

A Multi-pathway Modeling Approach to Assess the Threat of *Tuta absoluta* in South East Asia

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Abstract

1 Introduction

The world is witnessing a rapid increase in global trade and travel [9]. Due to this increased global connectivity—both international and domestic, no region is spared of threat from exotic species invasion [12]. Coupled with climate change and intensive agriculture, global food security and as a result, human health and social welfare [] is under great threat from these invasions. The South American Tomato leafminer or *Tuta absoluta* is a representative pest that has had devastating effects on tomato production world wide in the last decade.

Indigenous to South America, *T. absoluta* was accidentally introduced to Spain in 2006. Since then, it has rapidly spread throughout Europe, Africa, Western Asia, Indian subcontinent and parts of Central America over the past decade [6]. In South Asia, the pest was first reported by India in 2014 [13, 20]. By early 2016, it was discovered in the Kathmandu area of Nepal [3] and the Northern part of Bangladesh [11] in May 2016. Given the speed with which the pest is advancing, it poses an impending threat to mainland Southeast Asia. There is a great need to identify possible routes of introduction and likely spatio-temporal patterns of spread in this region. With tomato being a commercially important crop, this invasion has had significant global impact. For example, in Turkey alone, the annual estimated intervention cost is \$167M per year []. Due to extensive insecticide treatment in Europe, insecticidal resistance has been recently observed in populations [].

Overall, lack of effective natural predators has made integrated pest management (IPM) a challenging task.

Since tomato is among the top two traded vegetables (<http://www.fao.org>), it is strongly suspected that trade played a critical role in *T. absoluta*'s rapid spread [6]. Indeed, on multiple occasions it has been discovered in packaging stations []. It was observed that the spread pattern in Bulgaria was correlated with prime trade routes [15]. The Animal and Plant Health Inspection Service of the United States Department of Agriculture (USDA-APHIS) has instituted quarantine regulations for imports from regions where the pest is present [22]. (AA: pending: climate dependence and greenhouse; talk about Norway and Bulgaria).

Faced with the challenging task of preparing for invasion and responding to incursions of devastating pests and pathogens, decision makers are increasingly relying upon models of pest risk maps and spread as decision support tools. While models that create pest risk maps (e.g. CLIMEX) are useful to identify locations suitable for long-term establishment, spread models help get a better idea of the spatio-temporal dynamics of spread. The latter approach is particularly useful in planning for the possible threat from an invasive species [] through in silico experiments simulating hypothetical invasion scenarios. Together, these tools can be used to address questions such as which locations to monitor; what control measures to take (IPM practices, trade restrictions, etc.); what is the impact on the economy and health, and so on.

Although there is general consensus that vegetable and seedling trade is a primary driver of *T. absoluta* spread, previous modeling efforts have exclusively focused on ecological aspects. Two works [8, 21] provide risk maps based on CLIMEX []. Guimapi et al. [10] use a cellular automata approach to capture the global spread of the pest factoring in temporal variations and spatial distribution of vegetation, temperature and tomato production. In recent years the role of human-mediated dispersal is being increasingly accounted for by the modeling community (see for example, [7, 9, 17, 19]). In general, modeling human-mediated dispersal is a challenging task. (AA: need to develop this further; middle men, wholesale traders, etc., tuta biology)

In this work, we describe a network-based multi-pathway modeling approach to study the spread of invasive species. It is applied to study the invasion dynamics of *T. absoluta* with focus on the region of South East Asia. With the pest having already spread all over Bangladesh [], there is a high chance that it will be introduced to the study region soon. Motivated from past works in the context of human and livestock disease spread, we have developed a simple yet generic stochastic, spatially-explicit model to capture the pathways of natural and human-mediated spread. The model accounts for ecological factors (temperature, vegetation, host presence, etc.) as well as long-distance flow of host crops through trade (production, consumption, processing, imports and exports). Our data-driven model fuses multiple, noisy and disparate datasets. (AA:

