Using Species Distribution Modeling to Assess Illegal Trade Risk: A Case Study of US Imports of Endangered Mahogany (*Swietenia* spp.)

Sarah Pollack

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Committee:
Indroneil Ganguly
John C. Hermanson
Joshua J. Lawler
Suzanne M. Peyer

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Abstract

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Sarah Pollack

Chair of the Supervisory Committee:
Indroneil Ganguly
School of Environmental and Forest Sciences

Illegal logging threatens biodiversity and the global conservation of endangered species. To protect tree species from this threat, governments have enacted legislation against importing illegally sourced plant products. These laws, including the US Lacey Act Amendment of 2008, involve collecting information from importers on the scientific name and country of harvest of their plant products. For many species, a lack of consistent, comprehensive global distribution data makes validating these declarations difficult. I aimed to assist in this analysis by developing species distribution models for the American mahogany species (genus *Swietenia*). American mahoganies are high-value, high-demand tropical timber species restricted in international trade and known to be illegally logged and traded. I combined presence-absence species occurrence data from government forest surveys and presence-only species occurrence data from citizen science programs and herbarium collections for each *Swietenia* species. Both data types were modeled as dependent on climate variables, with the presence-only data also modeled as dependent on sampling bias predictors, such as distances to roads or cities. I combined the range maps generated by the models with previously compiled range country lists to create a global distribution for each species. I compared my range map predictions and the range country lists to a set of US import declarations of *Swietenia* species. Each declared species-country pair was classified as confirmed or unconfirmed based on the range country lists, and suitable or unsuitable based on the model output. By examining the unconfirmed, but climatically suitable, species-country pairs, I identified new range countries for *Swietenia* species that were poorly documented in the literature. I also found that many unconfirmed but suitable country-species pairs were from countries that did not contain *Swietenia* but did contain other, closely related species. Many of these species are endangered and/or regulated and produce wood that can be indistinguishable from *Swietenia*. These results show how species distribution modeling can expand knowledge of a species' global range and help identify patterns of potential illegal trade. While this study focused on US imports of *Swietenia*, these methods could be applied to any species or regulatory framework where knowing the country of harvest is necessary.

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This work is dedicated to all those whose lives and livelihoods are threatened by illegal logging.

1. Introduction

While wildlife trafficking and illegal fishing are well-known forms of environmental crime, illegal logging is in fact estimated to be the most valuable form of environmental crime worldwide (World Bank 2019). Illegal logging threatens the survival of endangered tree species, destroys critical habitats, depletes the world's carbon sinks, and increases the risk and impact of natural disasters such as wildfires and landslides (Reboredo 2013). Besides its environmental impacts, illegal logging also has tremendous social and economic costs, as it is carried out through violence and forced labor, steals natural resources from vulnerable communities, funds armed conflict and other forms of organized crime, and undercuts the legal wood industry (Reboredo 2013; Chimeli and Soares 2017; Araujo et al. 2024). In response to these threats, laws against illegal logging and associated trade have been passed around the world, but enforcement remains difficult due to challenges in detecting and identifying illegally sourced wood (Dormontt et al. 2015).

Trade in endangered tree species is controlled globally by international regulations such as the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and by national and local laws governing the harvest and sale of these species. Many countries have also adopted laws that criminalize the importation of plant products obtained in violation of another country's laws. For example, under the United States Lacey Act Amendment of 2008, the European Union Timber Regulation, or Australia's Illegal Logging Prohibition Act, it is illegal to import any wood or wood product made from a tree harvested illegally in any country (16 U.S.C. §§ 3371-3378; 2010 O.J. (L 295) 23; Illegal Logging Prohibition Act 2012). It is therefore critical to know the country where a tree was harvested to determine its legality by identifying the relevant local regulations on the harvest of the tree. These import regulations may then include a requirement for the importer to declare both the scientific name and country of harvest for their wood products (16 U.S.C. §§ 3371-3378; 2010 O.J. (L 295) 23; Illegal Logging Prohibition Act 2012).

Deliberately misdeclaring either or both the scientific name and the country of harvest is one way importers disguise their products' illegal origin (Chimeli and Boyd 2010; Colbourn and Swegle 2011). Misdeclaration of species can go undetected because many timber species have "lookalike" species. Two species are considered lookalikes when their wood is indistinguishable to the naked eye, which can occur both within and between genera (Gasson 2011). Country of harvest misdeclaration can also be difficult to detect due to the long, multi-national supply chains many products go through. Additionally, unlike for species identification, the visual properties of wood give little to no indication of its provenance (Gasson 2011). Misdeclaring either or both of these fields allows importers to circumvent laws that may be specific to the true harvest country or species. However, accidental misdeclaration can also occur for legal products due to confusions between scientific and vernacular names, or due to confusion between harvest and manufacturing countries (Colbourn and Swegle 2011).

One way species or country of harvest misdeclaration can be detected is through species-country mismatch. This occurs when a declaration lists a species that is not known to grow in the declared country of harvest, indicating that one or both of these must be incorrect. However, determining all the countries in the world where a species is present is not always a simple task, especially for species introduced well outside of their native ranges. When the question "does this species grow in this country?” is difficult to answer, another question one can ask is “could this species grow in this country?” Predicting the potential range of a species is one major application of species distribution modeling (SDM). SDM encompasses a broad range of methods and applications, but generally refers to any model seeking a relationship between where a species is (and is not) geographically located and the conditions present at these sites. These models can be used for many applications, including making geographic predictions of potentially suitable habitats when a species’ presence in a location is unknown (Guillera-Arroita et al. 2015). With respect to international trade and import policy, the primary application of species distribution models has been invasive species management (van Wilgen, Roura-Pascual, and Richardson 2009; Cook et al. 2019). While invasive species introduction is a major risk of international trade, the transport of illegally sourced wood products is another risk.

In this study, I investigated whether SDMs could assist in detecting species-country mismatch and analyzing import data for the genus *Swietenia*, which goes by the vernacular name American mahogany. There are three species in the genus: *S. macrophylla*, S. *mahagoni*, and *S. humilis*, and all three are native to the Neotropics (Lamb 1966). They are all listed on the CITES Appendix II, meaning their international trade is controlled to prevent overharvesting (United Nations Environment Programme – World Conservation Monitoring Centre [UNEP-WCMC] 2021). Illegal mahogany trade has been linked to instances of homicide and modern slavery in Brazil (Chimeli and Soares 2017; Araujo et al. 2024). Besides being high-risk, *Swietenia* is also a genus that illustrates the difficulty of obtaining global distribution data for timber species. For example, the introduced range for *S. macrophylla* could include as few as 17 to as many as 30 countries or territories, depending on the source (van Kleunen et al. 2019; Mayhew and Newton 1998).

In addition to species-country mismatch, I also investigated possible misdeclaration through mismatch between species and product type. Product types are classified in US import data by the Harmonized Tarriff Schedule (HTS) of the United States. These product classifications may specify a species name, genus name, or vernacular name for wood products (United States International Trade Commission [USITC] 2023). Therefore, it is possible for species-HTS code mismatch to also occur, when the declared species name does not match the scientific or vernacular name listed in the corresponding HTS code description. Like species-country mismatch, this indicates that either or both of these fields must be incorrect, either intentionally or inadvertently.

I developed a global SDM for each of the three *Swietenia* species, using a combination of point occurrence data from national surveys and public databases, along with climatic predictor variables known from previous research to affect their survival and distribution. Then, I used the SDM's climatic suitability predictions combined with existing country-level data on *Swietenia* distributions to categorize declared imports of *Swietenia* products to the United States. The goal of this work was to create the most accurate global picture of the range of all three *Swietenia* species, and to use this picture to detect potential patterns of illegal trade in US mahogany imports. To accomplish this goal, I asked four main questions about the trade data: 1. Are there additional range countries for *Swietenia* species present in the import declaration data that are not well documented in the literature? 2. Do declarations with species-country mismatch declare countries that contain lookalike species, indicating the possibility of species misdeclaration? 3. Does species-country mismatch occur more frequently in more finished products, indicating country misdeclaration due to supply chain confusion? 4. Are species-country mismatch and species-HTS mismatch related or separate phenomena?

2. Data and Methods

2.1 Study Genus

In this study, I focused on the three species in the genus *Swietenia: S. macrophylla, S. mahagoni*, and *S. humilis*. Together, these species are also referred to by their vernacular name American mahogany. While many other species are called “mahogany,” only the *Swietenia* species are considered to be “true” mahoganies (Helgason et al. 1996). For centuries, *Swietenia* species have been logged, milled and manufactured into ships, fine furniture, musical instruments and other high-value products (Lamb 1966). After extensive depletion of *S. mahagoni* in its native range, *S. macrophylla* became the primary species in trade, which it remains today (Anderson 2012). Currently, *S. mahagoni* is considered to be “commercially extinct,” although it remains in trade in smaller quantities (Groves and Rutherford 2015). Due to its smaller stature, *S. humilis* has never been as prized for timber as the other two species, but it is still considered at-risk today due to deforestation and habitat loss (Anderson 2012; Groves and Rutherford 2015).

All three *Swietenia* species are native to the Neotropics (Lamb 1966) and have also been introduced outside of their native ranges either as ornamentals or for timber production (Groves and Rutherford 2015). *S. mahagoni* is native to certain Caribbean Islands, such as Hispaniola and Jamaica, and the southern tip of Florida in the United States. *S. macrophylla* has the largest range of the three species, stretching from the Yucatán peninsula in Mexico through Central America and into the Amazon rainforest. *S. humilis i*s limited to the Pacific coast of Mexico and Central America, where it overlaps with *S. macrophylla* in certain areas (Lamb 1966). *S. macrophylla* has been introduced to the Caribbean, Asia, and the Pacific, including Puerto Rico, India, Indonesia, Fiji, and the Philippines (Mayhew and Newton 1998). *S. mahagoni* is also introduced in many of these areas (van Kleunen et al. 2019).

2.2 Initial Country Lists

Range country lists for each species were compiled from general biological databases and genus-specific literature. The databases used were Kew Plants of the World Online (POWO), the International Union for Conservation of Nature (IUCN), the Global Naturalized Alien Flora (GloNAF) database, and the Global Biodiversity Index Facility (GBIF) (POWO 2024; IUCN 2023; van Kleunen et al. 2019; GBIF 2024). Published books on *Swietenia* were also referenced for range-country information (Lamb 1966, Mayhew and Newton 1998). Because geographic information is available at differing levels of granularity, these lists were harmonized according to the International Organization for Standardization (ISO) 3166 country code system. Throughout this manuscript, “country” will refer to any region that has its own unique ISO-3166 code, although the independence and sovereignty of these regions vary and are sometimes disputed (e.g., French Polynesia, Puerto Rico, Taiwan). In total, there were 63 unique native and introduced countries for *S. macrophylla*, 63 for *S. mahagoni*, and 10 for *S. humilis*. For details and complete lists, see Appendix I.

2.3 Occurrence Data

To build the species distribution models, I combined two types of species occurrence data: presence-absence data and presence-only data. Presence-absence data are collected from a set of sampled sites that are searched and noted as either containing or not containing a given species. These collection efforts are often undertaken by government agencies or research institutions. The advantage of these data is that they carry information about both where a species is and where a species is not, which is critical for modeling a species' distribution. However, geographic coverage of presence-absence data tends to be limited, because of the time, labor, and resources required for their collection (Fletcher Jr. et al. 2019). By contrast, presence-only data are obtained mostly for citizen science programs and herbarium collections. These data are opportunistically rather than systematically collected, and only indicate locations where a species is present. As such, a geographic area with no presence-only occurrence points may indicate a lack of sampling effort rather than the actual absence of a species. However, the major advantage of presence-only data is their extensive geographic coverage and availability in comparison to presence-absence data (Fletcher Jr. et al. 2019). I made use of both presence-absence and presence-only occurrence data to take advantage of the benefits of both types of data.

Presence-absence data for *Swietenia* species were sourced from two national survey programs: the Forest Inventory and Analysis (FIA), carried out by the US Forest Service, and the Inventario Nacional de Forestal y Suelos (INFyS), carried out by the Mexican Comisión Nacional Forestal (CONAFOR). The FIA consists of a network of sample plots across the US states and territories, as well as Palau and the Federated States of Micronesia (United States Department of Agriculture [USDA] Forest Service 2023). Similarly, the INFyS consists of a network of sample plots across Mexico (CONAFOR 2019). Each dataset was limited to the regions that contained at least one plot with *S. macrophylla, S. mahagoni*, or *S. humilis*. For the FIA, these regions were Hawaii, Florida, Puerto Rico, the US Virgin Islands, Palau, and Micronesia. Data were obtained via the FIA DataMart (https://www.fs.usda.gov/research/products/dataandtools/tools/fia-datamart) by downloading the TREE and PLOT tables for each of the regions listed above. For the INFyS, these regions were the states of Guerrero, Oaxaca, Chiapas, Nayarit, Sinaloa, Durango, Campeche, Quintana Roo, Mexico, Puebla, and Jalisco. These data were obtained by downloading the "INFyS Arbolado 2015-2020" dataset from https://snmf.cnf.gob.mx/datos-del-inventario/, and then filtering for states containing *Swietenia* species. Across the two data sources, I obtained 152 occurrences of *S. macrophylla*, 13 occurrences of *S. mahagoni*, and 28 occurrences of *S. humilis*.

Presence-only data were obtained through the Global Biodiversity Information Facility (GBIF). GBIF is a publicly available database compiling species occurrence records from various herbariums, research institutions, and citizen science projects from around the world (https://www.gbif.org/; GBIF 2024). Data were downloaded from GBIF for each species individually, excluding records that did not contain coordinate values, or for which the coordinate values were flagged as suspicious (GBIF 2023a; GBIF 2023b; GBIF 2023c). This yielded 2032 occurrences of *S. macrophylla*, 114 occurrences of *S. mahagoni*, and 295 occurrences of *S. humilis*. Despite the limitations of presence-only data compared to presence-absence data, the number of presence-only occurrences available for each species was an order of magnitude greater than the available presence-absence data. Additionally, the presence-absence data span only four countries: the United States, Mexico, Palau, and the Federated States of Micronesia, while the presence-only data span dozens of countries across multiple continents. This illustrates the benefit of combining presence-absence and presence-only data in species distribution modeling.

