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Understanding of Pest Species Distribution on Land Use, Geographic Location, and Climate Factor using Species Distribution Modelling: Case Study in Java Island, Indonesia

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Abstract: Pest distribution has a broad impact across sectors, including agriculture, plantations, and forestry. The impacts are predicted to continue to increase in the future, so understanding pest distribution patterns is important as a basis for more effective pest management decision-making. This study aims to analyze the distribution of pests in Java Island based on land use, geographical location, and climate factors. A total of 2,777 individuals from 14 pest families in GBIF citizen science data were analyzed using a machine-learning-based Species Distribution Modeling (SDM) approach to map habitat suitability. Modeling was conducted using 12 WorldClim bioclimate variables: temperature (bio1, bio2, bio4-bio11), thermal (bio3), and rainfall (bio12). Model accuracy was evaluated using two metrics: Area Under the Curve (AUC) and Kappa. The results showed that most pest families were distributed across three land-use types, with a dominance on agricultural land and at elevations below 500 meters above sea level. Land Surface Temperature (LST) data shows that pests are generally found at temperatures between 15°C and 35°C. Among all bioclimate variables analyzed, annual rainfall (bio12) has the highest influence on habitat suitability. The model performs well, with an average AUC of 0.88 and a Kappa of 0.64, indicating that the predicted pest distribution is accurate enough for pest management planning in the study area. Information on the spatial distribution and potential habitats is needed to target natural treatments.

Keyword: habitat suitability, SDM modeling, pest distribution, pest management

INTRODUCTION

Pest populations are a global issue in the agricultural sector and a major cause of declining crop productivity and quality in many countries (Kasinathan *et al.* 2021). In modern agricultural systems, pests have proven to be a major threat to production efficiency and crop quality (Andargie *et al.* 2024). Pest investment and reproduction during the plant growth phase cause significant nutrient losses and can even lead to the complete death of plants in agricultural fields (Zhang and Lv 2024). This threat is even more significant in tropical regions, including Indonesia, where environmental conditions allow pests to thrive throughout the year. Various pests can reproduce faster, lay more eggs, and move into agricultural land more aggressively, resulting in more intensive attacks on crops (Singh *et al.* 2024). The increase in the per capita metabolic rate of insect pests is predicted to continue, further increasing total agricultural losses in the near future, especially in areas with open and monoculture agricultural systems (Deutsch *et al.* 2018).

Climate change is a considerable factor affecting the distribution and dynamics of agricultural pest populations. Changing climates, particularly global warming, have a direct impact on the geographical range of pests, increasing the risk of alien species invasions and the number of generations that can emerge in a single growing season (Skendžić 2021; Shrestha 2019). In addition, rising temperatures affect the phenology, voltinism, and interactions among pests, their host plants, and natural enemies. However, the response of pests to warm temperatures is not always uniform, as it depends heavily on physiological tolerance, specific environmental requirements, and microclimatic conditions in each region (Lehmann 2020). Pest distribution patterns also show how they adapt to specific geographical conditions, such as altitude and other environmental variables that can determine community structure and insect population diversity (Zhao *et al.* 2023). In fact, extreme weather events such as storms and floods can accelerate the spread of pests and plant diseases into areas previously unaffected, thereby disrupting the stability of local ecosystems (Alfizar and Nasution 2024). In addition to climate and geography, land use patterns also play an important role in determining pest distribution. Modern agricultural landscapes that tend to be homogeneous, such as large-scale monoculture systems, create conditions that support increased pest populations and spread (Nguyen and Nansen 2018). This distribution pattern shows that changes in land structure and use can expand the area of pest spread and increase the risk of more widespread attacks.

Sustainable pest management efforts require accurate spatial information on pest distribution and potential habitats to target control measures appropriately. One approach currently under development is pest distribution mapping based on data from the Global Biodiversity Information Facility (GBIF), which provides records of species occurrences from various global sources. This data collection is known as citizen science, an approach that ensures that everyone can access scientific data and information, thereby supporting sustainable research that provides broad benefits (Sherbinin *et al.* 2021). In fact, this approach can evolve into an informative form of social innovation and serve as a medium for education and the strengthening of scientific literacy in the community (Roche 2020). However, scientific information on the spatial distribution of pests on the island of Java remains very limited, which is considered one of the factors contributing to the inaccuracy of natural interventions to support predator species through forest area management to suppress pest populations. Therefore, this study was conducted to examine the distribution of pests, habitat suitability, and supporting bioclimate factors on the island of Java, thereby providing basic information to support integrated pest management in agricultural management.

METODOLOGI

Study Area

The study area is located administratively on the island of Java, Indonesia. The region includes six provinces: Banten, DKI Jakarta, West Java, Central Java, the Special Region of Yogyakarta, and East Java. Java Island has a land area of approximately 13,863,470.3 hectares and is located astronomically between 6°N to 9°N and 104°E to 114°E. With the largest population in Indonesia, Java also has a complex administrative structure comprising around 119 regencies/cities.

Research Design and Research Data

This research aims to identify pest species recorded on Java Island from various previous studies, reports, and researchers' findings in global databases. This research utilizes citizen science data that has been previously collected and/or recorded. Starting from retrieving citizen science data from the GBIF (Global Biodiversity Information Facility) database, and environmental data (Table 1). Environmental data used in the assessment of pest distribution include land-use data (Landsat-9 Operational Land Imager (OLI2) / Thermal Infrared Sensor (TIRS2)), bioclimatic data (WorldClim, Landsat-8 OLI/TIRS), and topographic data (Shuttle Radar Topography Mission (SRTM) - United States Geological Survey (USGS)). From the GBIF data, habitat suitability analysis for pest distribution is then carried out using bioclimatic variables and evaluated using topographic, climatic, and land-use data.

Pest Distribution Analysis

This study analyzed the distribution of insect pests across 6 orders: Coleoptera, Diptera, Hemiptera, Lepidoptera, Orthoptera, and Thysanura. The order is divided into 14 families, 130 genera, and 192 species. A

