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V.M. Tytar, <https://orcid.org/0000-0002-0864-2548>

I.I. Kozynenko

I.I. Schmalhausen Institute of Zoology of the NAS of Ukraine, Kyiv

E-mail: vtytar@gmail.com, kozynenko@gmail.com

Potential trends in invasion risk of the yellow-legged hornet, *Vespa velutina*, in Ukraine

Presented by Academician of the NAS of Ukraine I. G. Emelianov

*In the recent decade an alarming problem has risen about the invasion of *Vespa velutina* Lepeletier, 1836 (Hymenoptera: Vespidae) in European ecosystems. The species can cause serious damage to ecosystem biodiversity and in areas where it has been introduced, and can have serious impacts over beekeeping. Bioclimatic modelling suggests that under current climate conditions representatives of the invasive species have chances in the near term to invade a number of regions in Ukraine, especially in the west of the country, including Transcarpathia, and Crimea. Under predicted climate change the hornet will most likely extend its presence in Ukraine.*

Keywords: *Vespa velutina*, bioclimatic modelling, Ukraine.

Biological invasions are a major driver of global change, determining environmental and socio-economic impacts, whose frequency and magnitude are exacerbated by global trade and climate change [1]. In this respect, social insects are among the most successful invasive groups [2]. In the recent decade alarming concerns have risen about *Vespa velutina* Lepeletier, 1836 (Hymenoptera: Vespidae), also known as the Asian predatory wasp or the yellow-legged hornet, an invasive Vespine wasp [3]. The species can cause serious damage to biodiversity and ecosystems in areas where it has been introduced. In Europe, it was first recorded from southwest France in 2004 as an alien species [3, 4], identified as *V. velutina nigrithorax*, and has rapidly been extending its range of invasion. This hornet has now established in most of west Europe, including France, Italy, Spain, Portugal, Germany and the UK, and the invasion seems to be ongoing. The hornet has been shown to be a fast invader spreading with an invasion speed of around 78 km/year in France, but higher distances may be covered by accidental transportation [5].

Biological invasion by the hornet can cause several problems. Three major problems generally recognized are: 1) it can pose a threat, as a top predator of invertebrates, to native ecosystems; 2) it can be a strong stressor to native honeybees, which are *V. velutina*'s preferred prey, but can

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also prey on wild bees; 3) it may aggressively injure humans, stings are painful and damaging, and can even be fatal [6].

In Europe, in particular, *V. velutina* can have serious impacts over beekeeping [7]. Because of its impact, the hornet has been included by the European Union in the black-list of invasive alien species (Reg. EU 1141/2016) [8] for which it is mandatory to develop surveillance plans and actions to limit its spread as well as control and containment strategies.

In some European regions, predation of *V. velutina* has resulted in the loss of almost 50 % of bee hives, leading to the decreasing of beekeeping products and loss of revenue [7]. Since 2008, Ukraine has been ranked first in honey production among European countries (with a gross harvest of up to 75 thousand tons) [9], therefore the hornet's incursion of Ukraine could have disastrous consequences. For this reason, including environmental concerns, management programs are under urgent demand. Under such circumstances predicting the current and potential future distributions of introduced invasive species is of central importance to plan adaptation and management strategies. Current research has shown climatic models to be efficient in modelling the species distribution in Asia and its potential invasion range in Europe [10]. In this study we project climatic models under contemporary and future climate scenarios, in order to specifically assess the potential trends in invasion risk of *V. velutina* in Ukraine.

Materials and Methods. Species distribution models (SDMs) have proven to be useful tools for predicting the spread of invasive species and elucidating the importance of a wide range of environmental covariates considered to affect their occurrence [11]. As input, SDMs require georeferenced biodiversity observations. Localities for *V. velutina* were gathered from GBIF [12] and records found in the literature and Internet sources (for instance, <https://observation.org/>). Because many uncertainties are associated with SDM projections, particularly when it comes to building a SDM for a species expanding its home range in a new area, we used for the analysis only European records.

To avoid overemphasizing on sampled area, we selected points for model calibration using a subsampling regime to reduce sampling bias and spatial autocorrelation. We generated models using all available occurrence points and measured spatial autocorrelation among model pseudo-residuals by calculating Moran's I at multiple distance classes using the GeoDa software tool (<https://geodacenter.github.io/>). Moran's I is a widely used measure of spatial autocorrelation, ranging from 0 to 1, with values > 0.3 considered relatively large.

