**旱区作物逆境生物学国家重点实验室第一届研究生论坛报告安排**

| **序号** | **报告题目** | **报告人** | **所在学院** | **时 间** |
| --- | --- | --- | --- | --- |
| 1 | The FgKin1 kinase localizes to the septal pore and plays a role in hyphal growth, ascospore germination, pathogenesis, and localization of Tub1 beta-tubulins in *Fusariumgraminearum* | 罗永平 | 植保学院 | 8:40—9:00 |
| 2 | Resolving the inheritance of double ditelosomics in tetraploid wheat cultivar DR147 | 李 浩 | 农学院 | 9:00—9:20 |
| 3 | Responses of growth of spring root system on different types of water management in dryland | 李紫燕 | 资环学院 | 9:20—9:40 |
| 4 | Integrated Physiological and Quantitative Proteomics Analyses Reveal the Mechanisms for Adaptability and High Water-Use Efficiency in Apple Leaves under Moderate Drought | 周莎莎 | 园艺学院 | 9:40—10:00 |
| 茶 歇 | | | | 10:00—10:20 |
| 5 | *TaADF7*, an actin-depolymerizing factor, contributes to wheat resistance against *Puccinia striiformis* f. sp. *tritici* | 傅艳萍 | 生命学院 | 10:20—10:40 |
| 6 | Ecophysiological and Molecular Responses of Two Contrasting Populus Species to Nitrogen Deficiency | 罗 杰 | 林学院 | 10:40—11:00 |
| 7 | Effect of pre-infestation of tomato plants with Myzus persicae (Hemiptera: Aphididae) to *Bemisia tabaci* Biotype B (Hemiptera: Aleyrodidae) and related natural enemies | 谭晓玲 | 植保学院 | 11:00—11:20 |
| 8 | Function Characterization of TaER in Bread Wheat | 郑甲成 | 农学院 | 11:20—11:40 |
| 9 | Optimized tRNA allocation partially explains efficient translation in *Saccharomyces* *cerevisiae* | 毛圆辉 | 生命学院 | 14:30—14:50 |
| 10 | Summer fallow soil management - impact on rainfed winter wheat | 李富翠 | 资环学院 | 14:50—15:10 |
| 11 | Molecular Mechanisms of BAK1 regulating abiotic stress responses in plants | 张 珊 | 园艺学院 | 15:10—15:30 |
| 12 | Zygophiala wisconsinensis 在苹果表面的再传播 | 高 柳 | 植保学院 | 15:30—15:50 |
| 茶歇 | | | | 15:50—16:10 |
| 13 | Exogenous GA3 Application Can Compensate the Morphogenetic Effects of the GA-responsive Dwarfing Gene *Rht12* in Bread Wheat | 陈 亮 | 农学院 | 16:10—16:30 |
| 14 | 不同胁迫下小麦脱水蛋白*wzy1-2、wzy2*基因及启动子功能研究 | 朱维宁 | 生命学院 | 16:30—16:50 |
| 15 | Genome sequence of the canker pathogen *Valsa mali* reveals impressive arsenal of secondary metabolites | 尹志远 | 植保学院 | 16:50—17:10 |
| 16 | Genome-wide identiﬁcation and expression proﬁling of the cystatin gene family in apple (*Malus × domestica* Borkh.) | 谭延肖 | 园艺学院 | 17:10—17:30 |