Abstract: There is an urgent need to enhance agricultural production as well as productivity to meet the food demand of the growing population, estimated to be 10 billion by 2050, using a holistic and sustainable approach. The daily food sources for almost three-fourth of the global population, cereals and millets, are prone to several biotic factors and abiotic pressures. In particular, cereals and millet cultivation are limited by the polyphagous pink stem borer, *Sesamia inferens* Walker (Lepidoptera:Noctuidae) gaining national importance, since its larvae and pupae are concealed within the stem, none of the management measures have been found effective in controlling the menace. However, host plant resistance (HPR) is a reasonable and ecologically safe method wherein resistance mechanisms of crops could lower the stem borer infestation. The foremost challenge in understanding the mechanism would be to detecting the genes of interest in the crop using novel biotechnological approaches. The fundamental criterion for developing insect-resistant lines relies on recognizing the mechanism of plant resistance. The entire life cycle of this group of borers is completed or hidden within the stem, posing a hurdle in their management. Thus, molecular markers and Quantitative Trait Locus (QTL) mapping offer a more efficient approach to entomologists and plant breeders wherein they can work with traits like QTLs for stem borer resistance. In this review, an attempt has been made to provide an extensive summary of the host range and crop losses due to this borer, besides its taxonomic position, geographic distribution, bionomics, genetics of resistance, and molecular perspectives.

Keywords: *S. inferens*; cereals; millets; host plant resistance; molecular perspectives

1. Introduction

Plants with resistance coexisted with vulnerable insects for several decades until the domestication era. Consequently, challenging crops continued with the law of inheritance and natural assortment, which led to the evolution of host plant resistance. Investigation and improvement in research are pre-requisites to explore the host-plant relations and avail effective control measures against pests [1]. The crop improvement via plant resistance to insects includes plants transformed with insect resistance genes, termed as “substantial crop development.” The most notable attribute of Host Plant Resistance (HPR) is that it offers a farmer-friendly mechanism without specific knowledge and additional
investment. Thus, having the potential to reduce pesticide usage, slow down the development rate of resistance to insecticides, increase the activity of beneficial organisms, and ultimately reduce pesticide residue in agricultural produce. Host-plant resistance has the potential to be the most viable and sustainable method of pest control, and a variety resistant to such menacing pests would be most enviable [2,3].

Subsistence farmers in Europe, Asia and African countries mainly cultivate and consume small millets which contain high nutrients [4]. One of the chief producers of millets throughout the world is India [5], with 6–19 percent losses attributed to insect-pests [6]. Among all the insect-pests, stem borers are the most destructive assemblages infesting the millets [7–10]. The dominant stem borer species in India are the ragi pink stem borer, *Sesamia inferens* [Wlk] (Noctuidae); sorghum stem borer, *Chilo partellus* [Swinhoe] (Pyralidae) and the white stem borer, *Saluria inficita* [Wlk] (Pyralidae) [11].

*S. inferens* Walker (Noctuidae, Lepidoptera), also called Asian pink stem borer, gramineous pink stem borer, and ragi pink stem borer are highly polyphagous pests of all cereals and millets at different stages, causing severe yield loss. It is also referred to as “Goolabi tanna chhedak” and “khod kid” in North Indian states and Maharashtra, respectively [12] while in Gujarat, it is known vernacularly as “Gulabi gaabhmarani eyal” [13]. *Sesamia inferens* is a major insect pest of small millets, especially the pearl millet *Pennisetum glaucum* (Poales: Poaceae) however, it has shifted its infestation to other crops like barnyard millet. *S. inferens* occurrence was reported 30–35 percent in barnyard millet [14]. In India, the incidence of this group of pests has been documented in the states of Odisha, Karnataka, Andhra Pradesh, and Tamil Nadu. The larvae bore into the stem that causes a dead heart symptom in the early stage, promoting profused side-tillering with unproductive spikes. In later stages, peduncle and spike are damaged, leading to white ear symptoms [15].

Pesticides are a reliable tool to curtail the yield losses caused by stem borers and maintain sustainable production and productivity. However, stem borers are challenging to manage as the entire immature stages (larvae and pupae) hide inside the stem, besides the nocturnal nature of the adult moths. Climatic change with modern crop cultivation practices has hustled *S. inferens* to the status of major pests of millets in India [16].

Conventional breeding methods are time-consuming and labor-intensive, requiring skills for accurate evaluation and proficient selection of parents. DNA markers are used to overcome these issues by developing improved genotypes with specific traits. DNA markers and continuous improvement in molecular assays resulted in a successful molecular marker-assisted breeding (MAB) [17] program. This program is a superior breeding method as compared to traditional cum conventional methods [18]. In the early 1980s and 1990s, different types of DNA markers were developed for plants in molecular biotechnology. Moreover, DNA markers were also used in multiple fields of life sciences viz., evaluation of germplasm traits, gene mapping, QTL gene innovation and description of individual quality, biotic stress traits, abiotic stress performance, and up-gradation of the crop. Molecular studies have been developed as a dominant and consistent tool for the genetic exploitation of essential and defense traits in different plants.