2.4 Species Distribution Model and Predictor Variables

For the species distribution models, I employed the multispecies Poisson process (PP) model (Fithian et al. 2015). The multispecies PP model combines presence-absence and presence-only data for multiple related species to create a unique geographic distribution model for each species. In the model, the presence-absence data depend on the chosen environmental predictors (e.g., temperature, precipitation), while the presence-only data depend on these same environmental predictors in addition to predictors of the sampling effort (Fithian et al. 2015). Presence-only data are known to be spatially biased towards areas that are more accessible to and populated by humans (Di Cecco et al. 2021). This spatial bias is incorporated into the model of the presence-only data (Fithian et al. 2015).

I chose the multispecies PP model because it was uniquely suited to model three closely related species (i.e., *Swietenia* spp.) using a variety of occurrence data types. Both presence-absence and presence-only data are combined in a way that explicitly accounts for the different sampling methods of each data type, which is preferable to simple data pooling (Fletcher et al. 2019). Modeling all three species simultaneously allows the sampling effort function to be estimated using all available presence-only data. Modeling the presence-only data as a thinned version of the presence-absence data process accounts for the spatial biases known to be present in presence-only data (Fithian et al. 2015). While previous SDM studies on *Swietenia* have used machine learning techniques (e.g., MaxEnt; Navarro-Martínez et al. 2018; Sampayo-Maldonado et al. 2021; Herrera-Feijoo et al. 2023), I chose a generalized linear model (GLM) because it has been shown to have superior performance when transferring predictions to novel environments (Werkowska et al. 2017). Because my goal was to predict the ability of a given *Swietenia* species to grow in a particular country when the status of that species in that country is unknown, I selected a model that maximized transferability and was appropriate for the data available.

To build the model, I started with a set of climatic predictor variables based on the climatic tolerances of each *Swietenia* species (Lamb 1966; Lamprecht 1989; Mayhew and Newton 1998; Cornelius et al. 2004). First, I selected a subset of the 19 Bioclimatic variables available from WorldClim (https://worldclim.org/), a database of global weather and climate data collected from 1970 to 2000 (Fick and Hijmans 2017). I chose the most relevant subset for the *Swietenia* species, namely, annual mean temperature, maximum temperature of the warmest month, minimum temperature of the coldest month, annual precipitation, and precipitation of the wettest month. In addition, I obtained the average monthly precipitation dataset from WorldClim and used it to create a separate dry season dataset. Finally, I obtained potential evapotranspiration (PET) and aridity index data from the Global Aridity Index and Potential Evapotranspiration Database (Zomer, Xu, and Trabucco 2022).

Different spatial variables can bias the collection of presence-only species occurrence data (Kadmon, Farber, and Danin 2004; Stolar and Nielsen 2015; Monsarrat, Boshoff, and Kerley 2019; Di Cecco et al. 2021; Geurts, Reynolds, and Starzomski 2023). I selected a set of spatial variables as predictors of the spatial sampling bias: distance to nearest road (Kadmon, Farber, and Danin 2004; Stolar and Nielsen 2015; Geurts, Reynolds, and Starzomski 2023), distance to nearest town, city, or village (Monsarrat, Boshoff, and Kerley 2019; Di Cecco et al. 2021), population density (Stolar and Nielsen 2015; Di Cecco et al. 2021), and a binary indicator of the presence of a national park or other similar nature reserve (Geurts, Reynolds, and Starzomski 2023). Global population density data were obtained from the Center for International Earth Science Information Network (CIESIN) (CIESIN 2018). Locations of cities, towns, and villages were obtained as point data from OpenStreetMap, an open-source, collaborative geospatial database (https://www.openstreetmap.org/). The OpenStreetMap data were obtained for all countries containing presence-only records of a *Swietenia* species, except for the United States and Australia, which were limited to relevant states (Florida and Hawaii, and Queensland, respectively). Similarly, roads were obtained as line data, and national parks and nature reserves were obtained as polygons from OpenStreetMap (see Appendix II for details).

All predictor variables, both climate and sampling bias, were harmonized to the same raster grid resolution. I chose 2.5 arcminutes as it was the smallest available WorldClim resolution large enough to contain the size and uncertainty of the FIA and INFyS sample plots. FIA plot coordinates are "fuzzed" up to a mile away from their true location, resulting in a coordinate uncertainty value of up to 3200 meters (USDA Forest Service 2023). At a smaller raster resolution, this uncertainty value would cover multiple cells. In order to satisfy the assumptions of the multispecies PP model, one must assume the values of predictor variables are constant across sample sites (Fithian et al. 2015). Species occurrence data should be at a finer resolution than climate or other predictor data (Sillero and Barbosa 2020). Thus, all presence-only species records were filtered to include only records with coordinate uncertainty values under 4600 meters, which is approximately equivalent to 2.5 arcminutes at the equator.

WorldClim data were downloaded directly in 2.5-arcminute resolution. Aridity index and PET data were only available at 30-arcsecond resolution and were aggregated to 2.5 arcminutes using the “aggregate” function in the R package *terra*, using R version 4.3 (Hijmans 2023; R Core Team 2024). To create the dry season dataset, each raster cell was assigned a value for dry season length, which equaled the number of consecutive months averaging below 60 millimeters of precipitation over a 24-month period. These calculations were also carried out in R 4.3 (R Core Team 2024). According to the Koeppen-Geiger climate classification, a tropical climate experiences a dry season if at least one month averages below 60 millimeters of precipitation (Beck et al. 2018). Population density data were also downloaded directly at a 2.5-arcminute resolution.

Because the city, road and park data from OpenStreetMap were all obtained as vector data, they were converted to raster data using QGIS 3.22 Lima (QGIS.org 2023). For the city and road data, each vector dataset was first rasterized using the “v.to.rast” function in GRASS GIS version 8.3 (Geographic Resources Analysis Support System [GRASS] Development Team 2023). Then, distances to the nearest road or city cell were assigned to a raster grid using the “r.grow.distance” function. These processes were scripted in PyQGIS for each country layer, and then each layer was combined using the “r.series” GRASS function, taking the minimum value for any overlapping cells. Similarly, the parks data were rasterized using the “v.to.rast” function, then combined with “r.series” by maximum value, with 1 indicating cells inside parks and 0 indicating cells outside parks. Each raster grid was created at a 2.5-arcminute resolution and made to align with all other raster layers.

The underlying form of the multispecies PP model is an inhomogeneous Poisson point process, which generates points randomly in space accordingly to a spatially varying intensity function (Fithian et al. 2015). For a sufficiently small region A_i, such as a sample plot, the number of individuals of species k in plot i, N_{ik}, is approximately a Poisson random variable (Fithian et al. 2015). The mean of this Poisson random variable is equal to the area of A_i times the value of the intensity function at point s_i, $\lambda_k(s_i)$. The value of this intensity function varies spatially as a log-linear function of the covariates present there, in this case, our climatic predictors (Fithian et al. 2015). If $x(s_i)$ represents this vector of covariates and α_k and β_k are the intercepts and coefficients of our intensity function, respectively, we have that:

$$\log(\lambda_k(s_i)) = \alpha_k + \beta'_k x(s_i) \qquad (1)$$

and therefore:

$$\begin{aligned} N_{ik} &\approx Pois(|A_i|\lambda_k(s_i)) \\ &= Pois(|A_i| \exp(\alpha_k + \beta'_k x(s_i))) \qquad (2). \end{aligned}$$

The presence-absence data are thus modeled as a Bernoulli random variable with a complementary log-log link:

$$\begin{aligned} P(N_{ik} > 0) &\approx 1 - \exp(-|A_i|\lambda_k(s_i)) \\ &= 1 - \exp(-\exp(\alpha_k + \beta'_k x(s_i) + log|A_i|)) \qquad (3). \end{aligned}$$

The presence-only data, meanwhile, are modeled as a thinned version of the underlying inhomogeneous point process (Fithian et al. 2015). If the locations of individuals, in this case trees, are IPP($\lambda(s)$), then the locations of sampled individuals—the presence-only data points—are IPP($\lambda(s)b(s)$), where $b(s)$ represents the spatially varying sampling bias of the presence-only observation process (Fithian et al. 2015). Like the intensity function, the bias function is log-linearly dependent on spatial covariates $z(s)$. For species k at point i,

$$\log\left(b_k(s_i)\right) = \gamma_k + \delta' z(s_i) \qquad (4).$$

The key difference between equation 1 and equation 4 is that the coefficients of the site conditions do not vary by species in equation 4 like they do in equation 1. In equation 4, only the intercept varies by species. This is because the model assumes that while the underlying intensity of the presence-only sampling can vary by species, the effect of the covariates z, in this case distance to roads or cities, population density and locations of parks, on sampling effort are independent of the species being sampled (Fithian et al. 2015). Therefore, in the model, $\hat{\alpha}$, $\hat{\beta}$ and $\hat{\gamma}$ are each estimated individually for each species k, while $\hat{\delta}$ is estimated once by pooling all presence-only data across all species (Fithian et al. 2015). All of these parameters are estimated simultaneously by combining them into one large GLM using all of the data, with dummy variables introduced to differentiate between species and between presence-absence and presence-only data points. For more details, please refer to Fithian et al.'s "Bias correction in species distribution models: pooling survey and collection data for multiple species" (2015).

2.5 Model Fitting and Evaluation

Models were fitted in R version 4.3 (R Core Team 2024) using a modified version of the *multispeciesPP* package (Fithian 2014). The original *multispeciesPP* package did not allow varying plot sizes in presence-absence data, so the code was modified to allow for the different plot sizes between FIA and INFyS data (USDA Forest Service 2023; CONAFOR 2019). This modification was done through a fork of the original package on GitHub (https://github.com/sepollack/multispeciesPP). All other code and functionality remained the same between the two *multispeciesPP* versions. Climate predictor and bias predictor variable values were assigned to each presence-absence point (climate only) and presence-only point (climate and bias) using the “extract” function in *terra* (Hijmans 2023).

Two initial candidate models were considered, and each was modified following the same process. Model 1.1 included linear and quadratic terms for each of the five Bioclim variables selected (annual mean temperature, maximum temperature, minimum temperature, annual precipitation, and precipitation of the wettest month), dry season length, potential evapotranspiration ratio (PET), and an interaction term multiplying PET and annual precipitation. Model 2.1 was like model 1.1 except with aridity index replacing PET and the PET and precipitation interaction term. Aridity index is precipitation divided by PET (Zomer, Xu, and Trabucco 2023), so these two candidates were compared to see which better captured the humidity tolerances of the *Swietenia* species. After fitting models 1.1 and 2.1, I removed any predictors for each model that were not significant at the 0.05-level for all three *Swietenia* species, and re-fitted the models, labeling them 1.2 and 2.2. Finally, I removed any predictors from 1.2 and 2.2 that were not significant at the 0.05-level for at least two out of the three *Swietenia* species. So, a total of six models were compared, 1.1-1.3 and 2.1-2.3.

The goal of the model fitting process was to produce a model that was as simple as possible while still maximizing the predictive performance of the model in novel environments. Model predictions were generated using the “predict.multispeciesPP” function in *multispeciesPP*, which generates a value between 0 and 1 for every raster cell (Fithian 2014). Model performance was evaluated using two datasets for each species. The first dataset evaluated predictions at the country level. The suitability of each country was assessed using the maximum predicted value in that country for each species. This was to avoid biasing the suitability scores by the size or climatic diversity of the countries. For each species, the set of tested countries included every country from the compiled range lists (see 2.1) that did not have either presence-absence or presence-only data points for that species. The second test dataset was the plantation polygons for each species found in the Spatial Database of Planted Trees v2.0 (Richter et al. 2024). So, for each model, six datasets were tested, two data types per species.

To quantify model predictive performance, the area under the curve (AUC) value for the receiver operating characteristic (ROC) was calculated using the six test datasets. AUC values range from 0.5 to 1, with 0.5 indicating that the classifier is no better than random, and 1 indicating that it is perfect. The curve is generated by plotting the true positive rate against the false positive rate for every possible threshold value. Thus, the AUC value is independent of the chosen threshold, because it assesses the classifier at every possible threshold (Fielding and Bell 1997). Six AUC values were generated for each model, and the model with the highest average of these six was chosen as the best model, based on predictive performance. ROCs and AUCs were generated using the R package *pROC* (Robin et al. 2011).

After the best model was chosen, it was used to make country-level predictions for each species. To classify each country as suitable or unsuitable for each species, threshold values were chosen based on the ROCs for the country test dataset. A multitude of methods exist for determining threshold, and none is considered necessarily the best (Freeman and Moisen 2008). Instead, the choice of threshold depends on the intended use of the classifier. For example, in this instance, the goal of the model predictions was to determine whether a successful introduction of the given species to the given country is at all possible. Thus, a certain level of false positives is expected, and false negatives are more important to avoid. Thresholds were chosen using a minimum sensitivity approach, where the threshold value that reaches a minimum level of sensitivity (true positive) rate while maximizing specificity (true negative) is chosen (Fielding and Bell 1997; Freeman and Moison 2008). This minimum sensitivity value was set to 0.95.

2.6 Trade Data Analysis

Import data were obtained from the USDA Animal and Plant Health Inspection Service (APHIS) for January 2017 to March 2023. Each observation consists of one submitted import declaration containing text such as “swietenia,” “mahogany,” or similar. For each declaration, I obtained the year, HTS code, country of harvest, and scientific name, as all other fields were restricted due to protected trade data and privacy issues. No identifying information about the importers was contained anywhere in the data. The initial dataset contained 51,557 rows, representing 51,557 declarations filed during that time period. Because the scientific name field is a free text field, raw entered names had to be corrected for spelling. This was done through a program called BUSTER that determines which accepted plant scientific name most closely matches the entered text (Richardson et al. in review). For any entry that returned in a match in BUSTER, these names were evaluated individually, by comparing them to known scientific and vernacular names. All entries that I determined to either likely be a non-*Swietenia* species, or that were unintelligible, were removed. This reduced the size of the dataset to 47,215 declarations.

