会议注册

大会官网：http://www.plantprotein.org.cn/

注册费标准

注册类型	优惠注册（11 月 17 日前）	普通注册（11 月 17 日后）
参会代表	￥1500	￥1800
在读学生	￥1000	￥1300
公司代表	￥1600	￥1900

1. 注册会议请在网站上下载报名注册表，填写后发送至 **plantprotein_cll@163.com**。缴费前与报名负责人联系确认注册成功，以防出现遗漏影响参会。
2. 同单位 10 人以上团组注册，可享受注册费 8 折优惠。
3. 现场注册时请与会代表携带本人身份证，学生代表需携带学生证。已交费代表请带好汇款凭证，以备核对。
4. 注册代表权益：正式代表和学生代表，可以参加会议组织的所有活动。注册费包括会务费、资料费、12 月 18 日-20 日午餐及晚餐费用。
5. 退费说明：已交费的参会代表因个人原因不能参会或其他原因需要退款，请提前两周与会务组取得联系。
6. 退费原则：2016 年 11 月 1 日前退还所交款项的 100%，11 月 1 日-30 日退还所交款项的 60%，12 月 3 日及以后恕不退款。

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注意：请务必在汇款留言处注明参会人单位，姓名

报名注册联系人：

常丽丽，中国热带农业科学院，plantprotein_cll@163.com

征集论文摘要（abstract）范围及要求（参照附件模板）

投稿论文摘要（abstract）收录入会议论文摘要集。

参会代表的研究成果，均可投稿，具体要求如下：

征文范围：有关蛋白质组学及相关领域近年来研究的学术成果，以中/英文论文摘要形式投稿。

稿件要求：每篇论文摘要按正式发表论文要求撰写，300 字以内，使用 Word 软件撰写。文责自负（参照附件模板）。

字体要求：标题：宋体/Times New Roman，四号加粗。

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单位、地址、邮编、E-mail：宋体/Times New Roman，小五号居中。

摘要：宋体/Times New Roman，五号。

投稿方式：请将相应文件发送到邮箱 plantprotein_wd@163.com **，联系人：王丹。**

截止日期：论文摘要投稿截止日期为 2016 年 12 月 04 日

学术发言：大会和分会发言的参会代表请在注册当日（2016 年 12 月 17 日）将报告材料交至大会组委会，报告材料须为 Powerpoint 文件，存储于移动硬盘、USB 闪盘或光盘之中，大会提供笔记本电脑和幻灯放映设备，不接受个人电脑接入。如有特殊需求，请提前与大会会务组联系。

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摘要模板:

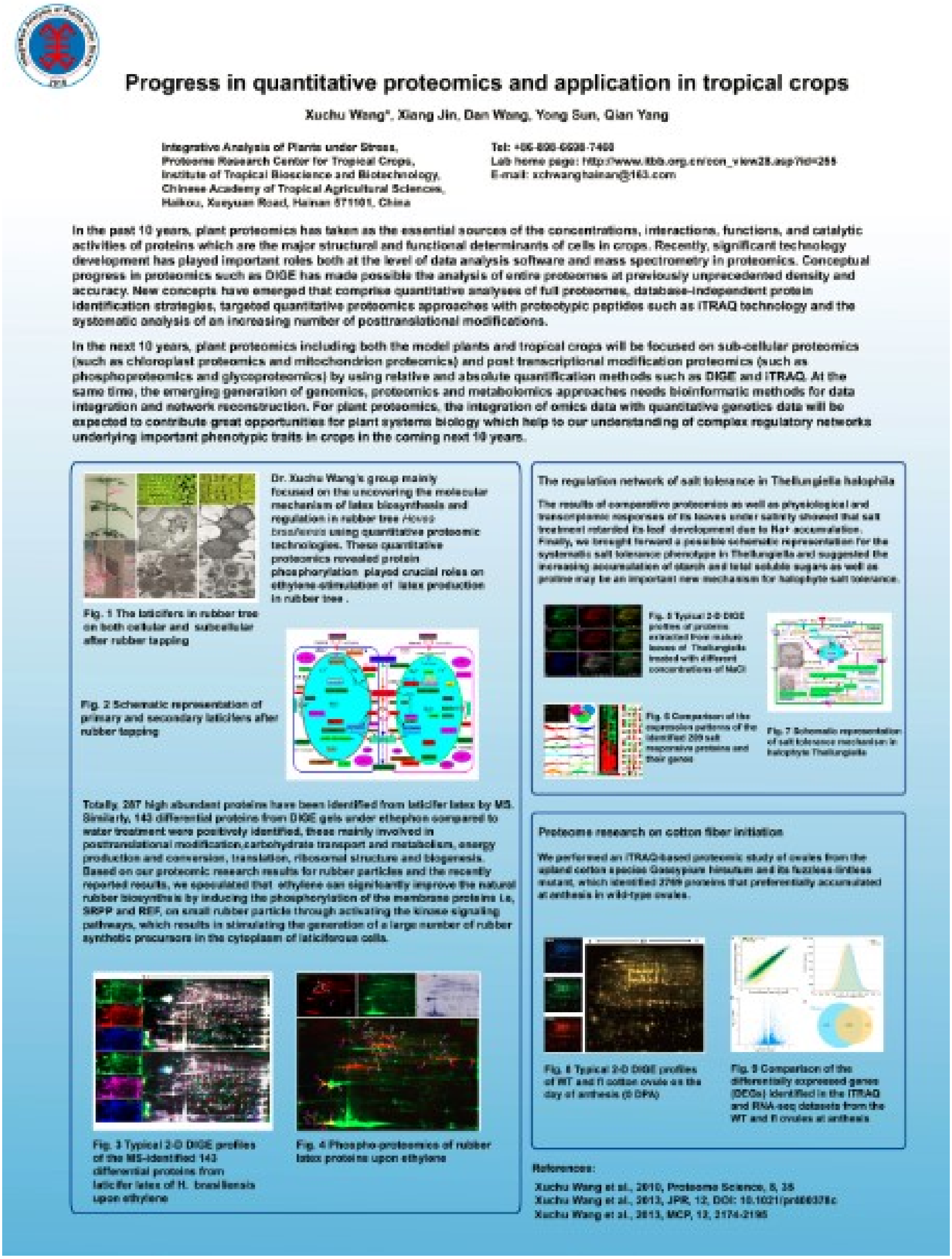
Comprehensive Proteomics Analysis of Laticifer Latex Reveals New Insights into Ethylene Stimulation of Natural Rubber Production

