

## Research article

# Spatial Distribution of Cotton Bollworm in Southeastern Shores of the Caspian Sea, Golestan Province, Iran

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## Abstract

### Keywords

cotton bollworm;  
Global Moran's I;  
hotspots;  
Local Moran's I

Cotton bollworm, *Helicoverpa armigera* Hübner (Lepidoptera: Noctuidae), is one of the major pests in the cotton fields, and threatens the sustainability of cotton production due to its polyphagous and cosmopolitan behaviors. Risk levels of moth distribution depend on spatial-temporal changes. Therefore, this study aimed at performing spatial-temporal analysis of *H. armigera* moth population in the southeastern area of the Caspian Sea (Golestan province, Iran) using the Geographic Information System (GIS). Almost weekly data (7-10 days), the moth distributions of *H. armigera* were collected from 65 cotton fields from May 30, 2020, to September 17, 2020. The moth's population maps of *H. armigera* were estimated using an Inverse Distance Weighting (IDW) interpolation method. Spatial autocorrelations and data clustering for the moth populations were performed by Moran's I analysis to highlight moth population hotspots on the shores of Caspian Sea. The result of the spatial analysis showed that moth of *H. armigera* distributed aggregation pattern during the cotton growing season. Interpolated maps (IDW) of *H. armigera* moth showed that almost all of the hotspots were located in the southeastern areas of the Caspian Sea.

## 1. Introduction

The cotton bollworm, *Helicoverpa armigera* Hübner (Lepidoptera Noctuidae), is a polyphagous insect (feeds on a wide range of crops) that is especially endemic in cotton [1]. It is recognized as a cosmopolitan pest in China, Pakistan, Central Africa, and Israel [2, 3]. In fact, almost all of *H. armigera* management programs focus on ecological models of population dynamics. An effective tool to collect forecasting data is the pheromone-bait trap, which simulates natural mating behavior in order to catch male *H. armigera* moths. Due to the tight relationship between the number of trapped moths and caterpillar emergence, measuring the male moths is an interesting method

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among entomologists for early infestation detection [4]. Although conventional statistical parameters such as dispersion indices can quantify fluctuations in populations and frequency distribution, such methods do not consider the spatial distribution of samples [5]. Since environmental factors, such as location, are considered as random factors in statistical analysis, they become a main source of error. Therefore, an alternative way is the use of spatial variables, which are reasonable and stochastic variables [4]. A new approach, using geostatistics was adapted which regarded the number of trapped moths as a random variable that was distributed continuously on the study area (spatial variable). Generated interpolated maps that analyzed moth distributions was able to be used to spatially distinguish changes of moth populations over time (as a type of change detection) [6]. Geostatistic methods with Geographic Information Systems (GIS) have been opening up new opportunities to estimate and characterize insect distributions [7]. There are numerous studies of pest distributions that involved analysis by Geostatistics based on GIS, and examples include studies of Rangeland Grasshopper (Orthoptera: Acrididae) [8], *Lygus hesperus* Knight (Heteroptera: Miridae) in lentils [9], *Rhopalosiphum maidis* F. (Homoptera: Aphididae) and its predator including *Harmonia axyridis* P., *Coleomegilla maculata* D., and *Coccinella septempunctata* L. (Coleoptera: Coccinellidae) in Iowa corn fields [7], *Scirtothrips dorsalis* (Thysanoptera: Thripidae) in Florida blueberry [10], and *Eurygaster integriceps* (Hemiptera: Scutelleridae) [11]. Geostatistic models are known as an environmental-friendly methods because their adoption may lead to a reduction in the use of chemical controls and because they tend to encourage focus on effective control at pest hotspots. The main objectives of the current research were to: (1) characterize the multi-temporal spatial distribution of *H. armigera* using geostatistical methods; (2) produce maps of moth distribution; and to (3) perform weekly change detection in patterns of moth population.

