Botrytis cinerea is the causal agent of gray mold of more than 1,400 plant host species. The disease can lead to substantial yield losses, especially of red raspberry and other small fruit crops in the US Pacific Northwest (PNW) and worldwide. Effectiveness of gray mold management in red raspberry remains limited due to incomplete understanding of the disease cycle. The bloom period of red raspberry is considered a critical window for B. cinerea colonization of this host, but the role of flowers in this disease remains unclear. The first objective of this research was to determine the infection pathways of B. cinerea on red raspberry under field conditions. Colonization incidence of red raspberry at bloom was limited, but significantly increased with fruit development and peaked on mature fruit. As fruit developed, different morphological parts became colonized by the fungus, suggesting multiple infection events throughout the season.

In the PNW, gray mold management programs on raspberry are based on protecting plants with fungicides throughout the production season, starting at bloom. It is, however, unknown if full-season fungicide programs are required to control B. cinerea effectively on raspberry. The second objective of this research was to study the effect of fungicide applications on B. cinerea colonization of raspberry in relation to plant development and test the floral infection hypothesis with genetic markers. Fungicide applications did not prevent or reduce flower colonization but significantly decreased fruit colonization. Pathogen genotypic diversity increased throughout the season and different genotypes colonized flowers, green and ripe fruit within raspberry inflorescence, suggesting that multiple fungal strains can colonize fruit at different developmental stages.

In the PNW, several small fruit hosts are grown in close proximity, but nothing is known about B. cinerea population biology on these hosts in this region. The third objective of this research was to investigate how evolutionary forces shape pathogen population structure on small fruit in the PNW. No association of B. cinerea with host was found, but populations were geographically differentiated at regional and farm scales, suggesting restricted gene flow. Evidence for local adaptation due to selection was detected with fungicide resistance markers.