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Image-based recognition using advanced neural networks can aid surveillance of *Agrilus* (Coleoptera, Buprestidae) jewel beetles

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Running title: Automatic image-based identification of *Agrilus* species

Abstract

The genus *Agrilus* includes two species, *A. planipennis* and *A. anxius*, that are of particular phytosanitary concern and that are regulated by the European Union legislation. This implies that phytosanitary agencies of all EU countries are obliged to establish specific surveillance programmes to verify the absence of these species from their territory. These activities commonly consist of the use of green-colored traps, which are however attractive not only for *A. planipennis* and *A. anxius* but also for a wide range of other *Agrilus* species. For this reason, much time and expertise is required to sort and identify specimens to species, impeding an efficient rapid response. In this study, we tested the efficacy of the Entomoscope, a low-cost, open-source photomicroscope that uses high-resolution digital imaging and allows a pre-trained CNN model to accurately detect, image and classify insect specimens, for automatic identification of 13 *Agrilus* species, including *A. planipennis* and *A. anxius*. The correct species was among the top five most probable predictions made by the trained CNN 94.5% of times. For most species, including *A. planipennis* and *A. anxius*, either no errors or only a few errors were made, whereas for a few native species misidentifications were more common. The trained CNN also efficiently classified as "unknown" species that were not used in the training process. These results provided proof of concept for an AI-driven surveillance system that can strongly aid in surveillance activities of *Agrilus* species.

Keywords

Agrilus planipennis, *Agrilus anxius*, Bronze birch borer, Deep learning, Early-detection, Emerald ash borer, Entomoscope

Introduction

The constant increase of global trade over the last hundred years, combined with deliberate plant introductions in the past and ongoing climate changes, has facilitated the movement among continents and the establishment likelihood of an increasing number of insects (Brockerhoff and Liebhold 2017; Pureswaran et al. 2022; Fenn-Moltu et al. 2023; Isitt et al. 2024). The genus *Agrilus* (Coleoptera, Buprestidae), one of the most species-rich genera of animals in the world (Jendek and Grebennikov 2023), is among the insect taxa that have taken the most advantage of these processes. More than 30 species have been already introduced and established outside their native range (Ruzzier et al. 2023), including the emerald ash borer *A. planipennis* Fairmaire, 1888, which has caused massive ecological and economic damage in North America (Kovacs et al. 2010; Klooster et al. 2018). For these reasons, the development of tools and strategies for early detection of accidentally introduced *Agrilus* species was identified as a research priority to trigger rapid response and reduce potential impacts in the invaded areas.

Among the numerous tools developed for *Agrilus* surveillance programs, baited or unbaited green traps set up at entry points and in their surrounding forests are currently adopted by several phytosanitary agencies worldwide (Evans et al. 2020; Imrei et al. 2020; Silk et al. 2020; Dodds et al. 2024; Duan et al. 2024; Santoiemma et al. 2024a). These traps were primarily developed based on lab and field studies targeting *A. planipennis* (Crook et al. 2009; Francese et al. 2010; Poland and McCullough 2014; Poland et al. 2019), but have been afterwards showed to be attractive also for a wide range of other species within the genus *Agrilus* (Rassati et al. 2019; Cavaletto et al. 2020; Le Souchu et al. 2024; Santoiemma et al. 2024a, Santoiemma et al. 2024b 2025; Khun et al. 2024). This allows practitioners to survey multiple species simultaneously, but much time and expertise is required to sort and identify specimens to species due to both the low interspecific morphological variation (Kelnarova et al. 2019) and the very high species richness of the genus (Jendek and Grebennikov 2023), impeding an efficient rapid response (Lyal and Miller 2020). Thus, novel technologies that can help to improve the efficiency of species identification are promptly needed.

Artificial intelligence (AI) systems are being increasingly adopted in entomology for various applications (Teixeira et al. 2023; Hartbauer 2024). Among them, AI is used to enhance the accuracy and speed of insect identification in the lab and in the field (Martinez et al. 2018; De Cesaro Júnior and Rieder 2020; Hartbauer 2024). Convolutional neural networks (CNNs) trained on image datasets have been shown to reliably classify insects at the family, genus or even species level (Valan et al. 2019; Ärje et al. 2020; Hansen et al. 2020; Wührl et al. 2022; Tannous et al. 2023; Marais et al. 2024). Exploiting this technology in surveillance activities for *Agrilus* species would, however, require that laboratories and plant health inspectors are equipped with an affordable device that can capture images of trapped specimens and, subsequently, automatically identify them to species. The Entomoscope, recently developed by the Karlsruhe Institute of Technology (KIT) (Wührl et al. 2024), might satisfy these needs. It is a low-cost, open-source photomicroscope that uses high-resolution digital imaging and allows a pre-trained CNN to accurately detect, image and classify insect specimens (Wührl et al. 2024). The Entomoscope has been tested so far on parasitoid wasps (Shirali et al. 2024), but its potential application in *Agrilus* beetle surveillance has not yet been investigated.

