A Social Network Analysis approach for identifying critical research areas in the management of Fall armyworm (Spodoptera frugiperda)

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Abstract

The fall armyworm (*Spodoptera frugiperda*) is threatening the world's food supply and causing negative effects on food production and rural livelihoods in numerous nations, resulting in socioeconomic consequences. Despite significant research, there is still no effective way to control this pest. To manage the fall armyworm, institutional or global collaboration is necessary, which involves mobilizing resources for research, promoting international cooperation, and sharing knowledge. The article employs the Social Network Analysis method to analyze the current research trends related to management techniques for the fall armyworm, which provides new insights into the relationships between different concepts and control strategies and how they are being implemented in the field. The study identifies important research concepts, popular topics, and key actors that have influenced a specific field of research related to managing an agricultural pest. The information collected can be useful for students, academics, practitioners, science policy-makers, and R&D management who are interested in dealing with this pest.

1. Introduction

The *Spodoptera frugiperda*, commonly known as the fall armyworm (FAW), is a lepidopteran insect from the family Noctuidae that poses a threat to global food security. It negatively impacts the rural livelihoods of millions of people and food production, resulting in socio-economic and health-related consequences (Abro et al., 2021). Originally native to the Americas (Luginbill, 1928), FAW has rapidly spread to neighboring countries and other regions of the continent, and was first discovered in West and Central Africa in early 2016 (Goergen et al., 2016). Within two years, it had nearly infested the entire sub-Saharan African region. FAW has since been detected in numerous Asian nations, such as India, Bangladesh, Sri Lanka, Thailand, Myanmar, China, Indonesia, the Philippines, the Lao People's Democratic Republic, Malaysia, Viet Nam, Cambodia, the Republic of Korea, and Japan, as well as in Sudan, Egypt, and Yemen. By early 2020, it had also reached Australia, Mauritania, Timor-Leste, and the United Arab Emirates, including mainland Australia, and has now been confirmed in 109 countries globally (FAO, 2022). FAW is a highly mobile and invasive insect that can travel over 100 kilometers in a single night and is considered a transboundary pest and a seasonal migrant (Rwomushana, 2019). The risk of its further spread and range expansion is a significant concern (FAO, 2022).

The FAW is a highly destructive insect pest that attacks a wide variety of plant species (Prasanna et al., 2018), numbering around 350 across 76 different plant families (Débora G Montezano et al., 2018). This insect poses a serious threat to over 80 important food crops such as maize, sorghum, soybean, cotton, barley, and wheat, and can significantly reduce crop yields (de Freitas et al., 2011; Malo et al., 2020; Marenco et al., 1992; Montezano et al., 2018; Overton et al., 2021; Pitre et al., 1983; Yang et al., 2020). FAW is a significant threat to the livelihoods of millions of smallholder farmers and consumers (Abro et al., 2021; Chimweta et al., 2020), where it could result in losses of up to US$13 billion annually in rice, sorghum, sugarcane, and maize (Abrahams et al., 2019). The economic impact and management of FAW must be understood, as it is spreading rapidly across the world. According to the Food and Agriculture Organization (FAO), FAW could result in annual losses of 8.3 million to 20.6 million metric tonnes of
maize for just 12 African nations and could cost between USD 2.5 billion and USD 6.2 billion (Day et al., 2017; Ferreira et al., 2010). The potential economic costs of phytosanitary measures to intercept FAW in the import or export of fresh produce have not yet been calculated (Abrahams et al., 2019; Health et al., 2018; Rwomushana 2019).

FAW is a mobile crop pest that quickly develops resistance to chemical pesticides, making population control challenging (Paredes-Sánchez et al., 2021). Inappropriate pesticide use can have negative impacts on humans and the environment, further increasing FAW resistance (Bolzan et al., 2019; Lira et al., 2020). Effective FAW invasion management requires an efficient pest recognition system. PCR and sequence-level techniques aid in detecting FAW behavior (Drès & Mallet, 2002; Montezano et al., 2019; Vélez-arango et al., 2008) and internal transcribed spacer 1 (ITS1)-based PCR primers have higher efficacy (Tsai et al., 2020). Quantitative real-time PCR (qRT-PCR) can analyze the expression profiles of various target genes, and examining the expression levels of multiple reference genes from FAW can aid in ensuring that future studies are more reliable (S. Han et al., 2021; Shu et al., 2021). Two S. frugiperda biotype strains, "rice or R" and "corn or C," differ in sensitivity to controls and preferred crops were recognized (Nagoshi & Meagher, 2004; Salinas-Hernandez et al., 2011; Vélez-arango et al., 2008). The Sf00067 loop-mediated isothermal amplification (LAMP) assay may allow genotype-based strain diagnosis (Osabutey et al., 2022). RNA interference (RNAi) has potential for controlling FAW and other Lepidoptera pests (Bettencourt et al., 2002; Bai-Zhong et al., 2020; Fite et al., 2022; Gregoriou et al., 2021; Gurusamy et al., 2020), is a gene silencing mechanism that can regulate chromatin modifications to inhibit or reduce the stability of targeted mRNA, leading to the destruction of specific mRNAs (S. Liu et al., 2020). This approach has been used in insect management strategies under field conditions by using double-stranded RNA (dsRNA) to silence target insect genes after ingestion (Dowling et al., 2016). This method has been effective in controlling major agricultural pests like FAW and other lepidopteran pests (De Schutter et al., 2021; Hernández-Soto et al., 2021; X.-H. Liu et al., 2020; Rosa et al., 2018; Tabashnik et al., 2017). CRISPR/Cas9-based genome editing has successfully been used in functional genomics research on major agricultural pests, and combining it with multiple sgRNA methods shows promise for achieving better results in genome editing for non-model insects like Lepidoptera (Chen & Palli, 2022; G.-H. Zhu et al., 2020).

