

Abstract

The diversity of reproductive strategies among angiosperms is considered as a key feature behind their success as one of the most species-rich group of land plants. Among them, the transition from outcrossing to selfing appears as one of the significant reproductive strategies altering the evolution of key sexual traits, underlying genes and speciation processes. Although the impact of transition to selfing on reproductive traits is well documented, its consequences on sex-specific selection at the trait and gene level remain unexplored. In this thesis, by combining developmental and comparative -omics approaches, I aimed at investigating the consequences of mating system shift on the evolution of male and female traits, underlying molecular mechanisms, and subsequent impact of this shift on establishing reproductive barriers in flowering plants. I focused on species that have undergone transitions to selfing across the plant model genera *Arabidopsis* and *Capsella*, with transition times ranging from 10k - 600k years old. In case studies 1 and 2 (CS1 and CS2), I investigated how the evolution of sexual traits and underlying molecular mechanism is impacted by the transition to selfing under the theoretical frame of sexual selection. Together with experimental approaches, I used transcriptomic data to identify the molecular mechanism underlying the evolution of the male and female gametophytic function in recently diverged sister lineages. I found that outcrossers, which experience strong sexual selection in nature, exhibited higher pollen performance and stricter female choice compared to selfers (CS1), consistent with predictions from modelling study (CS2). Additionally, I identified candidate genes involved in vesicle transport and cytoskeleton organization associated with pollen trait divergence, as well as genes related to auxin and stress responses that may explain differences in female choice through molecular crosstalk at the post-pollination stage (CS1). These results suggest that the transition to selfing can rapidly alter the intensity of sexual selection between outcrossing and selfing populations, driving the evolution of sexual traits and their associated gene expression patterns. In CS3, by conducting comparative proteomics in independent selfing lineages, I found that the pollen coat morphology evolved similarly in species exhibiting the selfing syndrome, such as *Arabidopsis thaliana* and *Capsella rubella* (CS3). Moreover, I identified differentially expressed pollen coat proteins that were significantly enriched for pathogen response functions in outcrossing species compared to their selfing counterparts across all three independent systems. These results reveal that both morphological and protein-level changes in the pollen coat have occurred similarly across independent transitions to selfing, demonstrating rapid convergent evolution of pollen coat functions related to defence and pathogen response, an aspect that was previously unknown. Finally, by performing reciprocal crosses and contributing to population genomic analyses between outcrossing and selfing *A. lyrata* lineages, I investigated whether the recent transition to selfing impacts hybrid seed lethality and selection on parent-specific imprinted genes (CS4 and CS5). I found that parental genomes in hybrid seeds interact negatively, leading to extensive hybrid seed lethality associated with endosperm cellularization disturbances (CS4). However, the work I contributed to did not detect differences of selection on imprinted genes between selfing and outcrossing populations of *A. lyrata*, suggesting that the transition to selfing has not significantly affected the evolution of these genes (CS5). These results indicate that, despite a relatively short divergence time, the transition to selfing can give rise to strong postzygotic barriers, causing hybrid seed inviability between two intraspecific *A. lyrata* lineages. Overall, my PhD thesis brings a novel

empirical contribution to our understanding of how mating system shifts impact the evolution of sexual traits and their underlying molecular and genetic elements, and how they drive the emergence of reproductive barriers and ultimately speciation.