In this study, we tested the efficacy of the Entomoscope and its associated CNN for automatic identification of *Agrilus* species collected in traps. We first trained the CNN using photos of 13 *Agrilus* species taken with the Entomoscope, and then determined the trained CNN accuracy in identifying them to species. Second, we tested the response of the trained CNN to specimens belonging to species that were not included in the training process. Our objective was to provide proof of concept for the use of AI applied through the Entomoscope in surveillance activities targeting *Agrilus* species.

Materials and Methods

Agrilus specimens

Specimens used for the training process of the CNN belonged to 13 *Agrilus* species, eleven native to Europe and two non-native to Europe, i.e., *A. anxius* native to North America, and *A. planipennis* native to Asia but already occurring in Europe (Table 1, Fig. 1). The native species were selected as they were commonly collected in trapping studies carried out in Europe targeting *Agrilus* spp. (Le Souchu et al. 2024; Santoiemma et al. 2024b, 2025), whereas the non-natives were selected because they are regulated by the European Union legislation and surveillance is mandatory in EU countries (EFSA et al. 2020a, Santoiemma al. 2024b). Specimens were collected in Poland, France, Slovenia and Canada (Table 1) using green multi-funnel traps set up in the canopy of oak-dominated forests or poplar stands. Depending on the country, trap-collecting cups were filled with mixture (2:1) of propylene glycol and water (Slovenia), mixture (1:1) of ethylene glycol and water (Poland), mixture (2:1) of monopropylene glycol and water plus a drop of liquid dish detergent (France), a saturated solution of table salt in water plus a drop of liquid dish detergent to reduce surface tension (Canada), or kept dry but integrated with a section of mesh impregnated with α-cypermethrin insecticide (Storanet®, BASF Pflanzenschutz Deutschland, Germany) (France). Specimens were preserved in ethanol until identification. Species-level taxonomic identifications were performed by Gianfranco Curletti, Eva Groznik, Maarten de Groot, Jerzy M. Gutowski, Alain Roques and Aurélien Sallé based on morphological traits, keys and other reference materials (Schaefer 1950; Farrugia 2007; Paiero et al. 2012).

Imaging

Agrilus specimens were photographed using the "plug-in" version of the Entomoscope, which requires connection to a computer with Microsoft’s Windows operating system (Wührl et al. 2024, see Fig. S1 for a picture and detailed description of the hardware). Two Entomoscopes, provided by the KIT, were used. One was installed in the laboratory of the DAFNAE department at the University of Padova, and the other was installed at the Entomology Museum of La Sapienza University of Roma. The software (ENIMAS) used for image acquisition is available free of charge from a GitLab repository (https://gitlab.kit.edu/kit/iai/ber/enimas) and Open Science Framework (OSF: https://osf.io/3vmrg/ with DOI:10.17605/OSF.IO/3VMRG) (Wührl et al. 2024). The software allows one to choose between two photo stacking methods, one implemented in ENIMAS itself and the other one via a connection with Helicon Focus. For this study, we used Helicon Focus (version 8.2.2). For the species used to train the algorithm, we used a minimum of 11 to a maximum of 59 specimens per species, without distinguishing between sexes. Each specimen was photographed from multiple angles, corresponding to five main points of view: dorsal, laterodorsal, lateral, lateroventral and ventral (Fig. S2). This approach allowed us to obtain comprehensive coverage of a specimen's morphology. However, depending on the specimen and the position in which it was captured and preserved (the "death position"), it was not always possible to obtain images from all five angles as, in some cases, the death position did not allow us to hold the specimen at a precise angle. Therefore, two to five complete images were taken of each specimen. Specimens were not manipulated by taxonomists (or at least to a minimal extent for the identification process) but instead kept in the natural death position to simulate as much as possible the conditions faced by phytosanitary inspectors during surveillance programs. All specimens were photographed completely submerged in ethanol (70%) to avoid distortion effects that can cause significant identification errors.

Most images were obtained by stacking 18–25 photos, but as many as 35 photos were used for when specimens that had particular characteristics such as open elytra or outstretched legs. The distance between one picture and another was set at 0.07–0.1mm (depending on the size of the specimen) to obtain a homogeneous focus. The image acquisition speed was set between 10% to 15%; a higher speed proved counterproductive for alcohol-preserved specimens, due to the vibrations that caused the specimen to move. The images were then merged using the stacking function of Helicon focus (with respective settings: Method B; Radius 8; Smoothing 4), to obtain a single focused image for each angle of the specimen.