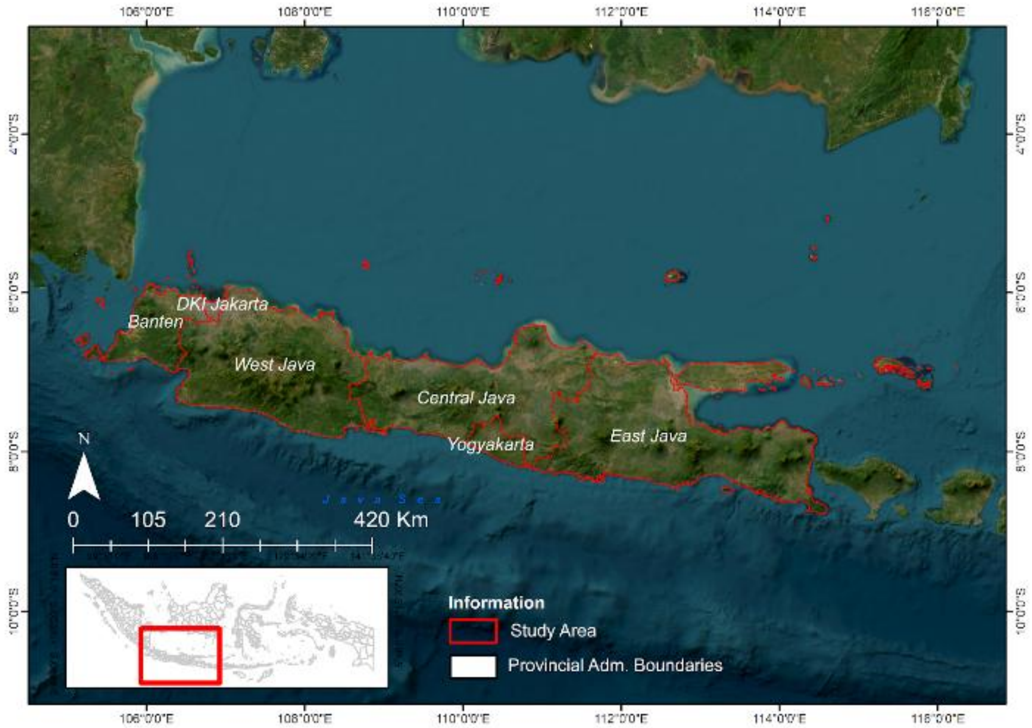

Figure 1. Research location in Java Island

pest distribution analysis was conducted to determine species distribution across geographic locations in the GBIF database (www.gbif.org). The GBIF platform provides global biodiversity data that is an important foundation in biogeographic and macroecological studies, and plays a role in monitoring the dynamics of environmental change over time (Smith *et al.* 2016). According to Luo et al. *et al.* (2021), GBIF data can also be used to track the spatial and temporal distribution of pests to support more effective pest control. In this study, GBIF data were downloaded using the rgbif package in R, which provides direct access to the database via the GBIF Application Programming Interface (API). This package has several primary functions, including occ_search(), occ_data(), and occ_download(), making it useful for obtaining relevant and accurate biodiversity data for insect pest distribution analysis (Chamberlain and Boettiger 2017).

Land Use Analysis

Land use analysis in this study utilizes GIS and remote sensing approaches in cloud computing Google Earth Engine (GEE). Utilizing Landsat 8 satellite data and classified using the machine learning Random Forest (RF) algorithm to obtain existing land use data in the pest record area on Java Island. The land use classification process on Landsat data is carried out over the time range 01-03-2024 to 30-12-2024, using cloud-masking techniques to obtain cloud-free images. Data processing for image calling and classification into three land-use classes is carried out entirely on the GEE cloud computing platform to obtain high-quality data efficiently (Gorelick *et al.* 2017).

Climate Condition Analysis

Climate condition analysis was conducted using land surface temperature (LST) data that represent the island of Java's climatic conditions. The LST data used is Landsat 9 data, with a temporal range from 01-01-2024 to 31-12-24, and includes an additional cloud-masking function to avoid image damage from cloud cover. Cloud masking plays a crucial role in remote sensing by correcting cloud and atmospheric effects and by identifying and removing pixels affected by clouds, shadows, or fog (Anzalone *et al.* 2024). The LST value is extracted using the area of interest boundary of the pest point.

Topographic Condition Analysis

Topographic analysis was conducted using SRTM-USGS (CGIAR/SRTM90_V4) DEM data and

Table 1. Data sources

Analysis	Data and Variable	Sources	Platform
Insect distribution	Global Biodiversity Information Facility (GBIF)	gbif.org	R Studio
Land use	Landsat USGS	earthexplorer.usgs.gov	GEE
Climate factor	Bioclimatic WorldClim	worldclim.org	R Studio
Topographic	Digital elevation model (DEM) SRTM USGS	earthexplorer.usgs.gov	GEE

Table 2. Bioclimate variable

Bioclimate variable	Description of Variabel	Unit
bio1	Annual Mean Temperature	°C
bio2	Mean Diurnal Range (Mean of monthly (max temp-min temp))	°C
bio3	Isothermality (bio2/bio7) (* 100)	%
bio4	Temperature Seasonality (standard deviation * 100)	°C
bio5	Max Temperature of Warmest Month	°C
bio6	Min Temperature of Coldest Month	°C
bio7	Temperature Annual Range (bio5-bio6)	°C
bio8	Mean Temperature of Wettest Quarter	°C
bio9	Mean Temperature of Driest Quarter	°C
bio10	Mean Temperature of Warmest Quarter	°C
bio11	Mean Temperature of Coldest Quarter	°C
bio12	Annual Precipitation	mm

processed in the GEE platform. This utilized GEE's spatial integration capabilities with satellite data, including SRTM-USGS DEM data. The GEE platform provides extraction of topographic information, such as elevation and slope, from the SRTM DEM dataset, which is used as a complement to satellite image data for mapping LULC change (Tesfaye *et al.* 2024). The DEM data is then analyzed to obtain elevation values for the GBIF-based pest-finding areas.

Habitat Suitability Modelling

This analysis uses the SDM (Species Distribution Modeling) approach in R and produces a habitat suitability index (HSI). The algorithm used for habitat projection is RF (Random Forest), which has a strong research record, with kappa values exceeding 80% (Lehmann *et al.* 2025). HSI insects are visualized with HSI values ranging from 0 to 1, which are categorized into several classes Li *et al.* (2022) reclassified habitat suitability into four categories: unsuitable habitat (0-0.2), low-suitable habitat (0.2-0.4), moderately suitable habitat (0.4-0.6), and highly suitable

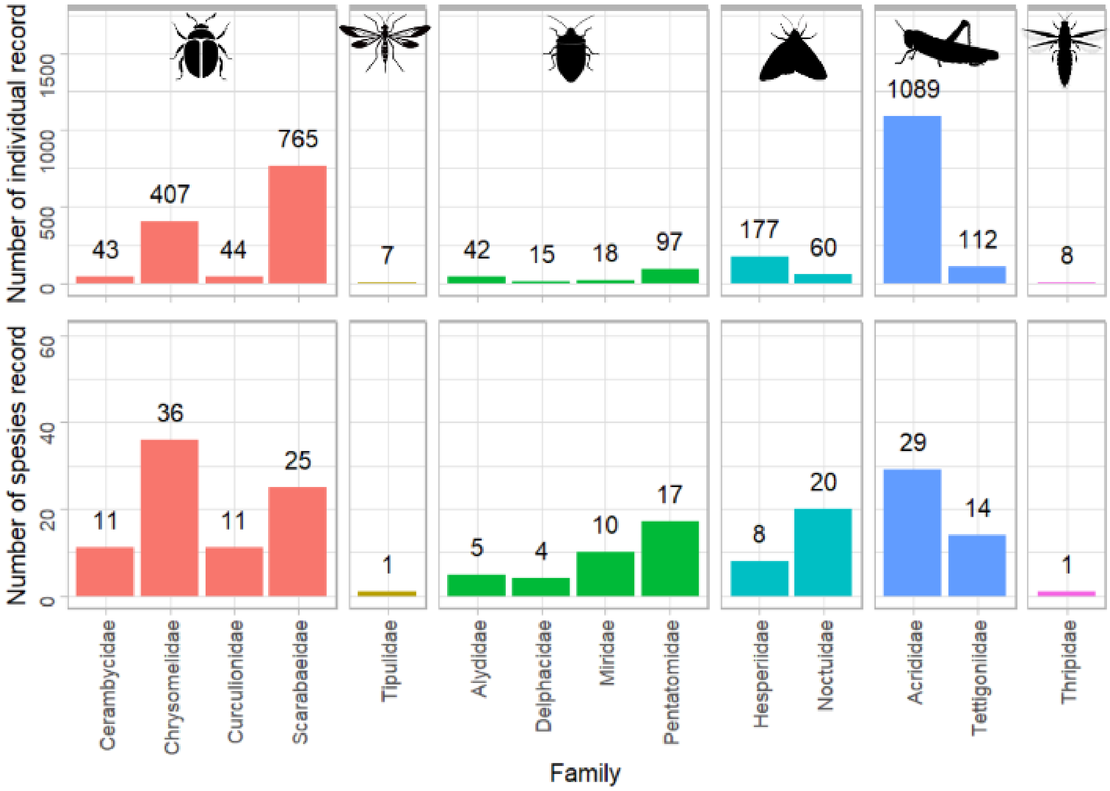

Figure 2. Statistically of species and individual distribution by pest family

habitat (0.6-1.0). The HSI prediction process was carried out using 12 bioclimate variables: temperature (bio1, bio2, bio4-bio11), thermal (bio3), and rainfall (bio12) (Table 2). To evaluate the habitat suitability model using two approaches, namely variable importance and accuracy. The variable importance value indicates each variable's influence on the spatial distribution of habitat suitability. Meanwhile, the accuracy value uses two metrics: AUC (Area Under the Curve) and kappa. The AUC and ROC curve values are not only used to evaluate the performance of the SDM model but also to assess the accuracy of habitat distribution predictions in general and to ensure the accuracy of modeling results without relying on specific threshold values (Yeh *et al.* 2021).