Identification and utilization of resistant cultivars are the cheapest, practicable, and environmentally friendly way to combat the insect pest problems. The identified resistant genetic resources can thus be utilized in a molecular breeding program with the aid of DNA markers. Improving the defense mechanism against insects and exploration of resistance genes is the only way to manage the stem borers using transgenic approaches [19]. Therefore, the development of stem borer resistant genotypes using molecular approaches to increase agricultural production is gaining importance. In subsequent sections, the host plant resistance mechanisms and molecular features of *S. inferens* like the mitochondrial genome, molecular categorization of heat shock proteins and Quantitative Real-Time PCR Analysis are summarized, which could help the researchers in planning future research.
1.1. Historical Perspectives

Foremost damage of the pink stem borer was observed in maize during 1914 by Fletcher in India. Afterwards it moved to finger millet, rice and wheat. Later on, the pink stem borer was confounded as a rigorous pest in many crops. The historical perspective of this pest is depicted in Figure 1.

![Figure 1. Historical perspectives of S. inferens.](image)

1.2. Pink Stem Borer—Host Range and Crop Losses

In South India, the pink stem borer has a broad host range that includes wheat, maize, sorghum, ragi, rice, sugarcane [20], and citronella grass in Bengal [21]. Besides, it has also been reported to infest sorghum in Gujarat [22]. In addition, the infestation was also reported [23,24] in rice, oats, barley, sugarcane, and some grasses, while Deole et al. [25] reported damage in maize crops in Chhattisgarh state. The other host plants of relatively lesser economic importance are Goose grass (*Eleusine indica* Poales: Poaceae), Spring grass (*Eriochloa procrera* Poales: Poaceae), Pearl barley (*Hordeum vulgare* Poales: Poaceae), Wrinkled grass (*Ischaemum rugosum* Poales: Poaceae), Lemon grass (*Cymbopogon citrates* Poales: Poaceae), Purple nutsedge (*Cyperus rotundus* Poales: Cyperaceae), Deccan grass (*Echinochloa colona* Poales: Poaceae), Barnyard millet (*Echinochloa crus-galli* Poales: Poaceae) Pigeon grass (*Setaria pumila* Poales: Poaceae), Sanwa millet (*Echinochloa frumentacea* Poales: Poaceae), Finger millet (*Eleusine coracana* Poales: Poaceae), Bahiagrass (*Paspalum scrobiculatum* Poales: Poaceae), Bajra (*Pennisetum glaucum* Poales: Poaceae), Sugarcane (*Saccharum officinarum* Poales: Poaceae), Italian millet (*Setaria italica* Poales: Poaceae) and Sorghum (*Sorghum bicolor* Poales: Poaceae). The grain yield loss varied from 25.7 to 78.9% in maize [15]. Similarly, Ghai et al. [26] recorded more than 11% damage in wheat. Butcheswera (1983) observed 25 to 80 per cent loss due to *S. inferens* in Maize. In addition, the yield losses of maize (DHM103) due to *S. inferens* registered that protected plot yielded 6210 kg/ha whereas unprotected plot yielded 5910 kg/ha [27].

1.3. Taxonomy of Pink Stem Borer

The pink stem borer was placed under the genus Leucania until 1856 [28]; however, in 1884, it was consigned to the genus Sesamia [29]. As per Lefroy [30], the pink stem borers were grouped into the genus Sesamia, order Lepidoptera, Family Noctuidae, and Subfamily Acronytinae. The synonym for *S. inferens* is *Leucania inferens* and *Nonagria inferens* [31,32]. Different species of Sesamia affect rice viz., *Sesamia botanephaga* (Tam and Bowden) (Africa), *Sesamia calamistis* (Hampson) (Africa),
Sesamia inferens Walker (Asia/Australia/Oceania) and Sesamia nonagrioides (Lefebre) (Africa). Rice and wheat were also found to be attacked by Sesamia epunctifera Hampson (Africa), Sesamiacretica (Lederer) (Africa/Europe/Middle East), Sesamia pennisetii (Tam and Bowden) (Africa) and Sesamia uniformis (Dudgeon) (Asia) [23]. The African pink stem borers, S. calamistis, S. botanephaga, and S. penniseti; pink stem borer or greater sugarcane borers, S. cretica and S. wiltshirei Rungs; Asian pink stem borer, S. inferens and shoot borer, S. uniformis dominate in the maize growing areas of the tropics. Sesamia species, which affected maize in the Mediterranean region of Europe and Africa, included S. nonagrioides and S. vuteria Mariani [33]. The prevalent pink stem borer species associated with millets in Asia, Australia, and Oceania are S. inferens [34].