Table 1: **Datasets** categorized by production, consumption, trade and pest information.

| Description | Source | Resolution | Year |
|---|----------------------------------|---|------|
| normalized difference vegetation index (NDVI) | NEO 2017 | 0.1 arc deg. \times 0.1 arc deg., Monthly | 2017 |
| Temperature | | | |
| Relative humidity | | | |
| Tomato production | FAO | | |
| Vegetable production distribution | MAPSPAM | 5 min. \times 5 min. | |
| Production seasonality | | Country level, Monthly | |
| Tomato consumption | | Country, Annual | |
| Population | Landscan | Grid level | |
| Per Capita Income | Country | 2013 | |
| Tomato import/exports | FAO | Country, Annual | 2013 |
| Major cities | | City/town | |
| City distances | Google Maps, Distance matrix API | City | 2017 |
| <i>T. absoluta</i> incidence reports | | | |

Will be developed further.)

2 Methods

(AA: Introduction para. based on HM inputs, main approach (stochastic ABM, multi-pathway model), structure and assumptions (production as proxy to population, etc.))

2.1 Data

We used diverse datasets in this analysis: vegetation, climate, production, international trade and travel, qualitative information on seasonal production and domestic trade dynamics. Table 1 summarizes the datasets used in our framework. While most of these datasets are open-source, the remaining were provided from local experts. Some of these datasets (such as temperature or NDVI) are obtained by direct measurements, while some are results of statistical imputation (some parts of FAOSTAT data for example) and models (MAPSPAM). For each country, we searched for reports and research articles to identify vegetable growing regions, seasons, important cities, consumption, etc. (see Supplementary Information).

2.2 *Tuta absoluta* biology and model assumptions

(AA: Mateus, Nico and Thierry: I will need some help here on justification of assumptions. If not, suggestions to do something else. Here are the assumptions:

- Amount of production is a proxy for tuta population. Crops accounted for: Tomato, potato, eggplant.

Should we take into account tobacco or pepper?

- When modeling trade, we consider tomato. Is this justified



- If tuta is introduced to a square region (25km x 25km), and if conditions are favorable, how many months does it take for this region to be infested? (your opinion). Currently, we are assuming one month as per Guimapi et al.'s assumption



)

2.3 Multi-pathway model

We use a discrete-time Susceptible-Infected (SI) epidemic model to simulate multi-pathway pest dispersal. See Figure 1 for an illustration. The focus region is overlaid with a grid of cell size 0.25 arc degree \times 0.25 arc degree. (AA: This corresponds ... at the equator, which is close to Guimapi et al.). Each cell can be in two states: susceptible (S) denoting pest free state or infected (I) denoting pest established state. Once the pest is established in a cell, the cell remains infected forever, a fair assumption considering that, historically, eradication of *T. absoluta* has not been successful. The only exception is United Kingdom where the pest was detected early []. The simulation takes place in discrete time steps, where each step corresponds to a month. The likelihood that a cell transitions from state S to I depends on (i) suitability of the cell for *T. absoluta* to establish at that time step (ii) influence of cells in state I in each pathway and (iii) level of infestation in each cell with state I .

Each cell v has the following time varying attributes: NDVI $V(v, t)$, temperature $T(v, t)$, vegetable production $P(v, t)$, and consumption $C(v, t)$, where t corresponds to a month. Since NDVI data is available at a much finer resolution (see Table 1), for each cell, we assign the maximum of the NDVI data points that fall in this cell for that month. For production, we consider the following vegetables: tomato, potato, eggplant and peppers. Annual country-level production data (in volume) is spatially disaggregated using MAPSPAM data on spatial distribution of vegetable production. Further, for each cell, this production was distributed temporally— one value for each month of the year using information on seasons (See Supplementary Information). (AA: pending: consumption, import/export)

There are three pathways in which a susceptible cell can become infected: short-distance dispersal, local human-mediated dispersal and long-distance dispersal. Short-distance dispersal captures the spread