The ROC curve represents the relationship between the True Positive Rate (TPR) and False Positive Rate (FPR), calculated as:

$$TPR = \frac{TP}{TP+FN} \text{.......(Eq.1)}$$

$$FPR = \frac{FP}{FP+TN} \text{.......(Eq.2)}$$

The AUC is defined as the integral of the ROC curve:

$$\text{AUC} = AUC \int TPR\, d(FPR)$$

RESULTS AND DISCUSSION

DISCUSSION

Pest distribution

Based on GBIF records, the family Acrididae had the largest distribution, with 1089 individuals across 29 species (Figure 2). In spatial terms, the family Acrididae has a distribution centered on Jakarta, Bandung, and Yogyakarta (Figure 3). In addition, the families Scrabaeidae and Chrysomelidae have distributions of 765 and 407 individuals across 36 and 25 species, respectively. While the families with the lowest distribution are the Thripidae and Tipulidae families, with a total of 8 and 7 individuals, respectively, divided into 2 and 1 species. The spatial distribution of the Thripidae family is centered in the Bandung and Demak regions. Meanwhile, the Tipulidae family has a spatial distribution centered in the Cianjur and Demak regions.

Pest distribution on land use

Based on land-use data (Figure 4), almost all families are distributed across all land-use classes. Especially in the agriculture class, such as the family Delphacidae (12 records), Thripidae (9 records), and

Tipulidae (5 records). In addition, some families show a significant distribution outside agriculture, such as the families Hesperiidae (58 records), Scarabaeidae (368 records), and Tettigoniidae (58 records), which are elevations <250 MSL. Some families, such as more distributed in the forest area class. In the built-up class, several families have a relatively high distribution compared to other classes, including Acrididae (535 records), Cerambycidae (20 records), Miridae (9 records), Noctuidae (30 records), and Pentatomidae (44 records).

Pest distribution on topographic condition

Based on elevation data, 14 families with 193 species have a distribution of 112 ± 151.9. A total of 12 of 14 families have a dominant distribution at elevations below 500 MSL. Families Alydidae, Cerambycidae, Chrysomelidae, and Curculionidae can be found at elevations <250 MSL. Some families, such as Hesperiidae, Miridae, Pentatomidae, Scarabaeidae, and Tettigoniidae, have a wide elevational distribution, indicating adaptability to elevations ranging from low to high altitudes. Meanwhile, Tipulidae can be found at elevations >1,000 MSL, and Thripidae are found between 500-750 MSL. This indicates that both families have habitat preferences in highland or mountainous areas.

Pest distribution on climate factor

Based on Land Surface Temperature (LST) data, 14 pest families have distributions ranging from 15° to 35° or 27° ± 2.7°. The Acrididae family has a minimum value of 17° and a maximum value of 33° and is dominant in the range of 26° to 28°. The family

Table 3. Pest species and number of record from GBIF, March 2025 collection

Family	Pest spesies (Number of record)
Acrididae	*Acrida cinerea* (4), *Acrida turrita* (2), *Aiolopus* sp. (1), *Anacridium javanicum* (1), *Bibracte cristulata* (1), *Bibracte deminuta* (5), *Bibracte hagenbachii* (3), *Bibracte maculata* (1), *Caryanda spuria* (272), *Chondracris rosea* (5), *Coptacra foedata* (56), *Locusta migratoria* (6), *Locusta migratoria migratorioides* (15), *Oxya chinensis* (1), *Oxya japonica* (9), *Oxya Serville* (11), *Patanga japonica* (1), *Phlaeoba antennata* (1), *Phlaeoba fumosa* (44), *Phlaeoba infumata* (1), *Phlaeoba* Stål (2), *Pseudoxya diminuta* (4), *Stenocatantops cornelii* (119), *Stenocatantops splendens* (3), *Traulia flavoannulata* (13), *Trilophidia annulata* (68), *Trimerotropis* Stål (1), *Tristria pisciformis* (1), *Valanga nigricornis* (370), *Valanga nigricornis melanocornis* (1), *Xenocatantops dirshi* (2), *Xenocatantops humile* (55).
Alydidae	*Leptocorisa acuta* (3), *Leptocorisa* Latreille (2), *Leptocorisa oratoria* (26), *Riptortus linearis* (3), *Riptortus pedestris* (1), *Riptortus* Stål (2).
Cerambycidae	*Acalolepta fuscomarmorata* (1), *Acalolepta rusticatrix* (4), *Anhammus dalenii* (1), *Apriona* Chevrolat (1), *Apriona cylindrica* (1), *Batocera* Dejean (3), *Batocera gigas* (5), *Batocera maculata* (1), *Batocera magica* (1), *Batocera numitor* (5), *Batocera parryi* (2), *Batocera rubus* (17).
Chrysomelidae	*Altica birmanensis* (14), *Altica* Geoffroy (59), *Anisodera* Chevrolat (1), *Anisodera fraterna* (1), *Aphthonoides beccarii* (1), *Aplosonyx* Chevrolat (20), *Aspidimorpha bataviana* (1), *Aspidimorpha deusta* (12), *Aspidimorpha dorsata* (4), *Aspidimorpha elevata* (6), *Aspidimorpha furcata* (6), *Aspidimorpha miliaris* (98), *Aspidimorpha sanctaecrucis* (14), *Aulacophora bicolor* (2), *Aulacophora indica* (2), *Aulacophora quinqeplagiata* (1), *Aulacophora similis* (1), *Basiprionota decempustulata* (2), *Basiprionota octopunctata* (1), *Callosobruchus maculatus* (325), *Cassida catenata* (2), *Cassida circumdata* (15), *Cassida ruralis* (1), *Chiridopsis punctata* (7), *Chiridopsis scalaris* (3), *Lema pectoralis* (2), *Lema praeusta* (10), *Lilioceris impressa* (10), *Monolepta signata* (8), *Oulema melanopus* (1), *Phyllobrotica* Chevrola (1), *Phyllocharis* Dalman (5), *Plagiodera* Chevrolat (3), *Platyxantha* Baly (2), *Podontia* Dalman (7), *Priostomus* Jacoby (1)
Curculionidae	*Coccotrypes* W.J.Eichhoff (4), *Dinoplatypus pseudocupulatus* (1), *Hypomeces pulviger* (4), *Hypomeces squamosus* (2), *Hypothenemus hampei* (4), *Javaulius subvirens* (1), *Peribleptus* C.J.Schoenherr(1), *Phytoscaphus triangularis* (16), *Platygaster* J.Faust(1), *Sternuchopsis* K.M.Heller(3), *Talanthia phalangium* (1), *Xanthochelus faunus* (6),
Delphacidae	*Javesella* sp.(1), *Nilaparvata lugens* (9), *Peregrinus maidis* (1), *Sogatella furcifera* (4)
Hesperiidae	*Baoris farri* (1), *Borbo cinnara* (7), *Cephrenes trichopepla* (1), *Cephrenes* Waterhouse & Lyell (2), *Erionota thrax* (63), *Hidari irava* (29), *Pseudocoladenia* Shirôzu & Saigusa (64), *Seseria affinis* (7)

Table 3 (*Continued*). Pest species and number of record from GBIF, March 2025 collection