Training setup and model architecture

The CNN was trained using a personal computer equipped with a NVIDIA RTX 4000 Ada Generation GPU, Intel Core i7-14700 2.10 GHz CPU and 32 GB RAM. Software: Python (v 3.10), PyTorch (v 2.0.1), CUDA (v 11.7), Anaconda software (v 2.6.0) and Visual Studio Code (v 1.95.3). For automated image classification tasks, we used the You Only Look Once (YOLO) framework for classification, specifically YOLO11 (Jocher et al. 2023; Khanam and Hussain 2024). YOLO is a deep learning model designed to process entire images in a single forward pass, making it efficient for fast applications (Redmond et al. 2016, 2025). We implemented YOLO models through Ultralytics, a framework that provides streamlined tools for training, evaluation, and deployment of YOLO-based models. The YOLO models (like any supervised machine learning model) must be "trained", i.e., they must be provided with data, in this case images, that can allow the CNN to learn how to recognize a particular object on its own, without having to compare it with any other data (Limberg et al. 2022). Learning strongly depends on the quality and quantity of the training dataset: if the dataset well represents the variability of insects (e.g., different species, poses, and light conditions), YOLO can generalize better. The model can "learn" either specific patterns (e.g., stripes or spots) or that certain general shapes (e.g., elongated or round) belong to a certain class (Redmond et al. 2016). In our study, each class (a term used in the machine learning context and not as taxonomic rank) corresponded to a different *Agrilus* species. Convolutional filters can detect repeating and invariant patterns, regardless of rotations, illumination, or scale. YOLO divides each image into a grid and simultaneously predicts: i) the probability that a cell contains an object of a particular class (i.e., species in our case); and ii) the parameters for the bounding box containing the object (Bochkovskiy et al. 2020). During the training, the models utilize various core configurations that influence the speed and the accuracy, such as learning rate, batch size and weight decay, but there are additional settings used to optimize the process, called argumentations. All YOLO argumentations are listed on the Ultralytics website at https://docs.ultralytics.com/modes/train/.

Images taken as described above were organized in three folders designated for CNN training, validation and testing (Table 1). For each species, 70% of the images were used for training, while the remaining 30% were equally divided into the folders designated for validation and testing. Although some species had more specimens than others, we decided to maintain the ratio 70:15:15 for each species. The image dataset was curated following the guidelines provided in Ultralytics' documentation, which supports various datasets and labels specific to YOLO classification. The data was preprocessed by resizing the images to match YOLO's input dimensions, normalizing pixel values at 640x640, and augmenting images through transformations (i.e. flipud, fliplr, mosaic, mixup, etc., see Table S1).

Training procedure

The training was conducted in Visual Studio Code (Microsoft 2024), an integrated development environment with Python (3.11.10) extensions, that allowed us to set up virtual environments and streamline package management for YOLO. Initially, all versions YOLO11 (i.e., *n*, *s*, *m*, *l* and *x*) were tested multiple times using a preliminary dataset with a reduced number of classes (i.e., fewer species). YOLO-n (nano) is the lightest, whereas YOLO-x (extra-large) is the most complex and accurate version but requires more computational resources. YOLO-*s*, *m*, and *l* fall between these two extremes, progressively increasing in complexity, number of parameters and accuracy at the cost of inference speed. In our case, the best-performing version was *x*. Consequently, only the *x* version was selected for the training procedure.

We used pre-trained models on ImageNet and fine-tuned them with training parameters that best suited our needs and our data. The training parameters, including batch size, learning rate and the number of epochs (where an epoch represents one complete pass of the training dataset through the algorithm) were defined as in Table S1. After training the model, its performance (i.e., the ability to assign a specimen to the correct species) was evaluated by analyzing the *results.csv* files generated in output directory, and by creating comparison charts. At this regard, two metrics of accuracy are usually considered: Top-1 and Top-5. Top-1 is the percentage of times the model's prediction with the highest probability corresponds exactly to the correct class. When the model makes a prediction, only the first result (the one with the highest confidence) is shown; if it is correct, then it counts as a correct assignment. Top-1 is a very strict indicator of performance, because it requires that the most probable prediction is always the correct one. Top-5, on the other hand, is the percentage of times the correct class is among the top five most probable predictions made by the model. When the model makes a prediction, the first five classes to which the prediction is associated are shown. If the correct class is among the top five choices of the model, it is considered a correct prediction. This value is more useful for evaluating how close the model is to the correct identification, even if it does not always choose the right class first. For our study, we decided to use the Top-5 metric because it predicts the five most probable classes, which is an important feature for surveillance purposes. In fact, it allows us to know which native species the model tends to confuse with the targeted non-native species, allowing phytosanitary personnel to conduct subsequent additional morphological or molecular confirmations.

Besides Top-5 accuracy, we also calculated the F1-score. The F1-score is a performance measure of a classification model that combines *precision* and *recall* into a single value. *Precision* measures how many of the predicted positive cases are correct. *Recall* measures how many of the actual positive cases the model correctly identified. We also used *pheatmap* (Kolde 2018) on RStudio to create a confusion matrix to graphically represent with a heatmap the accuracy of *Agrilus* species image classification and identification system.