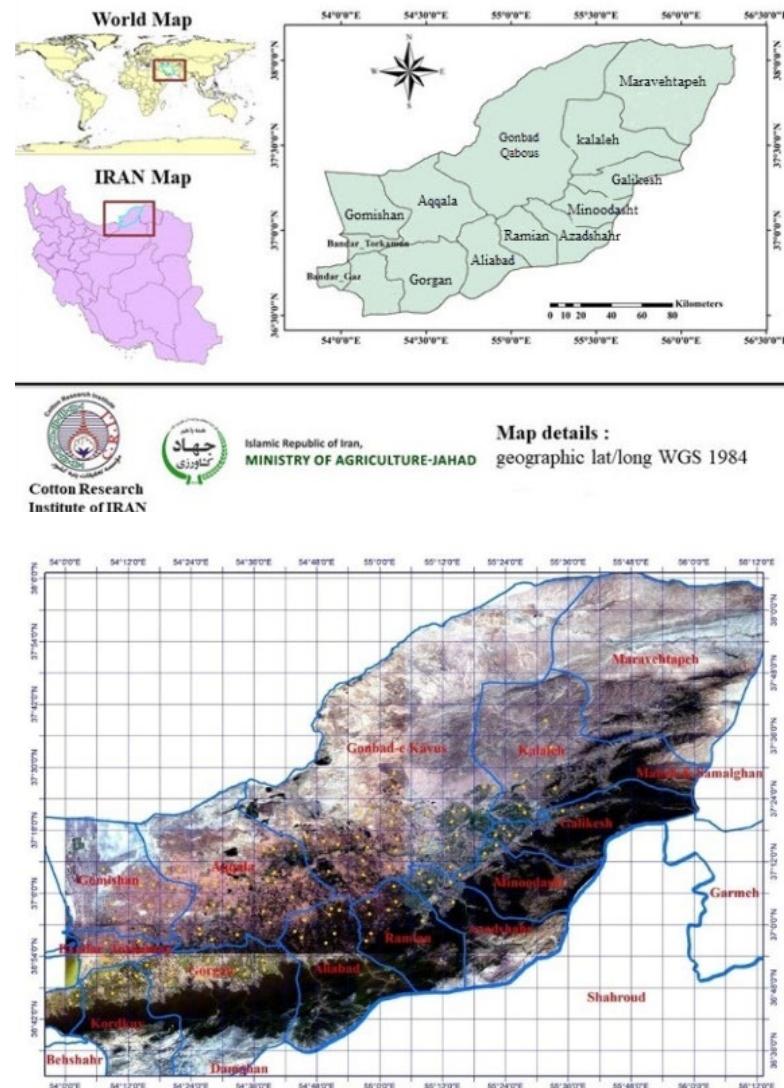
## 2. Materials and Methods

### 2.1 Study area and multi-temporal sampling program

The study was performed in the moderate and humid climate on the southeastern shores of the Caspian Sea in Golestan province, Iran, at latitude ranging from 36° 30' to 38° 10' N and longitude from 53° 50' to 56° 20' E (see Figure 1). The area occupies about 21400 km<sup>2</sup>. The mean annual temperature and rainfall are 16.8°C and 450 mm, respectively. Almost all of the agricultural communities include small landholdings of wheat, barley, canola, and broad bean as autumn crops. The dominant summer crops are soybean, cotton, and rice. The study area is the main natural fiber production region in Iran. The ground-truth data was mainly extracted from cotton agricultural fields. Aqqala, Gonbad-Qabous, and Gorgan with 33%, 31%, and 10%, respectively (percentage of cotton fields to other crops), are the highest cultivation areas of cotton while Minoodasht and Maravehtapeh lack cotton fields (Figure 1).

### 2.2 Moth sampling as ground-truth data

Pheromone-bait funnel tarps (five sex-pheromone traps for each place) were installed in 65 cotton fields across study area (about 20 m from each other and 1.5 m above the ground). Caught moths were identified (to make sure that they were cotton bollworm species) and their numbers were recorded weekly at every cotton field from May 30, 2020, to September 17, 2020. The number of trapped moths and their geographical coordinates were digitalized to build a geo-database for GIS analysis.