Family	Pest spesies (Number of record)
Miridae	*Calocoris javanus* (1), *Calocoropsis gedehensis* (1), *Helopeltis antonii* (1), *Helopeltis clavifer* (1), *Helopeltis cuneata* (2), *Helopeltis* Signore (1), *Lygus macgillavryi* (4), *Lygus malabarensis* (1), *Lygus parcepunctatus* (1), *Lygus suturalis* (3), *Lygus vittulicollis* (1), *Miridius rubrolineatus* (1)
Noctuidae	*Adisura marginalis* (4), *Agrotis ipsilon* (1), *Amyna axis* (1), *Amyna punctum* (1), *Axylia triseriata* (2), *Cerynea punctilinealis* (2), *Chrysodeixis eriosoma* (1), *Ctenoplusia limbirena* (2), *Elusa* Walker (1), *Eublemma accedens* (9), *Helicoverpa armigera* (2), *Helicoverpa assulta* (2), *Mythimna separata* (1), *Spodoptera* Guenée (1), *Spodoptera litura* (13), *Spodoptera picta* (9), *Thysanoplusia intermixta* (1), *Thysanoplusia orichalcea* (1), *Tiracola plagiata* (2), *Xestia c-nigrum* (1)
Pentatomidae	*Agonoscelis rutila* (7), *Antestiopsis cruciata* (1), *Antestiopsis Leston* (1), *Axiagastus* Dallas (1), *Catacanthus incarnatus* (2), *Cazira* (3), *Dalpada nodifera* (1), *Eurydema dominulus* (14), *Euschistus* Dallas (1), *Eysarcoris* Hahn (1), *Nezara* Amyot & Serville (2), *Nezara viridula* (54), *Piezodorus hybneri* (1), *Plautia crossota* (2), *Rhynchocoris* (1), *Scotinophara* (3), *Tetroda histeroides* (1)
Scarabaeidae	*Adoretus umbrosus* (1), *Amphitrichia constricta* (7), *Anomala antiqua* (2), *Anomala bicolor* (2), *Anomala inepta* (288), *Anomala pagana* (2), *Anomala pallida* (24), *Anomala rotundiceps* (3), *Anomala tricolorea* (1), *Anomala viridis* (58), *Callistethus drescheri* (1), *Callistethus trivittatus* (2), *Clyster itys* (1), *Heterorhina sexmaculata* (21), *Heterorhina sexmaculata imperatrix* (3), *Ixorida butona* (1), *Lepidiota stigma* (38), *Oryctes rhinoceros* (64), *Phyllophaga Harris* (2), *Popillia biguttata* (17), *Protaetia acuminata* (4), *Protaetia ciliata* (1), *Protaetia fusca* (21), *Thaumastopeus shangaicus* (1), *Walsternoplus schaumi* (1), *Xylotrupes gideon* (41), *Xylotrupes gideon gideon* (156)
Tettigoniidae	*Albertisiella acanthodiformis* (2), *Ancylecha fenestrata* (2), *Arnobia pilipes* (1), *Arnobia trichopus* (2), *Climacoptera ornata* (3), *Climacoptera parallela* (13), *Conocephalus longipennis* (2), *Conocephalus maculatus* (10), *Conocephalus melaenus* (56), *Mioacris brevifolia* (9), *Mioacris javana* (5), *Phyllomimus inversus* (1), *Salomona obscura javanica* (4), *Zulpha perlaria* (2)
Thripidae	*Chirothrips* Haliday (8), *Heliothrips* Haliday (1)
Tipulidae	*Tipula* Linnaeus (5), *Tipula tjibodensis* (2)

Delphacidae has a minimum value of 25.3° and a maximum value of 27.9°. While the Thripidae family has the same minimum and maximum values of 22.2°, these results indicate that both families tend to live in a stable or specific temperature range. In contrast, the distribution of the Hesperiidae, Miridae, and Tettigoniidae families shows that they tend to occur in locations with cooler ground surface temperatures. Meanwhile, some families, such as Curculionidae, Delphacidae, Noctuidae, Pentatomidae, and Scarabaeidae, have a fairly varied temperature distribution, spanning hot to cold areas.

Habitat suitability of pest

Spatial distribution of habitat suitability of pest

Based on the results of habitat suitability modeling, most of the central to eastern regions of Java Island show high habitat suitability for various insect families. Families such as Curculionidae, Pentatomidae, and Noctuidae have high concentrations in central to eastern regions, such as Kediri, Blitar, and Banyuwangi which are agricultural areas in the lowlands. Chrysomelidae, Miridae, and Tettigoniidae also show a wide distribution pattern with high habitat suitability in central areas such as Madiun, Nganjuk and Magetan. Meanwhile, Acrididae, Hesperiidae and Tipulidae are quite evenly distributed, especially in the eastern part such as Probolinggo and Pamekasan. Scarabaeidae, Cerambycidae and Delphacidae have high habitat suitability in central areas such as Jombang and Lumajang. Alydidae and Thripidae show a more limited distribution, only in some areas such as Brebes and Banyuwangi.

Model evaluation and accuracy of habitat suitability

The analysis of the effects of each climatic factor on pest habitat (Figure 8) shows that Annual precipitation (bio12) has the most significant contribution to habitat suitability. This indicates that annual precipitation is a significant factor in pest distribution. Variables Mean Diurnal Range (bio2), Isothermality (bio03), and Temperature Seasonality (bio4) also show the same influence, with median values

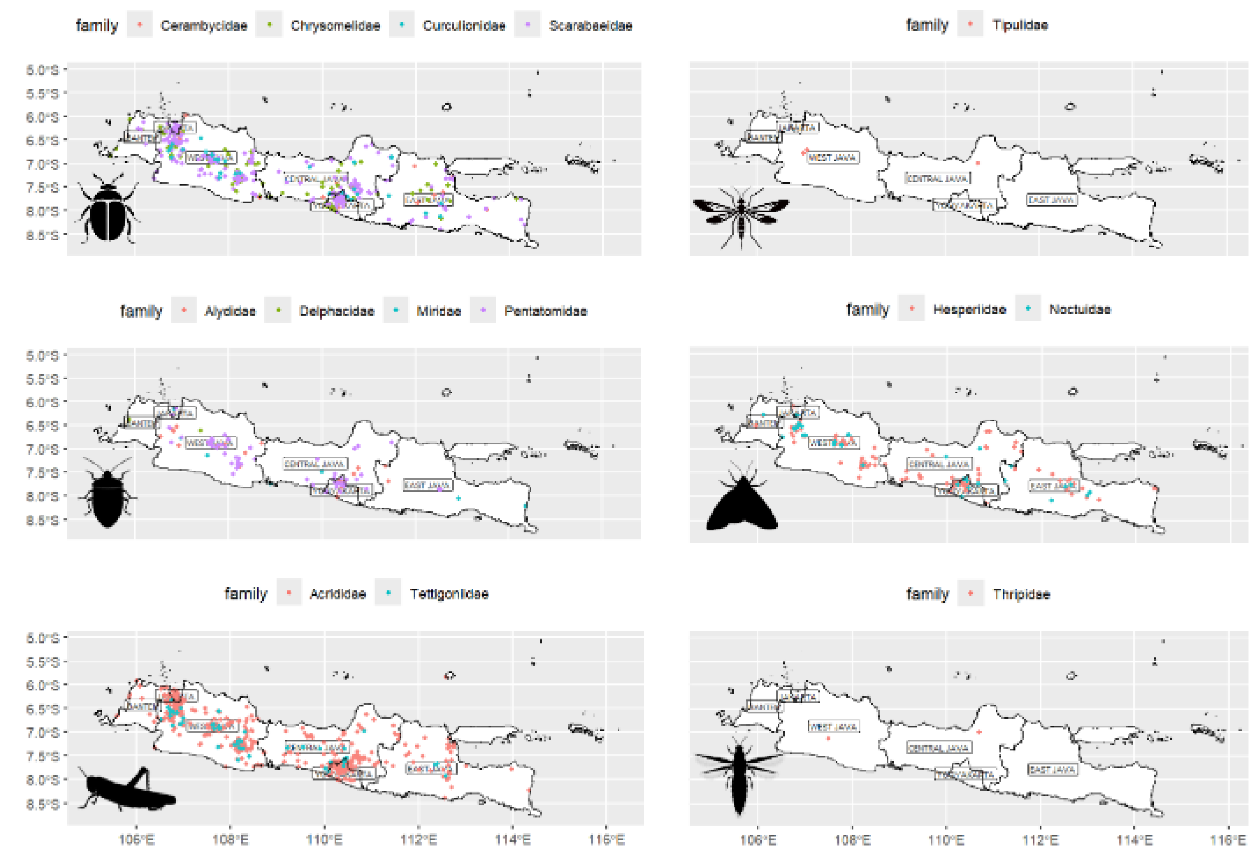

Figure 3. Pest spatial distribution by family and ordo

above average and a fairly wide distribution. Meanwhile, the other variables are below the mean line. This indicates that these variables have a reasonably low influence and contribution in this modeling.

