The Nilsson-Ehle Endowments fund (Nov.2021)• Presented postdoc projects three times in public with over 50 attendances and a poster presentation at the international conference |
| Oct 2015
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Nov 2019 | ● Researcher (IBMP, University of Strasbourg, Strasbourg, France)
Projects: three complex projects about the biological function characterization of histone methyltransferases in <i>Arabidopsis thaliana</i> (Wen-Hui Shen's lab) <ul style="list-style-type: none">• Discovered and proved histone proteins interaction with diverse genomic regions by implementing chromatin immunoprecipitation followed by qPCR assay and ChIP-seq analysis across three different projects• Generated over ten fluorescent-tagged transgenic materials for downstream genetic analyses through nuclei acid extraction, PCR, cloning and protein expression in bacteria, yeast and plants.• Identified interaction proteomics of three proteins through TAP technology in collaboration with Ghent-VIB center and immunoprecipitation followed by nano LC-MS/MS• Characterized a multi-protein complex through protein expression, protein extraction, western blotting and protein-protein interaction analyses |

EDUCATION

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| 2015-2019 | ● PhD in Molecular and Cell Biology (University of Strasbourg , Strasbourg, France) |
| 2012-2015 | ● MSc in Plant Protection (Zhejiang University , Hangzhou, China) |
| 2018-2012 | ● BSc in Plant Protection (Hainan University , Haikou, China)
Outstanding graduate (Top3, 2012); Miyoshi student (Top4, 2010&2012); The comprehensive scholarships' winner (top 10, 2008 to 2012) |

RELATED TRAINING COURSE

NBIS workshop-**Introduction to bioinformatic using NGS data**; SLUBI workshop-**Analysis of High Throughput Sequencing RNA-Seq**; NBIS workshop-**Epigenomics Data Analysis: from bulk to single cell**; SLU course-**Introduction to statistical learning**;

PUBLICATIONS LIST

- **Xue Zhang**, Alejandro Cárdenas, Susan Ducan, Stefanie Rosa* (in preparation). Single RNA molecules detection *in situ* by smFISH in *Arabidopsis* tissue cryosections
- **Xue Zhang**, Stefanie Rosa* (in preparation). Investigation of transcription coordination in convergent overlapping sense/antisense gene pairs at single locus level in *Arabidopsis thaliana*
- **Xue Zhang**, Julie Zumsteg, Mathiu Erhardt, Wen-Hui Shen and Alexandre Berr* (in preparation). The histone methyltransferase SDG26 is involved in the responses to cold stress in *Arabidopsis thaliana*
- **Xue Zhang**, Dominique Eeckhout, Geert De Jaeger, Wen-Hui Shen, Alexandre Berr* (in preparation). The histone methyltransferase SDG26 forms a multiprotein complex involved in the autonomous pathway to regulate *FLC* and *SOC1* expression in *Arabidopsis thaliana*
- **Xue Zhang**, Rozenn Ménard, Ying Li, Gloria M. Coruzzi, Thierry Heitz, Wen-Hui Shen and Alexandre Berr* (2019). SDG8 potentiates the sustainable transcriptional induction of the pathogenesis-related defense genes *PR1* and *PR2* in *Arabidopsis*. *Frontiers in Plant Science*, doi: 10.3389/fpls.2020.00277.
- Alexandre Berr, **Xue Zhang**, Wen-Hui Shen (2016). Reciprocity between active transcription and histone methylation. *Biologie Aujourd'hui*. 210 (4): 269- 282.
- Chulong Zhang, **Xue Zhang**, et al. (2018). *M. fengyangensis* bio-agent prep., CN104774770B, filed 03/28/2015, issued 01/05/2018.
- Lijuan Mao, Zhenzhu Su, Chulong Zhang, **Xue Zhang**, et al. (2018). Production of *Muscodor fengyangensis* bio-agent, CN104798820B, filed 03/28/2015, issued 02/09/2018.
- Xiaoxiao Feng, **Xue Zhang**, et al. (2017). A way to accelerate the growth of *M. fengyangensis* and the pre-treatment with activated carbon particles, CN104785231B, filed 03/28/2015, issued 07/28/2017