Lastly, we used the Class Activation Mapping (CAM) technique (Zhou et al. 2016) in VSCode using EigenCAM (Muhammad and Yeasin 2020) to highlight class-specific regions of images that have more weight on the classification results. This technique superimposes a heatmap over the images of each specimen, producing images where the areas are colored on a scale ranging from red to blue, where red is applied to areas with more relevance for the classification, and blue is applied to those with less (to no) relevance. Therefore, this can allow to spot the morphological characteristics or patterns that are used for the predictions.

All the images used for training and testing, as well as the scripts employed in the classification pipeline, are available in the Zenodo (www.zenodo.org) repository at the following DOI: https://doi.org/10.5281/zenodo.14998760.

Testing the response of the CNN to species not included in the initial training

To test the response of the trained CNN to specimens belonging to species that were not included in the training process, we added an additional class renamed "Unknown". In fact, YOLO does not include an "out-of-class" mechanism to exclude images that do not belong to any trained class, so it still tries to associate the image with the most similar species. When the image is very different from those used for training, the confidence level (max_conf) of the prediction is typically low. In our case, we set this confidence level to 0.5, meaning that the model will ignore all predictions with less than 50% confidence (Table S1). To test this mechanism, we used 19 images belonging to two native species that were not used for the training procedure (i.e., 8 images belonging to 2 specimens of *A. biguttatus* and 11 images belonging to 3 specimens of *A. convexicollis*, Table 1)

Results

Identification accuracy of specimens belonging to species used in the training procedure

Trained CNN (i.e., YOLO11x) showed a high Top-5 accuracy (94.9%) in assigning specimens belonging to the *Agrilus* species used in the training process and the F1-score value was 77.2%. The trained CNN correctly assigned the highest percentage of correspondence to the correct species 100% of times for 6 species, i.e., the non-native *A. planipennis*, and the native *A. betuleti*, *A. cuprescens*, *A. graminis*, *A. obscuricollis*, and *A. olivicolor* (Fig. 2, Fig. S3). For three of the other species, the trained CNN assigned the highest percentage of correspondence to the correct species between 90.0% and 95.0% of times (Fig. 2, Fig. S3). In particular, the native *A. angustulus* was identified with a 95% accuracy (two specimens out of 40 misidentified with *A. planipennis*), the native *A. laticornis* with a 94.5% accuracy (one specimen out of 18 misidentified as *A. graminis*), and the non-native *A. anxius* with 90.0% accuracy (two specimens out of 20 were misidentified as *A. sulcicollis*). The *Agrilus* species for which a misidentification was common were *A. viridis*, *A. pratensis* and *A. hastulifer*. For *A. viridis*, the trained CNN assigned the highest percentage of correspondence to the wrong species (*A. graminis*) 16 out of 21 times (Fig. 2, Fig. S3). For *A. pratensis*, the trained CNN assigned the highest percentage of correspondence to the wrong species 11 out of 12 times, i.e., 9 times to *A. obscuricollis* and 2 times to *A. cuprescens* (Fig. 2, Fig. S3). For *A. hastulifer*, the trained CNN assigned the highest percentage of correspondence to the wrong species 15 out of 16 times, i.e., 12 times to *A. graminis* and 3 times to *A. olivicolor* (Fig. 2, Fig. S3).

Considering class activation maps, to assign specimens to a certain species, the general shape of the body (pronotum and elytras) and the margins of the head (eyes and frons) were consistently used by the model (Fig. 3). Similarly, the shape of the abdominal sternites, the forehead, the area bearing the mouthparts (between clypeus, eyes margin and prosternum), and the clypeus itself were often used when the identification was based on pictures of the ventral part of the body.

Identification accuracy of specimens not belonging to species used in the training procedure

Considering specimens belonging to species not used in the training process, the trained CNN correctly assigned the highest percentage (100%) of correspondence to the class "Unknown" every time (Fig. 2, Fig. S3). This trend was valid both for the 8 specimens of *A. biguttatus* and 11 specimens of *A. convexicollis* (Fig. 2, Fig. S3).

Discussion

The genus *Agrilus* includes two species, *A. planipennis* and *A. anxius*, that are of particular phytosanitary concern due to the economic and ecological impacts they can have in the invaded areas (Baranchikov et al. 2008, 2014; Kovacs et al. 2010; Klooster et al. 2018; Evans et al. 2020) and as such, they are regulated by the European Union legislation (EFSA et al. 2020a, EFSA et al. 2020b). This implies that phytosanitary agencies of all EU countries are obliged to establish specific surveillance programmes to verify the absence of these species from their territory (Evans et al. 2020). These activities commonly consist of the use of green-colored traps, which are however attractive not only for *A. planipennis* and *A. anxius* but also for a wide range of other *Agrilus* species (Rassati et al. 2019; Cavaletto et al. 2020; Le Souchu et al. 2024; Santoiemma et al. 2024a, Santoiemma al. 2024b 2025). Here we showed that the Entomoscope, in combination with the trained CNN, strongly aid in very properly discriminating *A. planipennis* and *A. anxius* from other commonly collected native *Agrilus* species, a process that demands much time and taxonomic expertise. In addition, we showed that the trained CNN can efficiently classify as "unknown" species that were not used in the training process, which is a key feature to efficiently alert phytosanitary personnel when a potentially non-native species other than *A. planipennis* and *A. anxius* has entered the country.