Based on the results of the habitat suitability accuracy evaluation (Figure 9), two indices are used to measure model performance: AUC (Area Under the Curve) and kappa. These two indices show that the habitat suitability model based on the SSDM package in R generally predicts pest distributions well across several families. The results of the habitat suitability accuracy show that the average AUC is 0.88 and the kappa is 0.64. A high AUC indicates that the model performs very well at distinguishing habitat suitability for species presence. The families Delphacidae and Thripidae had the highest AUC values of 0.94. On the other hand, the families Cerambycidae and Tipulidae had the lowest values, 0.83 and 0.75, respectively. Meanwhile, the kappa value is highest in the family Delphacidae, at 0.8, indicating that the model can yield results consistent with the actual conditions. In contrast, the family Cerambycidae has the lowest kappa value among other families.

DISCUSSION

Pest distribution

Pest mapping using GBIF data is one solution for tracking affected agricultural areas. GBIF resources detected totaled approximately 2,777 records across 14 families, covering several land uses and threatening approximately 4,519,429 ha of agricultural areas in Java (Table 3; Figure 5). The Acrididae family, with the highest number of records (1,089), was distributed across built-up and agricultural areas. According to Rasiska *et al.* (2022), the Acrididae family in Bandung Regency, West Java, was primarily found in areas near nature parks. In agricultural areas of East Java, the most common pests are from the family Acrididae, especially *Oxya chinensis* (Ni'am *et al.* 2020). In line with the research of Prakoso and Kurniawan (2022), which found that the most common pests in rice fields in several villages in Karanggayam District, Central Java, were the Acrididae family (346 individuals), especially the species *Antractomorpha crenulata*, *Genusola mundata*, *Oxya hyla*, and *Valanga nigricornis*. Originating from the same order, Orthoptera, the family Tettigoniidae is dominantly distributed in the forest area class. According to Hosang *et al.* (2020), the Tettigoniidae family species *Segetes decoratus* is found only in Maluku. This pest predominantly attacks plantation crops, including sugar palm, banana, oil palm, pandanus, and coconut. In addition, another species, *Sexava coriacea*, is a significant pest of coconut plants and is widely distributed in North Maluku (Widyantoro 2023). In the same family, *Sexava nubila* caused damage to oil palm plantations around 2017-2022 in South Papua and North Maluku (Priwiratama *et al.* 2023). Based on several reports and studies, it can be concluded that Tettigoniidae are more abundant in eastern Indonesia, including Maluku, Lombok, Papua, and Sulawesi. Although widely distributed in the eastern region, research by Na'im and Nasirudin (2021) identified as many as 49 individuals of the Tettigoniidae family using light traps in the Jombang area, East Java.

Order Hemiptera from several families such as Alydidae, Delphacidae, Miridae, and Pentatomidae in this study were found to be dominantly distributed in the Built up area class. These results are in line with the research of Krinsky (2019), that Bed bugs can be found in high populations in built-up land such as hotels and houses, causing both physical and emotional stress. Family Pentatomidae has the most records in this order, which is 97 individuals. One of the important pest species on soybean plants is *Piezodorus hybneri*. According to Bayu and Tengkano (2014), *P. hybneri* is distributed in several provinces in Indonesia including East Java. Agricultural landscapes with forest cover also show a higher abundance of insect pests from the family Pentatomidae in food and non-food crop habitats, indicating that these pests have the ability to move and spread in various habitats (Leterza *et al.* 2023). In addition, *Helopeltis* spp. (Hemiptera: Miridae) is an important pest that attacks cocoa plants whose distribution covers Java and Sumatra (Indriati 2014). In the Special Region of Yogyakarta, the swallowtail species *Leptocorisa oratorius* (Hemiptera: Alydidae) causes significant damage to rice plants and the highest population is distributed in Sleman Regency at an altitude of 428 masl (Pratiwi *et al.* 2018). Furthermore, in the order Coleoptera which is divided into 4 families namely Cerambycidae, Chrysomelidae, Curculionidae, and Scarabaeidae. The highest number of individual records in this family is Scarabaeidae with a total of 765 individuals which are dominantly distributed in the forest area class. One of the pests that has a fairly wide distribution in Java Island is the lace ladybird (Coleoptera), as a stem borer on *Gmelina arborea* trees (Rahayu 2016). In addition to forest plants, this family also attacks plantation crops such as coconut and oil palm plants. *Oryctes rhinoceros* (Coleoptera: Scarabaeidae) was found to attack coconut plants and is the main pest of coconut in Tasikmalaya City (Ramadhan *et al.* 2020). In addition to coconut plants, *Oryctes rhinoceros* causes heavy damage to oil palm plants up to 64-71% in Bangsri Regency (Hasibuan 2024). Based on research conducted by Abduchalek *et al.* (2017), the results of

