The structure and sites of biochemical interaction of cotton defensive proteins and secondary metabolites

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Plain English summary:

A variety of proteins were purified from cotton seeds and were analysed by amino acid sequence determination (automated Edman degradation) and by state-of-the-art electrospray ionization mass spectrometry (ESMS). The amino acid sequences of about 40 vicilin-related cotton proteins were precisely defined. The molecular masses of the deduced sequences were in agreement with the masses observed by ESMS to within about 1-2 Da (i.e. to within the mass of 1-2 hydrogen atoms). A further major cotton seed protein was purified and shown to be a γ-conglutin-related protein with 2 component subunits and a molecular mass of 46250.3 ± 1.3 Da. The vicilin fractions and the γ-conglutin variously have anti-fungal activity against a wide range of fungi tested including the cotton pathogens *Fusarium oxysporum* and *Verticilium dahliae*. This precise work is potentially useful for classical and transgenic approaches to cotton plant breeding for pest resistance. Cotton leaves also contain anti-fungal components and a defensive component with larvicidal activity against the blowfly *Lucilia cuprina* and the mosquito *Aedes camptorhynchus*. Large-scale purifcation procedures were developed to enable further biological testing. Protein and non-protein fractions from cotton are variously active as inhibitors of animal cyclic AMP-dependent protein kinase and of the proteases trypsin and chymotrypsin.