

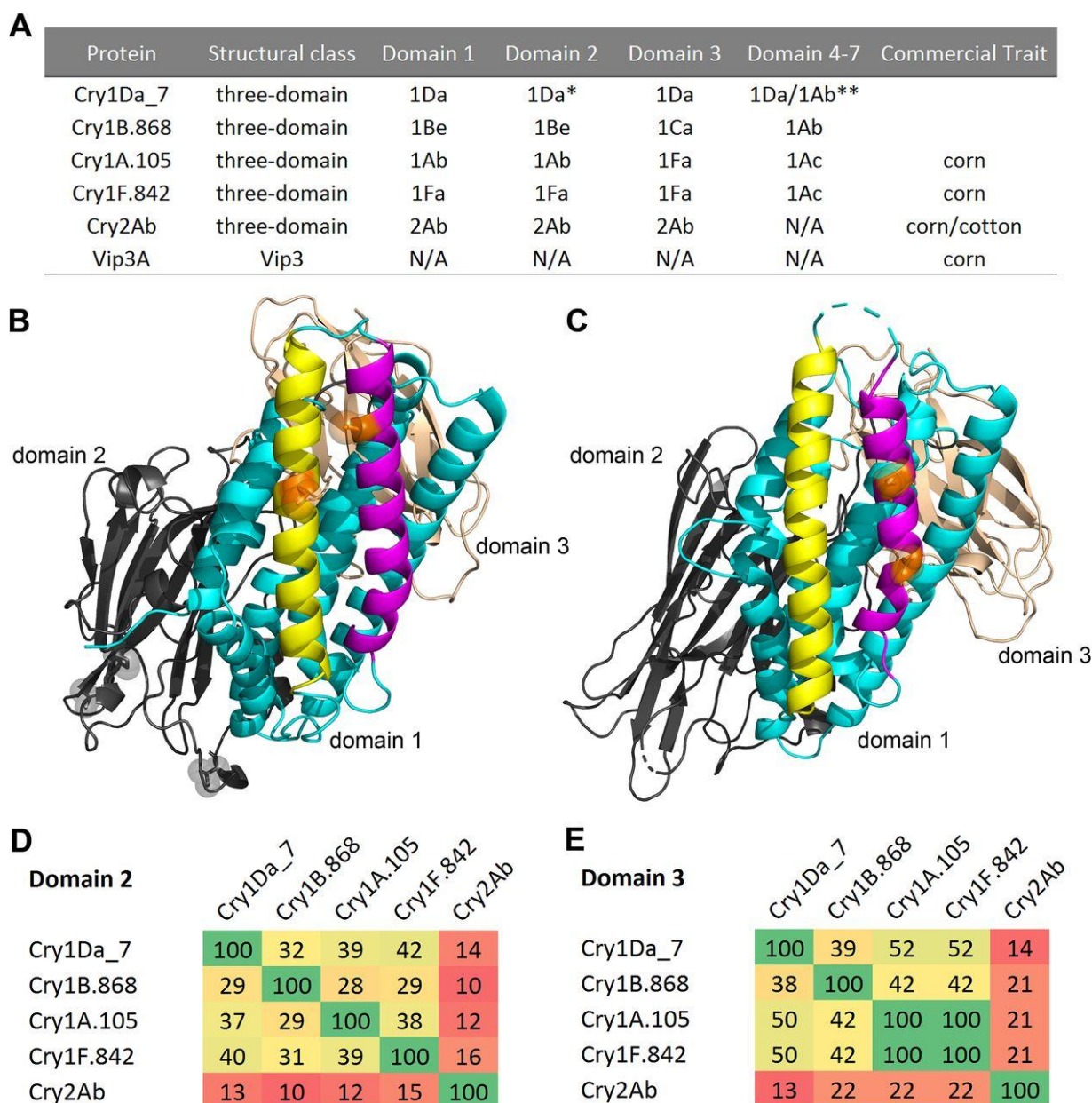


Figure 2 Sequence and structure relationship between Bt insecticidal proteins in current and next-generation above-ground traits (Adopted from Wang et al., 2019)

Image caption: (A) Protein sequence information on the different NIPs, indicated by Bt toxin holotype nomenclature. The asterisk indicates the Cry1Da domain, in which substitutions were made to enhance CEW activity. Domains 4 to 7 of the three-domain Cry1 proteins are protoxin domains that are digested in vivo and thus are not part of the active ingredient; the Cry1Da_7 active core was appended to both Cry1Da and Cry1Ab protoxin domains and tested separately (double asterisk). Cry2Ab does not have these protoxin domains. Vip3A is of a different structural class whose sequence is different and structurally distinct from those of three-domain Cry proteins. N/A, not applicable. (B) Crystal structure of Cry1Da_7-DIP showing the three-domain architecture of domain 1 (cyan), domain 2 (gray), and domain 3 (light pink) in cartoon representation as well as helix 3 (yellow) and helix 4 (magenta) in domain 1. The key domain 1-disabling cysteine substitutions V108C and E128C are highlighted with orange sticks and semitransparent spheres corresponding to their side chain. The gray sticks and semitransparent spheres in domain 2 indicate the side chains of substitutions (S282V, Y316S, and I368P) that confer increased CEW specific activity. (C) Model of the three-dimensional architecture of Cry1B.868-DIP protein in cartoon representation with the above-described color scheme. The key domain 1-disabling substitutions A160N and N167D are highlighted with orange sticks and semitransparent spheres corresponding to their side chain. (D) Percent sequence identity between domains 2 of FAW-active insecticidal proteins based on comparative sequence analysis by multiple-sequence alignment (74). (E) Percent sequence identity between these proteins in domain 3 (Adopted from Wang et al., 2019)