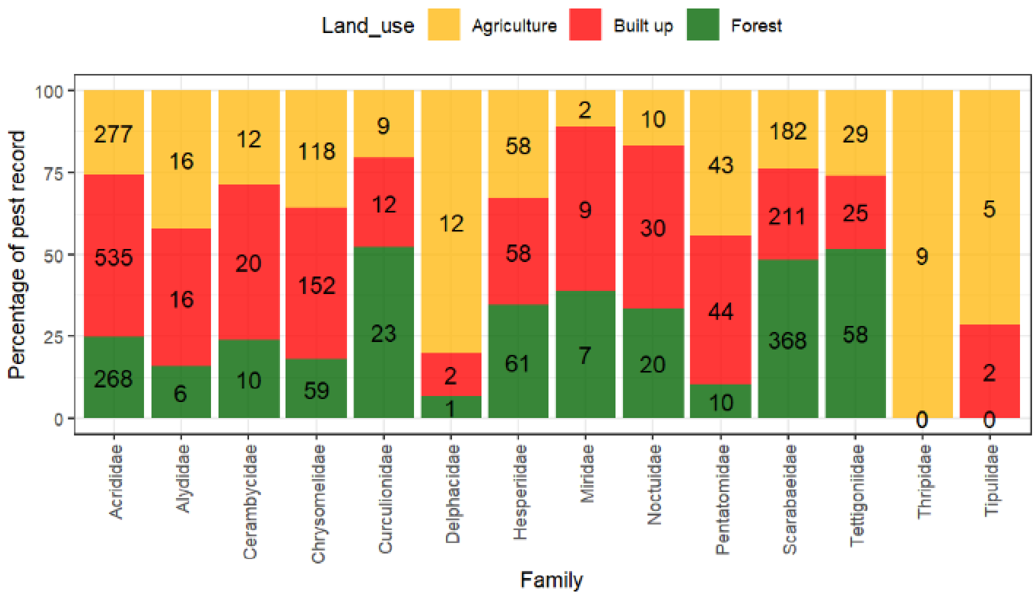

Figure 4. Land use for pest distribution in Java Island

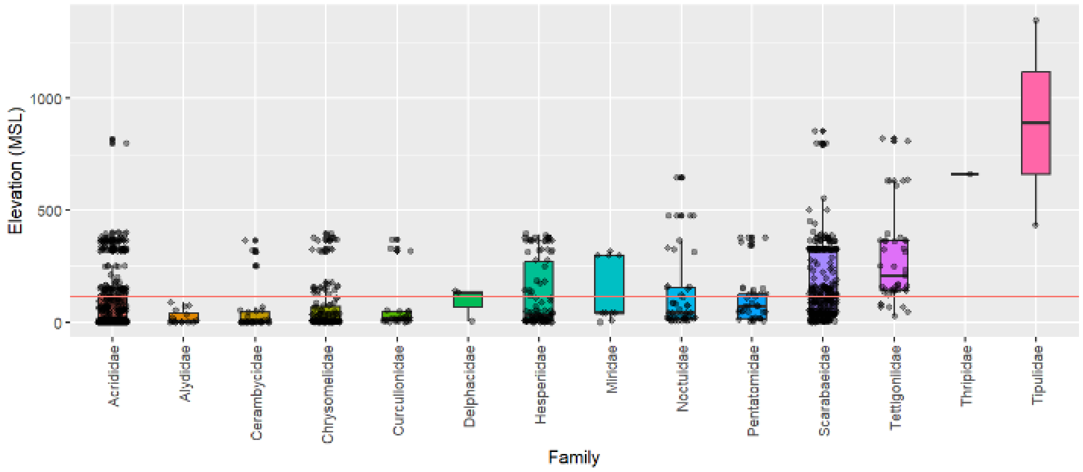

Figure 5. Elevation characteristics for pest distribution in Java Island (red line= mean, 112 MSL)

field surveys of cassava mealybugs (Hemiptera) show that the distribution of this pest can be found almost throughout Java Island with the most findings in West Java, this pest can be found at an altitude with a range of 15 masl to 850 masl.

Family Hesperiidae and Noctuidae are predominantly distributed in the Forest and Built-up area classes, with 177 and 60 individuals, respectively. This finding differs from Vahatalo's (2023) research, which compared the presence of Lepidoptera on previously forested built-up land with that in natural forests. According to him, the wider the built-up area, the fewer moths there are, but they can still live and fragment within it. In addition, the family is also found in agricultural areas. According to Triwidodo and Tanjung (2020), *Spodoptera exigua* (Noctuidae) is one of the main pests of onion plants, with distribution in several villages in Brebes, Central Java. Another study stated that the population distribution of insect pest species from the Noctuidae family, named *S. litura*, *C. chalcites*, and *Lamprosema indicata*, as well as species from the Chrysomelidae family, named *P. inclusa*, on soybean plants in Malang is quite diverse (Zahro *et al.* 2020). Based on pest identification results for shallot plants in Pati Regency, the species found were *Bemisia tabaci, Liriomyza chinensis, and Spodoptera exigua,* with *Liriomyza chinensis* being the most common pest (Apriyani *et al.* 2021). Based on the findings of this study, the Thripidae and Tipulidae families have the fewest species across land-use types. Based on the results of the GBIF record data analysis, there is only one species from the Thripidae family recorded in the GBIF record, named *Chirothrips Haliday*. This is not in line with the findings of Suabgyo *et al.* (2015), who reported that 15 species of thrips were found in West Java horticultural production

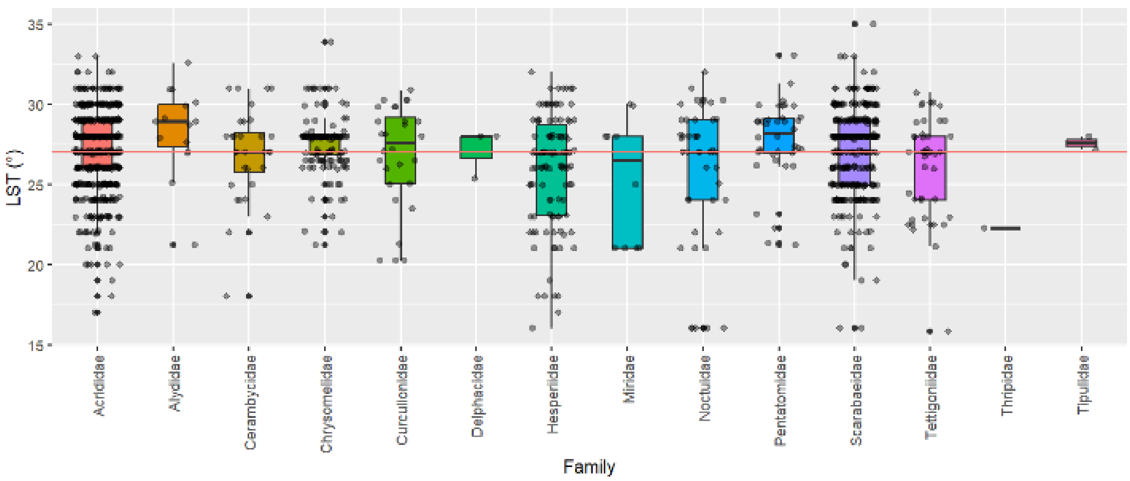

Figure 6. Land surface temperature for pest distribution in Java Island (red line= mean, 27)

centers, namely *Ceratothripoides brunneus, C. revelatus, Frankliniella intonsa, Megalurothrips typicus, M. usitatus, Scirtothrips dorsalis, Thrips aspinus, T. coloratus, T. hawaiiensis, T. javanicus, T. malloti, T. palmi, T. parvispinus, T. sumatraensis,* and *T. unispus*. The findings of Muhlison *et al.* (2016) also stated that the thrips species *Thrips javanicus* was found attacking star fruit plants in Blitar Regency during the dry season, with damage intensity ranging from 0.24 to 26.67%. We can infer from these two findings that several families of Thripidae are not recorded in GBIF.

Habitat, climatic and topographic support

The distribution of pest populations in an area can be influenced by factors such as habitat type, climate, and topography. Habitat diversity and topographic variation have a significant influence on pest distribution (Wang *et al.* 2023). Climate change causes extreme weather events, including floods and droughts, which can affect pest distribution (Kaur *et al.* 2023). Based on the results of HSI modeling, most areas with a high level of habitat suitability were distributed across the central to eastern part of Java Island, with administrative areas in Banyumas Regency, Yogyakarta, Blitar, Tulungagung, and Probolinggo. These areas are generally lowlands dominated by agricultural activities, thus supporting the presence of insect pests. This finding shows that landscape variation and local agricultural systems significantly affect the habitat suitability of each insect pest family, in line with Santoso *et al.* (2023), who found that insect diversity is higher in lowland areas intensively used for agricultural cultivation.

The results of the bioclimatic factor analysis (Figure 8) show that Annual Precipitation (bio12) is the most significant variable affecting the spatial distribution of insect pests. This variable shows the highest contribution among the bioclimatic variables, with values well above the mean line. This is in line with the findings of Jing *et al.* (2023), who found that annual rainfall is one of the important bioclimate variables for predicting the potential distribution of pests, with a