Despite extensive research and various approaches to manage FAW, a devastating pest that remains a global challenge when introduced to a new location, there is currently no single strategy for managing it. This article discusses the challenges posed by the Fall Armyworm (FAW) pest and the need for an integrated pest management strategy that involves community-based programs, science-based knowledge dissemination, and international cooperation. This article highlights the importance of research trend analysis in identifying emerging threats and developing effective pest management strategies. The article utilizes the Social Network Analysis (SNA) approach to identify research trends related to FAW management. SNA uses graph theory to analyze social networks and identify patterns and structures within the network (Barnes & Harary, 1983; Borgatti et al., 2010). The article analyzes publications covering different stages of FAW research over the past decade to gain insights into the relationships among different concepts and control tactics. Overall, SNA provides a powerful tool for
researchers to understand the dynamics of research communities and to identify emerging trends and research opportunities (Majeed et al., 2020; Scott et al., 2011; Zweig et al., 2016).

2. Methodology

2.1 Social network analysis (SNA)

The relationships between various players involved in collaboration can be visualized through the nodes and edges of a network graph. By using systematic knowledge, social networks can define the static and dynamic characteristics of a network structure. In this study, the SNA approach was used to investigate a collaborative community, with a focus on identifying specific actors' positions, rankings, significance, and influence within the network structure. The term "centrality" was used to describe this concept. Freeman (1978) proposed three basic measures of centrality that can be used to assess the significance of actors in a social network from various perspectives. The most commonly used metrics to assess an actor's contribution to a network are degree centrality, which represents the degree of collaboration of a node, and betweenness centrality, which refers to the possibility that a certain node will be found on the shortest path between other nodes (Wasserman & Faust, 1994). These measures can be applied to analyze various actors such as documents, authors, institutions, and countries as potential nodes in the network to identify their roles in FAW research.

The Web of Science (WoS) database was used to document research in the field by including Science Citation Index, Science Citation Index Expanded, Conference Proceedings Citation Index – Science, Index Chemicus as well as Social Science Citation indexes. The study was conducted from 1st January 2012 to 20th December 2022 for comparative purposes. The study used the key word "Fall armyworm or Spodoptera frugiperda" in the search string to extract research papers containing the term in title, abstract, author's keywords, and keyword plus (indexed words assigned to papers by WoS). The search strategy followed the approach of Yan and his co-workers, (Yan, Lee, & Lee, 2015) and only English-language articles were used. The search yielded 2326 documents, and data from each article was extracted in a plain text (.txt) format for analysis and the software RStudio-R version 4.2.2 package was used to undertake cluster as well as SNA analysis. Bibliometrics (as bibloioshiny), a tool created in 2017 by Massimo Aria and Corrado Cuccurullo, (Aria & Cuccurullo, 2017) is used for quantitative research in scientometrics and bibliometric analysis. It allows for bibliographic data import from several databases and enables the analysis of knowledge structures and co-occurrence matrix variations. These approaches facilitate to analyze knowledge structures like "Conceptual, Intellectual, and Social Structures" and reveal connections between important concepts by studying different co-occurrence matrix variations (Callon, Courtial, Turner, & Bauin, 1983). These strategies were used to establish the framework of the entire research topic.

3. Results
The article discusses the use of scientometrics, which involves using quantitative techniques to evaluate academic and research production, to identify global research trends in managing the agricultural pest fall armyworm. The study analyzes the expansion of publications, key journals, leading nations, institutions, and authors in this field to identify important research concepts, trending topics, and major actors in managing the pest. The study's findings can be valuable to students, academics, practitioners, science policy-makers, and R&D management by providing useful information and knowledge in this area of research.