1.4. Geographic Distribution

S. inferens is extremely polyphagous on different graminaceous plants and diminished the productivity of cereals and millets. It was accounted from Malaysia, Philippines, Taiwan, China, Japan, Bangladesh, Bhutan, Brunei, Hongkong, India, Indonesia, Korea, Nepal, Pakistan, Singapur, Srilanka, Thailand and Vietnam. The global geographic distribution of S. inferens is summarized in Table 1.

Table 1. Geographic distribution of S. inferens with different countries.

| Region | Reported Crop | Authors |
|--------|---------------|---------|
| Malaysia, Philippines, Taiwan, China,Japan, Bangladesh, Bhutan, Brunei,Hongkong, India, Indonesia, Korea,Nepal, Pakistan, Singapur, Sri Lanka,Thailand and Vietnam | Rice | [31,32,35] |
| Malaysia | | [36] |
| India | Wheat | [9,26,37] |
| Philippines | | [29] |
| Asia | | [31] |
| Bangladesh | Maize | [38] |
| India | | [9,21,39–41] |
| Malaysia | Sorghum, Johnson grass, Sudan grass | [28] |
| India | Millets | [37] |
| Asia | Sugarcane | [31] |
| India | | [9,29,39,42,43] |
| Asia | Guinea grass | [31] |
| India | | [37,39] |
| Asia | Graminaceous and Cyperus weeds | [31] |

1.5. Bionomics and Life History on Different Host Plants

The biology of S. inferens in Eleusine coracana was first examined by Krishnamurti and Usman [44]. The detailed review of each developmental stage of this insect is presented below. The life cycle of pink stem borer is depicted in Figure 2.
1.5.1. Egg

Agarwal and Siddiqui [45] recorded the eggs on the underside of the plant on rice. The freshly laid eggs are creamy white, semi-globose, flattened on the dorsal surface, measuring 0.6 mm in diameter with 0.6 mm length and 0.4 mm width [46]. The egg color ranges from creamy white to brown, and ash gray to finally becoming pinkish before hatching [47]. The developed embryo has a pink streak with a slight curl inside the shell on the fourth day, and on the sixth day, the larva is observed with a prominent head [33].

The yellowish eggs are spherical, placed in batches of 30–100 arranged in 2–3 corresponding lines in sorghum [48]. Egg laid pattern and place varies with the plant species. In sugarcane, about 50–150 numbers/cluster [49] of eggs are observed, while in rice, eggs are found either singly or in clusters of about 30–100 [32]. The egg number and place differ within the same crop and between the species. In rice, two to three rows of 15–91 eggs were noticed in the interior side of leaf sheath [50], while in basmati rice, it was in the third leaf sheath [51]. On maize, eggs were laid in 2–4 longitudinal rows in the lower leaf sheath, preferably the first and second leaf sheath in young plants [52].

The phyllotaxy played a crucial role in the number of eggs laid. Ateyim et al. [53] compared the eggs in different parts (upper, middle, and lower portions) of maize plants by *S. botanephaga* from Southern Ghana. They reported that the central portion of the plant had the highest amount of eggs (71.0 nos).

Age of plant also plays a crucial role in oviposition. The female moth preferred the 7th leaf sheath of the 11th leaf stage for fecundity in maize (35 days after germination) than 15 days after germination [54]. Similarly, the earliest and first leaf sheath recorded the highest number of eggs than the basal leaf sheath in maize [52,55].

The atmospheric temperature and humidity significantly influence the developmental system of insects. An incubation period of 7.5 ± 0.5 days is reported for pink stem borer in rice with 35.8 °C and 26.3 °C of maximum and minimum temperatures and a relative moisture content of 52–83% [56]. Similarly, Rothschild [57] from Malaysia reported 7–8 days of incubation period at 24–29 °C and 72–98% relative humidity (RH). The incubation period varied between the crops since the abiotic and biotic stresses greatly influence the insect’s growth and development and 5.34 ± 0.10 days’ incubation in
basmati rice [51], whereas 7.40 ± 0.38 days in wheat [58]. In maize, an incubation phase of 6–8 days and [33], 5–6 days [59] were reported.

1.5.2. Larva

The size of the larvae varies with season, accessibility, and availability of food sources. The larva is pinkish, even-textured, 30 mm length at full-grown upstage with red/brown color head, and encompasses six instars [48]. The fully grown larval body is segmented stout and robust. However, Dale [32] recorded a larval length of 20–26 mm in rice, whereas eight instars with an average length of 3.1, 4.3, 8.5, 12.7, 16.6, 21.3, 24.9, and 29.0 mm, respectively were recorded in sugarcane [49]. The grown larvae on maize crop were sturdy with a hard head capsule (orange-red), the body was purplish pink and white at the dorsal and ventral position respectively, 35 mm in length and 3 mm in width [33]. The full-grown larva in the maize crop was 30–35 mm long [60].

