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A computer model of the distribution of the tapeworm *Echinococcus multilocularis* in Ukraine

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Alveolar echinococcosis, caused by the larval form of the parasitic tapeworm Echinococcus multilocularis, affects a wide range of animal species, including domestic and wild livestock, and is a highly pathogenic helminthic disease for humans. Recently developed for the species habitat suitability maps are restricted to the border of the European Union and have left Ukraine outside the scope of this study. Our goal was to model and characterize the large-scale ecological niche of E. multilocularis in Europe, placing a particular emphasis on Ukraine, and to justify an assessment of the risk of E. multilocularis transmission in Ukraine under current environmental conditions. Using the CMCC-BioClimInd dataset and a Bayesian modeling approach, we developed a habitat suitability map for the species in Ukraine and distinguished corresponding risk areas. We anticipate the model will enhance future surveillance efforts and help to understand the epidemiological situation of the disease, especially under wartime conditions.

Keywords: Echinococcus multilocularis, bioclimatic modeling, Ukraine.

Introduction. Infectious diseases, including parasitic infections, are important health problems in both animals and humans, resulting in economic losses and severe malady [1]. Echinococcosis is considered a neglected zoonotic parasitic disease caused by the metacestode stages of the genus *Echinococcus* belonging to the family *Taeniidae*, order *Cyclophyllidea*, affecting a wide range of animal species including livestock and wildlife [2]. Alveolar echinococcosis, caused by

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the larval form of the parasitic tapeworm *Echinococcus multilocularis,* is an extremely dangerous helminthic disease of humans. In such cases, humans become incidental intermediate hosts and become infected through ingestion of eggs excreted in the feces of definitive hosts. Such fecal-oral infection may be acquired through contact with definitive hosts or through contamination of soil, food or possibly water [3]. The disease represents a serious public health threat in China, Siberia and central Europe. However, since the 1990s, the geographic ranges and incidence of human and animal disease in the Northern Hemisphere appear to be increasing [4]. In Europe, for instance, epidemiological studies conducted over the last two decades show that the disease has affected not only historically endemic areas but also neighboring regions [3, 5, 6].

In such circumstances, surveillance data are key to understanding the epidemiological situation and taking action in at-risk areas, as well as to prioritizing management. Fortunately, extensive and high-quality data on the occurrence of *E. multilocularis* are available in Europe due to its medical importance. Recently, this has allowed to establish the influence of climate and characterize the ecological niche of the parasite, and to make spatially explicit predictions of current habitat suitability for the species using species distribution modeling (SDM) [7]. SDMs have become one of the most widely used tools in ecology, based on correlating species occurrence with environmental data to draw ecological and evolutionary inferences. This family of methods has a wide range of applications, including identifying areas where a species may occur, which in itself is a prerequisite for monitoring [8], and determining their suitability based on the observed relationship of the species to environmental conditions. In the quoted work [7], authors have described suitability for *E. multilocularis* in each European country belonging to the European Union, so the corresponding habitat suitability maps are limited to the EU border and left Ukraine outside the scope of this study.

The **aim** of this paper is to fill this gap with the following objectives:

1) to model and characterize the large-scale ecological niche of *E. multilocularis* in Ukraine;

2) to substantiate the risk assessment of zoonotic transmission of the parasite in Ukraine under current environmental conditions.

Materials and methods. As input, SDMs require georeferenced biodiversity observations. Presence data were compiled from published records [7, 9], supplemented by Ukrainian sources [10, 11]. We excluded duplicate records and, as samples are often clustered at observer activity locations, we applied a spatial thinning approach. Records with a minimum distance of less than 10 km from each other were excluded using the "point thinning" tool in SAGA GIS (https://saga-gis. sourceforge.io/en/index.html).