### 3.1 Publication trends

A scientometric analysis was performed on 2326 documents extracted from the WoS database, and the articles were sorted according to their publication years. Figure 1 displays the growth and distribution of articles from 2012 to 2022, revealing a steady rise in the number of published articles related to *Spodoptera frugiperda* since 2018, with an overall growth rate of 11.81%. This suggests a growing interest in this research area in recent times. From 2012 to 2022, the 2326 articles were published in 522 source journals, with an average of 6.13 co-authors per document and 31.64% international co-authorship. The average age of the documents was 4.78, and the average citation per document was 12.72. Figure 1 displays the number of published items from 2012 to 20 December 2022, revealing a substantial rise in publications from 2018 to 2022. Exempt the year 2012, the largest decrease in publications occurred between 2013 and 2015. The graph indicates a gradual increase in publications during the middle period after a fluctuating trend between 2012 and 2017. The mean number of papers published per year was 444.36, with a standard deviation of 221.99. The right-skewed shape of the graph, which is consistent with the high standard deviation value, indicates an increasing interest and investment in research on managing *S. frugiperda*.

### 3.2 Most Global cited documents

The frequency and number of citations of articles can be used to evaluate the significance of a research topic or field. This is because the number of citations reflects the popularity of a paper among researchers in that domain. The most cited papers in this area of research are related to biological control, plant extract or metabolites, chemical insecticides, and pest resistance. Figure 2 shows the top 10 most cited articles in this specific research area. The top-ranked article on the invasion of the Fall Armyworm pest in West and Central Africa was authored by Georg Goergen and his colleagues. The paper presents genetic evidence for the worldwide spread of the pest and highlights the potential harm it could cause to maize crops. Débora G Montezano and colleagues authored an article in 2018 titled "Host Plants of *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in the Americas". The paper provides a comprehensive understanding of the host plants of the Fall Armyworm pest and suggests a new method for identifying them. This could help in studying host-parasite relationships, devising control strategies, and predicting invasion risks. The article "Surge in insect resistance to transgenic crops and prospects for sustainability" by Bruce E Tabashnik and Yves Carrière is ranked third. The article presents an overview of the increasing resistance of insects, including *S. frugiperda*, to the *Bacillus thuringiensis* (Bt) crystalline
proteins produced by transgenic crops. It also discusses the potential implications for sustainability. The remaining articles in the top ten rankings cover a variety of topics related to *S. frugiperda* and insect control. Some of these include the genetic basis of Cry1F resistance in *S. frugiperda* against Cry1F maize, the development of the baculovirus expression system as a gene expression platform, the mechanisms and potential uses of various insecticidal proteins, the use of secondary metabolites as natural insecticidal agents, the negative impact of spinosad on beneficial insects and soil, and the genetic basis of polyphagy in insect herbivores and its evolution.

### 3.2.1 Co-citation network analysis of documents

Co-citation analysis is a scientific method used to analyze relationships between elements in scientific literature in a particular field. It was independently introduced by Henry Small and Irina Marshakova in 1973 (Marshakova, 1973; Wei & Zhang, 2020). Co-citation analysis is an objective and reliable method that can be used to map subject-matter specialities, investigate the intellectual structure, and examine the structure and evolution of innovation research in a specific domain of interest. This method is considered valuable for identifying differences in research topics among publications (Braam *et al.*, 1991; G. Yu *et al.*, 2017; Rossetto *et al.*, 2018). Cluster and co-citation network analysis on WoS datasets, along with the Walktrap algorithm, were used to identify the primary domain of research in this topic between 2012 and 2022. This scientometric analysis can be used to examine the structure and evolution of innovation research in a specific domain of interest.

The co-citation network is a collection of references that have been cited together in various publications (M. Chen *et al.*, 2014). The topologies of the network are based on the 50 most frequently co-cited articles in the dataset, where each node represents a cited reference, and the edges indicate the co-cited relationships among papers (J. Zhu & Hua, 2017). The nodal colors denote the clustering of the network. The document co-citation network reveals four distinct clusters when the number of nodes is limited to 50, with the network's co-citation links primarily appearing in blue, indicating that these co-citations were prevalent during that time. The co-citation network analysis identified four distinct clusters, each represented by a unique color, which can be used to illustrate the topics of discussion. Cluster 1 (red) is mainly focused on research on the field-evolved resistance of *S. frugiperda* against transgenic maize, while cluster 2 (blue) includes topics related to outbreaks and biology of the FAW. Discussions on the resistance of *S. frugiperda* to synthetic insecticides are the dominant focus of documents in clusters 3 (green) and 4 (purple). Two key documents, "Field-evolved resistance to Cry1F maize by *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in Brazil" by Farias *et al.* (2014) and "Cry1F Resistance in Fall Armyworm *Spodoptera frugiperda*: Single Gene versus Pyramided Bt. Maize" by Huang *et al.* (2014), are located in cluster 1 identified as key documents that have mutual connection between clusters and play a significant role in knowledge exchange between nodes. Followed by the papers authored by Goergen *et al.* (2016) and Montezano *et al.* (2018) included in Cluster 2 and in cluster 4, Carvalho *et al.* (2013) and Gutiérrez-Moreno (2019) authored papers on the effects of cashew nut shell oil on insects and the resistance of fall armyworms to synthetic insecticides, respectively. The paper have the highest
betweenness (83.52928354) among the clusters is "Discovery and Characterization of Field Resistance to Bt Maize: *Spodoptera frugiperda* (Lepidoptera: Noctuidae) in Puerto Rico" authored by Storer et al. (2010).