We showed that the CNN that we initially trained had a generally high precision in assigning a given specimen to one of the 13 *Agrilus* species on which the training process was based. The correct species was in fact among the top five most probable predictions made by the model 94.5% of times. On the one hand this is not surprising given that the CNN we used, i.e., YOLO models, were already demonstrated to be very useful for automatic insect classification (Takimoto et al. 2021; Stark et al. 2023; Gao et al. 2024), including woodborers (Zhang et al. 2024). On the other hand, the high precision that we obtained at the taxonomic level that we targeted (i.e., species) is less common (e.g., Liu et al. 2023). For example, a study based on a previous version of the YOLO model showed a lower accuracy (i.e., 89%) in the identification of parasitoid wasps at the genus level (Shirali et al. 2024). Overall, these results indicated that the CNN we trained starting from pictures taken with the

Entomoscope can be considered a very promising model to be used for the automatic identification of *Agrilus* species starting from individuals collected in traps.

We also found that the degree of accuracy with which the trained CNN assigned specimens to the correct *Agrilus* species varied among species. For most of them, including the non-native *A. planipennis* and *A. anxius*, either no errors or only a few errors were made, whereas for others (i.e., the native *A. viridis*, *A. pratensis* and *A. hastulifer*) misidentifications were more common. This might be due to the characters used by the YOLO models to classify specimens. As for many others CNNs, YOLO models are only partially based on the same morphological characteristics (such as genitalia, hair distribution, size, etc.) (e.g., Volkovitsh et al. 2020) used by taxonomists but instead on the arrangement and intensity values in grayscale or Red-Green-Blue (RGB) of pixel clusters which are identified as discriminating features by the trained algorithm (Ganesh et al. 2021; Goodfellow et al. 2016; Redmon et al. 2016; Bochkovskiy et al. 2020). Class activation maps showed, for example, that, depending on the position of the specimen, the general shape of the body and the margins of the head, elytras and pronotum or the shape of the abdominal sternites, the forehead and the clypeus were used as main characters to discriminate among the tested *Agrilus* species. This can result in a very accurate classification of species that are well known to be difficult to distinguish from congeners (i.e., *A. obscuricollis*), but also to failures when it comes to discriminate between species that can be instead easily separated using classic taxonomic approaches (e.g., *A. graminis* and *A. pratensis*) (Schaefer 1950; Farrugia 2007; Paiero et al. 2012). Overall, these results indicate that the Entomoscope and the current version of the trained CNN can be very useful for surveillance of *A. planipennis* and *A. anxius*, but are not yet ready to identify to species level all native species collected in traps.

Finally, we found that the trained CNN correctly assigned the highest percentage (100%) of correspondence to the class “Unknown” when trying to identify specimens belonging to species not used in the training process. Several trapping studies showed that several *Agrilus* species can be collected when using green-colored traps in forest areas surrounding entry points (e.g., Santoiemma et al. 2024a, Santoiemma al. 2024b). These species might include native species present at low density or accidentally collected through the adopted trapping protocol, but also non-native species not initially targeted in the training process (e.g., non-regulated species). In this scenario, the capacity of the trained CNN to discriminate between known (i.e., species on which the training process was based on) and unknown species (i.e., species not included in the training process) can alert the phytosanitary personnel of the presence of a potential non-native species that should be further scrutinized via more classic morphological or molecular approaches. However, the chances that the "unknown" is a native species not included in the training of the CNN will increase with *Agrilus* species richness at the survey site; therefore, further efforts are necessary to increase the reference dataset with more native species.

Conclusions

By using the Entomoscope in combination with deep learning models we provide proof of concept for an AI-driven surveillance system capable of classifying the majority of *Agrilus* species with generally high accuracy. The open-source nature of this technology, combined with the relatively low cost of setting up and operating an Entomoscope, makes AI-based identification systems highly suitable for technology transfer initiatives. These systems could be integrated into training projects for phytosanitary personnel, foresters and environmental agencies, increasing knowledge on AI-based identification technologies, and encouraging their active participation in large-scale monitoring efforts. To further improve AI-based identification of *Agrilus* species, future research should explore the performance of other CNNs as well as hybrid approaches that integrate CNN-based image classification with other diagnostic methods, such as molecular tools. A multimodal approach, particularly in the initial training phases when large numbers of individuals need to be correctly assigned to their respective species, could significantly improve classification accuracy (Wuhrl et al.

