

МАСШТАБНОЕ ИССЛЕДОВАНИЕ ИНВАЗИИ ОПАСНОГО ВРЕДИТЕЛЯ ЯСЕНЕЙ – ЯСЕНЕВОЙ ИЗУМРУДНОЙ УЗКОТЕЛОЙ ЗЛАТКИ – В ЕВРАЗИИ: ВАЖНЫЙ ВКЛАД ГРАЖДАНСКИХ УЧЕНЫХ И НАУЧНОГО СООБЩЕСТВА

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LARGE-SCALE STUDY ON THE INVASION OF THE TREE-KILLER, THE EMERALD ASH BORER, IN EURASIA: INVALUABLE INPUT OF CITIZEN SCIENTISTS AND SCIENTIFIC COMMUNITY

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Organization and the first results of the large-scale study aiming at the exploration of invasion genetics of the Emerald ash borer in Eurasia are presented and discussed, and further perspectives of the research are drawn.

The Emerald ash borer (EAB), *Agrilus planipennis* Fairmaire, 1888 (Coleoptera: Buprestidae) is a dangerous East Asian pest which penetrated into North America, Russia (the European part and Siberia) and Ukraine, and continues spreading on the European and Asian continents killing ash trees, *Fraxinus* spp. (Oleaceae). This invasive beetle has not been recorded in Belarus yet, but its appearance in the country is not ruled out.

EAB is included in the Common List of Quarantine Pests of the Eurasian Economic Union (EEU), the organization, which, besides Russia, includes Armenia, Belarus, Kazakhstan and Kyrgyzstan. Furthermore, it is listed as an A2 quarantine pest for EPPO region, which includes 52 member countries. Given the quarantine status of the beetle, its progressive spreading, ecological consequences and economic losses associated with the spread, deeper studies of the beetle invasion are highly important and timely.

Thanks to the initiative of the EPPO Network of experts working on surveillance, monitoring, and control of the Emerald ash borer, *Agrilus planipennis* and a partial support of the Russian Science Foundation (RSF, grant No. 22-16-00075-P), with the involvement of citizen scientists and the colleagues-entomologists, we have gathered together a representative sampling set of EAB (larvae and adults) from the invaded regions of Russia and North America and from the native area (Far East). This material is used to explore the phylogeography of this tree-killer, defining genetic diversity of different geographic populations in invaded vs. native range and invasive haplotypes that keep spreading westwards. The first result of this large-scale study will be presented. We thank colleagues and volunteers from Russia and other countries for fruitful cooperation.