Each declaration was categorized in four ways by cross-referencing it with other datasets. First, each declaration was categorized as “confirmed” or “unconfirmed” based on whether or not the declared country of harvest was in the compiled range country list (see 2.1) for the declared species. Second, each declaration was categorized as “suitable” or “unsuitable” based on the predictions of the species distribution model for the combination of declared species and declared country of harvest (hereafter “species-country pair”). Third, each declaration’s declared species and declared HTS code (hereafter “species-HTS pair”) was assessed as a match or not, based on the product description for the HTS code. Finally, each declaration was categorized based on whether the declared country of harvest contained a lookalike species for the declared species.

Product descriptions for the HTS codes were sourced from USITC for the relevant year (USITC 2017, 2018, 2019, 2020, 2021, 2022, 2023). Each was categorized as either a “match” or “no match” for *Swietenia* species. Any description that specified a genus other than *Swietenia*, a vernacular name not known to refer to *Swietenia* (e.g., teak, meranti, sapele), or a non-wood material (e.g., bamboo, rattan, metal, plastic) was categorized as a “no match.” Any description that specified *Swietenia* or mahogany, or a broader category containing *Swietenia* (e.g., tropical wood, wood), or that did not specify a material, was categorized as a “match.” There were no HTS code descriptions that referred to a particular *Swietenia* species, only to the genus level.

Lookalike species information was sourced from the Checklist of CITES Species Identification Manual, which lists lookalikes for timber species (UNEP-WCMC 2020). Range countries for each listed lookalike species were sourced from Kew POWO (POWO 2024).

For any species-country pair that was classified as confirmed but unsuitable due to imperfect model predictions, that country was manually changed to suitable for the species. For every species-country pair that was categorized as both unconfirmed and suitable, I performed a literature search for additional information on the presence of that species in that country. I searched the country name and full species name in quotes in both Google Scholar and the University of Washington Libraries Catalog. Sources that confirmed the presence of the species in the country were compiled.

Rates of species-country mismatch and species-HTS mismatch were compared between chapters using Chi-square tests. Over 99% of the declarations were in chapters 44, 92, or 94, with the remaining under 1% of declarations grouped together as “Other.” Within chapters, rates of species-country mismatch were compared across subheadings (4-digit) codes. In chapters 44 and 92, subheading with cell counts fewer than 10 were grouped together as “Other.” Only three subheadings were present in the data for chapter 94, and only the two largest were compared as the third had only five declarations in total. Post-hoc grouping of subheadings was performed to identify the most significantly mismatching product types. Subheadings were grouped based on standardized residual values and groups were tested using Chi-square for homogeneity. Association between species-country mismatch and species-HTS mismatch was also tested for using Chi-square. Finally, rates of lookalike presence were tested across combinations of species-country pairs (i.e., confirmed-suitable, unconfirmed-suitable, unconfirmed-unsuitable). Tests were performed using the "CrossTable" function in the R package *gmodels* (Warnes et al. 2022). All 2x2 tests used Yates' continuity correction.

3. Results

3.1 Fitted Species Distribution Models and Predictions

The model with the highest average AUC value was model 2.2, with an average AUC of 0.849 across the six test datasets. The predictor variables in model 2.2 and their estimated coefficients are reported in tables 1-4. Complete AUC values for all test datasets and all models are reported in Appendix III.

Variable	**Estimated Coefficient**	**Standard Error**	**z-Value**	**P(>|z|)**
intercept	-14.852	0.832	-17.843	< 0.000
maximum temperature	13.720	1.275	10.785	< 0.000
maximum temperature squared	-11.244	1.041	-10.797	< 0.000
minimum temperature	22.708	1.198	18.949	< 0.000
minimum temperature squared	-10.094	0.518	-19.488	< 0.000
annual precipitation	2.353	0.520	4.522	< 0.000
annual precipitation squared	-1.224	0.289	-4.239	< 0.000
precipitation of wettest month	1.077	0.232	4.635	< 0.000
precipitation of wettest month squared	-0.772	0.163	-4.747	< 0.000
aridity index	-1.021	0.239	-4.270	< 0.000
dry season length	-0.516	0.122	-4.226	< 0.000

Table 1: Estimated coefficients and p-values for predictor variables in the distribution intensity function for *S. macrophylla*.

Variable	**Estimated Coefficient**	**Standard Error**	**z-Value**	**P(>|z|)**
intercept	-5.816	1.086	-5.356	< 0.000
maximum temperature	1.074	1.868	0.575	0.565

maximum temperature squared	-1.887	1.524	-1.238	0.216
minimum temperature	5.804	1.566	3.705	0.000
minimum temperature squared	-2.296	0.709	-3.239	0.001
annual precipitation	6.278	1.244	5.047	< 0.000
annual precipitation squared	-0.105	0.671	-0.156	0.876
precipitation of wettest month	-0.823	0.462	-1.780	0.075
precipitation of wettest month squared	0.297	0.205	1.451	0.147
aridity index	-7.412	0.863	-8.588	< 0.000
dry season length	-0.832	0.308	-2.705	0.007

Table 2: Estimated coefficients and p-values for predictor variables in the distribution intensity function for *S. mahagoni*.

Variable	**Estimated Coefficient**	**Standard Error**	**z-Value**	**P(>|z|)**
intercept	-12.268	0.941	-13.043	< 0.000
maximum temperature	16.347	1.709	9.568	< 0.000
maximum temperature squared	-14.402	1.339	-10.76	< 0.000
minimum temperature	12.692	1.301	9.758	< 0.000
minimum temperature squared	-6.204	0.601	-10.324	< 0.000
annual precipitation	6.850	0.765	8.957	< 0.000
annual precipitation squared	2.770	0.365	7.584	< 0.000
precipitation of wettest month	5.630	0.677	8.315	< 0.000
precipitation of wettest month squared	-9.157	1.075	-8.515	< 0.000
aridity index	-10.474	0.778	-13.456	< 0.000
dry season length	1.708	0.243	7.02	< 0.000

Table 3: Estimated coefficients and p-values for predictor variables in the distribution intensity function for *S. humilis.*

Variable	**Estimated Coefficient**	**Standard Error**	**z-Value**	**P(>|z|)**
S. macrophylla intercept	-15.588	0.212	-73.695	< 0.000
S. mahagoni intercept	-14.439	0.374	-38.57	< 0.000
S. humilis intercept	-12.268	0.941	-13.043	< 0.000
distance to road	-4.678	0.439	-10.666	< 0.000
distance to city	-2.522	0.195	-12.902	< 0.000
park presence	0.262	0.031	8.317	< 0.000
population density	0.14	0.004	35.072	< 0.000

Table 4: Estimated coefficients and p-values for predictor variables in the bias function for all three species.

Using the criteria set out in section 2.5, the cutoff values for each species were 0.928 for *S. macrophylla*, 0.529 for *S. mahagoni*, and 0.591 for *S. humilis*. This resulted in four incorrect predictions where a country from the compiled country list for a species was classified as unsuitable for the species. These were *S. macrophylla* in the Federated States of Micronesia, and *S. mahagoni* in Palau, Taiwan, and Curaçao. Additionally, there were three predictions of "suitable" that occurred purely based on the suitability of a minor outlying island of a country rather than the mainland of the country itself and were changed to "unsuitable." These were *S. macrophylla* and *S. mahagoni* in Portugal (Azores and Madeira) and *S. mahagoni* in France (Clipperton Island). Raster maps of climatic suitability for each species are shown in figures 1-3 below.

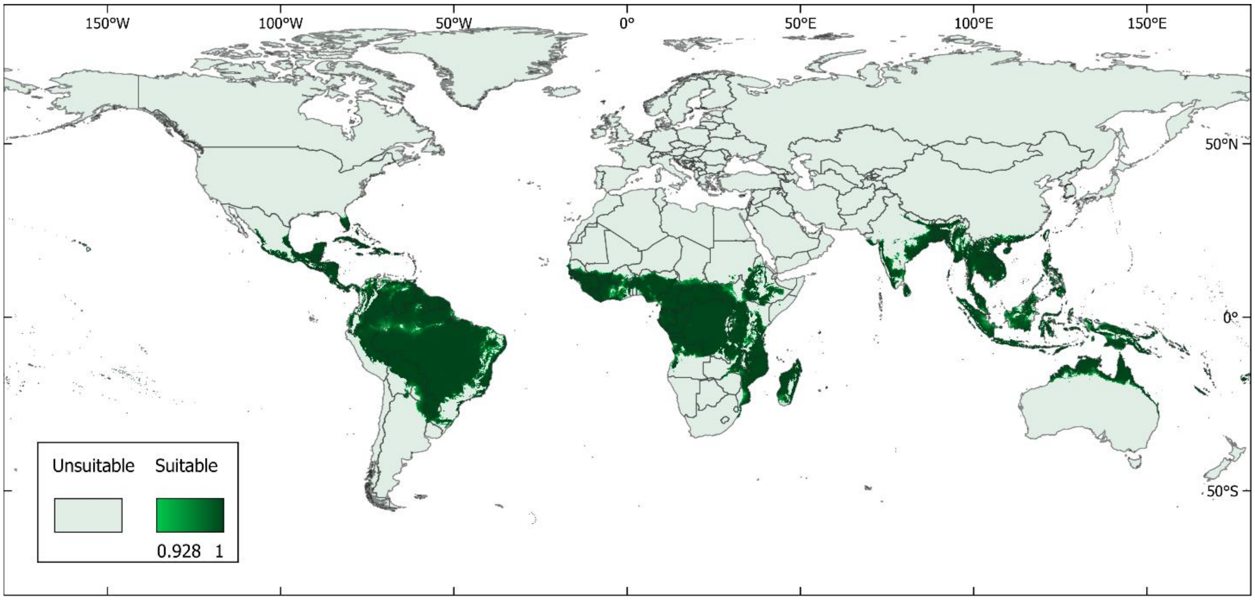

Figure 1: Climatic suitability map for *S. macrophylla*. Suitable raster cells are those with a predicted value greater than 0.928.

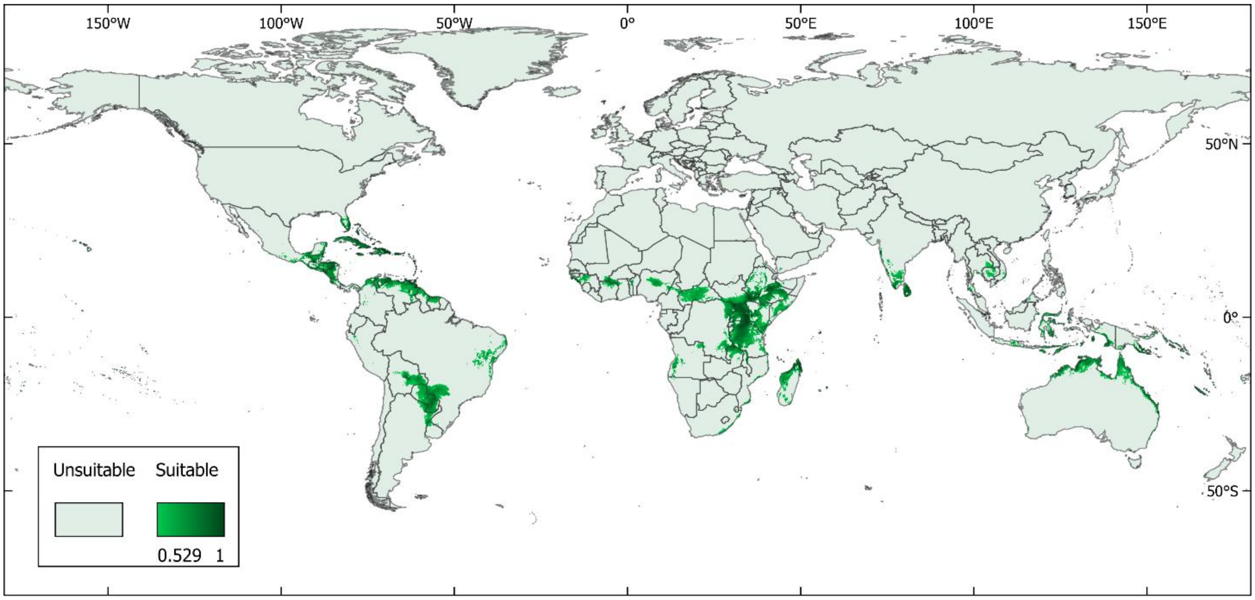

Figure 2: Climatic suitability map for *S. mahagoni*. Suitable raster cells are those with a predicted value greater than 0.529.

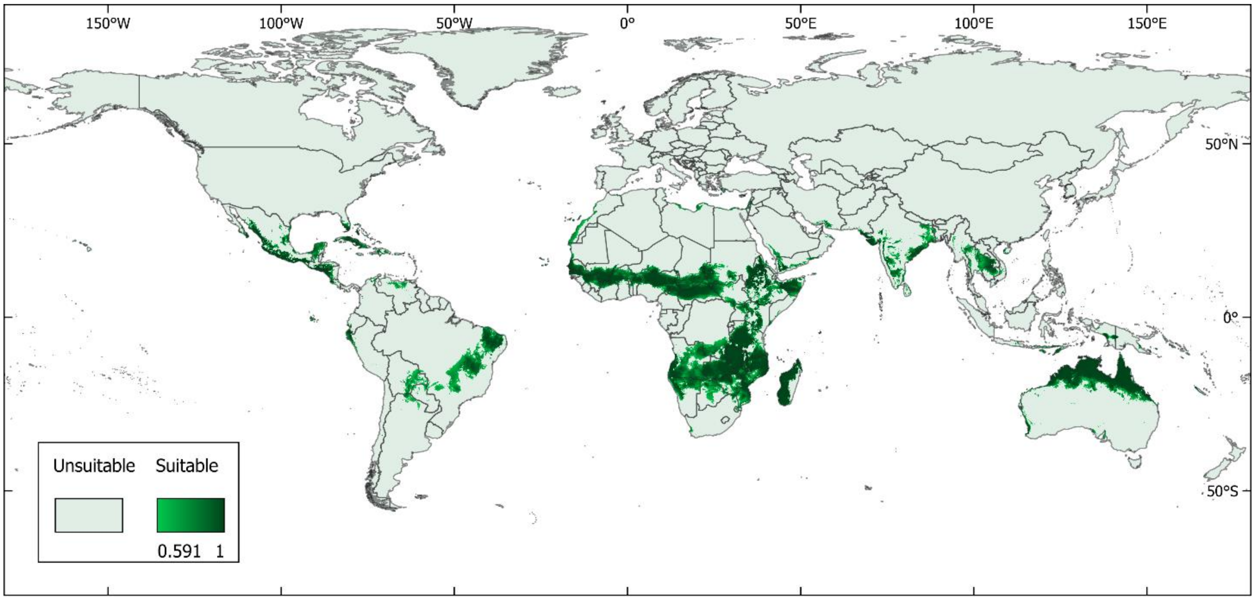

Figure 3: Climatic suitability map for *S. humilis*. Suitable raster cells are those with a predicted value greater than 0.591.