**Figure 1.** Study area (the Golestan province, Iran) and distribution of pheromone-bait trap throughout the study area; 5\* 5 (minute in the DMS coordinate system) grid cells (yellow points are monitoring farms)

### 2.3 Moran spatial autocorrelation analysis

The Moran spatial autocorrelation was used for spatial analysis of moth hotspots. Moran's Index can be used to measure the spatial difference between all samples [4]. For the spatial autocorrelation analysis of Moran's I, it is first necessary to obtain a standard score of Z or Z(I), and then the significance of the Moran spatial autocorrelation can be evaluated. The values of Global Moran's Index vary between 1 and -1. When the observations have similar values (a cluster pattern), the value of the Moran's I is close to +1. Otherwise, the value is close to -1, which occur when the

observations are scattered (dispersed pattern). Furthermore, the distribution pattern of the observations is considered random if the Moran's I is zero. The Global Moran's I was calculated by the following equation to describe the spatial correlation and spatial pattern of moth distribution (equation 1).

$$I = \frac{n}{S_0} \times \frac{\sum_{i=1}^n \sum_{j=1}^n W_{ij} (X_i - \bar{X})(X_j - \bar{X})}{\sum_{i=1}^n (X_i - \bar{X})^2} \quad (1)$$

Where  $X_j$  and  $X_i$  show the variable values in places  $j$  and  $i$ . Also,  $\bar{X}$  shows the mean of each field.  $W_{ij}$  is the spatial weight values of  $j$  and  $i$ . If  $j$  and  $i$  are neighborhood and non-neighbor, the value of  $W_{ij}$  is equal to 1 and 0, respectively.  $S_0$  also represents the sum of all the elements.

Local Moran's I was used to find differences in the number of trapped moths. Local Moran's I was displayed on interpolated maps to determine the difference in the number of moths over time and location (equation 2).

$$I_i = n (X_i - \bar{X}) \sum_{j=1, \neq i}^n W_{ij} (X_j - \bar{X}) \quad (2)$$

When  $n$  is the total number of variables,  $X_j$  and  $X_i$  are the numbers of moths in  $i$  and  $j$ , and  $W_{ij}$  is the spatial weight of  $j$  and  $i$ . The value of the local spatial autocorrelation coefficient must be greater than the expected coefficient to accept the spatial distribution pattern.

#### 2.4 Distribution map of moths

To obtain the distribution map of *H. armigera*, the deterministic interpolator was used in ArcMap software package (v.10.6, ESRI, CA) for the grid system (5 minute  $\times$  5 minutes DMS coordinate system). The Inverse Distance Weighted (IDW) interpolation was used to provide the population maps of moths. IDW is one of the interpolation methods which is in the form of a raster. The value of each raster cell (pixel) is calculated by averaging the known pixels at the same distance (weight for distance). Therefore, more weight is assigned to the nearest pixels and less weight to the farther pixels. In this method, the local effect on point data is eliminated by distance.

