

Pollen and Plant Reproduction Biology: Blooming from East to West

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The idea of assembling a Special Issue on Pollen Tube and Reproduction in *Molecular Plant* was conceived during the organization of the 2012 Pollen Biology International Symposium and Workshop held at the Shanghai Institute of Plant Physiology and Ecology (SIPPE), Chinese Academy of Science (CAS), 27–31 October 2012. Wei-Hua Tang of the SIPPE led the organization, with the support of Hong-Wei Xue, Director of SIPPE acting as Chair of the Organization Committee. The 2-d symposium was attended by about 100 international participants and focused on reports and discussions on the most recent research activities in the field. The 2-d workshop that followed provided a forum for in-depth introduction on various aspects of pollen and plant reproduction biology to about 200 graduate students, postdoctoral fellows, and new investigators to the field.

A comprehensive report of the Shanghai Symposium (contributed by Irene Lavagi, UC Riverside) had already appeared in the *Plant Reproduction Newsletter* published by the International Association of Sexual Plant Reproduction Research (www.iaspr.org). Here, we provide just a summary of the Symposium and how its theme is reflected in this Special Issue. Additionally, since the Shanghai Symposium and Workshop was conceived by the Pollen Biology Research Coordination Network (Pollen RCN from hereon, <http://pollennetwork.org>), a US National Science Foundation (NSF)-supported effort to achieve broad international participation in pollen research, we also briefly mention salient discussions of topics covered by two other Pollen RCN-sponsored meetings to highlight the vibrancy of the field and international collaboration among the pollen and plant reproduction research community.

The cell biological process of pollen tube growth and modeling of this dramatic polarized cell growth process were featured prominently at the Shanghai Symposium. The talks covered key cellular components of the cytoskeleton, the endomembrane trafficking system, regulators of ion (e.g. H⁺ and Ca²⁺) dynamics, and various aspects of the RAC/ROP GTPase molecular switch at the pollen tube tip. Perhaps more importantly, much of these discussions

focused on how these recent findings might be linked to the control of exo- and endocytosis and spatially and temporally regulated membrane expansion and wall deposition which together underlie the pollen tube tip-growth process.

The Shanghai Symposium represented a continuation of discussions started in the Second Annual Pollen RCN meeting that took place in August 2011 in Minneapolis, MN, USA (programs for the RCN annual meetings and the Shanghai Symposium and Workshop are available at <http://pollennetwork.org>). Pollen tube modeling was the featured topic of that meeting. It was apparent from these biological and computational discussions that knowledge of the pollen tube growth cell biological process is advanced enough to support the formulation of predictive modeling, which should help integrate the multiple facets of the pollen tube to provide a ‘systems understanding’ of this dramatic polarized cell growth process. The invited reviews of this Special Issue (Chebli et al., 2013; Guan et al., 2013; Hepler et al., 2013) provide excellent overviews of those areas as well as discussions on some of the unresolved questions in these areas. That these topics continue to be active areas of research is evidenced by at least six papers (Chen et al., 2013; Idilli et al., 2013; Li et al., 2013; Mähs et al., 2013; Wang et al., 2013) that were submitted in response to the call for papers for this Special Issue, as well as several previously accepted papers whose authors have opted for inclusion in this issue.

The Shanghai Symposium also featured many exciting talks on the recent discoveries in male–female interactions that underlie the reproductive process. Yan Zhang (Shangdong Agricultural University) summarized findings reported in many of these talks most humorously by commenting that ‘She’s the boss ...’ (Kessler and Grossniklaus,

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2011) but 'he's got to have ears!'. In this issue, the review by Dresselhaus and Franklin-Tong (2013) provides a timely perspective for the field, while T. Higashiyama's group reports on a continuing study on pollen tube attractant LURE from *Torenia fournieri* (Okuda et al., 2013). Efforts to unravel genetic mechanisms that underlie plant reproductive development continue to flourish, with several talks at the meeting reporting on findings of novel transcriptional regulators, epigenetic control, and RNA processing. Several papers (Cao et al., 2013; Hoffmann and Palmgren, 2013; Niu et al., 2013; Scarpin et al., 2013) on these topics are included in this Special Issue.