Xuchu Wang, Dan Wang, Yong Sun, Qian Yang, Lili Chang, Limin Wang, Xueru Meng, Qixing Huang, Xiang Jin, Zheng Tong.

Key Laboratory of Biology and Genetic Resources for Tropical Crops, Institute of Tropical Biosciences and Biotechnology, Chinese Academy of Tropical Agricultural Sciences, Haikou Hainan 571101, China. (Correspondence email: xchwanghainan@163.com)

Ethylene is a stimulant to increase natural rubber latex. After ethylene application, both fresh yield and dry matter of latex are substantially improved. Moreover, we found that ethylene improves the generation of small rubber particles. However, most genes involved in rubber biosynthesis are inhibited by exogenous ethylene. Therefore, we conducted a proteomics analysis of ethylene-stimulated rubber latex, and identified 287 abundant proteins as well as 143 ethylene responsive latex proteins (ERLPs) with mass spectrometry from the 2-DE and DIGE gels, respectively. In addition, more than 1,600 proteins, including 404 ERLPs, were identified by iTRAQ. Functional classification of ERLPs revealed that enzymes involved in post-translational modification, carbohydrate metabolism, hydrolase activity, and kinase activity were overrepresented. Some enzymes for rubber particle aggregation were inhibited to prolong latex flow, and thus finally improved latex production. Phosphoproteomics analysis identified 59 differential phosphoproteins; notably, specific isoforms of rubber elongation factor and small rubber particle protein that were phosphorylated mainly at serine residues. This post-translational modification and isoform-specific phosphorylation might be important for ethylene-stimulated latex production. These results not only deepen our understanding of the rubber latex proteome but also provide new insights into the use of ethylene to stimulate rubber latex production.

墙报模板:



Progress in quantitative proteomics and application in tropical crops

Xuchu Wang*, Xiang Jin, Dan Wang, Yong Sun, Qian Yang

Integrative Analysis of Plants under Stress,
Proteome Research Center for Tropical Crops,
Institute of Tropical Bioscience and Biotechnology,
Chinese Academy of Tropical Agricultural Sciences,
Haikou, Xueyuan Road, Hainan 571101, China

Tel: +86-898-6698-7400
Lab home page: http://www.itbb.org.cn/con_view28.asp?id=255
E-mail: xchwanghainan@163.com

In the past 10 years, plant proteomics has taken as the essential sources of the concentrations, interactions, functions, and catalytic activities of proteins which are the major structural and functional determinants of cells in crops. Recently, significant technology development has played important roles both at the level of data analysis software and mass spectrometry in proteomics. Conceptual progress in proteomics such as DIGE has made possible the analysis of entire proteomes at previously unprecedented density and accuracy. New concepts have emerged that comprise quantitative analyses of full proteomes, database-independent protein identification strategies, targeted quantitative proteomics approaches with proteotypic peptides such as iTRAQ technology and the systematic analysis of an increasing number of posttranslational modifications.

In the next 10 years, plant proteomics including both the model plants and tropical crops will be focused on sub-cellular proteomics (such as chloroplast proteomics and mitochondrion proteomics) and post transcriptional modification proteomics (such as phosphoproteomics and glycoproteomics) by using relative and absolute quantification methods such as DIGE and iTRAQ. At the same time, the emerging generation of genomics, proteomics and metabolomics approaches needs bioinformatic methods for data integration and network reconstruction. For plant proteomics, the integration of omics data with quantitative genetics data will be expected to contribute great opportunities for plant systems biology which help to our understanding of complex regulatory networks underlying important phenotypic traits in crops in the coming next 10 years.