**The Key concepts:** The fall armyworm has developed resistance to various control methods, such as transgenic plants and insecticides, which has led researchers to focus on developing combinations of Bt proteins and improving the effectiveness of insecticides through genetic and biochemical methods. Recent studies on the high-quality genome of *S. frugiperda* have emphasized the importance of resistance genes in causing insecticide resistance and the need for sustainable management and global attention to this issue. While research has focused on the invasiveness and adaptability of fall armyworm, attention has also been given to the emergence of resistant populations of *S. frugiperda* (Gui et al., 2022; B. Shu et al., 2021; Tay et al., 2022).

### 3.3. Core sources

Bradford's Law of Scattering, which was formulated in 1948, states that for a specific subject area, there are a few highly productive periodicals, a larger number of moderately productive ones, and a still larger number of constantly decreasing productivity. This is characterized by three zones: the top third (Zone 1 or core), which represents the most frequently cited journals in the subject and is of highest interest to researchers; the middle third (Zone 2), which includes journals with an average amount of citations; and the bottom third (Zone 3 or tail), which consists of the long tail of journals that are seldom cited and considered of marginal importance to the subject (Alabi, 1979; Sudhier et al., 2020; Venable et al., 2016; Vickery, 1948). The analysis of the clustering of journals based on Bradford's Law focused on 14 core journals (Fig. 4) that are highly influential and frequently cited in this field, making them a priority for researchers. During the relevant period, 779 articles (33.5% of the total) were published in this field, with an average of 4.456 (standard deviation 10.52) indexed in the WoS database. The core journals with the highest publication numbers are *Insects* (106), *Pest Management Science* (98), *Journal of Economic Entomology* (97), and *Plos One* (83), with a total citation of 2552 and an H-index of 26. Other core journals with lower publication numbers include *Scientific Reports* (66), *Journal of Invertebrate Pathology* (49), *Crop Protection* (46), *Journal of Pest Science* (45), *Florida Entomologist* (43), *Southwestern Entomologist* (32), *Environmental Entomology* (29), *Toxins* (29), *Insect Biochemistry and Molecular Biology* (28), and *Neotropical Entomology* (28). Figure 4 shows core journals and 61 journals were in Zone 2 with 783 articles, and 447 journals in the tail zone produced 764 articles.

### 3.4. Authors’ productivity and collaboration network

Celso Omoto, an effective entomology author, published 59 research articles (2012–2022), was accounting for 2.5% of total publications with a WoS h-index of 25. His research includes topics such as *S. frugiperda* resistance to genetically modified Cry1F maize, mutations conferring resistance to insecticides, and exploring target sites and mechanisms in resistant strains of *S. frugiperda*. Omoto also demonstrated the effectiveness of MON 810 Bt maize against fall armyworm, resulting in low resistance. Followed by the notable author Meagher RL, contributed 49 publications (2.1% of total), with recent
research focusing on S. frugiperda's resistance to Cry1F insecticidal proteins, atmospheric impact on flight patterns, and migration of fall armyworm moths using the Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT). He also developed models to trace fall armyworm populations geographically using genomic data. Wu Kong-Ming, is another top author in the field, has 44 publications (1.9% of total) and led the first team to identify the fall armyworm's genetic background and first chromosome-level genome, revealing a scaffold N50 of 12.9 Mb and 22,260 protein-coding genes using PacBio and Hi-C sequencing.

Figure 5 displays the top 10 most productive authors in fall armyworm research and their article count, citations, and impact. Recent FAW research has focused on several areas, including competition and resistance development among species, optimizing trapping methods, impeding resistance evolution, evaluating the efficacy of transgenic maize genes, understanding the role of SfABCC2 in FAW susceptibility to Cry1F, the importance of dynamic F-actin in virus invasion into the midgut cells, developing molecular markers for resistance mechanisms, assessing the impacts of transgenic and non-transgenic crops, and reducing FAW rearing expenses and infestation impacts. Recent research has also investigated genetic diversity, speciation mechanisms, identifying strains, natural enemies and predators, interactions during bio-control efforts, prey species selection impact on predator fitness, effects of invasions on host populations, and technological detection advances.

Improving collaborative networks can help researchers explore new research areas and conduct relevant investigations. Social network analysis is an effective tool for investigating scientific collaboration networks, allowing for the visualization of relationships and information between researchers (Vanni et al., 2014; Q. Yu et al., 2013). Insights gained from such analyses can be used to quantify levels of cooperation frequency in research practices (Salamati & Soheili, 2016). Collaboration can be identified by analyzing the co-authorship network and studying networking patterns or interactions among involved social actors. To depict academic communication and scientific research more accurately, co-occurrence connection analysis of authors, countries, and institutions can be conducted to evaluate various levels of cooperation (Franceschet et al., 2011; P. Han et al., 2014). Investigating intellectual connections between research topics is important for understanding the growth and evolution of research activities. Analyzing the collaboration network of authors can provide an indication of the similarity of research subjects and the strength and frequency of relationships, and produce a map that highlights clusters of authors involved in similar subject areas. This map provides insights into the authors' contributions to the research field (Borgatti et al., 2018; Newman, 2004).