3.2 Literature Search on Unconfirmed-Suitable Species-Country Pairs

A total of 48 unique unconfirmed but suitable species-country pairs were present in the trade data, 20 involving *S. macrophylla*, 19 involving *S. mahagoni*, and nine involving *S. humilis*.

Seven of these yielded evidence of species presence in country, two for *S. macrophylla* and five for *S. mahagoni*, and none for *S. humilis*. For many of these species-country pairs, the species is present in the country, but may not be part of the timber industry. For *S. macrophylla* in Papua New Guinea and Ghana, and *S. mahagoni* in Sri Lanka, the source described the species as present in purely experimental plantation plots (Bevacqua, Samaya, and Miller 2021; Darko et al. 2022; Tilakaratna 2001). *S. mahagoni* is present in Ghana only as roadside ornamental (Edusei et al. 2021). *S. mahagoni* is also recorded as a non-native or invasive species in natural forests in Fiji and Vietnam (Franklin, Keppel, and Whistler 2008; Tuan et al. 2022). Only in Guatemala was there evidence of *S. mahagoni* as present as a timber production species in plantations (Richter et al. 2024). A complete list of checked species-country pairs is available in Appendix IV.

3.3 Lookalike Species and Species-Country Mismatch

All three *Swietenia* species are considered lookalikes of one another and may also be confused with other tropical timbers such as *Khaya* spp. or *Entandrophragma* spp. (UNEP-WCMC 2020). In declarations that had an unconfirmed but suitable species-country pair, the declared country of harvest contained a *Swietenia* lookalike 82.211% of the time. This rate was much lower for other types of species country pairs, with 31.580% of declarations with a confirmed country of harvest containing a lookalike, and just 4.915% for declarations with unconfirmed and unsuitable countries of harvest. Comparing rates of lookalike presence across all three species-country pair types (confirmed-suitable, unconfirmed-suitable, unconfirmed-unsuitable) produced a chi-square value of 2367.2 and a p-value much smaller than 0.001. Pairwise comparisons between the three categories also all yielded p-values well under 0.001, indicating that these rates of lookalike are likely to all be truly different.

The most frequently declared unconfirmed country of harvest was Cameroon (Fig. 4), which was declared for both *S. macrophylla* and *S. mahagoni*, and for multiple product types, mostly 4409 (shaped wood) and 9202 (other string instruments). Cameroon has many native lookalike species for *Swietenia*, including *Entandrophragma angolense, E. candollei*, *E. cylindricum*, *E. utile*, *Khaya anthotheca*, *K. ivorensis*, and *K. senegalensis* (POWO 2024). *Khaya* spp. were added to CITES Appendix II in 2022 due to overharvesting and declining populations in Africa (UNEP-WCMC 2022). While no *Entandrophragma* species are CITES-listed, they are considered "vulnerable" by the IUCN and are exploited heavily for their valuable timber in their native regions of West and Central Africa, including illegally (Kasongo Yakusu et al. 2021).

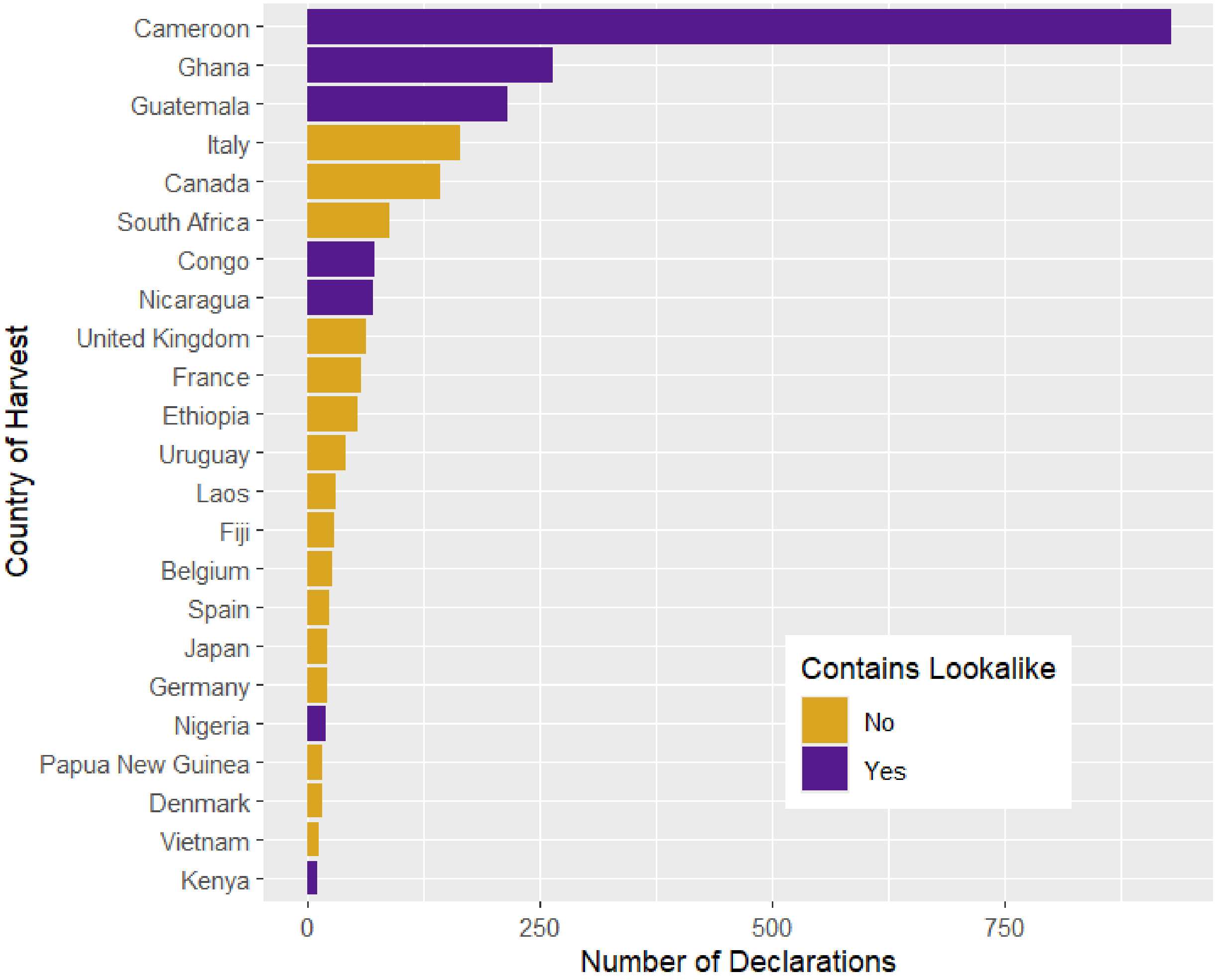

Figure 4: Unconfirmed countries of harvest declared for *Swietenia* spp., 2017-2023. Countries declared fewer than ten times not included.

3.4 Rates of Species-Country Mismatch by HTS Code

The trade data were grouped into four categories based on HTS chapter: 44 (wood and articles of wood), 92 (musical instruments and parts), 94 (furniture), and “Other”. “Other” encompassed the fewer than 1% of declarations outside these three chapters. Rates of species-country mismatch differed among the categories (chi-squared = 869.350, p < 0.000) (Fig. 5). Post-hoc grouping revealed no significant difference between chapter 92 and “other” (chi-squared = 1.415, p = 0.234), which had species-country mismatch rates of 5.604% and 7.045%, respectively. Chapter

92 was significantly lower than these two categories, with a species-country mismatch rate of 1.458% (chi-squared = 398.89, p < 0.000). Chapter 44 had a significantly higher rate than chapters 92 and “other,” with a species-country mismatch rate of 9.133% (chi-squared = 143.77, p < 0.000).

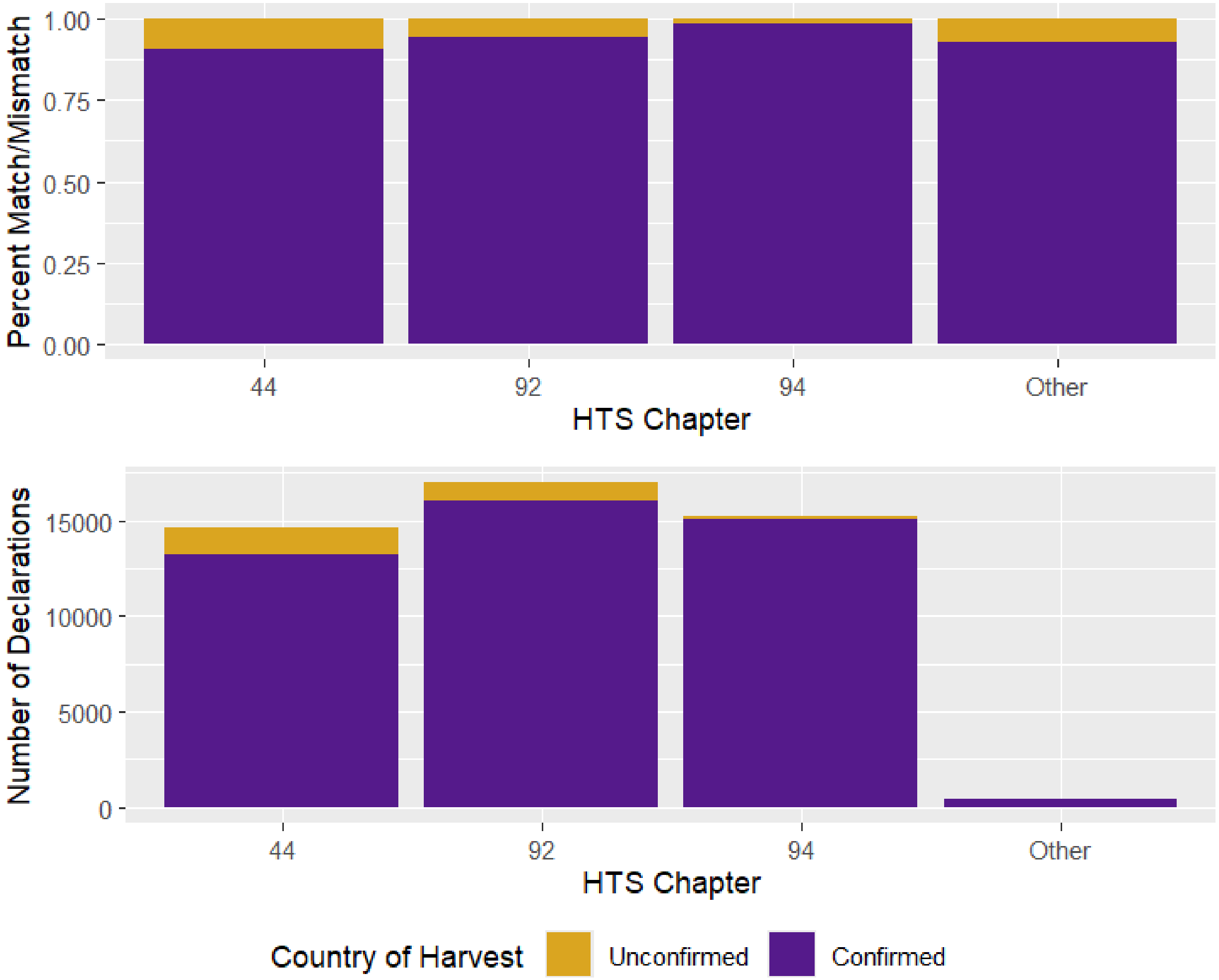

Figure 5: Rates of species-country mismatch across HTS chapters. Chapter 44 = wood and wood products, chapter 92 = musical instruments and parts, chapter 94 = furniture, etc. “Other” encompasses the 21 other chapters across which the remaining less than 1% of declarations were scattered.

Within chapter 44, the chapter with the highest rate of species-country mismatch, rates also varied among subheadings, from as low as 1.095% to as high as 33.121% (Fig. 6). Subheadings refer to different, more specific product types within chapter 44 (e.g., 4407 is for lumber/sawn wood). Rates were compared among all subheadings; those with fewer than ten declarations in a category were lumped into "Other" (4401, 4402, 4403, 4410, 4415, 4416, 4417). Chi-squared comparison among all ten categories was highly significant (chi-squared = 744.82, p < 0.000). Post-hoc testing supported seven distinct groups (see Table 5).