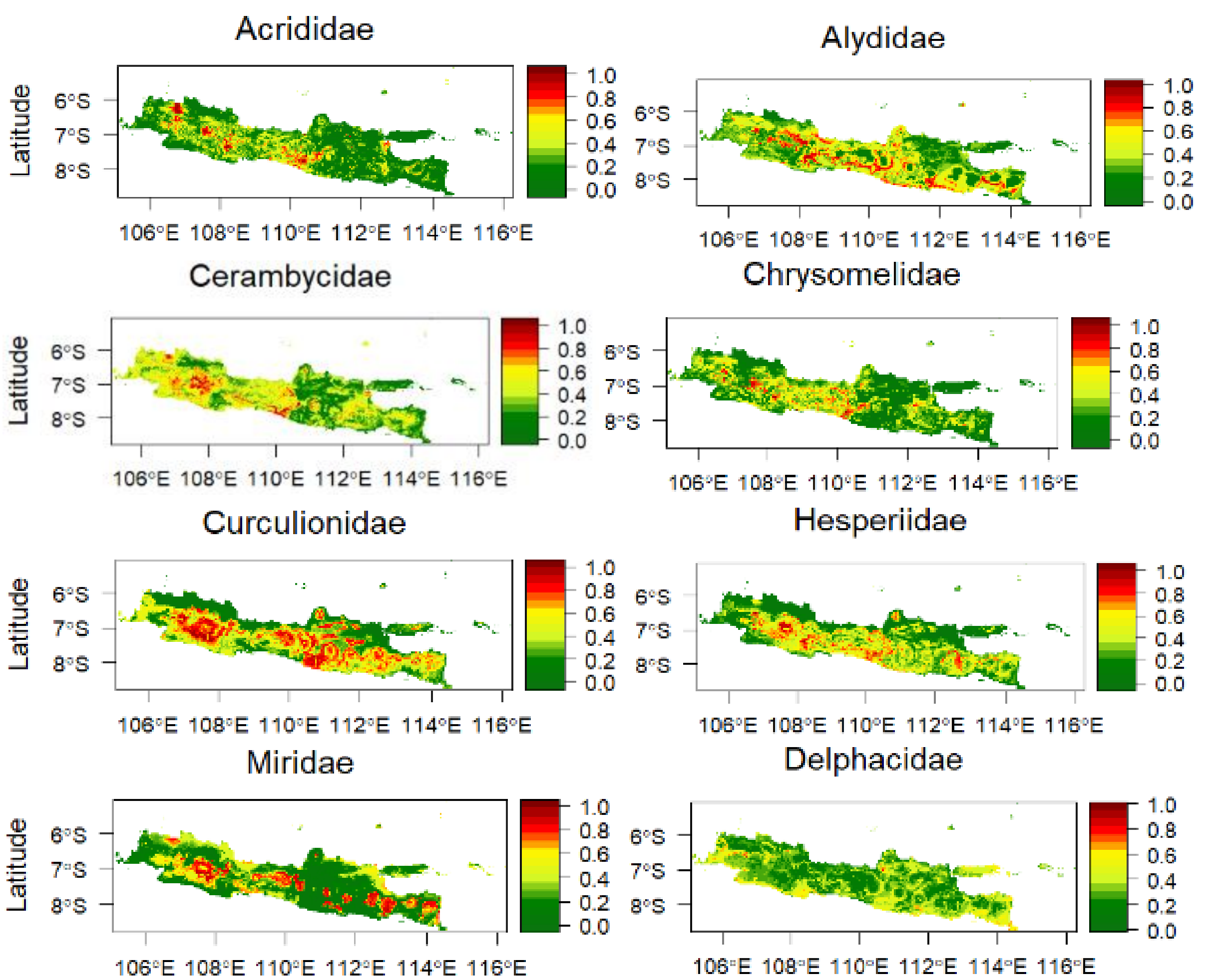

Figure 7. Habitat suitability index

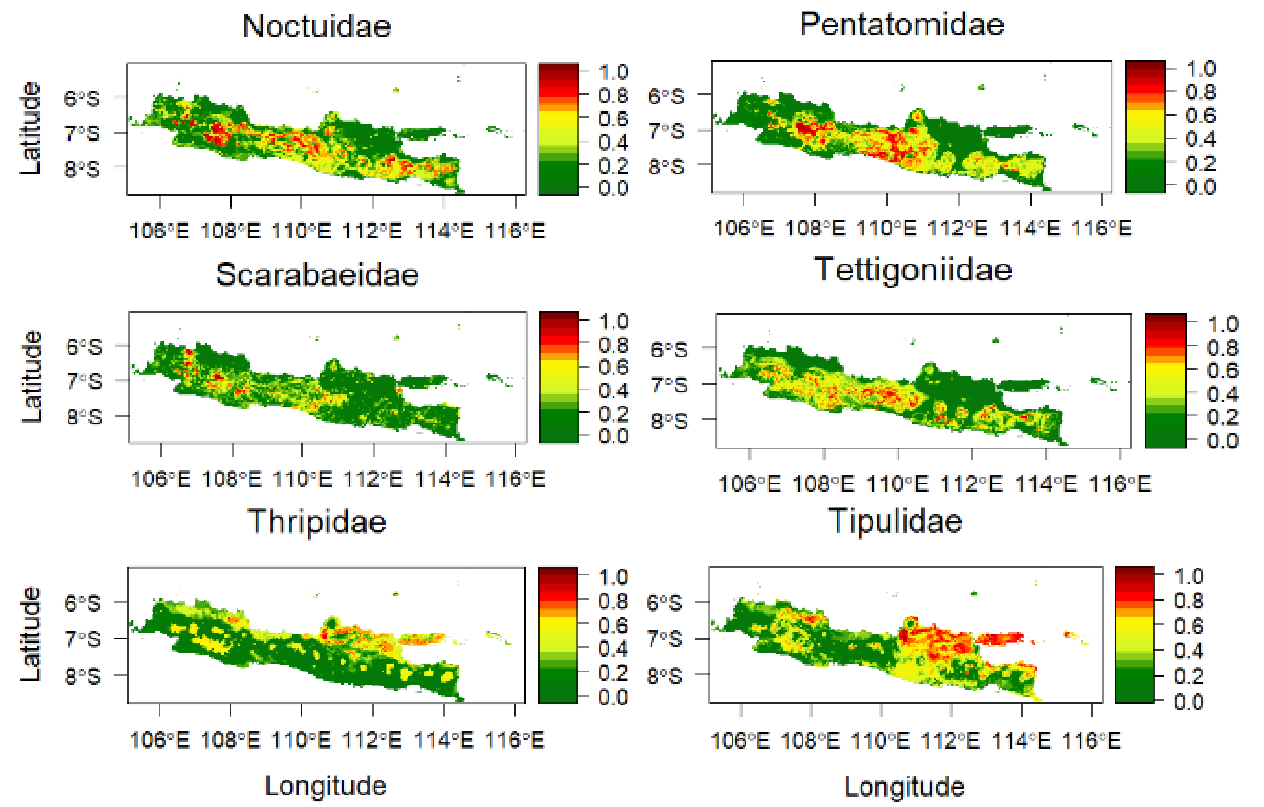

Figure 7 (Continued). Habitat suitability index

value of 8.7%. According to Li *et al.* (2025), the distribution of *Anthonomus eugenii* (Coleoptera: Curculionidae) is strongly influenced by temperature and rainfall, with an optimal annual temperature range of 6.01-26.53 °C. In addition to annual rainfall, Mean Diurnal Range (bio2), Isothermality (bio3), and Temperature Seasonality (bio4) also contribute significantly. The analysis showed that the contribution of bio2 variables to the distribution of Hemiptera was 18.17%. However, the study by Li *et al.* (2024) found that the bio2 variable is a key factor contributing to the distribution of *E. onukii* pests (Hemiptera), accounting for 23.57%. In addition, Zanzana *et al.* (2025) showed that the larval population was higher in the dry season than in the rainy season. Research by Teppa-Yotto *et al.* (2021) also found that *Spodoptera frugiperda* has high habitat suitability in tropical regions with warm, humid conditions and cannot survive at temperatures below 12.6°C. In addition, Coleoptera are more commonly found in areas with stable thermal conditions, proximity to the sea, and low human populations (He *et al.* 2024). Based on aspects of natural habitat, research by Holusa and Kalab (2023) showed that *Gryllotalpa gryllotalpa* (Orthoptera) thrives more readily in wetlands, such as gardens near rivers, that are simply managed. Such environmental conditions provide abundant nesting sites and food sources. Global climate change also adds to the complexity of these dynamics, as it may expand the areas suitable for both crops and pests and increase the risk of overlap between agricultural areas and natural habitats for pests (Grünig *et al.* 2020).