2022). This would be particularly beneficial for species that are difficult to distinguish based on morphological characteristics alone. A major future advance would be the development of real-time processing capabilities, allowing field-based identification without the need for extensive laboratory infrastructure (Brydegaard et al. 2024; Chiavassa et al. 2024). A cloud-based or mobile application linked to the Entomoscope could allow users to upload images and receive automated identifications in real time, greatly increasing the accessibility and practical applicability of the system. Such an innovation would not only facilitate rapid species identification in phytosanitary surveillance but also contribute to broader biodiversity assessment initiatives.

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CRediT authorship contribution statement

Valerio Caruso: Writing - original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization, Visualization; **Hossein Shirali:** Writing – review & editing, Methodology, Formal analysis; **Christophe Bouget:** Writing – review & editing; **Pierfilippo Cerretti:** Writing – original draft, Conceptualization, Supervision, Funding acquisition; **Gianfranco Curletti:** Writing – review & editing, Data curation; **Maarten de Groot:** Writing – review & editing, Resources; **Eva Groznik**: Writing – review & editing, Resources; **Jerzy M. Gutowski:** Writing – review & editing, Resources; **Christian Pyliatuk:** Writing – review & editing, Resources, Methodology; **Alain Roques:** Writing – review & editing, Resources; **Aurelién Sallé:** Writing – review & editing, Resources; **Jon Sweeney:** Writing – review & editing, Resources; **Lorenz Wührl:** Writing – review & editing, Methodology; **Davide Rassati:** Writing – original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization, Visualization, Funding acquisition, Project administration

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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FIGURES

Figure 1. Examples of pictures taken using the Entomoscope to some of the Agrilus specimens used during the training process. (A) A. angustulus, (B) A. anxius, (C) A. cuprescens, (D) A. graminis, (E) A. hastulifer, (F) A. laticornis, (G) A. obscuricollis, (H) A. olivicolor, (I) A. planipennis, (J) A. pratensis, (K) A. sulcicollis, (L) A. viridis. Note: the pictures are not to scale with each other.