### 3. Result and Discussion

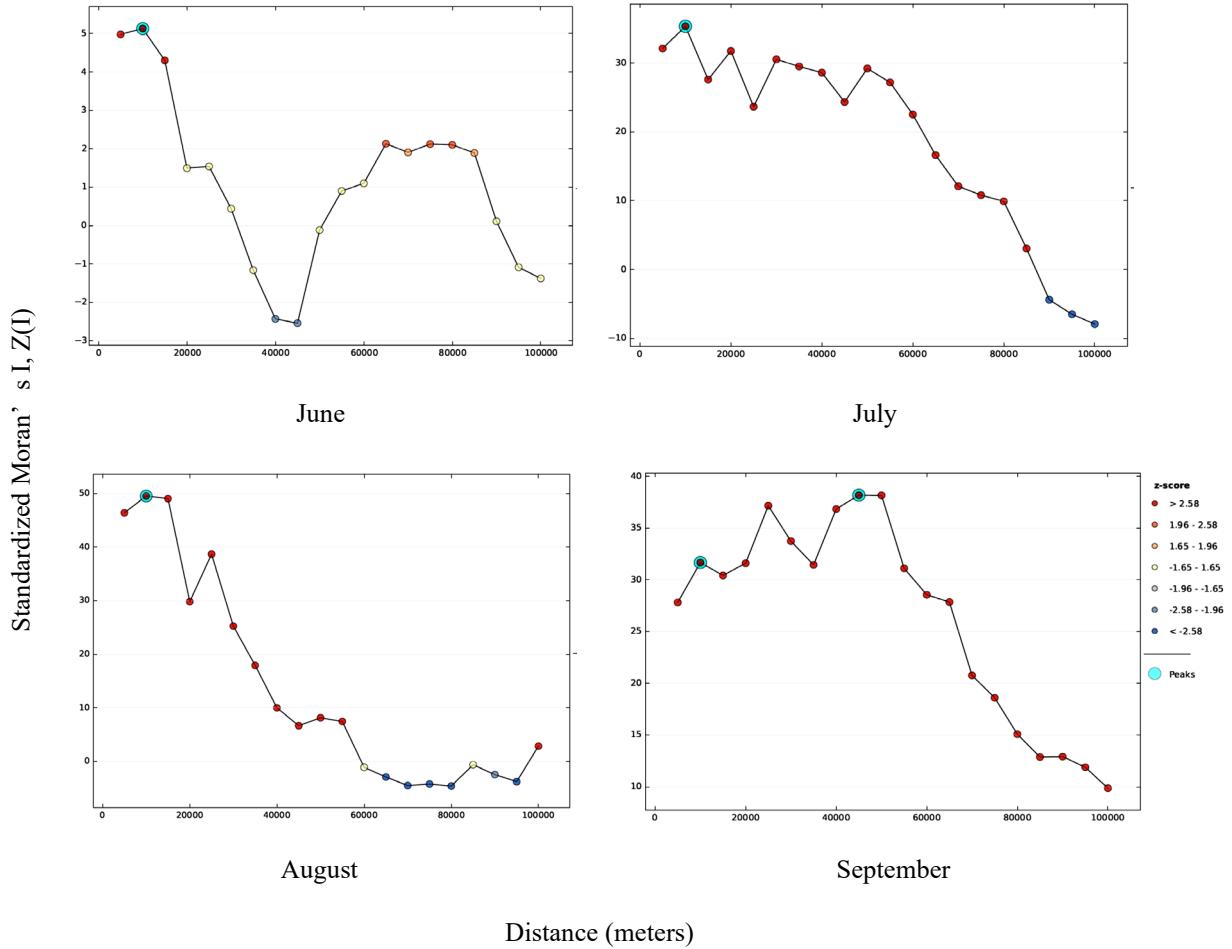
Table 1 shows the Global spatial autocorrelation for all monitoring periods of moth population. According to Table 1, the values of Moran's I were significantly positive which indicates the clustering of neighboring points in all sampling periods. This phenomenon presented not only a strong spatial correlation between sampling points but also an aggregated distribution of the moth population in the study area. A key point in any sampling program is the effect of the distance between sampling locations on the final accuracy. The distance between sampling fields is the main source of changes to the Moran's I. Spatial correlograms were used to show changes of the Global Moran's I relative to the distances between the trapped moths during the monitoring periods [12]. With increasing distance, the values of the Global Moran's I decreased over the sampling periods, which indicated an inverse correlation between the spatial correlation of moth samples and the distance (Figure 2). In total, the optimal distance that produce the maximum Global Moran's I was

**Table 1.** Spatial autocorrelation (Global Moran's I) of the distribution of cotton bollworm moth from May 30 to September 17, 2020