The analysis of authors' collaboration networks identified 15 clusters, with clusters 3, 1, and 4 being the most dominant (represented in Green, Red, and Purple colour respectively). Wu Kong-Ming had the highest degree of betweenness centrality (276.045) among the authors, with Xiao Yutao (108.206) and Yang Xianming (105.584) following closely behind. Despite having divergent research interests, these authors were significantly involved in a research collaboration network. Wu Kong-Ming collaborated mostly with authors from other clusters (3 & 2), even though they were located within the same cluster. Cluster one's actors have shared several key research concepts, including immigration, monitoring,
management, early warning, and forecasting of spatiotemporal changes and migration of FAW. Additionally, there is a focus on genetic background/genome editing and the mechanisms of rapid adaptation behind the invasion and resistance of fall armyworms, with the aim of improving management strategies.

A group of authors, including Wu Qiu-Lin, He Li-Mei, Zhao SY, and Yang Xianming, are collaborating closely with Wu Kong-Ming. Celso Omoto has the second highest betweenness centrality score (126.230) among the authors, indicating a strong position in the collaboration network. Shu Benshui and Meagher RL also play important roles in the network with high betweenness centrality scores of 72 and 65.557, respectively. These authors are distributed across clusters 4, 5, and 3, which focus on researching the molecular and genetic basis of insect resistance, the development of insecticide resistance mechanisms, and transgenic corn expressing Bt toxins with an objectives of establishment of insect resistance management (IRM) strategies. Authors Bernardi O, Bernardi D, and Horikoshi RJ collaborated significantly with Celso Omoto in cluster 3. In cluster 4, there was a significant collaboration between authors Meagher RL and Nagoshi RN, Williams Trevor and Caballero Primitivo, and Negre Nicolas and d'Alencon E. Authors Serrao JE and Zanuncio JC from clusters 7 and 6 collaborated with authors Cespedes CL and Alarcon J from clusters 10 and 15, respectively, on research related to bio-control and bio-insecticides of FAW. Authors Ferreira C and Terra WR, and Wanderley-Teixeira V and Teixeira AAC collaborated significantly in the domain of molecular research and gene expression of FAW, belonging to clusters 11, 3, 14, and 9, respectively. Authors Peiffer M and Felton G, from clusters 12 and 8, respectively, have important research collaboration in the field of FAW-microbial interaction. Figure 6 displays the authors significantly involved in FAW research collaboration networks with node centrality.

Although each author’s importance is acknowledged, it may be relevant to consider their respective institutions and countries in evaluating their contribution to the field. Publication numbers can be used to evaluate the contribution of each institution, region, or country in the relevant field. The upcoming sessions aim to showcase notable partnerships between authors, institutions, and nations in the realm of S. frugiperda management research, evaluating the existing state of international research collaboration and identifying prominent actors with established research networks and dependable relationships. The collaboration network analysis used the same parameters and algorithm as the co-citation network analysis.

### 3.5 Institutions: productivity and collaboration network

In this research field, there are a total of 1945 institutions involved. Figure 7 displays the top 10 institutions that have been most productive in related research publications as per the data from Web of Science. The ‘Institute of Plant Protection’ is ranked first and has produced 146 articles exclusively in this field of research. In doing so, they have collaborated with 377 authors from 82 institutions spanning six different countries. In recent times, there have been studies focused on improving cultural methods, and one of the newly identified sustainable pest control methods is the use of wheat-based intercropping systems. The push-pull strategy is used to manage pests by emphasizing the role of host plants, among other innovative concepts (Liu et al., 2022). Researchers have studied the seasonal migration patterns of
the fall armyworm to develop effective control measures, and new techniques for monitoring its movements have been proposed (Ge et al., 2022; He et al., 2021; H. Zhang et al., 2022). Novel modeling techniques have been developed to predict the distribution of the FAW by considering ecological and climatic factors (Du et al., 2022; Zhao et al., 2022). Improvements to the monitoring system have led to the creation of a particular mix of pheromones that can draw in fall armyworms. The pheromone components and the sensory neurons and pheromone receptors responsible for sex allocation have been identified (Wang et al., 2022; Zhong et al., 2022). Additionally, methods have been developed to increase the efficiency of producing Telenomus remus, a natural agent used to manage fall armyworms (W. Chen et al., 2022), and cost-effective synthetic diets have been developed for the fall armyworm rearing process (Shishuai et al., 2022). A safer and effective alternative to pesticides for controlling the fall armyworm is proposed using entomopathogenic nematodes. Potential of fall armyworm as a biological agent against alligator weed, Alternanthera philoxeroides has been obtained (Jin et al., 2022). Recent studies have highlighted the importance of the SfPAE and SfPO2 genes in the fall armyworm's innate immune system, which is crucial in defending against Bt toxins (Banerjee et al., 2022; X. Huang et al., 2022; Li et al., 2022). Chlorantraniliprole and carbaryl have been identified as effective in controlling the fall armyworm, along with methyl benzoate as a botanical pesticide and DBN3601T corn expressing Cry1Ab and Vip3Aa19 (S. Zhao et al., 2023). These findings have the potential to reduce the need for pesticide usage (S. Yang et al., 2022; Y. Yang et al., 2022).