The total larval duration varies significantly with different seasons and crops. Six larval instars with 24 days of larval duration in rice crops [56], while eight instars with 42 days of the larval duration in sugarcane [49]. On the contrary, six instars in May–October and eight instars in November–December in rice [47]. Eight instars in wheat in about 53 days of the larval period during October–December and 85 days during November–February [58]. Larval period of 22–36 days was reported in maize crop [33] while in basmati rice eight larval instars with a mean larval duration of 68 days were documented [51]. However, six instars with a total period of 23–29 days were also reported in maize [59].

1.5.3. Pupa

The obtect pupa is 9 to 14 mm long with a head area of pupa covered with bluish dust, and the remaining the body is dark brown [46]. In contrast, pupae of S. inferens in sugarcane were robust and brownish, with a tapering abdomen that carried two small “bumps” in the front of the genitalia [49]. They measured 15 to 17 mm in size; females were larger with broad abdomen than males and devoid of any markings making the sex determination easier for the pupa. In addition, a 12 to 18 mm long reddish-brown pupa was observed by Litsinger [31]. Smaller size of the male pupa (having 9th sternite guarded by two pads) compared to female pupa was noticed (having bursa copulatrix on the 8th sternite) [61]. In maize, 17–20 mm long female pupa and male pupa 14–16 mm of length were reported [60]. The female pupae were bigger than males in all the studies. It was reported that the length and width of 10.00 ± 0.26 and 2.05 mm, respectively, were recorded for male pupa, whereas 12.58 ± 0.32, and 2.55 mm were recorded for female pupa [58]. The abdominal spiracles were an outstanding feature with a slit-like, slightly raised opening [59]. The pupal period was low, about 12 days during summer, while 36 days in winter in rice [46], and 9–11 days in sugarcane [49]. Furthermore, various researchers reported the pupal period as 7–10 days [33], 12–15 days [60], and 7–12 days [59] on maize. In wheat, the pupal duration for males as 37 days, and 38 days for females, during the winter season [58].

The stalk with the emergence hole pointed out the presence of the pupa of S. inferens by Atwal and Chaudhari [56] in rice, and it was observed amid the leaf sheath and stem (Khan et al. [23] Dale [32]). Sekhar et al. [33] reported pupation in the leaf whorl, tassel, ears, and stem of maize. Similarly, Nagarjuna et al. [59] observed that pupation occurred inside the stem of the maize crop. Singh [58] observed that S. inferens pupated in the soil near the foot of the wheat plant. However, the majority of the pupation occurred inside the stubbles of rice plants or within/near its base. Pupation occurred inside the stem, with the biology completing in around fifty days [48].

1.5.4. Adult

The copulation rate was higher in one-day aged female (90%) moths than a five-day-old female (40%) [16]. The adult fecundity was reported as 300 eggs in sugarcane [62], whereas 300 to 600 eggs in rice [46]. Fecundity of 405 eggs, with the highest eggs (174 nos), acquired from second day-old adults [55] in maize.
The adult emerged with rudimentary wings that later expanded entirely in about 30 min. The maximum adult emergence was 79% and occurred between 7 pm and 6 am [49]. Evening and night hours [34] were optimum for noctuid pink stem borer oviposition. The sex ratio was as follows 1:1 and 1:1.04 in rice [47,58] and 1:1 in wheat [58] from India. Adult longevity in wheat was reported as seven days for females and five days for males [58]. Similarly, adult longevity of 5–7 days in females and 3–5 days in males on maize [59].

Straw-colored medium-sized moth with copper streaks on the forewing and milky hind wings was recorded on maize [60]. Straw-colored moths with dark brown streaks on the forewings and hind wings with three black spots were also reported [48]. The antennal type made the sex determination easier for the moths, *S. inferens*. The males had a pectinate antenna and mid-longitudinal dark brown triangular streak in the straw-colored forewings [59]. The length of males (10 mm) and females (14 mm) in rice crops [50]. The body length varied from 14–17 mm, and the wingspan was about 33 mm on maize [33]. The pest also completed 4–5 generations per year [48].

1.6. Seasonal Abundance

Early planted crop undergoes a higher injury level than late-planted crops. Besides, it was also observed that *S. inferens* was active from July to October [14]. Akhter et al. [63] noticed the occurrence of *S. inferens* in rice from September to April in Pakistan. The pink stem borer hides in the stubbles of rice within the extended stem from October to March and moths emerge from mid-April. The egg is laid starting from spring season on wheat, barley, and rice [40]. It was observed that a higher rate of larvae and the nocturnal moth activity were detected on maize from the second week of March in Chandigarh [64]. Sidar et al. [65] reported that *S. inferens* first appeared on maize during August, with about 10% dead heart and reached its peak with 60% dead heart symptoms during September.

The dead heart percentage showed an insignificant, positive association with high temperature, dampness, and daylight, whereas a negative correlation with low temperature, wetness, and rainfall. Sidar et al. [65] showed a highly significant negative correlation for dead heart symptoms with wind velocity.