Dr. Xuchu Wang's group mainly focused on the uncovering the molecular mechanism of latex biosynthesis and regulation in rubber tree *Hevea brasiliensis* using quantitative proteomic technologies. These quantitative proteomics revealed protein phosphorylation played crucial roles on ethylene-stimulation of latex production in rubber tree.

Fig. 1 The laticifers in rubber tree on both cellular and subcellular after rubber tapping

Fig. 2 Schematic representation of primary and secondary laticifers after rubber tapping

Totally, 287 high abundant proteins have been identified from laticifer latex by MS. Similarly, 143 differential proteins from DIGE gels under ethephon compared to water treatment were positively identified, these mainly involved in posttranslational modification,carbohydrate transport and metabolism, energy production and conversion, translation, ribosomal structure and biogenesis. Based on our proteomic research results for rubber particles and the recently reported results, we speculated that ethylene can significantly improve the natural rubber biosynthesis by inducing the phosphorylation of the membrane proteins i.e, SRPP and REF, on small rubber particle through activating the kinase signaling pathways, which results in stimulating the generation of a large number of rubber synthetic precursors in the cytoplasm of laticiferous cells.

Fig. 3 Typical 2-D DIGE profiles of the MS-identified 143 differential proteins from laticifer latex of H. brasiliensis upon ethylene

Fig. 4 Phospho-proteomics of rubber latex proteins upon ethylene

The regulation network of salt tolerance in Thellungiella halophila

The results of comparative proteomics as well as physiological and transcriptomic responses of its leaves under salinity showed that salt treatment retarded its leaf development due to Na^+ accumulation. Finally, we brought forward a possible schematic representation for the systematic salt tolerance phenotype in Thellungiella and suggested the increasing accumulation of starch and total soluble sugars as well as proline may be an important new mechanism for halophyte salt tolerance.

Fig. 5 Typical 2-D DIGE profiles of proteins extracted from mature leaves of Thellungiella treated with different concentrations of NaCl

Fig. 6 Comparison of the expression patterns of the identified 209 salt responsive proteins and their genes

Fig. 7 Schematic representation of salt tolerance mechanism in halophyte Thellungiella

Proteome research on cotton fiber initiation

We performed an iTRAQ-based proteomic study of ovules from the upland cotton species Gossypium hirsutum and its fuzzless-lintless mutant, which identified 2769 proteins that preferentially accumulated at anthesis in wild-type ovules.

Fig. 8 Typical 2-D DIGE profiles of WT and fl cotton ovule on the day of anthesis (0 DPA)

Fig. 9 Comparison of the differentially expressed genes (DEGs) identified in the iTRAQ and RNA-seq datasets from the WT and fl ovules at anthesis

References:

Xuchu Wang et al., 2010, Proteome Science, 8, 28
Xuchu Wang et al., 2013, JPR, 12, DOI: 10.1021/pr400378c
Xuchu Wang et al., 2013, MCP, 12, 2174-2195

会议地址和住宿宾馆

会议地址：中国-海南大学思源学堂报告厅：海南省海口市人民大道 58 号。

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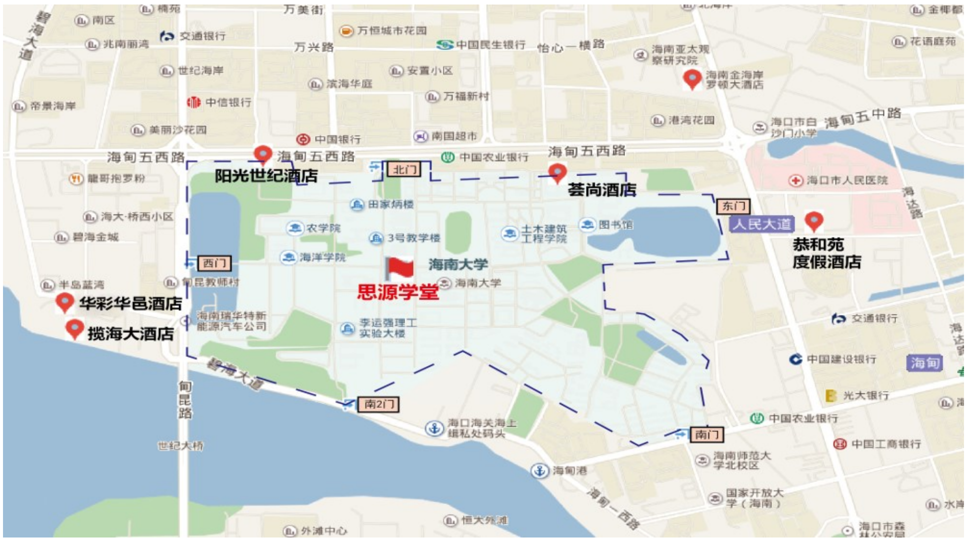
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