SDMs are primarily climate-driven and this makes sense because climate is a chief driver of environmental suitability. Core 19 bioclimatic parameters were downloaded as raster layers from the CHELSA website (<https://chelsa-climate.org/>) [13] for current (1981-2010) and future conditions (2011-2040, according to the GFDL-ESM4 model). These variables represent a combination of means, extremes, variability and seasonality of temperature and precipitation data that are known to influence species distribution and have previously been used for insect niche modelling. Climate variables often show high collinearity and most SDM approaches require the selection of one among strongly correlated variables. Such selection was carried out using the "removeCollinearity" function in the "virtualspecies" R package (<http://borisleroy.com/virtualspecies/>). Because climate variables are commonly skewed or have outliers, the Spearman correlation method was employed. SDMs were generated using Bayesian additive regression trees (BART), a powerful machine learning approach. Running SDMs with BARTs has recently been

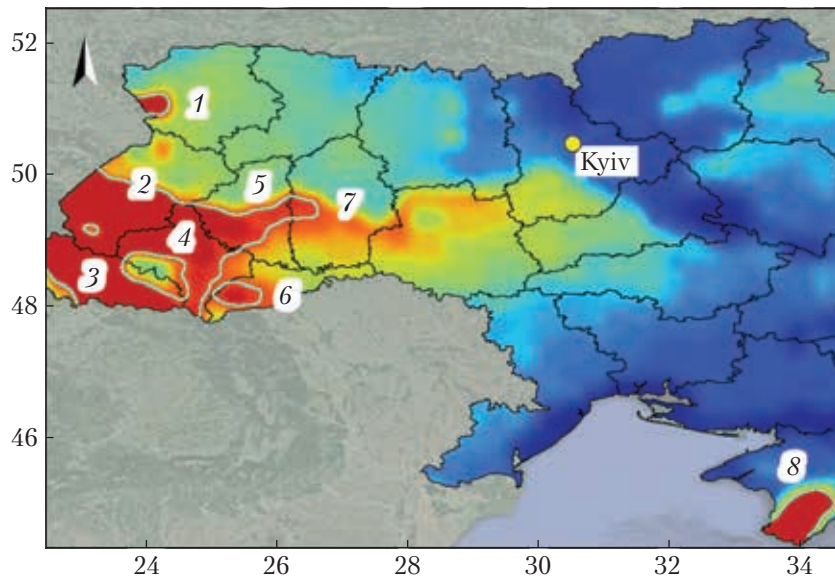


Fig. 1. Predicted habitat suitability for *Vespa velutina* in Ukraine under current climate with warmer colors representative of higher suitability. The blue line depicts the accepted threshold. 1 – Volynska; 2 – Lvivska; 3 – Zakarpatska (Transcarpathia); 4 – Ivano-Frankivska; 5 – Ternopilska; 6 – Chernivetska; 7 – Khmelnytska oblasts; 8 – Crimea

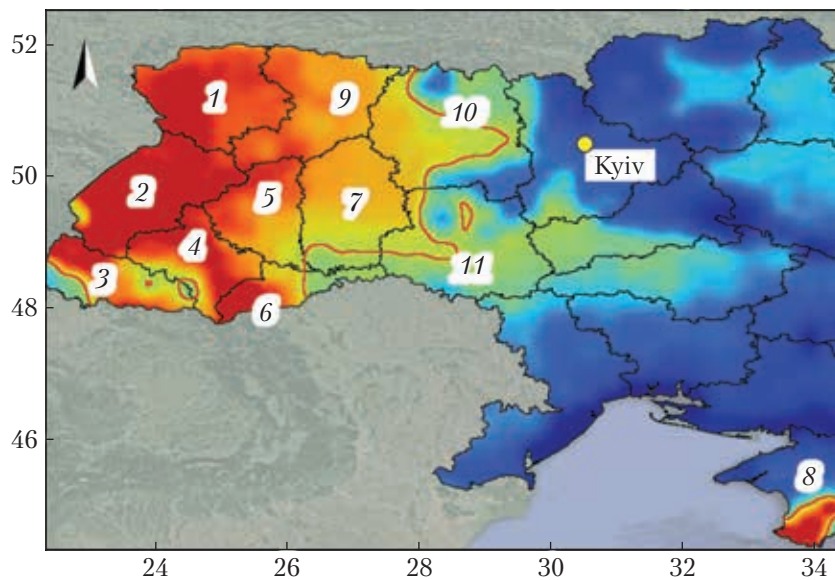


Fig. 2. Predicted habitat suitability for *Vespa velutina* in Ukraine under future climate with warmer colors representative of higher suitability. The red line depicts the accepted threshold. 1–8 as in Fig. 1; 9 – Rivnenska; 10 – Zhytomyrska; 11 – Vinnytska oblasts

facilitated by the development of an R package, “embarcadero” (<https://github.com/cjcarlson/embarcadero>), being highly effective at identifying informative subsets of predictors and ranking them according to their importance. The algorithm computes habitat suitability values ranging from 0, for fully nonsuitable habitat, to 1, for fully suitable habitat. Also the package includes methods for sorting out the effect of selected variables on habitat suitability. We used the 10th percentile training presence logistic threshold value to distinguish between suitable and non-suitable areas. This threshold value is considered to provide a better ecologically significant result when compared with more restricted threshold values.

