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Whole-Genome Assembly and Analysis of a Chili Pepper Cultivar (*Capsicum* sp.*)* in the Philippines

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Capsicum sp., commonly known as pepper, is one of the most important crops in the Philippines, valued for its economic, culinary, and cultural significance. However, genomic resources for locally adapted cultivars remain scarce, limiting progress in breeding and crop improvement. In this study, we report the draft genome assembly of a commercially available chili pepper cultivar in the Philippines. A hybrid genome assembly strategy was employed, integrating long reads from PacBio and Oxford Nanopore sequencing technologies, with error correction and polishing performed using high-accuracy short reads from MGI sequencing. Assembly was carried out with Hifiasm, and raw sequence quality and coverage were evaluated using SeqKit, confirming the suitability of the data for assembly. Assembly completeness was further assessed using BUSCO, providing a measure of conserved gene content and genome quality. While detailed assembly statistics and gene annotation are still underway, this draft genome provides a valuable genomic resource for *Capsicum* research. It will support future studies on functional genomics, genetic diversity, disease resistance, and local adaptation, contributing to the improvement and long-term sustainability of chili cultivation in the Philippines.