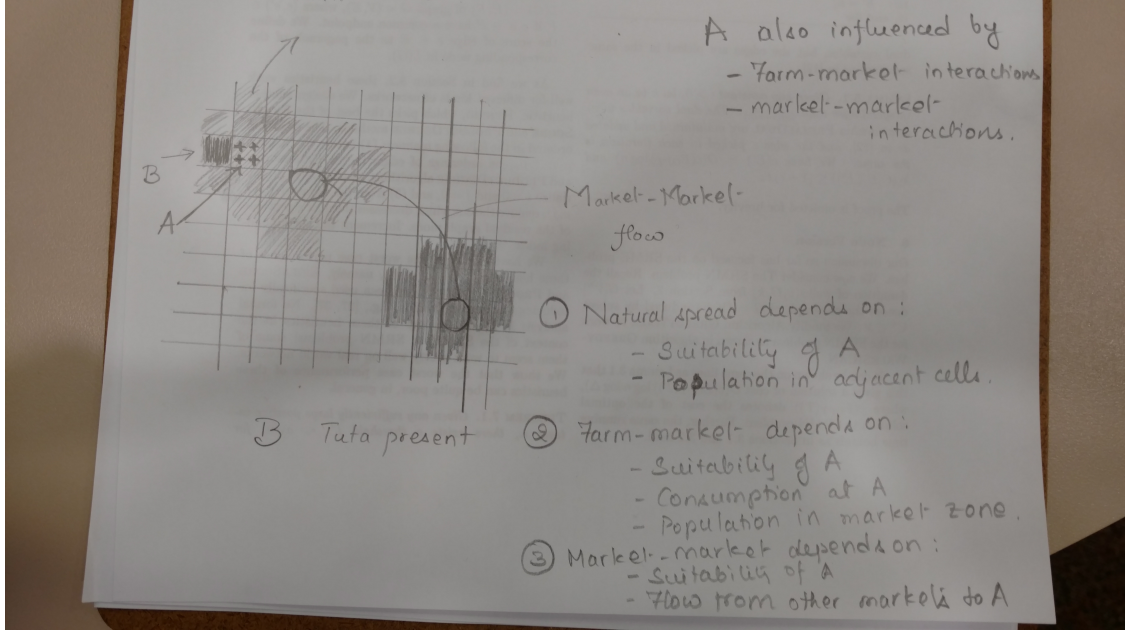


Figure 1: Schematic of the model.

through natural means, from an infected cell to its adjacent susceptible cells. Local human-mediated dispersal captures the spread due to “local” interactions, i.e., farm–city–farm spread. Here, a cell can be influenced by infected cells catering to markets in the same city. Long-distance human-mediated dispersal corresponds to spread through city–city trade. Here, a cell can be influenced by inflow of considered host crops from markets in pest infested regions into the market or city close to the cell.

The suitability of a cell v (in state S) for pest establishment at time t is denoted by $\epsilon(v, t)$. (AA: pending, but mostly based on Guimapi) The level of infestation in a cell v at time t is denoted by $\rho(v, t)$ (which is 0 when the cell is in S state). It depends on host presence at time t . (AA: pending: The infectiousness of a cell is a function of when the pest was introduced and population of the pest in the cell. Here, population is modeled as a function of the amount of production (measure of reservoir, see Carrasco may be) in the given time step.)

Short distance dispersal. At any time step, a cell’s state is influenced by its Moore neighborhood of range r . When range $r = 1$, it corresponds to the adjacent cells (eight at most) and when $r = 2$, it corresponds to $r = 1$ neighbors and cells adjacent to them. The Moore neighborhood of v is denoted by M_v .

$$p_s(v, t) = \alpha_s \epsilon(v, t) \left(1 - \exp \left(- \sum_{v' \in M_v(r)} \rho(v', t) \right) \right), \quad (1)$$

1 where α_s is a tuning parameter for this pathway.