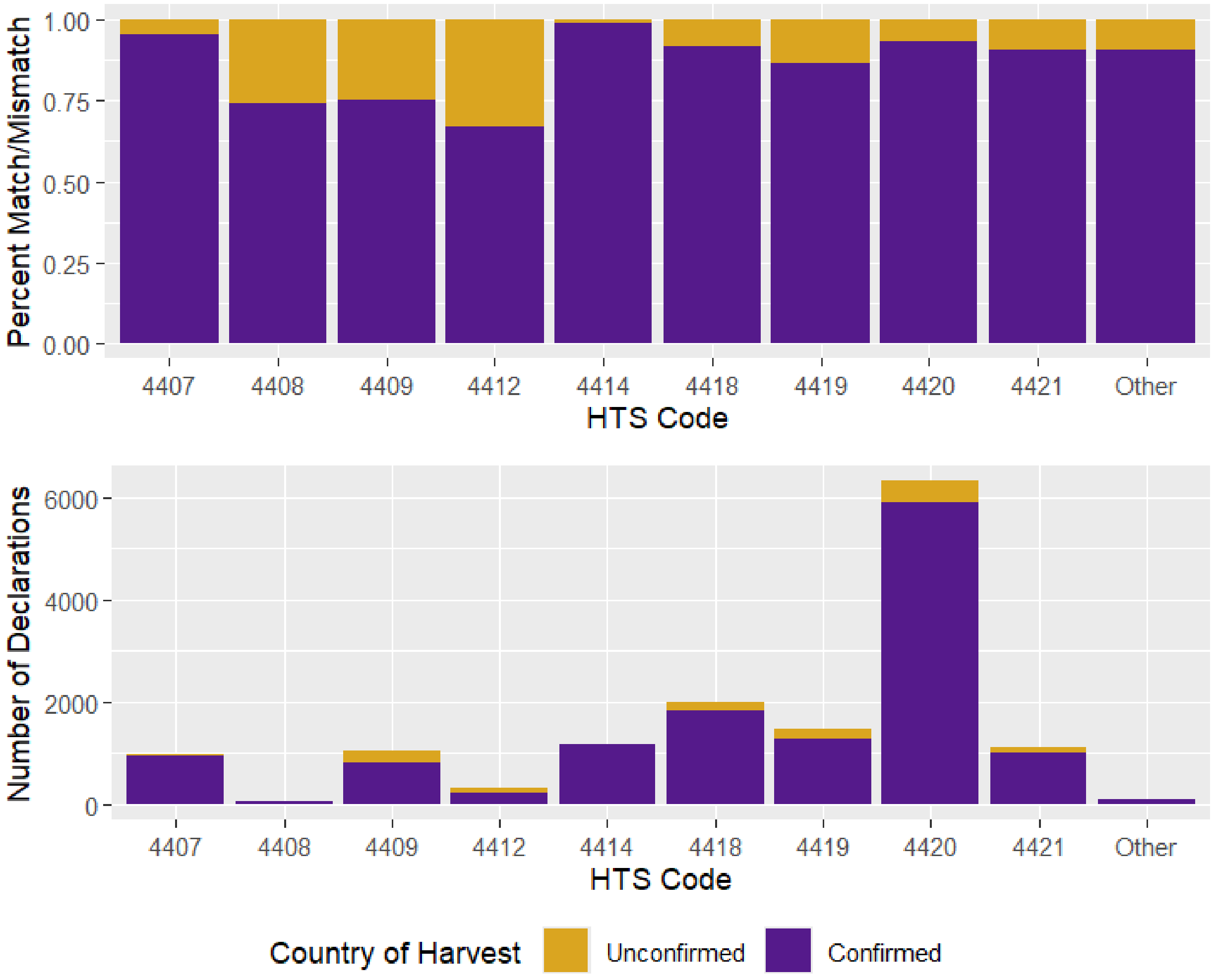

Figure 6: Rates of species-country mismatch across subheadings within chapter 44. "Other" includes all subheadings that contained fewer than ten declarations in either category. Post-hoc groupings and product descriptions are available in Table 5.

Group	**Species-Country Mismatch Rate**	**Product Description(s)**	**Post-hoc Test Results**
4414	1.095%	Wooden frames	4414 vs 4407: chi-sq = 24.907 p < 0.000
4407	4.694%	Lumber/sawn wood	4407 vs 4420: chi-sq = 5.236 p = 0.022
4420	6.677%	Marquetry, jewelry boxes, ornamental items	4420 vs 4418, 4421, Other: chi-sq = 4.296 p = 0.038
4418, 4421, Other	8.487%	Builders' joinery and shingles; All other miscellaneous	4418 vs 4421 vs Other: chi-sq = 1.094 p = 0.579 4418, 4421, Other vs 4419: chi-sq = 37.740 p < 0.000
4419	13.499%	Tableware and kitchenware	4419 vs 4408, 4409: chi-sq = 20.063 p < 0.000
4408, 4409	24.690%	Veneering; shaped wood	4408 vs 4409: chi-sq = 0.004 p = 0.949
4412	33.121%	Plywood	4412 vs 4408, 4409: chi-sq = 25.587 p < 0.000

Table 5: Post-hoc groupings of subheadings within chapter 44 by species-country mismatch rate.

Declarations in chapter 92 had lower rates of species-country mismatch than those in chapter 92, and they varied less widely among subheadings as well (Fig. 7). Within chapter 92, subheadings 9205 (wind instruments), 9208 (other musical instruments), and 9209 (parts and accessories) were grouped into the "Other" category due to having cell counts fewer than ten and were compared against the remaining four subheadings. Across all five groups, species-country mismatch rates were significantly different (chi-squared = 33.732, p <0.000), but these differences were less extreme than in chapter 44 (Fig. 6). Rates ranged from 3.579% for 9207 and 9.747% for the “Other” category. Post-hoc testing indicated just three groupings, with 9201, 9202, and 9206 not being significantly different from one another (chi-squared = 3.2971, p = 0.192). 9207 had a significantly lower species-country mismatch rate than this group (chi-squared = 16.236, p < 0.000), and the “Other” category was significantly higher than the middle group (chi-squared = 8.246, p = 0.004).

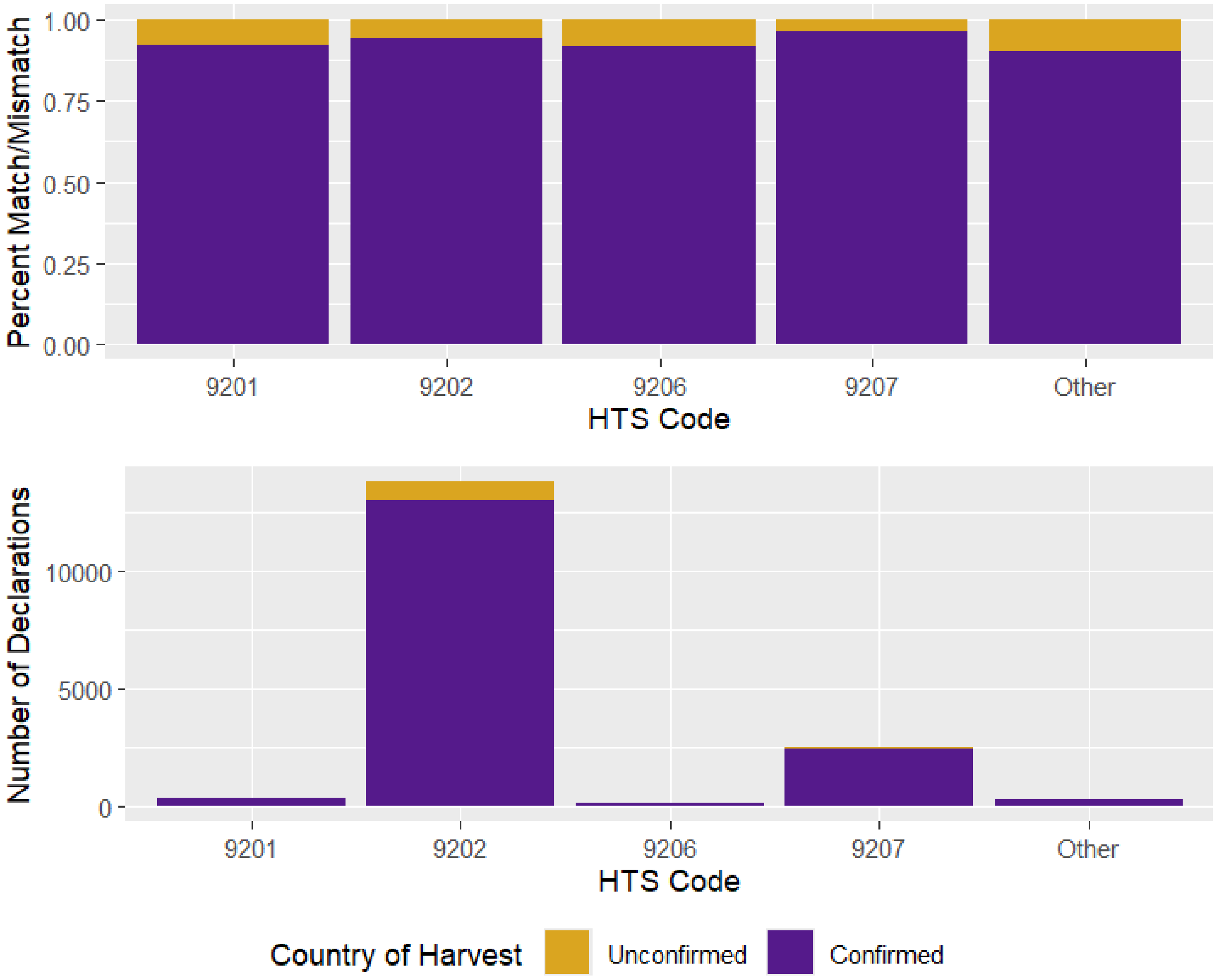

Figure 7: Rates of species-country mismatch across subheadings within chapter 92. 9201 = pianos, 9202 = other string instruments, 9206 = percussion, 9207 = electronically amplified instruments. “Other” includes all subheadings that contained fewer than ten declarations in either category.

Chapter 94 had the lowest rate of species-country mismatch and only three subheadings declared in the trade data (Fig. 8). Additionally, 9405 had only five total declarations and was therefore excluded from the chi-squared testing. Subheadings 9401 and 9403 had significantly different rates of species-country mismatch (chi-squared = 213.251, p < 0.000). No post-hoc testing was performed as the initial test was only 2x2.

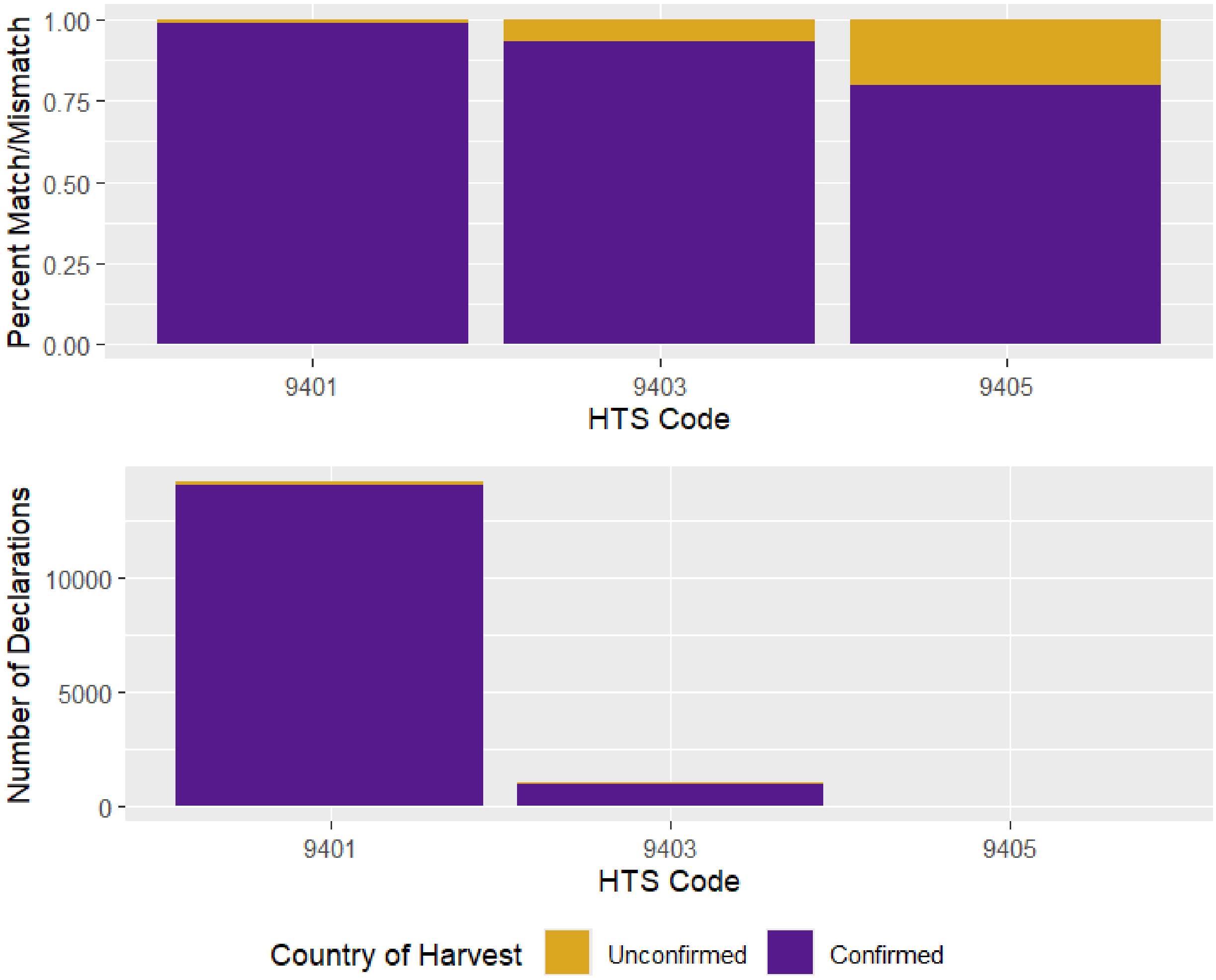

Figure 8: Rates of species-country mismatch across subheadings within chapter 94. 9401 = seats, 9403 = other furniture, 9405 = light fixtures.

3.5 Species-HTS Code Mismatch

Species-HTS code mismatch was analyzed for chapters 44 and 94 as chapter 92 does not contain material types in its product descriptions. Chapters outside these three were automatically mismatching, and very infrequently declared, and therefore also excluded. Within chapters 44 and 94, mismatching descriptions either specified a different type of wood, or in chapter 94, a material other than wood. 57.299% of these mismatching declarations were because the HTS description specified a different tropical wood (teak, meranti, *Cedrela*, sapelli, *Khaya*, *Tabebuia, Myroxylon balsamum, Shorea*, other tropical). However, only 3.138% of these mismatches were due to another wood commonly called “mahogany” (*Khaya, Myroxylon balsamum, Shorea,* meranti, sapelli) (Fig. 9).