Interval periods*	Global Moran's I	Z-score			
			p-value	Z-score	pattern
May 30 - June 9, 2020	0.720	6.583**	0.01	<-2.58	
9 - 17 June, 2020	0.999	25.689**	0.05	-2.58 to -1.96	
17 - 24 June, 2020	0.915	39.800**	0.1	-1.96 to -1.65	Dispersed
24 - 30 June, 2020	0.992	40.274**			
June 30 - July 8, 2020	0.965	43.039**			
8 - 15 July, 2020	0.996	41.214**	-----	-1.65 to 1.65	Random
15 - 21 July, 2020	0.990	43.314**			
21 - 29 July, 2020	0.993	44.231**	0.1	1.65 to 1.96	
July 29 - August 3, 2020	0.996	42.162**	0.05	1.96 to 2.58	Clustered
3 - 11 August, 2020	0.990	39.738**	0.01	>2.58	
11 - 18 August, 2020	0.999	46.462**			
18 - 29 August, 2020	0.997	37.127**			
August 29 - September 5, 2020	0.999	43.558**			
5 - 10 September, 2020	0.996	45.100**			
10 - 17 September, 2020	0.910	28.127**			

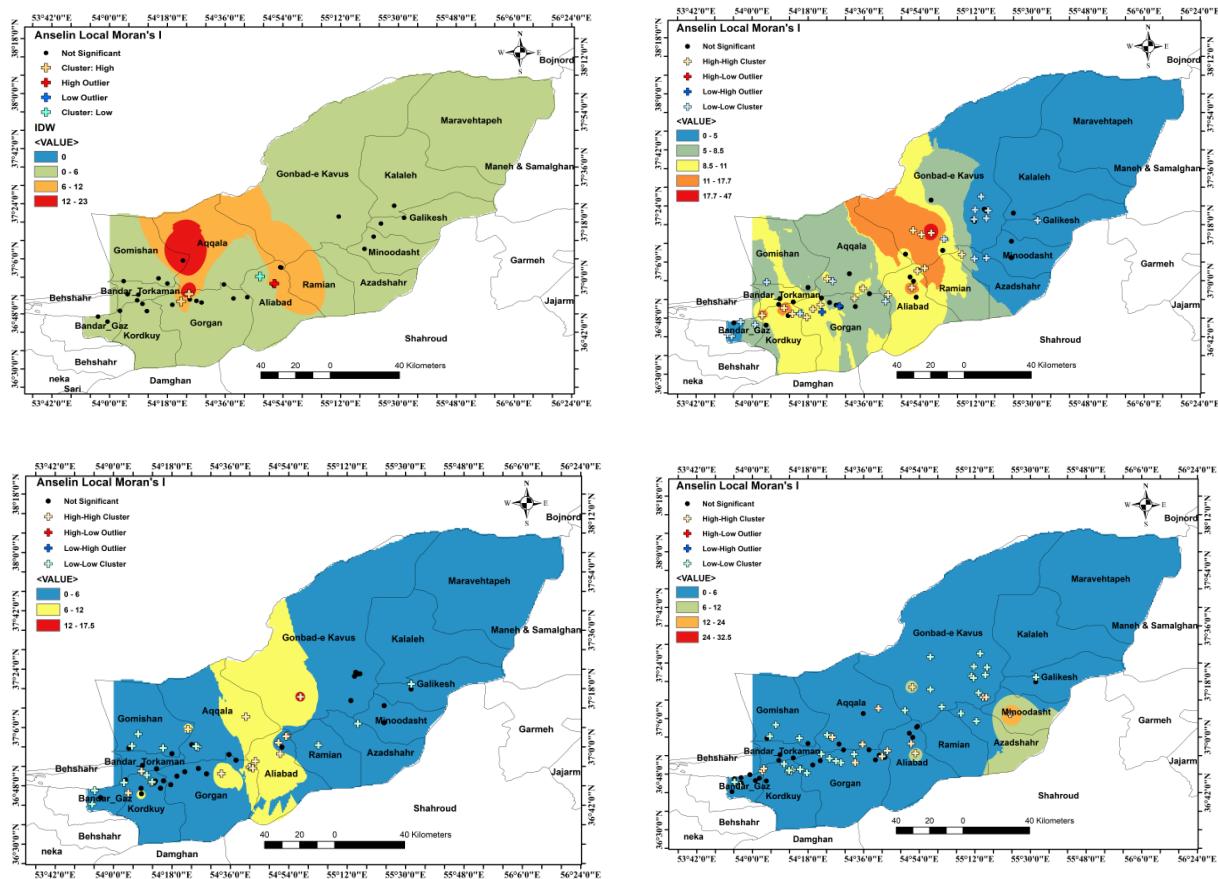
\*According to Z-score, all moth samplings followed as clustered distribution during monitoring periods or adults of *H. armigera* formed an aggregated distribution.