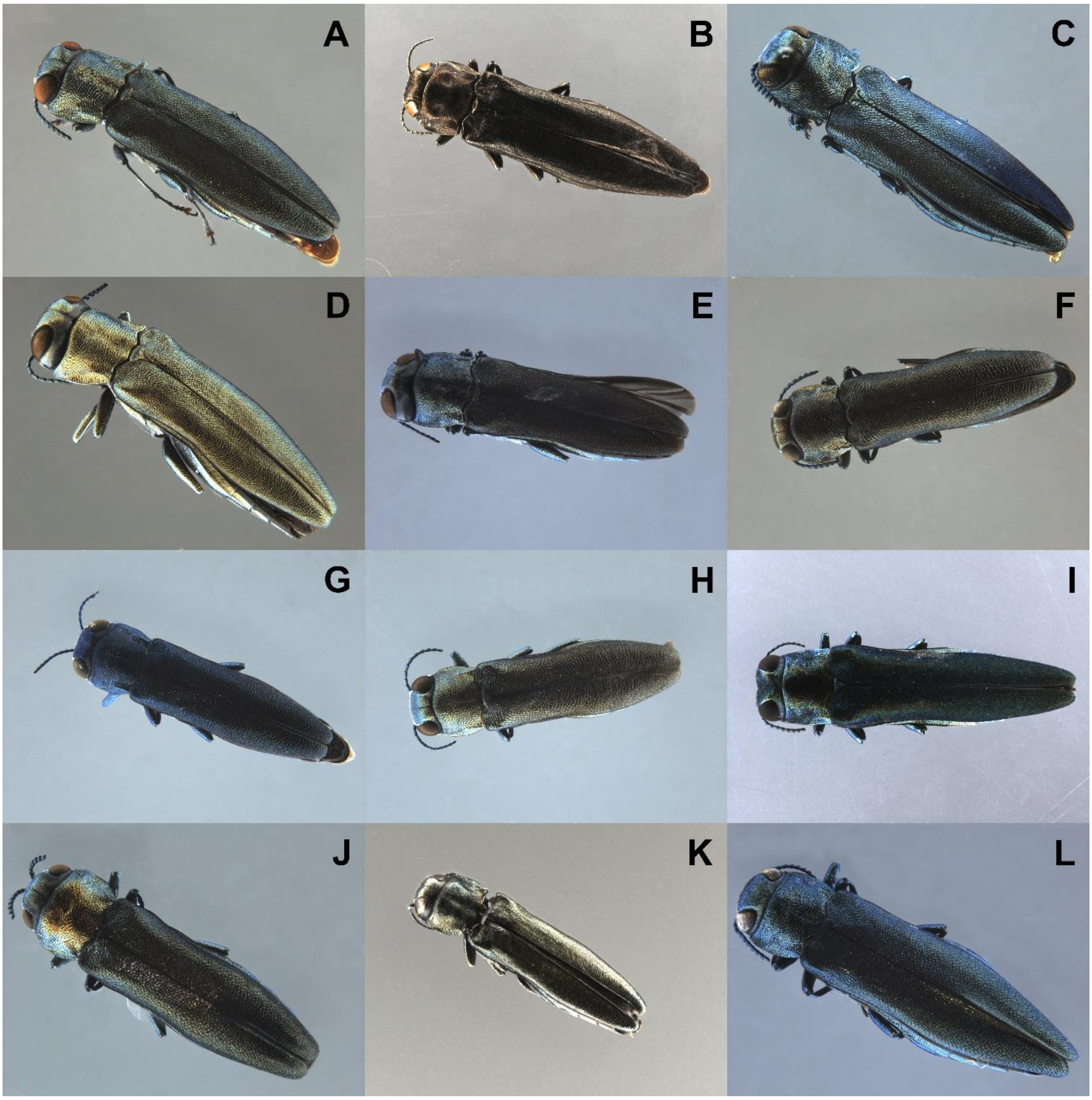


Figure 2. Confusion matrix with classification results of the YOLO11x model. Real species indicate the true species identity. Predicted species indicate the species to which the model assigned analyzed specimens. N = number of specimens for each species employed in testing process. The degree of accuracy is reported both in the form of numerical values, showing both the percentage and the absolute number of specimens that were assigned to a given species, and color-coded with blue for correct predictions and red for incorrect ones (light blue and red are associated with low degree of prediction, both correct and incorrect).

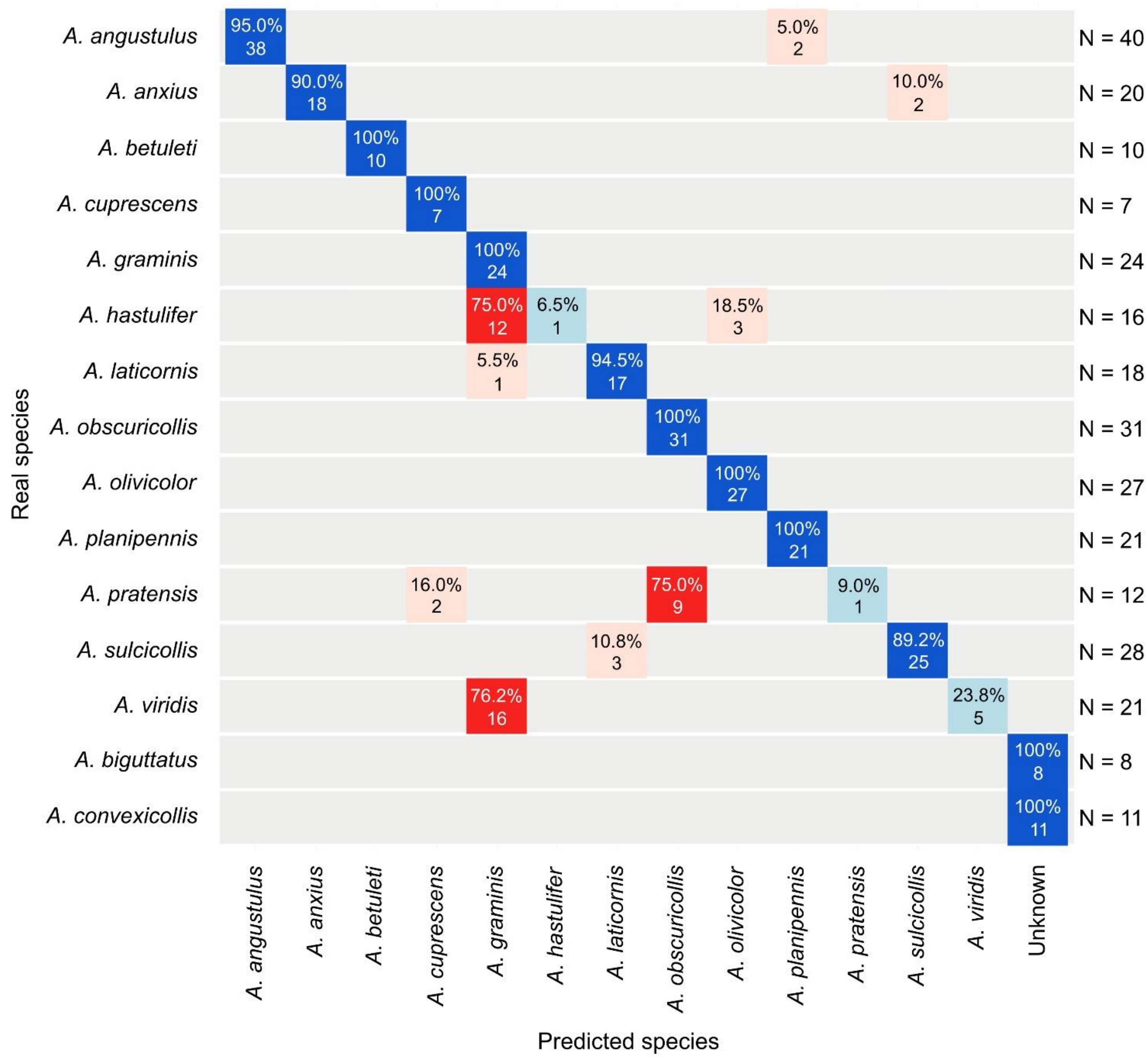
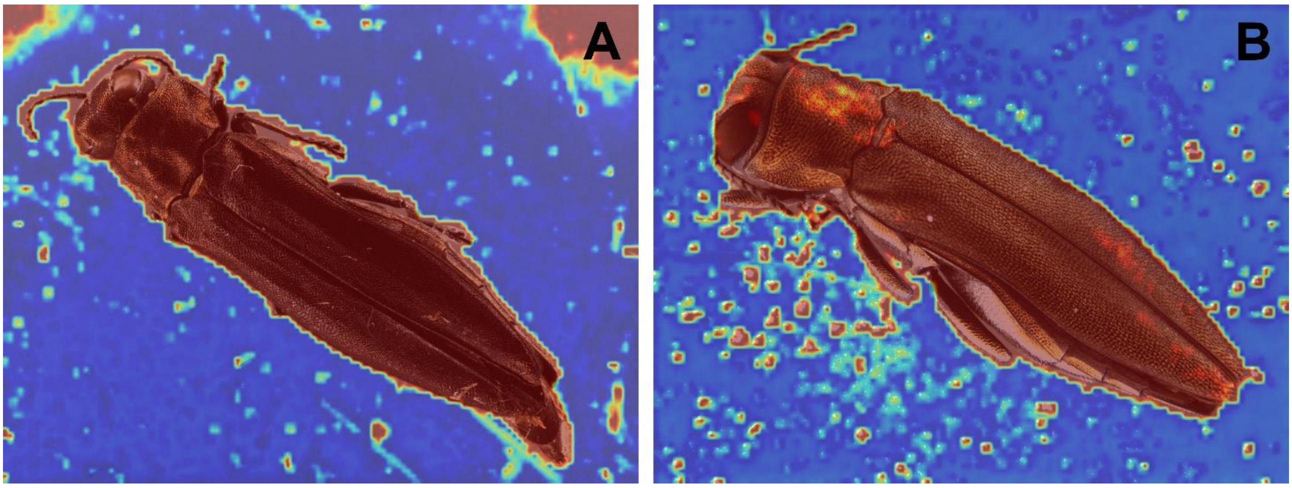