The 'Universidade De Sao Paulo' takes the second spot for being the most productive institution, while 'Universidade Federal De Vicosa' follows closely with 144 and 125 published articles, respectively. The latest research from these institutions focuses on the biology, ecology, and management of the fall armyworm, covering various aspects such as taxonomy, behavior, food preferences, damage, population, geographic distribution, and control techniques. They have developed a "species-specific molecular marker" that can detect S. frugiperda DNA in predator's gut contents, enabling the identification of potential biological control agents against this pest (Maggio et al., 2022). The analysis of the gut microbiome has also identified the presence of Enterococcus and Pseudomonas, and variations in the gut metabolome based on the diet or host plant, particularly in larvae of host-adapted C or R' strains (Oliveira et al., 2022). According to recent research, S. frugiperda caterpillars are sensitive to both biotic and abiotic stimuli, as revealed in the vibroscape study (Turchen et al., 2022). However, there has been a gradual increase in resistance to Emamectin benzoate over the last few years (Garlet et al., 2022; Muraro et al., 2022), and susceptibility to various insecticides has also varied regarding the evolution of FAW resistance. A recent study has identified the potential insecticidal effects of compounds such as N, N-dimethylaniline and 1,2,5-trithiepane on S. frugiperda caterpillars (Campos et al., 2022). Additionally, the "competitive exclusion" factor has been discovered to accelerate the development of pest resistance to insecticides by increasing the probability of genetic fixation of resistance alleles (Malaquias et al., 2022). The growing resistance of FAW to insecticides can have implications for insecticide resistance management strategies and genetically modified crops, according to a fitness cost analysis (Padovez et al., 2022; Garlet et al., 2022). Observations under commercial field conditions have shown reduced effectiveness of Bt. maize hybrids in controlling S. frugiperda (Valicente et al., 2022). However, various
approaches can be taken to mitigate the impact of insect resistance evolution on GMO crops (Tomé et al., 2022). Recent research has revealed that Bt. crops do not harm non-target species and can reduce the fertility of resistant individuals (Souza et al., 2022; Zuim et al., 2022). Figure 7 summarizes the top 10 most productive institutions and their number of publications. Around, 40% of these institutions are from the United States, 30% from China, 20% from Brazil, and 10% from Spain. The United States dominates research in this field, followed by China.

3.5.1 Collaboration network; The institutions’ collaboration network analysis identified a total of 48 nodes representing institutes or universities in the FAW research community, which were distributed across 7 clusters in the institutional collaboration network. We measured the degree, betweenness, and closeness centrality of each institution in the network to determine their significance and contribution to disseminating knowledge throughout the community. The Fig. 8 displays the institutions that are significantly involved in the FAW research collaboration networks and their centrality. Eight institutions occupy the top positions in both degree and betweenness centrality ranking lists, with a small variation in order. This reflects their key role and significance in transmitting knowledge related to FAW research. The top eight institutions in the FAW research collaboration network, ranked by their centrality measures, are the Institute of Plant Protection, which has the highest cumulative degree (1) and betweenness (200.283), followed by Universidade de Sao Paulo, University of Florida, Texas A and M University, Universidade Federal de Vicosa, Pennsylvania State University, South China Agricultural University, and the Center for Medical, Agricultural and Veterinary Entomology. The research on FAW covers various fields such as invasion, migration, damage, monitoring, control measures, IPM, and biology. However, there is significant institutional collaboration in genomic research related to FAW management, including gene mutation, evolving resistance to insecticides or GM crops, mechanisms of resistance, and enhancing alternatives such as Bt toxins, bio-insecticides, and other alternatives.