2 **2.4 Human-mediated dispersal**

3 For the human-mediated dispersal, we identify major cities in each country (See Supplementary Information).
4 (AA: pending: based on population of cities and how many grid cells are assigned to it) We partition the
5 grid by assigning each grid cell to its nearest city in the country to which it belongs to. This is motivated
6 by the fact that major cities have trade infrastructure such as wholesale markets, traders and distributors as
7 well as high consumption [5]. Local human-mediated dispersal is modeled as the interaction between cells
8 belonging to a city. Long distance human-mediated dispersal is modeled as trade flows of considered host
9 crops from one city to another. For a city i , $L(i)$ denotes all cells which are assigned to it. (AA: Need to talk
10 about choice of crops for trade)

Local human-mediated dispersal. Here, the cell's state is influenced by the infected cells in its locality through the marketing chain. In general, it is hard to model the local dynamics as there are several actors in bringing the commodities from farm to market to consumers. Further, these are country and commodity specific. See for example Kethonga et al. [16] for the typical structure of marketing chains and Rebaudo et al. [18] for modeling human interactions in the context of invasive species spread. Here, we use a simple approach. Every cell v is influenced by cells in its locality L based on their infectiousness. (AA: should we add a distance kernel? Also, is this mean field approximation?) The expression is similar to that of (1).

$$p_\ell(v, t) = \alpha_\ell \epsilon(v, t) \left(1 - \exp \left(- \sum_{v' \in L} \rho(v', t) \right) \right), \quad (2)$$

11 where α_ℓ is a tuning parameter for this pathway.

Trade network construction. We model the flow of vegetables among markets based on the following assumptions: (i) The total outflow from a city depends on the amount of produce in its surrounding regions and imports from countries outside the focus region at time t , and (ii) the total inflow depends on total consumption, processing demand and exports from the city to countries outside the focus region. More details are given in the Supplementary Material. The flows are estimated using a doubly constrained gravity model [2, 14]. For a city i , let O_i and I_i denote total outflow and total inflow respectively. The flow F_{ij} from

city i to city j is given by $F_{ij}(t) = a_i(t)b_j(t)O_i(t)I_j(t)f(d_{ij})$, where, d_{ij} is the time to travel from i to j , and $f(\cdot)$ is the *distance deterrence function*: $d_{ij}^{-\beta} \exp(-d_{ij}/\kappa)$, where β and κ are tunable parameters. The travel times were computed using Google API (AA: cite) (See Supplementary Information for more details). The coefficients a_i and b_j are computed through an iterative process such that the total outflow and total inflow at each node agree with the input values [14]. Overall, we will have 12 networks representing flows for each month. The outflows and inflows are calculated as follows:

$$O_i(t) = \sum_{v \in L(i)} P(v, t) + \text{Ex}(i, t), \quad (3)$$

$$I_i(t) = \sum_{v \in L(i)} C(v) + \text{Im}(i, t) + \text{Pr}(i, t), \quad (4)$$

1 where, Ex, Im and Pr are the exports, imports and processing demand respectively at this locality.

Long-distance human-mediated dispersal. Given a locality j , let its total infectiousness be denoted by $\rho_T(j, t) = \sum_{v' \in L(j)} \rho(j, t)$. Suppose cell v belongs to locality i . Then, the probability of cell v transitioning from S to I due to long-distance dispersal is given by,

$$p_{\ell d}(v, t) = \alpha_{\ell d} \epsilon(v, t) \left(1 - \exp \left(- \sum_{v' \in L(j)} F_{ji} \rho_T(j, t) \right) \right). \quad (5)$$

2 Here, $\alpha_{\ell d}$ is a tunable parameter for this pathway and i is the locality to which v belongs to. The influence
3 depends on total infectiousness of a locality and the flow from that locality to the locality i .