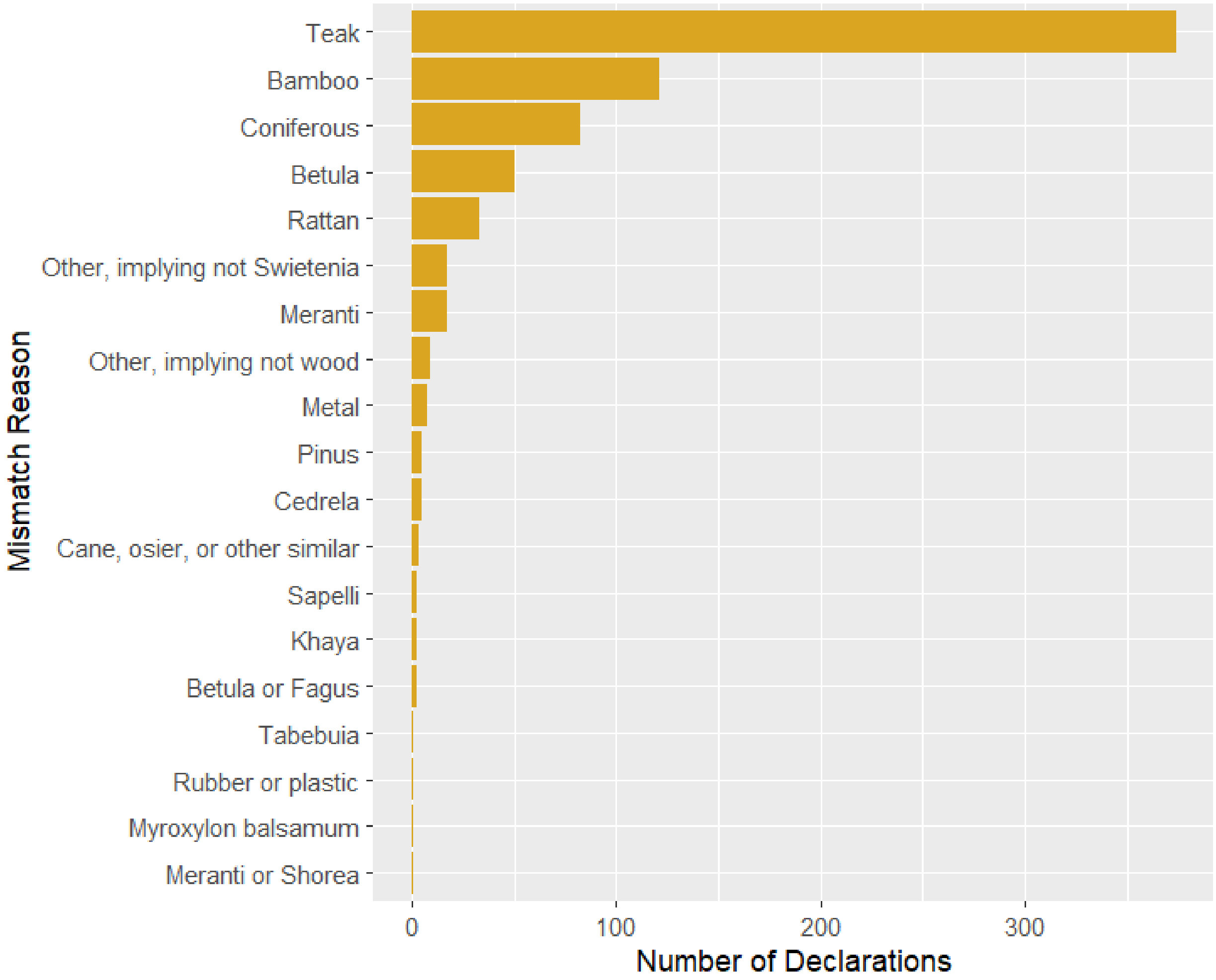

Figure 9: Counts of reasons for species-HTS mismatch in declarations of *Swietenia* spp., 2017-2023.

Within chapters 44 and 94, there were eight subheadings that contained at least one instance of species-HTS mismatch (Fig. 10). Rates of mismatch varied among these (chi-squared = 694.121, $p < 0.000$), with a broad range between the smallest (0.449%) and largest (37.838%) rates. Post-hoc testing supported five distinct groupings of subheadings with different mismatch rates. Detailed test results are in table 6.

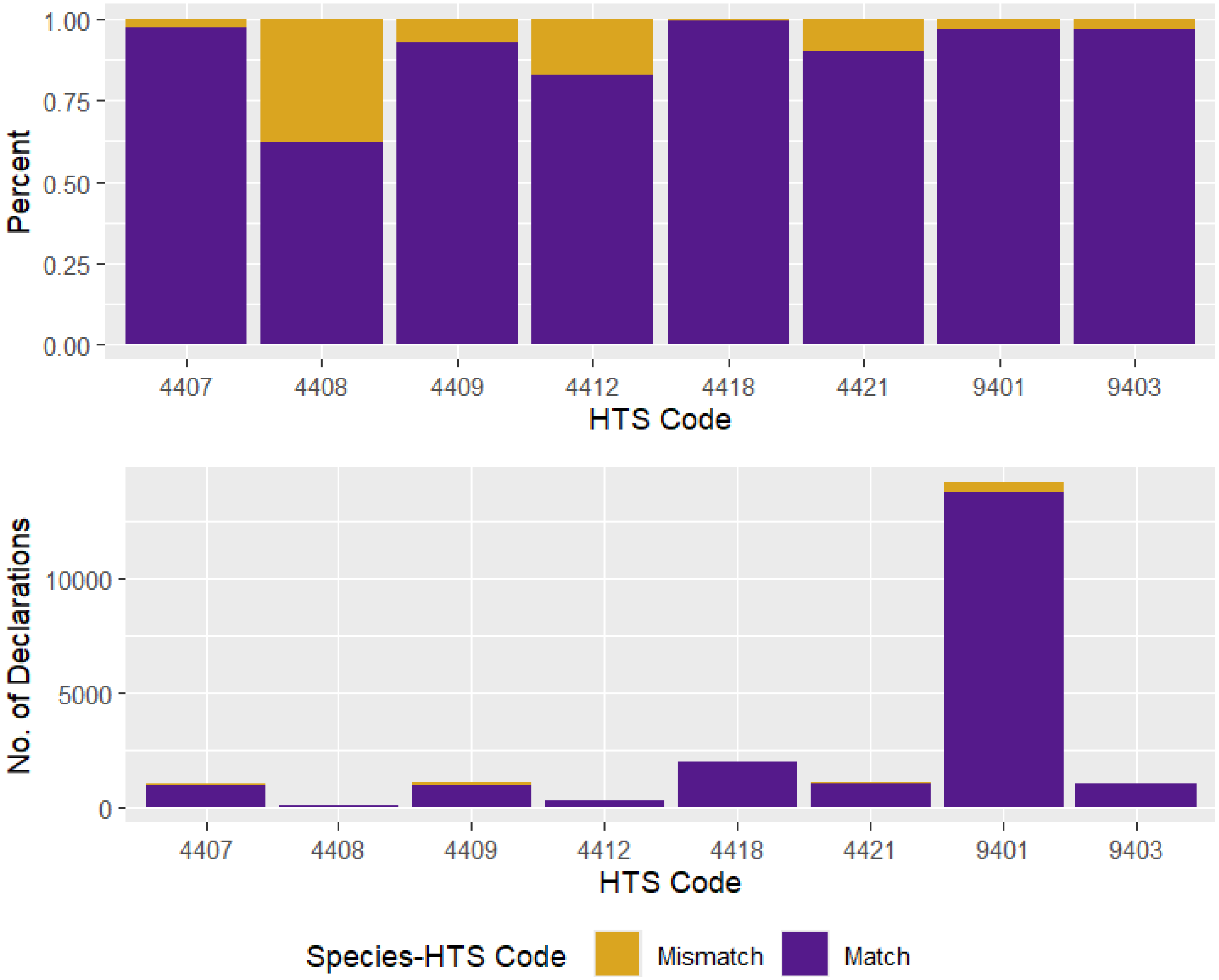

Figure 10: Rates of species-HTS code mismatch across subheadings within chapters 44 and 94. Subheadings with a rate of are 0% not included. Post-hoc groupings and product descriptions are available in Table 6.

Group	**Species-HTS Code Mismatch Rate**	**Product Description(s)**	**Post-hoc Test Results**
4418	0.449%	Builders' joinery and shingles	<u>4418 vs 4407, 9401, 9403</u>: chi-sq = 38.482 p < 0.000
4407, 9401, 9403	2.863%	Lumber/sawn wood; Seats; Other furniture	<u>4407 vs 9401 vs 9403</u>: chi-sq = 0.657 p = 0.720

Group	**Species-HTS Code Mismatch Rate**	**Product Description(s)**	**Post-hoc Test Results**
			4407, 9401, 9403 vs 4409, 4421: chi-sq = 198.04 p < 0.000
4409, 4421	9.536%	Shaped wood; All other miscellaneous	4409 vs 4421: chi-sq = 4.186 p = 0.048
4412	17.197%	Plywood	4409, 4421 vs 4412: chi-sq = 21.47 p < 0.000
4408	37.838%	Veneering	4412 vs 4408: chi-sq = 14.094 p < 0.000

Table 6: Post-hoc groupings of subheadings within chapter 44 and 94 by species-HTS code mismatch rate.

Across all of the declarations, there was not a significant correlation between species-country mismatch and species-HTS code mismatch (chi-squared = 0.269, p = 0.605). Even in subheadings that had high rates of both types of mismatch, such as 4408 and 4412, there were still very few declarations with both species-country mismatch and species-HTS mismatch.

4. Discussion

While previous species distribution modeling applications to international trade have focused on the risks of invasive species, this work demonstrates how SDM can assist in detecting import misdeclaration and risk of illegal trade. Detecting species-country mismatch is one key component of detecting misdeclaration, and accurate range information is critical for detecting species-country mismatch. But, accurate global range information is not always available from existing literature or databases, or may scattered and fragmented across sources. There were 167 unique species-country pairs in the *Swietenia* import data, and by combining existing range information with the SDM, I was able to reduce this to just 48 species-country pairs that needed to be researched individually. Additionally, five of these species-country pair searches yielded evidence that the declared species was present in the declared country.

The main drawback to using model predictions to analyze other data is the risk of incorrect predictions. When assessing the climatic suitability of all the areas where a species may or may not be present, it is expected that many predictions will be “false” positives, as the area may be climatically suitable for the species, but the species may not have, for example, geographic access to the area. However, there were four instances of false negatives in the SDM predictions, where a country with known *Swietenia* presence was predicted to be unsuitable for the species. All four of these occurred in island countries, where room for error is small, as an island may only be the size of a handful of raster cells. Additionally, three of these were Pacific Island nations, where weather station data is sparse, and WorldClim relies more heavily on interpolation (Fick and Hijmans 2017). Finally, three of these four were also for *S. mahagoni*, the species with the fewest number of available occurrence data points to train the model. These all underscore the necessity of good quality data for building a good quality model. Despite these drawbacks, the SDM predictions still performed well overall and were able to correctly predict both previously known and previously unknown range countries for *Swietenia*.

By categorizing import declarations by species-country mismatch, species-country suitability, and species-HTS mismatch, I was able to find broad-scale evidence of misdeclaration and potential illegal trade in the *Swietenia* import data. Declarations with species-country mismatch were frequently declared with countries of harvest containing native *Swietenia* lookalikes (Fig.

4), significantly more frequently than declarations without species-country mismatch. This indicates the possibility that these lookalikes are being passed off as *Swietenia*. Chapter 44 had the highest rates of species-country mismatch, particularly at the subheading level (Figs. 5-6). Some chapter 44 subheadings had mismatch rates higher than 20%, while no other chapter had a subheading above 10% (min. 10 declarations). One possible explanation for species-country 6mismatch is confusion between country of harvest and country of origin, which may be different if the wood was harvested in one country and the product was manufactured in another (Colbourn and Swegle 2011). However, the smaller rates of species-country mismatch in musical instrument and furniture product categories than in rawer wood product categories such as 4408 and 4409 indicate that innocent supply chain mistakes are not the main driver of species-country mismatch in the *Swietenia* import data. Finally, species-country mismatch and species-HTS code mismatch were not significantly associated with one another, meaning that declarations with one type of mismatch were not necessarily more likely to have the other. This indicates that these two types of mismatch are coming from different sources, meaning multiple potential streams of illegal wood are entering the United States.

By identifying the most frequently mismatching subheadings and the most frequently declared mismatching countries and HTS codes, and investigating these further, I was able to identify multiple potential methods of misdeclaration occurring in the trade data. The first is the aforementioned possibility that lookalike species are being declared as *Swietenia* to obscure the true species if it is of illegal origin. This occurred in both declarations with species-country mismatch and species-HTS code mismatch. There were also indicators of misdeclaration for financial incentives, such as to avoid paying duties. Finally, some patterns of misdeclaration do have a potential legal or innocent explanation but may also represent illegal activity.

Cameroon was the most frequently declared country of harvest in declarations with species-country mismatch (Fig. 4). Within subheading 4409, which had the third-highest rate of species-country mismatch (Fig. 6), Cameroon was declared in over 90% of the misdeclarations. Cameroon was also frequently declared for subheading 9202, which had a relatively low rate but a high volume of country-species mismatch (Fig. 7), as it was one of the most frequently declared subheadings for *Swietenia* overall. Cameroon is home to several *Swietenia* lookalikes, including *Entandrophragma angolense, E. candollei, E. cylindricum, E. utile, Khaya anthotheca, K. ivorensis,* and *K. senegalensis* (POWO 2024). *Khaya* and *Entandrophragma* are both genera whose timber is sought after and valued on the international market (UNEP-WCMC 2022; Kasongo Yakusu et al. 2021). Despite efforts to curb illegal logging in Cameroon, it persists, both through individual loggers and abuse of logging permits and concessions by companies (Frankline et al. 2020). *E. candollei* and *E. cylindricum* are two of the most logged species in Cameroon, and while Cameroon does not export much wood directly to the United States (Ngaba et al. 2023), products made of wood harvested in Cameroon may still come to the US via other countries. As *Swietenia* spp. are entirely absent from Cameroon, these declarations must contain some form of misdeclaration, either species or country of harvest. Given the presence of *Swietenia* lookalikes and high rates of illegal logging in Cameroon, these imports may actually be *Entandrophragma* or *Khaya* species.