To evaluate the potential distribution of *E. multilocularis*, we used the Bayesian additive regression trees (BART) approach. BART is a tree-based machine learning method based on the Bayesian approach to classification and regression trees (CART). BART is defined by the prior distribution and likelihood for event return predictions, which allows us to quantify prediction uncertainty and estimate marginal effects of covariates. The BART method is a technique that deals with non-linear and non-monotonic relationships between response and predictor variables, and allows estimating the probability of presence of a species or its populations. Running SDMs with BARTs has been facilitated by the development of the R package, "embarcadero" (https:// github.com/cjcarlson/embarcadero). The package also includes methods for sorting the effects of selected variables on habitat suitability and constructs appropriate response curves. We used a 10-percentile training presence score threshold to distinguish between suitable and unsuitable

areas. Model performance was evaluated using the area under the curve (AUC) of receiver operating characteristic (ROC), true skill statictic (TSS), and the continuous Boyce index (CBI). The AUC ranges from 0 to 1, where scores below 0.5 indicate discrimination worse than random and a score of 1 indicates perfect discrimination. TSS ranges from −1 to +1, where +1 indicates perfect agreement between predictions and observations, and values of 0 or less indicate agreement no better than random classification. Finally, the CBI varies from −1 for an inverse model to 0 for a random model to 1 for a perfect model. For estimating the CBI a R script was employed (https://github.com/jmrmcode/contboyceindex).

Taking into account that the most common definitive host of the parasite is the widespread fox, and that a wide variety of intermediate rodent hosts are available as prey for this predator, habitat is hardly a limiting factor [7]. Climate, in contrast, is critical for the survival of the oncosphere contained in the egg during the winter outside the warm-blooded host. Primarily SDMs at broad geographic scales are climate-driven and this makes sense because climate is a chief driver of environmental suitability. For instance, eggs of *E. multilocularis* can persist in climatic conditions of southwestern Germany for more than half a year, but that they are sensitive to elevated temperatures, to desiccation and to very low temperatures [12]. In the present study, we used 35 bioclimatic indicators of the CMCC-BioClimInd dataset [13]. These indicators represent combinations of mean, extreme, variable and seasonal values of temperature and precipitation, potential evapotranspiration, which are known to influence species distributions. For modeling purposes, the corresponding rasters were resampled to a 5 arc-minute resolution.

The obtained SDMs were reclassified into different areas of potential habitat suitability. Using the "classify" tool in SAGA GIS, we defined these thresholds based on Jenks natural breaks, which maximizes the similarity of numbers in groups by minimizing each class average deviation from the class mean, while maximizing each class deviation from the means of the other groups.

Maps of habitat suitability in the GeoTIFF format were processed and visualized in SAGA GIS, statistical procedures were performed in PAST (https://past.en.lo4d.com/windows).

Results and discussion. After removing duplicate records and point thinning, which reduced sampling bias and spatial autocorrelation (Moran's $I < 0.3$, p-value < 0.01), a total of 796 occurrences across Europe were taken into consideration. This number of encounter records is considered more than sufficient to generate reliable species distribution models.

The ROC curve of the final model based on current climate shows "excellent" predictive power with the training AUC score of 0.925 and corresponding TSS value of 0.737, which are sufficiently high to make confident predictions. Using the 10 percentile threshold of 0.546, the CBI too evidences good performance of the model (0.856, $t = 14.901$, df = 81, p-value $< 2.2 \cdot 10^{-16}$).