Figure 3. Example of class activation heatmaps obtained for pictures of A) *A. anxius* and B) *A. laticornis* (dorsal views). Colors range from blue to red based on the weight that areas had in classification: blue areas are regions with the least weight in classification, red areas are regions with the highest weight in classification, and the intensity of the red increases with the importance of the detected area.



TABLES

Table 1. Number of specimens photographed and number of pictures used to train, validate and test the CNN for each species. Countries where specimens of each species were collected are also indicated. *indicates species non-native to Europe. [+]indicates species used to test the response of the trained CNN to species not included in the initial training process.

Species	No. of specimens	No. of pictures for training	No. of pictures for validation	No. of pictures for testing	Country of collection
Agrilus angustulus (Illiger)	59	189	40	40	France, Poland, Slovenia
Agrilus anxius Gory *	35	96	20	20	Canada
Agrilus betuleti (Ratzeburg)	16	46	10	10	Poland
Agrilus cuprescens (Ménétries)	11	36	7	7	Poland
Agrilus graminis Kiesenwetter	46	115	24	24	France, Poland
Agrilus hastulifer (Ratzeburg)	28	74	16	16	France, Poland
Agrilus laticornis (Illiger)	36	85	18	18	France, Slovenia
Agrilus obscuricollis Kiesenwetter	47	144	31	31	France, Poland, Slovenia
Agrilus olivicolor Kiesenwetter	44	124	27	27	France, Slovenia
Agrilus planipennis Fairmaire *	34	95	21	21	Canada
Agrilus pratensis (Ratzeburg)	21	55	12	12	France, Poland
Agrilus sulcicollis Lacordaire	47	130	28	28	France, Poland, Slovenia
Agrilus viridis (Linnaeus)	40	98	21	21	Poland
Agrilus biguttatus (Fabricius) [+]	2	-	-	8	Slovenia
Agrilus convexicollis Redtenbacher [+]	3	-	-	11	France