about 10 Km, which was used as a criterion for local Moran's clusters. The local Moran's I highlights the hotspots, that is the area where the moths have the highest density. The local Moran's I can be used as an indicator of spatial patterns and the existence of spatial outliers. Spatial outliers are data point in collected data that are radically different from the neighborhoods. After transforming moth data to normality, the clusters formed based on the values of local Moran's I were presented in Figure 3. According to local Moran's I clustering, the majority of the sampling points were not significantly different. In other words, the number of trapped moths were in the average range of the different areas. Spatial data with higher and lower values than neighboring points are known as high outliers and low outliers, respectively (Figure 3). The result of interpolated maps of *H. armigera* adults is presented in Figure 3. It showed that most of the hotspots were located in the southwestern parts of Golestan province. The above-mentioned areas, known to be ecological niches of *H. armigera*, were in agreement with studies of Kriticos *et al.* [13] who reported that *H. armigera* was found in areas that naturally had extended periods of rainfall with higher soil moisture, like the southeastern parts of the Caspian Sea. The current result showed the month of June was starting point it corresponded to the sudden increase in Global Moran's I, which continued until September. This was in agreement with Milonas *et al.* [14] who used spatial patterns of the *H. armigera* populations to timely perform controlling tactics. In the current study, by monitoring the flight activity of 1<sup>st</sup> (the overwintering



**Figure 2.** Standardized spatial correlograms of *H. armigera* distribution from May 30 to September 17, 2020; the first peak is the optimal distance where the  $Z(I)$  reached a maximum value. This optimal distance was used for detecting moth hotspots and outliers by Local Moran's I.

pupae), 2<sup>nd</sup> and 3<sup>rd</sup> cotton bollworm generations, the month of May proved to be the time of overwintering moth emergence, which was in agreement with the results of Mironidis *et al.* [15] who reported diapause terminated between mid-April and early May, and adult emergence occurred within a 4- to 6-week period from late April to early June. Spatial distribution from interpolated maps for cotton bollworm moth depicted a clustered distribution which was confirmed by Milonas *et al.* [14]. The host availability as one of the main factors that affected the spatial distribution pattern of *H. armigera* could be ignored due to polyphagous behavior of *H. armigera* and wild plant availability.



**Figure 3.** Distribution maps of *H. armigera* moth based on IDW model during form May 30 to September 17, 2020

#### 4. Conclusions

Based on the present study, the IDW method was able to highlight areas with a high density of *H. armigera* moth and represent thematic maps of cotton bollworm. Hotspots are of great importance for control programs because they can be targeted. Hotspot zones showed that the shore of the Caspian Sea had a tendency to host *H. armigera*. Therefore, farmers should perform continuous monitoring during growing season, even if they get involved in crop rotation with non-host crops. We guess that crop rotation does not significantly affect the distribution changes of *H. armigera*. The smallholder survives on crop residues and the high flying potentials of the moth restrict the value of crop rotation. Mixed cropping, including intercropping, is an interesting agricultural system which involves growing two or more species or cultivars of the same species simultaneously in the same field. Mixed cropping has the potential to replace sole crop systems for the control of *H. armigera*, especially in developed countries.

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