Flowering is a tightly regulated physiological process that is essential for seed production and proliferation in the majority of higher plants. The vegetative to reproductive transition is controlled by diverse exogenous and endogenous cues that trigger distinct genetic pathways, all of which converge at floral integrators. Recent studies in *Arabidopsis thaliana* have shown that some of these integral molecules act as mobile florigens. These conserved phosphatidylethanolamine-binding proteins (PEBPs) are synthesized in leaves and migrate to the shoot apex to form a floral activation complex (FAC) that ultimately prompts reproductive specificity. In sugarcane (*Saccharum officinarum*), several PEBP florigen candidates have been discovered. One of these genes, *ScFT2*, causes extremely late flowering and a dramatic change in shoot architecture. Later analysis revealed that 8 amino acids were fortuitously added to the C terminus of *ScFT2*, creating a synthetic variant. This research aims at characterizing the molecular mechanism behind this novel protein, termed *ScFT2-OSCAR*. The effect of the additional amino acids will be tested to determine if OSCAR or *ScFT2* is responsible for the vegetative phenotype, and if the 8 amino acid additions can alter shoot architecture when added to other PEBP orthologs. An interaction assay will be conducted to determine if *ScFT2-OSCAR* interferes with FAC formation by competitive inhibition of endogenous PEBP signalling, and to identify new undiscovered entities involved in floral regulation. *ScFT2-OSCAR* will also be overexpressed in other plant species to determine whether this protein can act as a novel universal anti-florigen for agricultural applications.