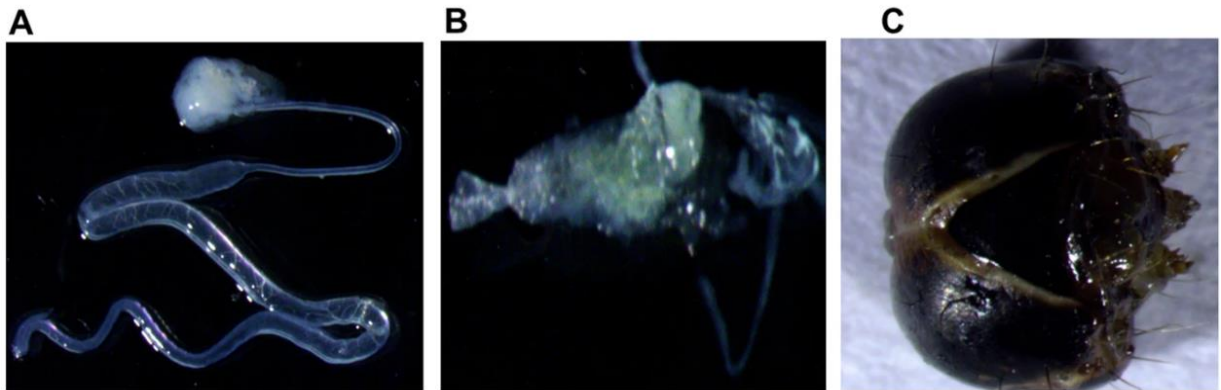


In silico* identification of effector proteins from generalist herbivore *Spodoptera litura

Team of scientists at DBT's National Institute of Plant Genome Research (NIPGR), New Delhi, isolated labial, mandibular and ventral eversible glands of *Spodoptera*. A high throughput transcriptome analysis in the salivary glands of the insect was done for identification of the effector proteins, and 267 proteins from salivary gland proteins were predicted to be potential effector proteins. Detoxifying enzymes, glucose oxidase, chemosensory proteins, calcium ion binding proteins, clip domain serine proteinases, lipases, phospholipases and peroxidases are the major potential effector protein families identified in this study. Functional and mechanistic characterization of these insect effector proteins will provide deeper insight into the insect-mediated suppression of plant defense and how to overcome it.



Salivary glands present in *S. litura* after dissection a) Labial salivary gland b) Ventral eversible gland c) Head

Spodoptera litura or common cutworm is one of the most destructive insect pests of agricultural crops, with more than 120 host plants globally. Related species, *Spodoptera frugiperda* (Fall armyworm) is a devastating pest and has caused great damage to maize in India and world over. *Spodoptera* can parasitize many plant hosts by overcoming the plant immune system and effectors proteins, secreted by the insect into plant cells, are responsible for this ability. Effector proteins are secreted out from salivary secretion.

Link: <https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-020-07196-4>

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