1.7. Crop Damage

The neonate pink stem borer larvae remain in groups inside the leaf sheath and feed on the epidermal layer. The original site of its feeding is the bottom-most leaf sheath. Gummy liquid oozes out with water-soaked laceration appearing outside of the affected leaf sheath due to the early instars feeding.

Ultimately, through leaf sheath feeding, the larvae reach the central primordium which consequently leads to the formation of parallel rows (2–3 mm size) which are widely spread in the leaves and later gets extended and become streaks. In extreme cases, bored midrib concludes with tunneling symptoms on leaf blades, showing ragged manifestation in plants. The emerging points of the stem infested in the end, get dried and developing a dead heart symptom. Thus, leading to the expansion of abundant side tillers at the vegetative stage and “white ears with unproductive spikes at the reproductive stage which bore chaffy grains in cereals and millets. As a result, vegetative stage infestation and reproductive stage damage finally led to grain loss as well as fodder reduction. The maximum stem damage was noted between the first to fifth internodes with approximately 2–5 exit holes per plant. The stem tunneling was horizontal that occasionally moved to nearby internodes. The outer portion of the lowermost stem showed circular cuts filled with frass [66]. A single caterpillar triggered profuse infestation in numerous plants. Once the stems dehydrated, the larvae left the old tunnels at the earliest and settled in new tunnels [67]. The two-leaf stage was observed as a critical stage for *S. inferens* damage [68] in maize.
1.8. Genomics of Defense to S. inferens

“The prerequisites and criteria in resistant molecular breeding against the target pests are understanding the genomics level of host plant defense and evaluation of the number of responsible genes imparting resistance to a plant-feeding insect pest” [69]. Mather [70] called it as the backbone of Generation Mean Analysis (GMA), developed and promoted the effectiveness of scaling check to recognize and understand the heredity and genetic material underlying quantitative behavior such as insect resistance genes. GMA is a fundamental tool to study the genomics of an organism. GMA was successfully utilized in maize to understand the inheritance of resistance to Mediterranean corn borer (MCB) [71]. Furthermore, the heredity of resistance against MCB recommended quantitative inheritance [71,72]. GMA is specified as a relatively easy and consistent tool [72,73]. Besides, the genetic source of defense mechanism against S. inferens was reported in maize in India. Santosh et al. [74] illustrated that negative additive and dominance effects, and positive additive x dominance (j) and dominance x dominance (l) epistatic interaction affects the management of the S. inferens resistance in maize. The effective inbred line improvement can be accomplished through the association of pedigree breeding coupled with a cyclical breeding procedure (Figure 3). Insect resistance is mainly regulated by additive x additive (i), followed by dominance (d) and additive (a) gene effects. The effects of inbred lines and their reaction to S. inferens were studied in maize [75]. The lines used in the study are depicted in Table 2. In DMRE2 X CML287, epistasis (i, j, and l) was not observed and was insignificant (expression resistant to S. inferens).

![Flow chart of cyclic breeding method.](image)

**Table 2.** Effects of inbred lines and their reaction to S. inferens in Maize.

| S.No | Name of the Inbred Lines | Source Germplasm | Reaction to Pink Stem Borer |
|------|--------------------------|-------------------|-----------------------------|
| 1    | DMRE1                    | PT963128          | Resistant                   |
| 2    | DMRE2                    | Antigua Gr.1      | Resistant                   |
| 3    | CML287                   | Population 24     | Susceptible                 |
| 4    | CML451                   | Pool 25           | Susceptible                 |

The reciprocal recurrent selection (RRS) method creates a platform for horizontal resistance against insects, which cannot be broken by the environmental condition. Inherited resistance against S. inferens was confirmed in maize [75]. Nevertheless, details on the genetics of the insect resistance are sparse [74]. One significant constraint in conventional breeding is a prolonged time, which could be rectified through combined biotechnological approaches. However, the study is limited to S. inferens infesting millets that require further research for better understanding.
2. Quantitative Trait Loci (QTLs)

Understanding of various mechanisms on resistance against insect infestation, especially pink stem borers, is of utmost need. Antixenosis diminishes the contact between insects and plants, and antibiosis affects the growth and development of larvae when the plant is utilized for food. However, non-preference and antibiosis against borers are lacking [76]. The development of a resistant variety is the best way for borer management because the larvae and pupae hide within the stem. Thus, characterizing the pink stem borers resistance mechanism using quantitative trait loci [71] method to overcome the borers [19] infestations is a necessity. The genes linked by a unique trait within the genome are known as quantitative trait loci (QTLs). Although the recognition of QTLs by phenotypic illustration is not feasible, the quantitative trait variance could be successfully identified by molecular markers during 1980. QTL generally starts with a combination of genotypes (molecular markers) and phenotypic data. The genotypic data are placed on the genetic map by linkage mapping approaches through markers. Analytical methods have facilitated the detection of one or numerous QTL on every chromosome [77]. Despite the above facts, the genome of barnyard millet with QTL for *S. inferens* is unexplored.