3.6 Country productivity and collaboration network

Figure 9 shows the 10 most productive countries in FAW research based on publication numbers and intra- or inter-national collaboration, out of 97 contributing countries. China tops the list with the largest number of publications (1409), followed by the USA (1400), Brazil (1226), Mexico (344), India (255), France (219), Argentina (175), Germany (153), Spain (131), and the UK (129). China, USA, and Brazil collectively contributed over half (57%) of global productivity in this research field, with China alone accounting for almost one-fifth (19.9%) of worldwide publications. Additionally, around two-thirds (67.9%) of published articles involved single-country participation (SCP), while one-third (32%) involved collaboration with other countries or multiple country participation (MCP). Recent findings in these countries have paved the way for research in diverse areas, including the development of early detection models, accurate identification, and understanding of climatic factors that limit the spread, as well as biotic and abiotic factors affecting the life cycle, behavior, and adaptation of FAW. FAW research involves investigating various critical aspects, including the combined effects of synthetic and non-synthetic toxins, innovative insecticide development, pheromone detection molecular mechanisms, bioassays of entomopathogenic fungi, population, genomic, and gene expression analysis, modification of dsRNA
nanoparticles/protamine sulphate/lipid delivery systems to enhance RNA interference, microRNA-mediated techniques, CRISPR/Cas9-based genome editing for gene editing/knockout, agronomic research, host plant resistance/FAW tolerant Bt. Maize or GM crops, FAW gut microbiome studies, genomic recombination research, and host plant self-limiting male strain OX5382G. Additional research has focused on evolving resistance and insecticide tolerance in the field, host plant metabolites, FAW gut microbiome studies, and integrated management of FAW, including entomo-culture, which examines protein-rich food production using insect cells, all of which are significant contributions to FAW research.

3.6.1 Countries’ Collaboration network; The collaboration network of countries has formed 9 clusters due to the involvement of 50 out of 97 nodes/countries. The size and edges connecting nodes in the collaboration network represent the influence and strength of cooperative relationships between nations, which greatly impact the production of research articles at an international level. The network shows significant communication between the two main communities: one comprising China, USA, India, France, Germany, United Kingdom, Australia, Switzerland, Canada, Belgium, Netherlands, Italy, Cameroon, and Czech Republic; and the other comprising Brazil, Mexico, Argentina, Spain, Colombia, Chile, Austria, New Zealand, and Uruguay. The USA has the highest number of collaborations with other countries (61 in total) and has produced 431 documents, with significant collaboration from Brazil contributing to around 20% of this output. Other countries that have high levels of collaboration with other nations include China (48 countries and 297 documents), Brazil (40 countries and 129 documents), France (37 countries and 114 documents), and the United Kingdom (32 countries and 106 documents). The collaboration networks between different countries and the frequency of document production are depicted in Fig. 10.

3.7 Trending research topics

The study identified popular research topics related to the invasion and control of fall armyworms based on keywords and keyword plus used by researchers. The top three trending research topics for each year were illustrated in Fig. 11. Despite the common/scientific name of pest "Resistance" was the most frequently discussed topic. The authors of the study have identified the most popular and frequently discussed research topics related to the invasion and control of fall armyworms, based on the keywords and keyword plus used by researchers over a certain period of time. This provides valuable insight into the specific areas of interest among researchers. Figure 11 illustrates the top three trending research topics for each year. Despite the species being commonly referred to as fall armyworms, the topic of "Resistance" had the highest frequency of discussion (348). Research in this area has focused on the challenges posed by the acquisition and evolution of resistance in FAW, which has rendered existing management techniques ineffective. There is a pressing need for resistance management strategies in response to the development of resistance to various pesticides and transgenic crops. The current trending research area for this topic is to discover the genetics and resistance mechanisms involved in the evolving resistance of this species, as highlighted by recent studies (Muraro et al., 2022; Nhim et al., 2022; Okuma et al., 2022; L. Zhang et al., 2020).
Discovery and expression of insecticidal protein genes from Bt in transgenic crops is a popular research area (100–200 frequency). Bt T405 has been found to combined Cry1, Cry2Aa, Cry2Ab, and vip3A1, in addition to a wide range of FAW-susceptible toxins (Cry) and proteins (vegetative insecticidal proteins) (Schnable et al., 2009; Barcellos et al., 2023; Garlet et al., 2022; Hernández-Martínez et al., 2013). Sathyan et al. (2022) discovered protein-coding genes for potential FAW insecticidal toxins, including Cry1Ac32, Cry1Ab9, Cry1Aa6, Cry1Ac5, Cry1Aal8, Cry1Ab8, Cry1Ab11, Cry2Aa9, Cry1la40, Cry2Ab35, Cyt, Vip3Aa7, and tpp80Aa, as well as genes that may enhance virulence such as phospholipase C, chitinase, immune inhibitor A, cell wall hydrolases, sphingomyelinase, hemolysin Xh1A, and urease subunit coding genes. Delanthabettu et al. (2022) identified several genes, including Cry1I, Cry3, Cry7, Cry8, Cry14, Cry26, and Cry55, across 12 different natural Bt strains. Machado et al. (2020) suggest that improving toxin efficacy and plant resistance to FAW is a major research area. Recent developments include transgenic crops with genes targeting multiple mechanisms, using CRISPR/Cas9 and Bt toxin assays, and exploring proteins like cadherin (SfCad) to enhance synergism (Bai-Zhong et al., 2020; Soares Figueiredo et al., 2019). The recent trending topic of *S. frugiperda* involves exploring the genetic basis and inheritance of resistance to insecticides, as well as studying biochemical mechanisms, translocation, adjuvant/synergistic effects, and gene silencing/RNA interference to induce susceptibility. Cannibalism, phenology, and biological control methods, such as using Bt, entomopathogenic viruses and fungi, are also being considered. Researchers are actively investigating the effectiveness of these control agents and their combinations with insecticides as part of integrated pest management strategies (Stenberg et al., 2021; Pidre et al., 2019; Schroeder et al., 2019; Visconti et al., 2019; Zaghloul et al., 2017; Villamizar et al., 2004; Rivero-Borja et al., 2018).

