Speaker: Matthew Tucker, University of Adelaide
Talk Title: Using spatial transcriptomics to discover new genes influencing cereal grain development

Abstract: Cereal grains are produced after fertilization of the ovule, a complex structure that is located deep within the flower. While transcriptional profiling has revealed many details about major genes involved in ovule and grain development, remarkably little is known about the specific molecular signatures of different cell types and how these might contribute to variation in grain size and composition. Over a number of years, we have applied techniques such as fluorescence-assisted cell sorting and laser microdissection in multiple species to capture and transcriptionally profile different ovule cells and tissues contributing to grain development. This has led to the discovery of genes involved in epigenetic pathways, transcriptional regulation, and cell wall composition, many of which contribute to female fertility and/or grain size. While generally successful, these techniques have presented challenges in terms of time, cost, staffing expertise, resolution, and infrastructure. As a result, we have shifted focus towards alternative spatial transcriptomic methods such as Visium with the aim of improving resolution, reproducibility and data quality. In this presentation I will discuss how we are applying spatial transcriptomics as part of a broader strategy to find and characterize new genes and cell types, and to piece together cell-autonomous versus non-cell-autonomous effects of transcription factors involved in ovule and seed development.