2.1. Barnyard Millet Genome

Five *Echinochloa* species were sequenced from various regions of India, including Tamil Nadu, especially the complete chloroplast genome sequence of *Echinochloa frumentacea* (139593 bp). It has close relatives to *Echinochloa oryzicola* and *Echinochloa crus-galli* [78] (Table 3). The sequence is available to plot the quantitative trait locus (QTL) for insect resistance. Besides, this newly illustrated chloroplast genome of *E. frumentacea* offers a valuable source for linkage mapping analysis [78].

| Crop Description | Accession Number | Genome Size | Country          | Reference |
|------------------|------------------|-------------|------------------|-----------|
| *Echinochloa frumentacea* cultivar CO(KV)2 chloroplast, complete genome | KU242342.1 | 139593 bp | Tamil Nadu, India | [78] |
| *Echinochloa crus-galli* var. crus-galli chloroplast, complete genome | KJ000047.1 | 139800 bp | China | [79] |
| *Echinochloa crus-galli* var. praticeola chloroplast, complete genome | KR822686.1 | 139846 bp | China | [80] |
| *Echinochloa crus-galli* chloroplast, complete genome | KR822684.1 | 139857 bp | China | [80] |
| *Echinochloa crus-galli* var. crus-galli chloroplast, complete genome | KR822685.1 | 139860 bp | China | [80] |
| *Panicum virgatum* chloroplast, complete genome | NC_015990.1 | 139619 bp | USA | [81] |
| *Zea mays* chloroplast, complete genome | NC_001666.2 | 140384 bp | Germany | [82] |
| *Setaria italica* chloroplast, complete genome | KJ001642.1 | 138833 bp | USA | [83] |

2.2. Phylogenetic Analysis of *Echinochloa frumentacea*

Phylo-geographical outline of existing heritable differences in organisms is extremely valuable in enlightening demographic records and widely recognized as a tool for exploring the origin
and the dispersal path of a species [84]. Four sequences covering complete chloroplast sequences of Echinochloa sp. and one Setaria italica sequence with the out-group, Brachypodium distachyon were aligned using Clustal W [85]. The multiple sequence alignment was done and subsequently trimmed in MEGA v.6 which has developed at Pennsylvania State University, University Park, PA, USA [86]. Phylogenetic interactions were analyzed using [87] neighbor-joining method coupled with bootstrapping [88]. Evolutionary distances were calculated by the P-distance method [89] using MEGA v.5 which has developed at Pennsylvania State University, University Park, PA. Bootstrap values (1000 iterations) were deliberated based on more than 70% majority rule and confidence limits.

The phylogenetic analysis of the sequences using tree construction showed 99% homology with the Echinochloa sp. (Figure 4). The sequence can thus be used in mapping analysis to explore the insect-resistant genes (QTL) since QTL mapping for pink stem borer resistance is unidentified in the barnyard millet genome.

![Cladogram of Echinochloa frumentacea using chloroplast genome sequences](image)

**Figure 4.** Cladogram of Echinochloa frumentacea using chloroplast genome sequences (The sequences were retrieved from NCBI).

### 2.3. The Mitochondrial Genome of S. inferens

Mitogenomics is extensively used as a useful molecular marker to describe phylogenetic conjecture, identify the species, phylogeography, the investigation of population configuration and dynamics, and molecular evolution at the genomic level [90]. Thus, insect mitogenomes would amplify the richness of information for phylogenetic study and evolutionary natural science.

Currently, mitogenomes are considered an important strategy in pest control. The usefulness of this study is to improve the progress of scientific databases and support future population genetics studies, especially in Lepidopteran insects. The mitochondria-targeted genomes (mitogenomes) were isolated from 393 species of herbivores, together with 241 species of phytophagous insects. Thirty-six mitogenomes from these were sequenced from 6 super-families of Lepidoptera (biggest order) including Bombycoidea (7 species), Geometroidea (1 species), Papilionoidea (14 species) Pyraloidea (6 species), Tortricoidea (3 species) and Noctuoidea (5 species) namely, old world bollworm, American white moth, gypsy moth, the bag-shelter moth and the pink stem borer [91–94]. The insect mitogenome is a closed-circular duplex molecule, about 14 to 20 kb in size. The 13 protein-coding genes (atp6, atp8, cox1, cox2, cox3, cob, nad1, nad2, nad3, nad4, nad5, nad6, and nad4L genes); large and small ribosomal RNA genes (rrnL and rrnS), 22 tRNA genes, account for energy generation, electron transport mechanism and process of oxidative phosphorylation [95]. Silencing protein-coding genes can lead to the prevention of transcription, such as amino acid synthesis, which is essential for
the growth and development of insects. This novel technique became important in the pest control program. In addition, Wei et al. [96] reported that the AT-rich region, present in the insect mitochondrial genome and an initiation site is in charge of the transcription and replication of the genome.