4 2.5 Validation and sensitivity analysis

5 •

6 2.6 Computational aspects

7 Developed using a variety of software: Python, PSQL. Run on clusters, etc.

8 3 Results

9 (AA: Still working on it. Many parts of 3.1 will be moved to SI)

1 What is our contribution here?

- 2 • analysis of production and distribution both at the international as well as domestic level
- 3 • identifying pathways of introduction and locations of likely entry
- 4 • Understanding spatio-temporal spread of the spread for various hypothetical scenarios.

5 **3.1 Trends in production and trade: a country-level analysis of vulnerability**

6 Here, the objective is to study the dynamics of country-level production and trade flow of various hosts of
7 *T. absoluta* and thereby identify the possible roles these countries could play in the introduction and spread of
8 the pest in this region. To this end, we used data from FAOSTAT– the most recent being for year 2013

9 **General trend.** We aggregated the tomato production per year in the region for years 2004 to 2013 and
10 normalized each quantity by dividing it by the maximum value. To capture the level of internal trade, we
11 computed the sum of trade flows for tomato between countries in the region. This is plotted in Figure 2a
12 (plot “Internal trade”). There is a steady increase in the production and amount of internal trade, with more or
13 less the same rate of change for both quantities. We also considered the total quantity of tomato imported
14 by the focus region from countries outside the region. For every pair of countries, FAOSTAT potentially
15 provides two estimates of commodity flow, one by the source country (called “Import Quantity”) and the
16 other by the destination country (“Export Quantity”). We took the average of the two before aggregation.
17 Similarly, for each year we also computed the total quantity of tomato exported by the focus region. Both
18 these sets of quantities were normalized by dividing by their respective maximum values. While the exports
19 (Figure 2a plot “Exports”) have risen steeply in the recent years, the imports generally indicate a downward
20 trend (“Imports”). However, there is a lot of discrepancy in reporting import (or export) figures, particularly
21 the commodity flows with countries outside the region. The filled curves shows the difference in these
22 estimates when considered individually.

23 **Production.** Among the countries listed in the FAOSTAT dataset, Indonesia is by far the largest producer
24 (\approx 1M tonnes) followed by Phillipines and Malaysia (\approx 200K tonnes each). FAOSTAT does not have tomato
25 production data for Vietnam and Cambodia. However, alternate data sources (personal communication)

1 indicate that Vietnam is the second largest producer ($\approx 400\text{K}$ tonnes) (see [23] for 2005 information). The
 2 data also indicates that Indonesia is the largest producer of eggplants in the region, followed by Philippines.

3 **Trade.** The network capturing tomato trade within the focus region, imports from *T. absoluta* affected
 4 countries and exports to countries which have not reported *T. absoluta* is shown in Figure 2b. The network
 5 was constructed using data from FAOSTAT Trade matrix (Table 1). We note that except for Philippines, there
 6 is a lot of trade activity between countries. Malaysia and Singapore serve as major hubs for tomato trade
 7 with considerable amount of trade among themselves, within the focus region and beyond. Being the largest
 8 producers in the area, Vietnam and Indonesia play the role of source nodes with mainly exports to other
 9 countries. Philippines does not report any fresh tomato trade with other countries. However, it does report
 imports of processed tomato []. (AA: Betweenness centrality)

