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Data Article

Data of *in vitro* synthesized dsRNAs on growth and development of *Helicoverpa armigera*

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ABSTRACT

The data presented in this article is related to the research article "RNAi of selected candidate genes interrupts growth and development of *Helicoverpa armigera*" (Chikate et al., 2016) [1]. RNA interference (RNAi) is emerging as a potent insect pest control strategy over current methods and their resistance by pest. In this study we tested 15 different *in vitro* synthesized dsRNAs for gene silencing in *Helicoverpa armigera*. These dsRNAs were specific against *H. armigera* enzymes/proteins such as proteases like trypsins (*HaTry2*, *3*, *4* and *6*), chymotrypsin (*HaChy4*) and cysteine proteases such as cathepsin (*HaCATHL*); glutathione S-transferases (*HaGST1a, 6* and *8*); esterases (*HaAce4, HaJHE*); catalase (*HaCAT*); super-oxide-dismutase (*HaCu/ZnSOD*); fatty acid binding protein (*HaFabp*) and chitin deacetylase (*HaCda5b*). These dsRNAs were fed to second instar larvae at an optimized dose (60 μg/day) for 3 days separately. Effects of dsRNA feeding were observed in terms of larval mass gain, percentage mortality and phenotypic abnormalities in later developmental stages of *H. armigera*. These findings might provide potential new candidates for designing sequence-specific dsRNA as pesticide in crop protection.

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Specialization Table

Subject area	Biology
More specific subject area	RNAi and Biochemistry
Type of data	Tables and Figures
How data was acquired	Workflow of primer designing, *in vitro* dsRNA synthesis and its stability
Data format	Raw
Experimental factors	We selected major enzyme/protein classes in *H. armigera* for gene silencing by feeding them specific dsRNA
Experimental features	Each dsRNA fed to 30 insects
Data source location	CSIR-National Chemical Laboratory, Pune, India
Data accessibility	Data is presented in this article

Value of the data

- This data will be useful to the other investigators to follow the same system for implementing in the field experiments by using nanoparticles for the stability of dsRNA.
- Environmental parameters need to be integrated in these experiments hence environmental factors can be explored for its concrete use in the ground level.
- The data support the development of further experiments on the use dsRNA in other devastating insect pests.
- Findings from this work will be valuable for designing potent dsRNA as pesticide in crop protection.

1. Data

Here, we demonstrated the use of dsRNA in pest control and various aspects *viz*. dsRNA stability, concentration and amplicon size were assessed based on ingestion by *Helicoverpa armigera* (Figs. 1 and 2). In the data, 15 dsRNAs targeting various *H. armigera* enzymes/proteins have been shown in terms of larval mass reduction post 96 and 144 h of dsRNA exposure (DPE) (Chikate et al. [1]). These dsRNAs were seen to be played role at larval and pupal level by reduction in mass (Fig. 3A, B and C). Upon ingestion of dsRNA by *H. armigera*, reduction in larval mass, abnormal phenotypes, egg laying capacity, gene silencing and enzyme activity pattern was successively studied.

2. Experimental design, materials and methods

2.1. Sequence analysis and primer designing

Based on earlier studies in our laboratory [2–4] we selected major enzyme/protein classes in *H. armigera* for gene silencing by feeding them specific dsRNA. These involved 15 mRNAs belonging to proteases (6), glutathione *S*-transferases (3), esterases (2), catalase (1)/super-oxide-dismutase (SOD) (1), fatty acid binding protein (1) and chitin deacetylase (1). Green fluorescent protein (GFP) was used as a negative control while glyceraldehydes phosphate dehydrogenase from *H. armigera* (GAPDH) was used as positive control. Sequence analyses for each of these target mRNA class was performed using CLUSTAL W and primers containing gene-specific sequence adapted to T7 promoter sequence in inverted orientation were designed manually (Fig. 1). These were around 45 bp long primers, devoid of self-complementarily or secondary structures giving amplicon of around 200–500 bp. The primer sequences, amplicon sizes for preparation of dsRNA of each mRNA are listed in Table 1. To check the