Mitogenome of *S. inferens* revealed that the secondary formation of tRNA and rRNA genes AT-rich regions elucidate its genomic features, gene order, and the nucleotide composition of PCGs (protein coding genes). The stem-and-loop structure of the AT-rich region was only observed in *S. inferens*, but not in other noctuid moths, a unique feature of *S. inferens*. Thus, the herbivore mitogenomes helped in determining the phylogeny of Noctuoidea [97]. Understanding more about this imperative pest could facilitate the improvement of techniques for its control. Moreover, the complete genomics of the *S. inferens* is useful for the synthesis of species/gene-specific primers. The gene-specific primers play a vital role in molecular breeding. A specific insect could be identified, isolated, and amplified by PCR using these primers. The sequence results could further be used for research in the molecular breeding program, ultimately establishing insect species-specific markers.

2.4. Temperature Shock Proteins in *S. inferens*

Temperature preference determines the life history parameters of insects. Highly conserved and endogenous proteins known for temperature stresses were identified as “Heat shock proteins (HSPs)” [98]. HSP are incredible proteins present throughout the organism. Manipulation of HSPs is imperative in pest management since it involves the regulatory roles of the physiology of insects. The small heat shock proteins (sHSPs), namely, Sihsp21.4, Sihsp20.6, and Sihsp19.6, were isolated and characterized from the members of α-cristallin [98]. In addition, the three complementary DNA encoded proteins of 187, 183, and 174 amino acids with average molecular weights of 21.4, 20.6, and 19.6 kDa, respectively, were also illustrated in *S. inferens*. The results showed that sHSP genes play an imperative role in the physiology of *S. inferens* and could be used in pest management programs after the exploitation of sHSPs genes [98]. In *S. inferens* the small heat shock proteins (sHSPs) gene expression was studied using qRT–PCR that detected the elevated expression of Sihsp21.4 gene in the heads of *S. inferens* larvae which infers lower gene expression and where the fold appearance was high in eggs (Sihsp20.6 and Sihsp19.6) [98]. The exact roles of different HSPs are still not entirely tacit [98], and additional investigations on HSPs are needed to manage the economically significant insects.

2.5. Quantitative Real-Time PCR Analysis in *S. inferens*

The real-time polymerase chain reaction (RT-PCR) is presently the most precise, responsive, sensitive, and accurate tool for gene expression analysis. In qRT-PCR, data are standardized using ideal reference genes, which helps control internal deviation and diminish the inaccuracy between samples. Meng et al. [99] recorded seven reference candidate genes to study the genetic expression of *S. inferens* viz., 18S rRNA (18S ribosomal RNA), EF1 (elongation factor 1), GAPDH (glyceraldehyde-3-phosphate dehydrogenase), RPS20 (ribosomal protein S20), TUB (tubulin) and ACTB (β-actin). The results revealed that all seven genes were used in normalizing gene expression under different investigational circumstances. Further, the results showed that three genes (RPS13, RPS20, and EF1) were the most favorable to regularize gene expression profiles in various insect segments, viz foregut, midgut, and hindgut [99]. The genes, GAPDH, 18S rRNA, and EF1, wereexcellent in normalizing expression with subject to reproductive organs [99]. These studies thus described that the reference genes analysis is useful to compute genetic expression in *S. inferens* precisely. However these studies on gene expression in *S. inferens* are inadequate and need to be more exploredusing novel molecular approaches. Thus, reference genes were used to study the gene expression profile level without insect infestation as well as by challenging insect infestation in any plants.

Improvement of SSRs (simple sequence repeats) and its application in heritable multiplicity study of Indian population of *S. inferens* were studied by Anthony Reetha and Mohan [100]. In which, six SSRs illustrated the hereditary divergence among *S. inferens* population with respect to their host sorghum, sugarcane, maize and rice field populations of *S. inferens* noted with a low level of
inter-population gene flow. Also, the differences among the populations indicate only a moderate scattering ability of *S. inferens*. Hence, it is pertinent to the re-evaluate the gene flow of sympatric *S. inferens* populations linked with dissimilar host plants within its distribution range.

Moreover, an effective method to establish a marker associated with insect resistance traits, especially plants showing insect resistance genes, should be studied and evaluated for future research, mainly in the small millets and cereals against *S. inferens*.

3. Status of Pink Stem Borer, *S. inferens* on Cereals and Millets

3.1. Finger Millet, *Eleusine coracana*

The finger millet (*E. coracana* L.), often referred to as “small seeds with bigger health benefits,” is a vital small grain millet broadly cultivated in different parts of India, and Africa, providing sustained food for small farmers in many countries. Although among the millets, it ranks 6th in production in India [101], it showed a downtrend from *S. inferens* damage [102] that causes severe damage across the country throughout the year. In South India, it often was affected by *S. inferens* when cultivated in winter [103]. Ragi crops were found to be the most preferred host for *S. inferens* in irrigated conditions [104].