The next-most frequently declared mismatching country of harvest was Ghana (Fig. 4). While there is evidence of both *S. macrophylla* and *S. mahagoni* presence in Ghana, they are limited to being either ornamental or experimental trees and are not part of the timber industry (Darko et al. 2022; Edusei et al. 2021). Ghana was the most frequently declared mismatching country of harvest in subheadings 4412 and 4420. Eight Swietenia lookalike species are native to Ghana, four in genus *Entandrophragma* and four in *Khaya* (POWO 2024). Illegal logging of *E. candollei, E. angolense, E. cylindricum, E. utile, K. ivorensis*, and *Khaya* spp. has been documented in Ghana throughout the 2000s and 2010s (Boakye 2015; Gyamfi, Derkyi, and Brobbey 2021; Amoah et al. 2019). While regulations against illegal logging exist in Ghana, enforcement is often not carried out for a variety of reasons, such as corruption and lack of resources (Boakye 2020). These declarations may, therefore, represent another instance of illegally logged *Khaya* and/or *Entandrophragma* entering the US disguised as *Swietenia*. However, it is worth noting that in subheading 4412, the HTS codes declared with a country of harvest of Ghana refer to "mahogany," meaning either *Swietenia* or *Khaya*, and may represent a confusion between vernacular and scientific names rather than intentional misdeclaration.

Guatemala was the third-most declared mismatching country of harvest (Fig. 4). All of these mismatching declarations had species *S. mahagoni*, as *S. macrophylla* and *S. humilis* are native to Guatemala (Lamb 1966). However, my species-country pair searches revealed that *S. mahagoni* is in fact present in Guatemala. The Spatial Database of Planted Trees (SDPT) v2.0 contains registered timber plantation data from the Guatemala Forestry Incentives Database (Richter et al. 2024). In this registry are multiple mixed-species timber plantations in Guatemala growing *S. mahagoni*. These declarations are then not an actual instance of species-country mismatch, but rather represent the lack of distributional data on *Swietenia* spp. and the importance of planted forest data in examining import declarations.

In terms of species-HTS code mismatch, the second-most mismatching product category was 4412 (plywood) (Fig. 10). Within the declarations under 4412, over 90% of the mismatch came from declaring an HTS code that referred to *Betula* spp. (birch) on the face ply. While most plywood is subject to a rate of duty under the US tariff schedule, for example 8% for plywood with a face ply of mahogany, the one exception is plywood with face ply of *Betula*, which is free (USITC 2023). This creates an obvious financial incentive for importers to declare their plywood products as having a face ply of *Betula*, regardless of the actual species. These mismatches are then likely a result of misdeclaration for tax evasion rather than trying to obscure the illegally logged origin of a product.

Subheading 4408 (veneering) had the highest rate of species-HTS mismatch (Fig. 10), and the majority (60.714%) of this misdeclaration came from HTS codes that specify “dark red meranti, light red meranti, and meranti bakau” (USITC 2023). “Meranti” is a common name for the genus *Shorea*, which is native to south and southeast Asia, and “red meranti” refers to a subset of these species that produce reddish wood (Tsumura et al. 2011). Although there are no CITES-listed *Shorea* species, many of the “red meranti” species are on the IUCN Red List, including *S. rotundifolia*, which is critically endangered (IUCN 2023). These threatened red meranti species are largely native to Malaysia and Indonesia, where they are known to be illegally harvested (Tsumura et al. 2011; Ng et al. 2022; Rangkuti et al. 2022; Purwaningsih and Kintamani 2018). India was the declared country of harvest for all declarations with a meranti HTS code under subheading 4408. There are *Shorea* species native to India, such as *Shorea robusta*, which is common and a key species in India’s timber industry (Nandy, Ghosh, and Singh 2021).

However, according to Trade Data Monitor (TDM), India also imported large volumes of red meranti logs (440341) and red meranti sawn wood (440725) from 2017-2023, primarily from Malaysia (Trade Data Monitor LLC). Without knowing whether these declared products were *Shorea robusta*, some more vulnerable *Shorea* species, or *Swietenia*, it is difficult to say which form of misdeclaration this represents or how it occurred. Still, since all 4408 products are free to import to the US regardless of species (USITC 2023), the reason for misdeclaration is not a financial one.

The number one cause of species-HTS mismatch in the *Swietenia* trade data was teak (Fig. 9), which occurred exclusively in subheading 9401 (seats). This subheading had a relatively low mismatch rate, but this is because it was also one of the most frequently declared subheadings overall. Again, all rates of duty across 9401 are free (USITC 2023), so there is no financial incentive to misdeclare product types. The majority of these misdeclarations were declared from Indonesia, although Indonesia was also the most frequently declared country of harvest for all 9401 products (and indeed all *Swietenia* products), HTS match or no match. Teak (*Tectona grandis*) is a major timber plantation species throughout the global tropics, but Indonesia is estimated to have the second-most teak plantation area in the world, after India (Midgley et al. 2015). Despite the teak in Indonesia being grown on plantations, it is still at risk of illegal logging, where the trees are stolen from plantations for financial reasons (Lee et al. 2018). Again, without knowing the true species of the declared products, it is difficult to ascertain the mechanism and incentive behind this form of misdeclaration.

Throughout US import declarations of *Swietenia* spp. products from 2017-2023, there is evidence for potential misdeclaration of species, product type, and country of harvest, all of which are illegal under the US Lacey Act Amendment of 2008 (16 U.S.C. §§ 3371-3378). While intentional misdeclaration is a known method for importing illegal wood, the extent to which it occurs, and for which species, remains largely unknown (Wiedenhoeft et al. 2019). From these import data, there is evidence that valuable, at-risk tropical African and Asian woods may be entering the US disguised as *Swietenia*, which is not native to these continents. Previous research on wood misidentification revealed instances of products in the US sold as *Swietenia* that were in fact *Shorea* or *Entandrophragma* species (Wiedenhoeft et al. 2019). This corroborates the evidence in the Lacey import data that showed declarations of *Swietenia* from *Entandrophragma* range states and under HTS codes for *Shorea* spp. Without access to the shipments themselves and their accompanying documents, it is impossible to say what the true species of these imports were, or whether they were logged illegally. However, due to the occurrence of species-country and species-HTS mismatch, there is at minimum some form misdeclaration occurring, whether intentional or unintentional. There are likely to be illegally logged wood products that do not result in species-country mismatch in import declarations. Still, this work represents a starting point into the as yet unknown prevalence of misdeclared and/or illegally-sourced imported wood on the US market.

Clearly, more research is needed to identify where and how illegally logged wood is entering the US market, especially studies investigating the imported products themselves. Trade data analysis can assist in this work by identifying which product types, species, and countries of harvest contain patterns of suspicious activity and should be prioritized for further investigation. In particular, species distribution modeling can be a key tool in correctly identifying species-country mismatch in the absence of reliable or easily accessible country-level range data on species. The potential applications of such analysis are not limited to timber species or to the Lacey Act. With several countries having adopted similar import laws and thousands of endangered species in trade, there are a multitude of trade flows that could be inspected for similar patterns of risk indicators.

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Appendix I: *Swietenia* Range Country Lists

Country Name	Lamb 1966	Mayhew and Newton 1998	Kew POWO	IUCN	GloNAF	GBIF
Antigua and Barbuda		Introduced	Introduced[1]			
Australia		Introduced				Present
Bangladesh		Introduced	Introduced			
Bolivia (Pluri-national State of)	Native	Native	Native	Resident		Present
Brazil	Native	Native	Native	Resident	Naturalized	Present
Belize	Native	Native	Native	Resident		Present
China						Present
Colombia	Native	Native	Native	Resident		Present
Costa Rica	Native	Native	Native	Resident		Present
Cuba		Introduced	Introduced		Naturalized	Present
Dominica			Introduced[2]		Alien	Present
Dominican Republic		Introduced	Introduced			
Ecuador	Native	Native	Native	Resident		Present
Fiji		Introduced			Alien	
Micronesia (Federated States of)			Introduced[3]			Present
Grenada		Introduced	Introduced[2]		Alien	
French Guiana		Introduced	Introduced	Resident		Present
Guadeloupe		Introduced	Introduced[1]			Present
Guatemala	Native	Native	Native	Resident		Present
Guam		Introduced	Introduced[4]		Alien	Present
Guyana		Introduced		Uncertain		
Honduras	Native	Native	Native	Resident		Present
Haiti		Introduced	Introduced			
Indonesia		Introduced	Introduced			Present
India		Introduced	Introduced			Present
Jamaica		Introduced	Introduced			
Comoros			Introduced			
Cayman Islands			Introduced		Alien	

Country Name	Lamb 1966	Mayhew and Newton 1998	Kew POWO	IUCN	GloNAF	GBIF
Lao People's Democratic Republic			Introduced		Alien	
Saint Lucia		Introduced	Introduced[2]			
Sri Lanka		Introduced				Present
Myanmar		Introduced				Present
Northern Mariana Islands			Introduced[4]		Alien	
Martinique		Introduced	Introduced[2]		Alien	Present
Montserrat		Introduced	Introduced[1]		Naturalized	
Mauritius		Introduced				
Mexico	Native	Native	Native	Resident		Present
Malaysia		Introduced	Introduced[5]			Present
New Caledonia						Present
Nicaragua	Native	Native	Native	Resident		Present
Panama	Native	Native	Native	Resident		Present
Peru	Native	Native	Native	Resident		Present
French Polynesia						Present
Philippines		Introduced			Naturalized	Present
Puerto Rico		Introduced	Introduced		Naturalized	Present
Palau			Introduced[3]			Present
Solomon Islands		Introduced	Introduced			
Seychelles		Introduced	Introduced			Present
Singapore						Present
Suriname		Introduced				
El Salvador			Introduced	Resident		Present
Thailand		Introduced	Introduced		Naturalized	Present
Tonga		Introduced				
Trinidad and Tobago		Introduced	Introduced			Present
Taiwan, Province of China		Introduced	Introduced		Naturalized	Present

Country Name	Lamb 1966	Mayhew and Newton 1998	Kew POWO	IUCN	GloNAF	GBIF
Tanzania, United Republic of		Introduced				Present
United States of America		Introduced			Naturalized	Present
Saint Vincent and the Grenadines			Introduced[2]		Alien	
Venezuela (Bolivarian Republic of)	Native	Native	Introduced	Resident		Present
Virgin Islands (U.S.)		Introduced	Introduced[1]		Naturalized	
Viet Nam			Introduced			Present
Vanuatu		Introduced	Introduced			
Samoa		Introduced				

Table A1.1: Range country lists for *S. macrophylla*. Footnotes indicate verbatim locality where presence inferred from broader geographic area. 1: Leeward Islands, 2: Windward Islands, 3: Caroline Islands, 4: Marianas, 5: Borneo.

Country Name	Lamb 1966	Kew POWO	IUCN	GloNAF	GBIF
Antigua and Barbuda		Introduced[1]	Introduced	Alien	Present
Anguilla		Introduced[1]	Introduced	Alien	Present
Barbados			Introduced	Alien	Present
Bangladesh		Introduced			
Saint Barthélemy		Introduced[1]	Resident	Alien	Present
Bermuda					Present
Bolivia (Plurinational State of)					Present
Bonaire, Sint Eustatius and Saba		Introduced[1]			Present
Brazil					Present
Bahamas	Native	Native	Resident		Present
China		Introduced			Present
Colombia					Present
Cuba	Native	Native	Resident		Present

Country Name	**Lamb 1966**	**Kew POWO**	**IUCN**	**GloNAF**	**GBIF**
Curaçao					Present
Dominica		Introduced[2]	Introduced	Alien	Present
Dominican Republic	Native	Native	Resident		Present
Micronesia (Federated States of)		Introduced[3]			
Grenada		Introduced[2]		Alien	Present
Guadeloupe		Introduced[1]	Introduced		Present
Guam		Introduced		Alien	
Guyana					Present
Honduras					Present
Haiti	Native	Native	Resident		Present
Indonesia		Introduced			Present
India		Introduced		Naturalized	Present
Jamaica	Native	Native	Resident		Present
Japan					Present
Kenya					Present
Saint Kitts and Nevis		Introduced	Introduced		Present
Cayman Islands	Native	Native	Resident		Present
Lao People's Democratic Republic		Introduced		Alien	
Saint Lucia		Introduced[2]	Introduced	Alien	
Saint Martin (French part)		Introduced	Introduced		Present
Northern Mariana Islands		Introduced		Alien	
Martinique		Introduced[2]	Introduced	Alien	Present
Montserrat		Introduced[1]	Introduced		Present
Mauritius					Present
Mexico					Present
Malaysia					Present
Mozambique				Alien	
Nigeria					Present
Panama					Present
Peru					Present
French Polynesia					Present
Philippines				Naturalized	Present
Puerto Rico		Introduced			Present
Palau		Introduced[3]			
Réunion		Introduced			Present
Seychelles					Present
Suriname					Present

Country Name	Lamb 1966	Kew POWO	IUCN	GloNAF	GBIF
El Salvador					Present
Sint Maarten (Dutch part)		Introduced			Present
Turks and Caicos Islands	Native	Native	Uncertain		Present
Thailand		Introduced			Present
Trinidad and Tobago		Introduced			
Taiwan, Province of China		Introduced		Naturalized	Present
Tanzania, United Republic of					Present
United States of America	Native	Native	Resident		Present
Saint Vincent and the Grenadines		Introduced[2]	Introduced	Alien	
Venezuela (Bolivarian Republic of)		Introduced			Present
Virgin Islands (British)		Introduced[1]		Alien	
Virgin Islands (U.S.)		Introduced[1]			Present
Mayotte					Present

Table A1.2: Range country lists for S. *mahagoni*. Footnotes indicate verbatim locality where presence inferred from broader geographic area. 1: Leeward Islands, 2: Windward Islands, 3: Caroline Islands.