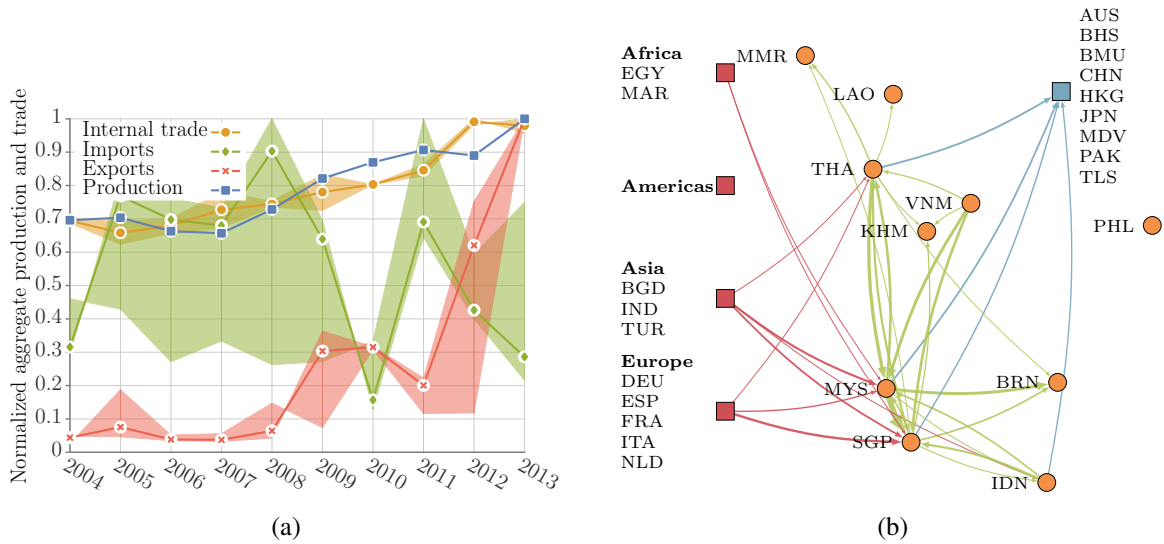


Figure 2: **Country-level production and trade of tomato in the focus region.** (a) General trends of overall production and trade in the region over a decade. The trade data presented for each year is the average of total quantity reported by importing countries and exporting countries. (b) The trade of tomato in the focus region. The network was created using data from FAOSTAT 2013. The trade between countries of the focus region is represented by green edges. Also shown are imports from *T. absoluta* affected countries categorized by region. The edge thickness is a function of the trade volume. (AA: China to be shown separately)

11 **Risk of invasion through the trade pathway.** The network structure does indicate a high risk of introduc-
 12 tion of *T. absoluta* through trade. In particular, our analysis of how the network has evolved over the years
 13 (Supplementary Information) shows that while the basic network structure does not vary much, the imports
 14 from *T. absoluta* infested countries is steadily increasing. By virtue of being important hubs, there is a high

chance that the pest will enter through the ports of Malaysia and Singapore, and spread to Thailand, Brunei and Indonesia due to their high interactions with these neighbors. Further, it is possible that *T. absoluta* can invade through trade of alternate hosts such as eggplants, potatoes, etc. (see Supplementary Information for networks of alternate hosts.) We also analyzed how the network structure evolved observe much variation in the network structure across years. (AA: Monitoring quality)

3.2 Seasonal domestic production and trade

3.3 Spatio-temporal dynamics of *T. absoluta* spread

4 Discussion

- increased thrust towards greenhouse production. How it is threatened.
- generic framework (modular)
- In discussion: talk about keeping it simple. Trade is complex in general; farmer, wholesaler, retailer, distributor, etc. But for the purpose of spread we don't consider much.
- Key challenges:
 - different years, spatial resolution
 - need to scoure literature (statistics, on supply-chain research, economics, value-chain projects)
 - type of data: statistics, surveys
 - data is biased: mostly for big cities

4.1 Related work

- Garrett, Robinet, [4], Boroughs work
- position our work here
- Carrasco: why it can't be used here. too much detailed biology, decades of work.
- tuta stuff
- Bulgaria

- Garrett and Robinet stuff
- general international food trade Zoltan, Rebaudo, Carrasco
- recent work on biology of tuta
- modeling of livestock diseases [4]

4.2 Shortcomings and extensions of the model

- does not account for damage done by the pest. Production remains the same.
- very flexible. For example, long-distance dispersal can include other pathways such as travel within the same framework.
- wind not included
- complex interactions of food systems not included. talk about Carrasco work.
- country specific modeling is required for flows and other aspects too.
- interventions?

5 Conclusion

Acknowledgments

- Hoa
- Aunu
- Yousuf

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