Although *S. inferens* has the ability to withstand freezing temperatures, the critical ecological restriction for the existence of insects is low winter temperature [98]. Pink stem borer injury starts when the crop is 30-days-old. Some of the resistant and tolerant genotypes are listed in Table 4.

### Table 4. Resistant and tolerant genotypes of Finger millet against *S. inferens*.

| Crop Category | Reported by |
|---------------|-------------|
| Finger millet, *Eleusine coracana* | - PRM 9002, KOPN 933, OEB 28, RAU 8 and Champabati [103] |
| KM 1 RAU 1, RAU 3, INDAF 7, INDAF 8, HR 154, HR 374, HR 1523, PES 110, PES 400, WR 9 and VL 110 | - [105] |
| PES 9, PES 144, PES 224, KM 1, KM 14, HR 228, JNR 1008 and T 36-B | - [106] |
| - VL 109, VR 530, PR 202, HR 374 | - [107] |

3.2. Maize, *Zea mays*

Maize hybrids against *S. inferens* revealed that CP 828 recorded the lowest infested plants (3.87%), cob damage (3.92%), dead hearts (4.04%) and 13 pinholes with a straw yield of 96.54 q/ha and grain yield of 44.69 q/ha, confirming it as the most tolerant variety [59]. Six inherited cultivars viz., WNZPBTI 9 (3.2), WNZPBL 8 (3.5), CML 338 (3.6), WNZ EXOTIC POOL DC2 (3.1), CML 424 (3.2), WNZPBL 9–1 (3.4) recorded leaf injury rating less than the resistant variety CM 500 (3.8). It was considered as a resistant line in maize against pink stem borer, *S. inferens* [109]. The period of extension from young one to adult was prolonged in resistant maize compared to the susceptible genotype. The HQPM-1 resistant genotype recorded 35.84 days of the larval growth period, being low in susceptible genotype, Sugar 75 (34.90 days). Furthermore, the growth index was higher in Sugar 75 (1.68) compared to the resistant cultivar, HQPM-1 (1.48). Some resistant and susceptible cultivars are listed in Table 5 [25].
Table 5. Resistant and susceptible cultivars of Maize against *S. inferens*.

| Crop        | Category | Susceptible | Resistant                                                                 |
|-------------|----------|-------------|---------------------------------------------------------------------------|
| Maize, *Zea mays* |          |             | The entries namely, 221267-A, full season maturity line 221267-D, PAC-9703, BIO-9637, PAC-9735, medium stage maturity line KH-5354, BIO-9691, 127868, JKM14095MMH-1765 and R-51 (Early maturity) |
|             |          |             | IC331939, IC340368, IC369174, IC369184, IC406420, IC549985, IC549990, IC569669, IC547811 | 110 |
|             |          |             | DC-2, HKI-193-2 and E-62 WP-21, E-63 and HKI-193-1 | 111 |

3.3. Barnyard Millet, *Echinochloa frumentacea*

The barnyard millet germplasm against *S. inferens* showed that DHBM 99–6 (2.63%) followed by DHBM 99–7 (2.91%) and TNEF-204 (3.94%) recorded less dead heart and were considered resistant to *S. inferens*. However, DHBM-33 recorded the highest dead heart (16.36%) symptom and was regarded as susceptible [112]. However, the study on varietal screening of barnyard millet against *S. inferens* is still in infancy stage.

4. Conclusions

The polyphagous pink stem borer, devastating the cereals and millets and has gained national importance. Nevertheless, none of the management measures have been found to be effective for controlling this pest successfully since its larvae and pupae are sheltered within the stem. Crop losses due to this borer consistently reveal an increasing trend. There is huge demand to overcome such a notorious pest in an eco-friendly manner. But, none of them had exhaustively reviewed about *S. inferens* menace completely on cereals and millets. With this issue, we illustrated about bionomics, host plant resistance and molecular perspectives of *Sesamia inferens* with recent updates. In this context, useful genetic variations exist in many wild relatives as well as native cultivars of plants, which are yet to be exploited for crop improvement. Traditional approaches of breeding technique face limitations in the resistant cross-breeding program such as a slow-moving operation, prolonged time, and complicated method of detecting a specific gene due to the presence of quantitative traits at several loci. Hence, without markers, the screening program never completes. However, recent biotechnological interventions act as a platform to provide and execute new avenues for pest control with access to novel gene fragments, capable of developing genetically modified genotypes with defense genes against herbivores. Moreover, biotechnology is a modern science to overcome the harmful effects of pests that hindered millet advancement, using the host plant resistance approach.

**Funding:** This review did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

**Acknowledgments:** Sincere thanks to Center of Innovations, TNAU for providing an enormous knowledge source and support for this review paper.

**Conflicts of Interest:** No conflicts of interest have been declared by all authors.
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