**Molecular Basis of Grain Calcium content in Pigeonpea through Comparative Proteomics Analysis**

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Pigeonpea (*Cajanus cajan* (Linn.) Millsp.)is an important legume crop known for its high nutritional significance. Calcium, a vital mineral element in plants and animals, plays an indispensable role in structure and signaling. Understanding the genetic variation and molecular mechanisms underlying the uptake, transport, accumulation of calcium in grains is of utmost importance. A study was conducted to elucidate the molecular mechanisms underlying the calcium accumulation and transport thoroughly, between low and high calcium lines of pigeonpea through comparative proteomic analysis. The results revealed membrane protein (C24H6.13 and C2G11.09), calcium transporting ATPase, sarcoplasmic reticulum histidine-rich calcium-binding protein and calcium-binding protein for calcium uptake, transport, storage, and regulation in grains. A significant differential abundance was noted in proteins associated with calcium-binding, transporters, calcium-dependent signaling pathways, and calcium storage organelles. These findings help in the identification of genes for high grain calcium content in pigeonpea opening an avenue for calcium biofortification in Pigeonpea.

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