Country Name	Lamb 1966	Kew POWO	IUCN	GBIF
Costa Rica	Native	Native	Resident	Present
El Salvador	Native	Native	Resident	Present
Guatemala	Native	Native	Resident	Present
Honduras	Native	Native	Resident	Present
Mexico	Native	Native	Resident	Present
Nicaragua	Native	Native	Resident	Present
Belize			Resident	
India				Present
Mauritius				Present
United States of America				Present

Table A1.3: Range country lists for S. *humilis*.

Source Name	**Citations**	**Methods/Notes**
Lamb 1966	Lamb, F. Bruce. 1966. *Mahogany of Tropical America: Its Ecology and Management*. Ann Arbor, MI: The University of Michigan Press.	
Mayhew and Newton 1998	Mayhew, J. E., and A. C. Newton. 1998. *The Silviculture of Mahogany*. Wallingford, UK: CABI Publishing.	
Kew POWO	POWO. 2024. "Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew." http://www.plantsoftheworldonline.org/ (accessed April 8, 2024).	Localities taken from individual species pages for each *Swietenia* species.
IUCN	IUCN. 2023. The IUCN Red List of Threatened Species. Version 2023-1. https://www.iucnredlist.org (accessed April 15, 2024).	Localities taken from individual species pages for each *Swietenia* species. Verbatim terms (introduced, resident, uncertain) recorded.
GloNAF	van Kleunen, Mark, Petr Pyšek, Wayne Dawson, Franz Essl, Holger Kreft, Jan Pergl, Patrick Weigelt, et al. 2019. "The Global Naturalized Alien Flora (GloNAF) Database." *Ecology* 100 (1): e02542. https://doi.org/10.1002/ecy.2542.	Localities taken from Plant View page for *S. macrophylla* and *S. mahagoni*. No information available for *S. humilis*. Verbatim terms (naturalized, alien) recorded.
GBIF	GBIF: The Global Biodiversity Information Facility. 2024. *What is GBIF?*. https://www.gbif.org/what-is-gbif (accessed April 15, 2024). Chamberlain, S., V. Barve, D. Mcglinn, D. Oldoni, P. Desmet, L. Geffert, and K. Ram. 2024. *rgbif: Interface to the Global Biodiversity Information Facility API*. R package version 3.7.8, https://CRAN.R-project.org/package=rgbif.	Accessed via R package *rgbif:* occ_data(scientificName = "Swietenia_[species]", hasGeospatialIssue = FALSE, hasCoordinate = TRUE, limit = 100000). All countries in dataset recorded as "Present." Pulled June 2023.

Table A1.4: Detailed citations and methods for each source listed in tables A1:1-3 above.

Appendix II: OpenStreetMap Data Sources

	City Data	**Road Data**	**Park Data**
OpenStreetMap Keys and Values	**place=city, place=town, place=village, place=hamlet**	**highway=motorway, highway=trunk, highway=primary, highway=secondary, highway=tertiary**	**boundary=national_park, leisure=nature_reserve, boundary=protected_area**
Data Type	**Point**	**Line**	**Polygon**
Sources by Country:			
Taiwan	Geofabrik	Geofabrik	Overpass Turbo
Indonesia	Geofabrik	Geofabrik	Overpass Turbo
Florida	Geofabrik	Geofabrik	Overpass Turbo
Hawaii	Geofabrik	Geofabrik	Overpass Turbo
El Salvador	Geofabrik	Geofabrik	Overpass Turbo
Seychelles	Geofabrik	Geofabrik	Overpass Turbo
Colombia	Geofabrik	Geofabrik	Overpass Turbo
Sri Lanka	Geofabrik	Geofabrik	Overpass Turbo
Martinique	Humanitarian OpenStreetMap Team	Humanitarian OpenStreetMap Team	Overpass Turbo
Malaysia	Geofabrik	Geofabrik	Overpass Turbo
Australia (Queensland only)	Geofabrik	Geofabrik	Overpass Turbo
Guatemala	Geofabrik	Geofabrik	Overpass Turbo
Nicaragua	Humanitarian OpenStreetMap Team	Humanitarian OpenStreetMap Team	Overpass Turbo
Dominican Republic	Geofabrik	Geofabrik	Overpass Turbo
Puerto Rico	Geofabrik	Geofabrik	Overpass Turbo
Curacao	Humanitarian OpenStreetMap Team	Humanitarian OpenStreetMap Team	Overpass Turbo
Bahamas	Geofabrik	Geofabrik	Overpass Turbo
Vietnam	Geofabrik	Geofabrik	Overpass Turbo
India	Geofabrik	Geofabrik	Overpass Turbo
Singapore	Geofabrik	Geofabrik	Overpass Turbo
China	Geofabrik	Geofabrik	Overpass Turbo
Guadeloupe	Geofabrik	Geofabrik	Overpass Turbo
Myanmar	Geofabrik	Geofabrik	Overpass Turbo
Costa Rica	Geofabrik	Geofabrik	Overpass Turbo

	City Data	**Road Data**	**Park Data**
OpenStreetMap Keys and Values	**place=city, place=town, place=village, place=hamlet**	**highway=motorway, highway=trunk, highway=primary, highway=secondary, highway=tertiary**	**boundary=national_park, leisure=nature_reserve, boundary=protected_area**
Data Type	**Point**	**Line**	**Polygon**
Sources by Country:			
Mexico	Geofabrik	Geofabrik	Overpass Turbo
Bolivia	Geofabrik	Geofabrik	Overpass Turbo
Belize	Geofabrik	Geofabrik	Overpass Turbo
Honduras	Geofabrik	Geofabrik	Overpass Turbo
Panama	Geofabrik	Geofabrik	Overpass Turbo
Brazil	Geofabrik	Geofabrik	Overpass Turbo
Thailand	Geofabrik	Geofabrik	Overpass Turbo
Cuba	Geofabrik	Geofabrik	Overpass Turbo
Bonaire, Sint Eustatius, and Saba	Humanitarian OpenStreetMap Team	Humanitarian OpenStreetMap Team	Overpass Turbo
Jamaica	Geofabrik	Geofabrik	Overpass Turbo
United States (Hawaii and Florida only)	Geofabrik	Geofabrik	Overpass Turbo

Table A2.1: Sources for OpenStreetMap data. Only features that matched the listed key-value pairs and data type were collected for each region. Geofabrik data were downloaded as country- or state-level extracts from http://download.geofabrik.de/ and then filtered by key-value pair and data type. Humanitarian OpenStreetMap Team (HOT) data were downloaded from the HOT Export Tool (https://export.hotosm.org/v3/) by specifying the relevant area boundary, key-value pairs, and data type. Overpass Turbo data were downloaded via the Overpass Turbo API (https://overpass-turbo.eu/), using queries specifying boundary, key-value pairs, and data types. All map data copyright OpenStreetMap contributors (https://www.openstreetmap.org/).

Appendix III: AUC Values for All Candidate Models

Model	**Plantation Test Dataset**			**Country Test Dataset**			**Mean**
	S. macrophylla	*S. mahagoni*	*S. humilis*	*S. macrophylla*	*S. mahagoni*	*S. humilis*	
1.1	0.820	0.957	0.886	0.758	0.812	0.812	0.841
1.2	0.827	0.975	0.884	0.827	0.743	0.813	0.845
1.3	0.827	0.911	0.876	0.827	0.841	0.802	0.847
2.1	0.806	0.866	0.889	0.813	0.865	0.810	0.841
2.2	0.820	0.907	0.887	0.825	0.850	0.807	0.849
2.3	0.823	0.867	0.867	0.838	0.870	0.794	0.841

Table A3.1: Area under the curve (AUC) values for all candidate models tested. Plantation data came from the Spatial Database of Planted Trees v2.0 (Richter et al. 2023) and consisted of known *Swietenia* plantation polygons located in Mexico and Guatemala. Country data were countries with known presence of *Swietenia* spp. but no occurrence data available for model training data.

	1.1	**1.2**	**1.3**	**2.1**	**2.2**	**2.3**
bio1	x			x		
bio5	x	x	x	x	x	x
bio6	x	x	x	x	x	x
bio12	x	x		x	x	
bio13	x	x	x	x	x	x
bio1^2	x			x		
bio5^2	x	x		x	x	x
bio6^2	x	x	x	x	x	x
bio12^2	x	x	x	x	x	
bio13^2	x	x	x	x	x	x
PET	x	x				
PET x bio12	x	x	x			
AI				x	x	x
dry season length	x	x	x	x	x	x

Table A3.2: Variables included in each candidate model. The bio variables refer to the Bioclim dataset from WorldClim (Fick and Hijmans 2017). Bio1 = annual mean temperature, bio5 = maximum temperature of the warmest month, bio6 = minimum temperature of coldest month, bio12 = annual precipitation, bio13 = precipitation of wettest month; PET = potential evapotranspiration, AI = aridity index.

Appendix IV: All Unconfirmed-Suitable Species-Country Pairs

Country	Species	Present	Source
Cameroon	*Swietenia macrophylla*	0	
Papua New Guinea	*Swietenia macrophylla*	1	Bevacqua, Robert F., Jonae N. Samaya, and Ross H. Miller. May 2021. *Mahogany in Micronesia.* https://www.uog.edu/_resources/files/wptrc/Mahogany_Final.pdf (accessed July 4, 2024). Dobunaba, J. and T. Kosi. 2001. "*Hypsipyla* Shoot Borers of Meliaceae in Papua New Guinea." In *Hypsipyla Shoot Borers in Meliaceae. Proceedings of an International Workshop, Kandy, Sri Lanka 20-23 August 1996*, edited by R. B. Floyd and C. Hauxwell, 33-36. Canberra: Australian Centre for International Agricultural Research.
Kenya	*Swietenia macrophylla*	0	
Ethiopia	*Swietenia macrophylla*	0	
Uruguay	*Swietenia macrophylla*	0	
Gabon	*Swietenia macrophylla*	0	
Angola	*Swietenia macrophylla*	0	
South Africa	*Swietenia macrophylla*	0	
Congo, Democratic Republic of	*Swietenia macrophylla*	0	
Nigeria	*Swietenia macrophylla*	0	
Cambodia	*Swietenia macrophylla*	0	
Congo	*Swietenia macrophylla*	0	
Ghana	*Swietenia macrophylla*	1	Darko, C. B., E. Opuni-Frimpong, S. A. Owusu, B. Kyere, and A. J. Storer. 2022. “Sustainability of Mahogany Production in Plantations: Does Resource Availability Influence Susceptibility of Young Mahogany Plantation Stands to Hypsipyla Robusta Infestation?” *International Journal of Forestry*

Country	Species	Present	Source
			Research 2022 (1): 5588184. https://doi.org/10.1155/2022/5588184.
Hong Kong	*Swietenia macrophylla*	0	
Central African Republic	*Swietenia macrophylla*	0	
Cote D`Ivoire	*Swietenia macrophylla*	0	
Japan	*Swietenia macrophylla*	0	
Madagascar	*Swietenia macrophylla*	0	
Bahamas	*Swietenia macrophylla*	0	
Liberia	*Swietenia macrophylla*	0	
Myanmar	*Swietenia mahagoni*	0	
Guatemala	*Swietenia mahagoni*	1	Richter, Jessica, Elizabeth Goldman, Nancy Harris, David Gibbs, Melissa Rose, Suzanne Peyer, Sarah Richardson, and Hemalatha Velappan. 2024. *Spatial Database of Planted Trees (SDPT Version 2.0)*. World Resources Institute. https://doi.org/10.46830/writn.23.00073.
South Africa	*Swietenia mahagoni*	0	
Ghana	*Swietenia mahagoni*	1	Edusei, G., J. B. Tandoh, R. Edziah, O. Gyampo, and H. Ahiamadjie. 2021. “Chronological Study of Metallic Pollution Using Tree Rings at Tema Industrial Area.” *Pollution* 7 (1). https://doi.org/10.22059/poll.2020.306742.855.
Fiji	*Swietenia mahagoni*	1	Franklin, Janet, Gunnar Keppel, and W. Arthur Whistler. 2008. “The Vegetation and Flora of Lakeba, Nayau and Aiwa Islands, Central Lau Group, Fiji.” *Micronesica* 40 (1/2): 169–225.
Italy	*Swietenia mahagoni*	0	
Nicaragua	*Swietenia mahagoni*	0	
Viet Nam	*Swietenia mahagoni*	1	Tuan, Nguyen Thanh, Diego I. Rodríguez-Hernández, Vu Cong Tuan, Nguyen Van Quy, Maxwell C. Obiakara, and Joshua Hufton. 2022. “Effects of Tree Diversity and Stand

Country	Species	Present	Source
			Structure on Above-Ground Carbon Storage in Evergreen Broad-Leaved and Deciduous Forests in Southeast Vietnam.” *Dendrobiology* 88 (September): 38–55. https://doi.org/10.12657/denbio.088.003.
Cameroon	*Swietenia mahagoni*	0	
Sri Lanka	*Swietenia mahagoni*	1	Tilakaratna, D. 2001. "Hypsipyla Shoot Borers of Meliaceae in Sri Lanka." In *Hypsipyla Shoot Borers in Meliaceae. Proceedings of an International Workshop, Kandy, Sri Lanka 20-23 August 1996*, edited by R. B. Floyd and C. Hauxwell, 3-6. Canberra: Australian Centre for International Agricultural Research.
Spain	*Swietenia mahagoni*	0	
Guinea	*Swietenia mahagoni*	0	
Congo, Democratic Republic of	*Swietenia mahagoni*	0	
Senegal	*Swietenia mahagoni*	0	
New Zealand	*Swietenia mahagoni*	0	
United Arab Emirates	*Swietenia mahagoni*	0	
Central African Republic	*Swietenia mahagoni*	0	
Costa Rica	*Swietenia mahagoni*	0	
Uganda	*Swietenia mahagoni*	0	
Spain	*Swietenia humilis*	0	
China	*Swietenia humilis*	0	
Brazil	*Swietenia humilis*	0	
South Africa	*Swietenia humilis*	0	
Indonesia	*Swietenia humilis*	0	
Italy	*Swietenia humilis*	0	

Country	Species	Present	Source
Laos	*Swietenia humilis*	0	
Viet Nam	*Swietenia humilis*	0	
Malaysia	*Swietenia humilis*	0	