In terms of bioclimatic indicators, the most important for SDM construction were: 1) seasonality of temperature; 2) seasonality of precipitation; 3) average temperature of the warmest quarter; 4) average temperature of the driest month; 5) average temperature of the wettest quarter; 6) ombrothermal index of summer and previous month. Basically, both temperature and precipitation seasonality, encompassing 34% of the variability, appear to play a critical role in influencing the persistence of the parasite and affecting its distributional pattern. This primarily indicates the vulnerability of the species to seasonal temperature fluctuations, especially when it drops sharply to freezing levels, thus increasing the corresponding index (Fig. 1). Notably,
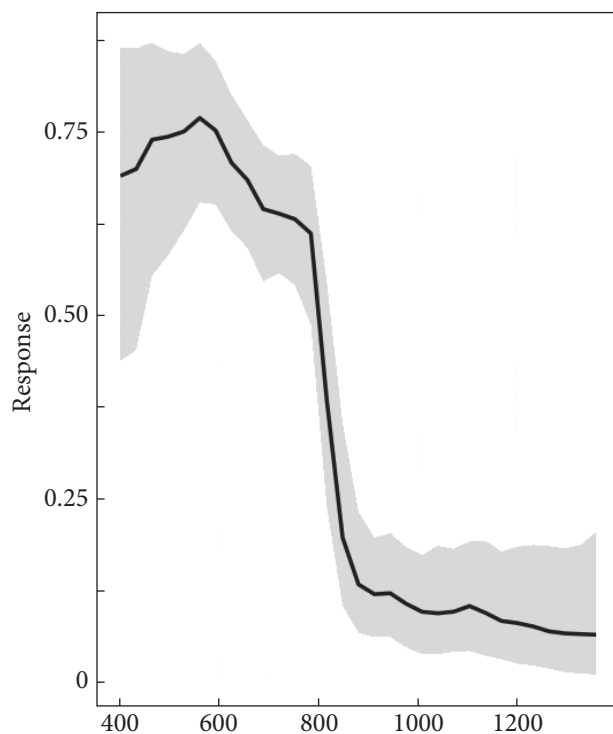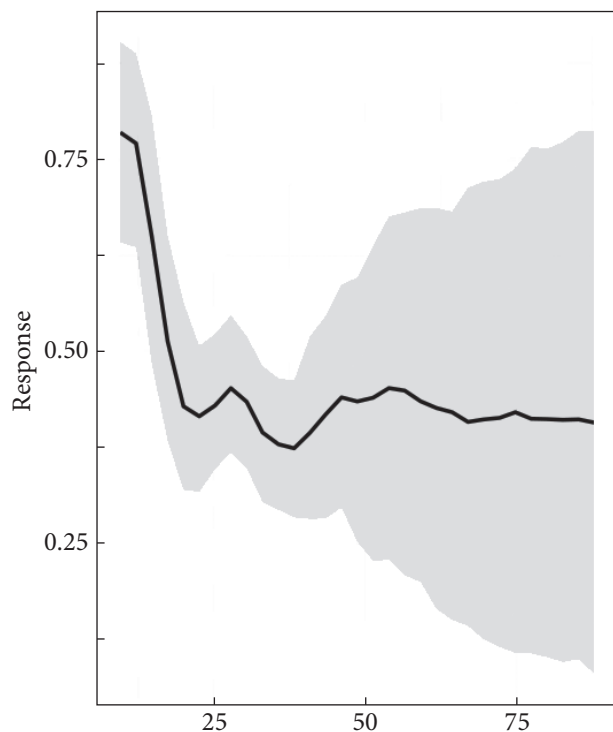
Fig. 1. Partial dependence plot for temperature seasonality; units — standard deviation × 10. Response — habitat suitability score, gray area — 95% confidence interval

this increase occurs along a longitudinal gradient (Spearman's *r* = 0.95, *p*-value < 0.01). Secondly, habitat suitability forms a negative relationship with precipitation seasonality (Fig. 2) and confirms a possible negative impact of drought periods on egg survival and transmission of the parasite, as previously suggested [7].

Among the variables highlighted by the BART algorithm as important variables worthy of attention is the "ombrothermal index of summer and previous month", with a contribution of 16.2%. Previously, this index has hardly been used as a covariate in the creation of SDMs. In general, ombrothermal indices relate precipitation to temperature and can be used to better characterize the bioclimatology of any study region and, perhaps more importantly, to predict what vegetation should be found there [14]. In our case, the corresponding partial dependence plot for this covariate shows an increase in habitat suitability (up to 60%) in places where the index reaches higher values and where the optimum of the assumed vegetation is winter deciduous forests, and in mountains — coniferous forests. This clearly echoes previously published results [7], despite the fact that covariates explicitly related to forest were not used in our modeling.

Coincidentally, we found a relatively strong correlation between the considered

Fig. 2. Partial dependence plot for precipitation seasonality; units — coefficient of variation expressed as a percentage. Response — habitat suitability score, gray area — 95% confidence interval

