Epigenetic and Phenotypic Responses of Apple Trees (*Malus domestica* Borkh) to Climate Variability Across European Orchards

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Abstract

Climate change poses a major challenge to perennial fruit crops such as apple (*Malus domestica*), which have limited capacity for rapid genetic adaptation due to their long lifespans and clonal propagation. Phenotypic plasticity and epigenetic mechanisms, including DNA methylation, may enable such long-lived species to adjust to environmental variability. This study investigates how contrasting climatic conditions shape methylation marks and phenotypic traits in apple trees cultivated across two European orchards located in Spain and France. These orchards are five years old and consist of clonally propagated apple trees, ensuring genetic uniformity across sites. We selected trees exhibiting contrasting flowering time phenotypes. Buds were sampled from these individuals and sequenced using Oxford Nanopore long-read technology to screen genome-wide DNA methylations and identify epigenetic signatures associated with environmental resilience. This work aims to elucidate the role of plasticity in climate adaptation, providing insights into the epigenetic mechanisms underpinning stress tolerance in perennial crops. Ultimately, the findings will inform climate-resilient breeding strategies, improve sustainable orchard management, and contribute to safeguarding food production in an era of increasing environmental instability.