SDM Model Evaluation

The SDM model provided visual distribution results with measurable accuracy, as indicated by AUC and Kappa (Figure 8), and variable importance (Figure 7). Figure 8 shows that the accuracy ranges from 0.5 to 0.9 and reveals fundamental differences between the families. Of the 12 variables, only three had a strong influence and were above the average of 8.32 (Figure 7). This shows that, in developing a spatial prediction model for pests in Java, it is sufficient to use four variables: bio2, bio3, bio4, and bio12. This is consistent with the research of Fan *et al.* (2020), which found that bio12 is the primary bioclimate factor for pest distribution. Another study, Huang *et al.* (2024), showed that temperature and rainfall have an important influence on pest populations and survival. The daily average temperature variable is among the most influential factors shaping the potential geographic distribution of pests (Jing *et al.* 2023). The average AUC value obtained reached 0.88, indicating high habitat

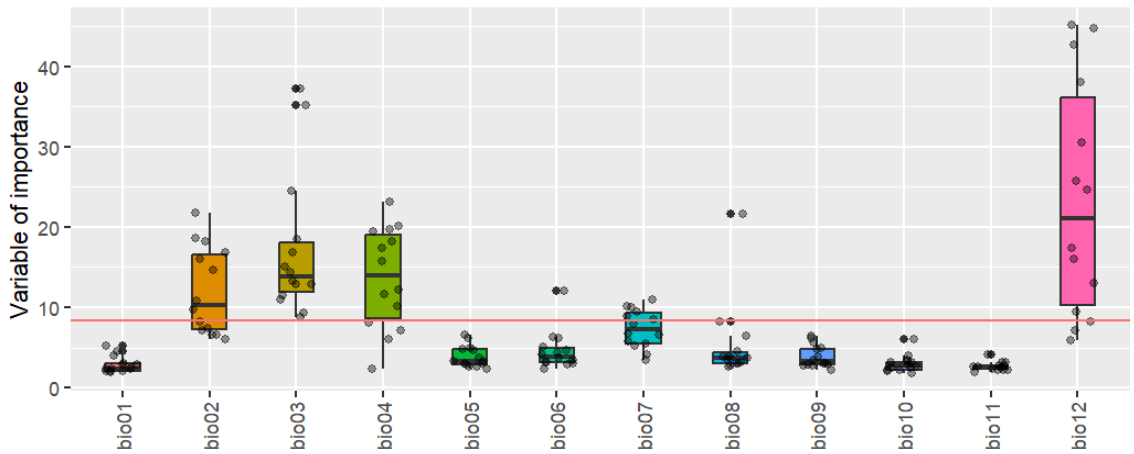

Figure 8. Variable importance of bioclimatic variables (red line= mean 8,32)

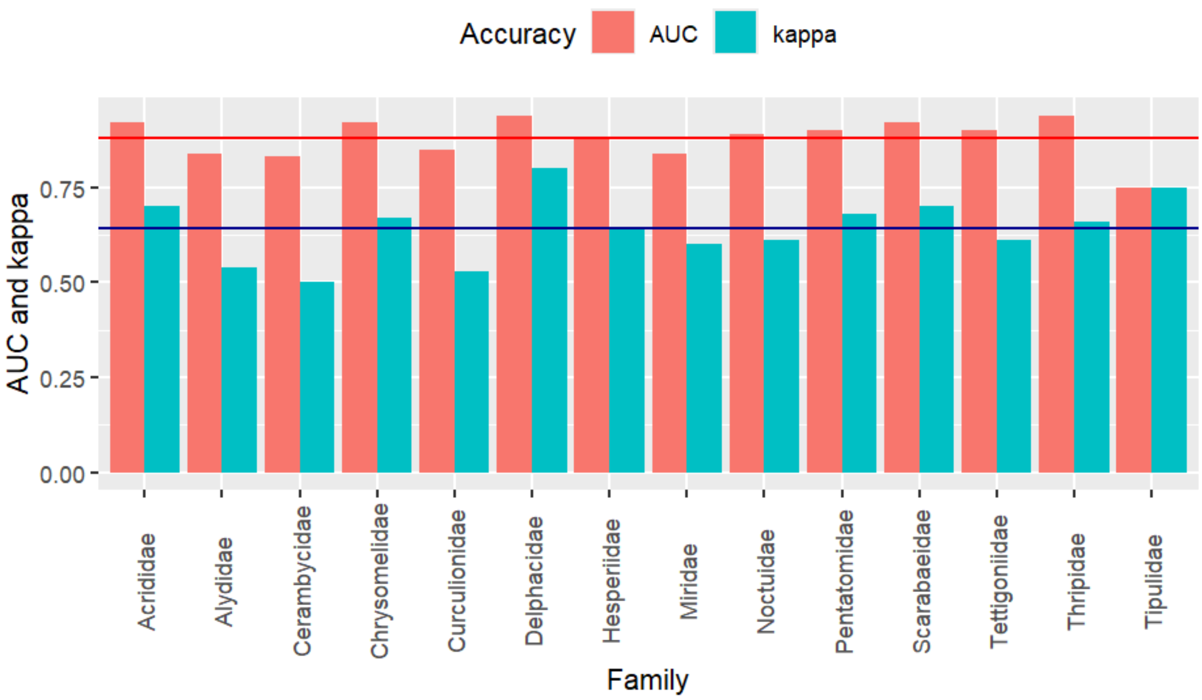

Figure 9. Accuracy of habitat suitability modelling

suitability. As in the research of Agboka *et al.* (2024), the resulting modeling obtained a very high AUC value of > 0.9. Low AUC values are found in several families, such as Alydidae, Cerambycidae, and Curculionidae, which are classified as having moderate habitat suitability, with an accuracy range of 0.4-0.6, indicating that habitat suitability remains moderate. Variations in low AUC values across scales can occur due to data limitations and the near-identity of habitat types at all scales (Rusch *et al.* 2012).

Limitations of GBIF data and SDM modeling approaches

Some species, such as *Antractomorpha crenulata*, *Ceratothripoides brunneus*, *C. revelatus*, *Frankliniella intonsa*, *Megalurothrips typicus*, *M. usitatus*, *Scirtothrips dorsalis*, *Thrips aspinus*, *T. coloratus*, *T. hawaiiensis*, *T. javanicus*, *T. malloti*, *T. palmi*, *T. parvispinus*, *T. sumatraensis*, and *T. unispus*, were not found in GBIF data records in Java. GBIF databases often exhibit spatial biases, particularly toward high-altitude sites, areas with high population density, and higher herbarium density (De Araujo *et al.* 2022). These spatial biases can compromise the accuracy of species distribution modeling, resulting in inaccurate predictions (Beck *et al.* 2014). In SDM modeling, each model can make different assumptions about how species are distributed in the environment, suggesting that if these assumptions do not match the species' characteristics or the area under study, the predictions may be incorrect (Jimenez and Soberon 2020). For example, some SDM models can produce poorly calibrated predictions, leading to overestimates despite low accuracy (Norberg *et al.* 2019). This highlights the importance of more complete and precise recording in the GBIF database, which can improve the spatial accuracy of SDM model predictions and support better decision-making on species conservation.

CONCLUSIONS

This study shows that land-use factors, geographic location, and climatic conditions significantly influence pest distribution in Java. Most pest families are distributed across all land-use classes, except Thripidae, which is found only in agricultural areas. The Acrididae family was recorded most frequently, with a total of 1,089 individuals, while Tipulidae was the least, with only 7 individuals. Based on geographical factors, the majority of pests were found at elevations below 500 meters above sea level, while Tipulidae were found at elevations above 1,000 meters above sea level. In terms of climatic factors, pests mainly were distributed at ground surface temperatures between 15°-35°C, and annual rainfall (bio12) proved to be the most influential factor in determining habitat suitability. These findings are important for the development of more targeted spatially-based pest control strategies, including in natural enemy conservation and buffer zone management. However, the modeling approach remains vulnerable to spatial bias, so data improvements are needed to enhance the accuracy and suitability of future species distribution modeling results.

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