The pollen and plant reproduction biology field is moving towards an era where 'systems understanding' is fast becoming a necessity as well as a reality. To facilitate research on this front, the Third Annual Pollen RCN meeting in Tucson, Arizona, USA, 1–3 March 2013 was organized to accomplish two goals: to serve as a forum for updates on the latest technologies and approaches in the field and to provide a platform to introduce and equip pollen and plant reproduction biology researchers with computational tools for undertaking a systems biology approach.

The Tucson meeting featured a special session for computational approaches in pollen and reproduction biology in collaboration with the NSF-funded iPlant Collaborative (www.iplantcollaborative.org). Steve Goff, Director of iPlant Collaborative, gave an overview as to how they provide a comprehensive environment for systems biology research and discussed in great detail how researchers could use iPlant Collaborative for storage, organization, analysis, and sharing of large-scale data sets. Two presenters highlighted online computational resources in iPlant Collaborative: Bisque and CoGe, to analyze imaging and comparative genomics data, respectively. To complement these presentations, three pollen biology researchers presented examples of high-throughput research that employed computational tools. Exciting details on the recent RNA-seq analysis of pollen gene expression (Loraine et al., 2013) and visual analysis of this data with Integrated Genome Browser (<http://bioviz.org/igb/>) were presented. The availability and utility of pollen tube tracker in the iPlant Collaborative's Bisque server to automatically track multiple, overlapping pollen tube trajectories in fluorescent time-lapse images were also discussed. A highlight of this session was that, once the oral presentations concluded, the presenters were available at five work stations equipped with appropriate hardware and software to showcase the computational approaches and tools discussed in the oral presentations. This set up facilitated personal and productive interactions between presenters and attendees—an aspect critical for effective computational presentations to biologists.

Many other challenging and emerging aspects of pollen and plant reproduction biology were also covered at the Tucson meeting. Attendees learned about the latest

advances on the use of pollen grain as a model to understand calcium signaling and membrane dynamics, unravel the genetics, biochemistry, and physiology of exine and aperture formation in pollen walls, and gain insights into the communications among pollen-foraging honey bees. The pollen tube continues to be an important model to understand various aspects of a growing plant cell. The utility of pollen tube in understanding the molecular connections between actin filaments and exocytic vesicles, unraveling the complex mechanisms of callose plug deposition, and investigating the molecular determinants of incompatibility in intra- and inter-specific crosses were presented. Several novel and high-impact approaches to unravel pollen tube biology were also discussed. Some examples include genetics of post-pollination non-random mating to understand success of certain pollen over others, ecotype variability to decipher the physiology of pollen germination, variable-angle epifluorescence microscopy to examine the organization and dynamics of the actin cytoskeleton, transcriptome-assisted functional genomics of pollen tube–pistil interactions, transcriptome of pollen tube to identify genes with roles in micropylar guidance, and a novel molecular probe to understand the role of reactive oxygen species in pollen tube functions.

Beyond the discussions at the scientific frontier, we believe that an important achievement from these recent gatherings is the learning experience they provided to young scientists joining the field of plant reproduction. The Workshop that followed the Shanghai Symposium provided a forum for in-depth exposure of theoretical, computational, and technical aspects important to research in pollen and plant reproduction biology. Nearly half of the attendees of the Second and Third Pollen RCN meetings were graduate students or post-doctoral fellows. These young researchers responded to talks with insightful and provocative questions, exhibiting their fearless thinking of how to tackle the unsolved challenges confronting this exciting field. Additionally, they actively engaged in discussions with senior scientists and established new collaborations. It is therefore not an understatement that the future is indeed very bright for pollen and plant reproduction biology research.

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