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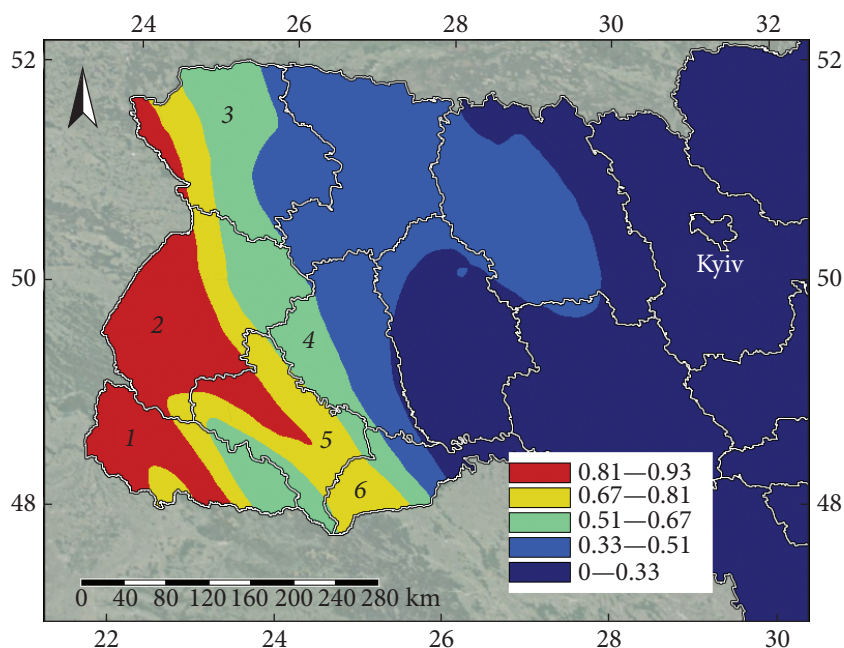*ISSN 1025-6415. Dopov. Nac. akad. nauk Ukr. 2024. No 5*

Fig. 3. Map of bioclimatic habitat suitability for *Echinococcus multilocularis* in Ukraine divided into five suitability classes: very low (navy blue), low (blue), moderate (green), high (yellow), and very high (red); the corresponding ranges of habitat suitability are presented in the legend. Oblasts: *1* — Zakarpatska (Transcarpathia); *2* — Lvivska; *3* — Volynska; *4* — Ternopilska; *5* — Ivano-Frankivska; *6* — Chernivetska

ombrothermic index and aboveground forest biomass (Spearman's $r = 0.65$, *p*-value < 0.01); forest biomass data sourced from https://iiasa.ac.at/.

We divided suitable areas for parasites into five suitability classes, according to the natural discontinuity classification methodology implemented in SAGA GIS (Fig. 3). According to the created habitat suitability map, large areas of Lvivska and Zakarpatska oblasts are very highly suitable for the parasite in terms of survival and transmission. In this respect following oblasts are Ivano-Frankivska, Volynska, Chernivetska, and in the end Ternopilska.

Conclusion. Mapping of potential habitats of *E. multilocularis* projected the cestode to be capable of establishing in portions of western Ukraine. The urgency of the problem is exacerbated by the fact that Russia's armed aggression has forced millions of citizens to leave their homes in search of safety and temporarily relocate mainly to the western regions of the country, away from the war zone. We expect that the developed SDM can be useful for predicting disease risk in Ukraine, help guide future research and support effective planning and decision-making in the public health sector.

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КОМП'ЮТЕРНА МОДЕЛЬ ПОШИРЕННЯ ЦЕСТОДИ *ECHINOCOCCUS MULTILOCULARIS* В УКРАЇНІ

Альвеолярний ехінококоз, спричинений личинковою формою паразитичного черва *Echinococcus multilocularis*, уражує широкий спектр видів тварин, як свійських, так і диких, і є високопатогенним гельмінтозом людини. Нещодавно розроблені карти придатності середовища існування цього паразита обмежені кордоном Європейського Союзу, Україна залишилась поза сферою дослідження. Метою роботи було змоделювати і детально охарактеризувати екологічну нішу *E. multilocularis* в Україні та оцінити ризики зараження *E. multilocularis* за поточних екологічних умов. З використанням набору даних CMCC-BioClimInd і баєсівського підходу до моделювання розроблено карту придатності середовища існування для виду в Україні і виділено відповідні зони ризику. Очікується, що ця модель буде корисним інструментом для виявлення паразита і допоможе зрозуміти епідеміологічну ситуацію щодо захворювання, особливо під час воєнних дій та масового переміщення населення на захід країни.

Ключові слова*: Echinococcus multilocularis, біокліматичне моделювання, Україна.*