**Metabolomics and proteomics integration unveil how secondary cell wall thickening in peanuts helps in resisting aflatoxin accumulation**

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Aflatoxin contamination, caused by *Aspergillus flavus*, significantly threatens food safety and human health. However, the molecular and biochemical pathways need to be better understood. Different approaches have been explored previously, including genetic mechanisms, cellular defense mechanisms such as secondary cell wall thickening, utilization of biocontrol agents, and the identification of resistance or susceptibility-associated genes. These studies have unveiled potential targets for precision breeding in peanuts to resist *Aspergillus* infection and subsequent aflatoxin contamination. However, due to the complexity of this trait, these studies have yet to fully elucidate the overall resistance mechanisms during *Aspergillus* infection in peanut. Our study adopted an integrative approach using metabolomics and proteomics using contrasting peanut genotypes-transgenic peanut expressing 4RNAi (resistant) and WT-ICGV 91114 (susceptible), to uncover the underlying resistance mechanisms by identifying regulatory events governing cellular processes such as enzyme activity, post-translational modifications, and gene expression during *Aspergillus* infection. Notably, changes in protein expression often precede alterations in metabolite levels, indicating regulatory events at the proteomic level. Integrating metabolomics and proteomics provided complementary insights into the metabolic and protein profiles associated with the production of phenylpropanoids, flavonoids, and fatty acids, shedding light on crucial pathways involved in inhibiting aflatoxin production. Furthermore, our study delves into host-pathogen interactions at the molecular level, elucidating how plants recognize fungal pathogens, activate defense responses, and adjust their metabolism to counteract aflatoxin production. This comprehensive and multidimensional analysis lays the groundwork for breeding peanut with reduced aflatoxin levels and implementing sustainable solutions to agriculture-related challenges.

**Keywords:** Aflatoxin, Fatty acids, Flavonoids, Metabolomics, Phenylpropanoids and Proteomics.