Ongoing bio-control investigations aim to determine the crucial parasitoids and natural enemies regulating the population of *S. frugiperda*. Over 100 parasitic organisms have been identified, including commonly encountered Hymenopteran species such as *Trichogramma* spp., *Chelonus* spp., *Apanteles* spp., *Cotesia marginiventris, Meteorus laphygmae*, and *Dipteron* species such as *Archytas marmoratus, Lespesia archippivora*, as well as predator species such as Hemipteran, species *Zelus* sp., *Orius* sp., *Podisus* sp., Neuropteran species *Chrysoperla* sp., Dermapteran species *Dorus taeniatum*, and Hymenopteran species *Trichogramma atopovirilia, Trichogramma pretiosum*, and *Chelonus insularis*. Recent identification of vital parasitoids in several African countries has led to the adoption of *Telenomus remus* in China and Brazil as part of the FAW control program (Arthurs & Dara, 2019; Jaraleño-Teniente et al., 2020; Agboyi et al., 2020; Caniço et al., 2020; Kenis et al., 2019; W. Chen et al., 2021). In summary, the investigation highlights the research areas receiving significant attention regarding the invasion and control of fall armyworms, including resistance management strategies, genetic and resistance mechanisms, and insecticidal protein genes from *Bacillus thuringiensis*. Other areas of research such as cannibalism, phenology, biological control, and integrated pest management strategies are also important for controlling the FAW population.

4. Discussion & Conclusion
This article explores the persistent problem of the invasion of fall armyworm in the agriculture sector and its impact on food security. The prevention and control of this pest have remained a challenge, requiring further research and action to reduce the risks associated with this pest. The article identifies an increase in the number of articles published on FAW management research over the past ten years, with an increase in the typical number of authors, institutions, and countries involved in publications. This suggests that researchers place a high value on collaboration. Collaboration among researchers, institutions, and nations is essential for enhancing the quality of research. The study emphasizes the need for multiple collaborations, especially between institutions and nations, to further research and sustainable management of *S. frugiperda*. The article also identifies the top academics, institutions, and nations involved in FAW management research and the critical role played by actors with high centrality in the development of collaborative networks. Brazil, China, and the United States are the most active nations and centers of research on FAW regulation. The findings have implications for encouraging further collaborative research in FAW management, particularly between institutions and nations, for the sustainable management of this pest.

This paper provides a comprehensive definition of scientific collaboration in the field of *S. frugiperda* research, which has not been extensively explored before. However, the exclusion of non-English publications and the possibility of a biased database may fluctuate the accuracy of the results. Even though, the paper systematically describes collaboration at different levels of author, institution, and nation, and highlights the increasing number of publications and popular research topics in this field. The study emphasizes the importance of encouraging collaborations between institutions and nations for sustainable *S. frugiperda* management. The paper also identifies important research concepts and influential actors in this field, providing valuable insights for students, academics, practitioners, science policy-makers, and R&D management. Overall, the insights from this study could help researchers and policymakers focus their efforts and resources more effectively to manage the spread of fall armyworms and minimize the damage they cause.

Declarations

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Figures

**Figure 1**

Annual scientific production for the interval 2012-2022.
**Figure 2**

The top 10 most global cited journal articles.
Figure 3

**Co-citation network of Documents: a)** The nodes in the graph represent documents that are frequently cited together within a community, which is labeled by the author(s) and year of publication. The color of the nodes indicates the community that shares a similar perception, while the size of the nodes corresponds to the total number of links within the network. The edges in the graph represent the co-citations between documents and are represented by their width and color tone, which were also used in the collaboration network analysis. The graph was created using the automatic layout function in the R-package. **b)** Node centrality of documents.
Figure 4

Shows Bradford’s law; names of core sources/journals.

Figure 5

The number of publications with annual citation of the top 10 most productive authors.
Figure 6

a) The structure map of authors' collaboration network, b) Node centrality of Authors’
Figure 7

Top 10 most productive institutions in the field of FAW management.
Figure 8

a) The structure map of institutional collaboration network, b) Node centrality.
Figure 9

Country scientific production and top 10 productive countries.

Country Collaboration Map

Figure 10

World map of countries' collaboration network.
Figure 11

Trending research topic on *S. frugiperda* for the period 2012-2022.