Metabolomic profile of commercial and dwarf tomato cultivars

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Tomato (*Solanum lycopersicum*) is one of the most important vegetable crops in the world. Due to its diploid genome, it is a model species essential for research on fleshy fruits. Tomato cultivation requires essential inputs like irrigation and fertilizers, a need intensified by climate change impacts threatening global food security. Breeding programs commonly use wild species and improved cultivars to develop resistant varieties resistant to pests and biotic stress. Dwarf gene plants show promise, offering both morphological adaptations and resilience to saline and water stress. Despite their benefits, these plants exhibit gaps in chemical composition which can be addressed by untargeted metabolomics using gas chromatography-mass spectrometry (GC-MS). This technique enables the analysis of small molecules, offering deeper insights into the plant metabolome and revealing correlations between metabolites, quality, and yield. Metabolomics, the comprehensive study of metabolites within a biological system, is commonly used for identifying biomarkers and understanding the biochemical pathways that contribute to plant stress resistance. This study aimed to identify compounds contributing to resistance against both abiotic and biotic stresses, thereby enhancing understanding of genetic adaptability in hybrids derived from dwarf and wild plants sourced from the Tomato Genetic Improvement Program at the Federal University of Uberlândia (Monte Carmelo, Brazil). The specific objectives were to profile the metabolic differences between dwarf and commercial cultivars and to link these differences to stress resistance traits. The analysis was performed on macerated leaflets processed with an extracting solution and cell disruptor. The extracted samples were dried, subjected to derivatization, and analyzed by gas chromatography-mass spectrometry (GC-MS). Data processing utilized MS-Dial 5 and MetaboAnalyst 6.0 software with significance set at $p < 0.05$. The analysis identified 52 significantly different compounds, with 36 showing higher abundance in the dwarf cultivar and 16 in the commercial cultivar. Specifically, dwarf plants had higher levels of 5 amino acids, 8 carbohydrates, and 8 carboxylic acids, while commercial plants exhibited higher levels of 1 amino acid, 9 carbohydrates, and 5 carboxylic acids. The increased metabolites found in the dwarf plants, particularly carbohydrates and amino acids, are strong candidates for important compounds related to defense mechanisms through stress tolerance or damage control proteins. Elevated amino acid levels may indicate increased activity of amino acid biosynthesis pathways and relate to cellular energy dynamics, intracellular redox balance, and act as stress biomarkers. The significant expression of these biomarkers highlights the potential of metabolomics in elucidating physiological mechanisms that contribute to productivity and resistance in dwarf gene plants, thereby enhancing our understanding of the metabolic mechanisms in this cultivar.

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