

Bridging Agri-Science and Technology: Decoding Pre- and Post-Pollination Molecular Changes in *Aquilegia* Using Comparative Transcriptomics

Mankirat K Pandher^{1*}, Ana Alcaraz Echeveste^{1*}, Rene K Romo^{1*}, Marianellie Bravo^{1*}, Rakesh Kaundal² and Bharti Sharma¹

¹Department of Biological Sciences, Cal Poly Pomona, and ²Department of Plants, Soils, and Climate, and Bioinformatics Facility, Center for Integrated BioSystems Utah State University, Logan

Impact on California Agriculture: Fruit development is a key process and has an immense economic impact on agricultural and horticultural crops. Despite carpels being the most crucial organs in plants that produce seeds, studies in horticultural crops that determine the genetic control of ovary, ovule, and seed development are rare. In the proposed study, we aim to unravel the genetic and molecular bases of carpel development using *Aquilegia coerulea* as a model system. *Aquilegia*, commonly known as columbine, is a popular horticultural plant and a native of California. In 2019, the horticulture sector in California reported revenues amounting to \$2.63 billion, highlighting its critical economic role within the agricultural landscape. This underscores the importance of advancing our understanding of plant reproductive biology.

Rationale/Introduction: Carpels bear the female reproductive organs of plants. Matured and fertilized carpels form fruit, and ovules develop into seeds. For the continuity of a plant species, timely pollination and fertilization are essential to ensure a successful seed set.

Experimental Approach: We have deployed developmental, molecular, and transcriptomic approaches to understand the genetic networks underlying seed formation. *Aquilegia coerulea* “Krigami” plugs were grown to an 8-leaf stage in the Cal Poly Pomona greenhouse. Plants were vernalized at 6 °C for 4 weeks. Post-vernalizations plants flowered in four weeks. Carpels from three developmental stages were collected. RNA was extracted from dissected carpels. Libraries were prepared for RNA sequencing. Reference-based transcriptome analysis was performed using the R pipeline. The data obtained was analyzed, and differential gene expression and cluster analysis were performed.

Major Conclusions: This study has identified crucial candidate genes that influence carpel and ovule development. The outcome of this research provides valuable data to better understand the gene expression changes that carpels undergo pre- and post-fertilization.

*Student researcher