Model performance was assessed using measures of accuracy. Firstly, the threshold-independent receiver operating characteristic (ROC) approach, where the calculated area under the ROC curve (AUC) is considered as a measure of prediction success. A rough classification guide for the AUC is the traditional academic point system: poor (0.5–0.6), fair (0.6–0.7), good (0.7–0.8), very good (0.8–0.9) and excellent (0.9–1.0). Secondly, the true skills statistic (TSS). TSS values of -1 indicate predictive abilities of not better than a random model, zero indicates an indiscriminate model and $+1$ a perfect model; TSS values > 0.6 are considered to be useful to excellent.

Maps of habitat suitability in the GeoTIFF format were processed and visualized in SAGA GIS (<https://saga-gis.sourceforge.io/en/index.html>).

Results and Discussion. In total of 26511 nonduplicate records of *V. velutina* were collected from European localities, including a number from Greece, Cyprus, and one questionable from Romania. A minimum distance of 204 km was detected, at which Moran’s $I < 0.3$ ($p = 0.001$). To subsample our dataset such that all occurrence records were separated by this minimum distance we used the “point thinning” module in SAGA GIS. The procedure greatly reduced sampling bias and spatial autocorrelation. In the end, we retained 302 occurrence records. This number of occurrence records is considered more than sufficient to generate robust species distribution models.

The employed variable selection analyses retained 7 variables with a Spearman’s pair-wise rank correlation coefficient $\rho < |0.7|$. These are: mean diurnal air temperature range (bio2), temperature seasonality (bio4), mean daily maximum air temperature of the warmest month (bio5), mean daily minimum air temperature of the coldest month (bio6), precipitation amount of the wettest month (bio13), precipitation amount of the driest month (bio14), and precipitation seasonality (bio15).

The ROC curve of the final models based on current and future climates shows “excellent” predictive power with average training AUC scores of 0.953 and 0.952, respectively. The corresponding TSS values are 0.791 and 0.804, respectively, which are sufficiently high to make confident predictions.

In terms of the bioclimate, around 70 % of the variance in the models is explained by 4 variables: bio2, bio4, bio6 and bio13, the first three of which are temperature-related. For instance, bio2 is an important meteorological indicator associated with global climate change, which describes the within-day temperature variability and reflects weather stability. Increasing such range has been shown to reduce population viability of ectotherms, although the strength and direction of the effect can depend on the mean temperature [14].

Mapping the potential occurrence of *V. velutina* using CLIMEX projected the hornet to be capable of establishing in most of Europe [15]. Figs. 1 and 2 represent the predicted distribution of *V. velutina* in Ukraine under current and the future climatic conditions, respectively. Accord-

ing to maximum habitat suitability as a measure of risk, oblasts in Ukraine can be ranked in the following order: Crimea > Zakarpatska > Lvivska > Ivano-Frankivska > Volynska > Ternopilska > Chernivetska > Khmelnytska. This regards current climate. Under the future climate scenario more oblasts are predicted to be affected by the hornet and their ranking in terms of invasion risk appears as: Chernivetska > Lvivska > Crimea > Ivano-Frankivska > Zakarpatska > Volynska > Ternopilska > Rivnenska > Khmelnytska > Zhytomyrska > Vinnytska.

Results of these predictions provide a tentative theoretical reference framework for the prevention of the spread of *V. velutina* in Ukraine, because only bioclimatic dimensions of the ecological niche have been considered. Nevertheless, this may help in establishing relevant monitoring programs and elucidating the socio-economic consequences of such invasion.

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V.M. Tytar, <https://orcid.org/0000-0002-0864-2548>

I.I. Kozynenko

Інститут зоології ім. І.І. Шмальгаузена НАН України, Київ

E-mail: vtytar@gmail.com, kozynenko@gmail.com

ПОТЕНЦІЙНІ ТЕНДЕНЦІЇ РИЗИКІВ ІНВАЗІЇ ЖОВТОНОГОГО ШЕРШНЯ *VESPA VELUTINA* В УКРАЇНІ

В останнє десятиліття виникла серйозна проблема щодо інвазії *Vespa velutina* Lepeletier, 1836 (Hymenoptera: Vespidae) в екосистемі Європи. Вид може завдати істотної шкоди біорізноманіттю екосистем у районах, де він був інтродукований, а також негативно вплинути на бджільництво. Біокліматичне моделювання свідчить про те, що за сучасних кліматичних умов представники виду мають шанси найближчим часом з'явитися у низці областей України, особливо на заході країни, у тому числі Закарпатті, та в Криму. За прогнозованих змін клімату шершень, найімовірніше, продовжить поширюватися в Україні.

Ключові слова: *Vespa velutina*, біокліматичне моделювання, Україна.