



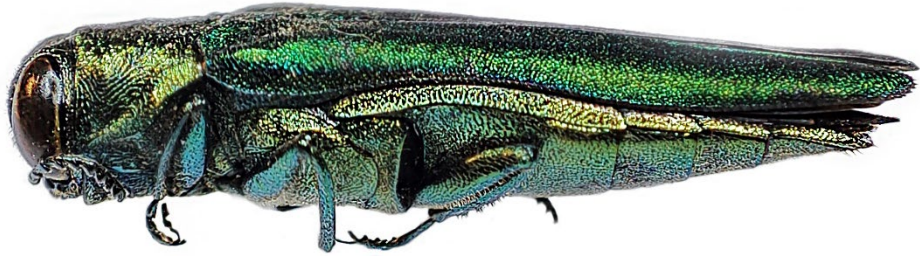
Molecular genetics of the Emerald ash borer invasion in European Russia and Eastern Europe



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The emerald ash borer, *Agrilus planipennis*



Natural range:

East Asia (Russian Far East, China, Mongolia, Japan, Taiwan)

Invasive range:

North America

European part of Russia + Siberia

Ukraine, Belarus (new)

Host plants:

Fraxinus spp.

Damage in the natural range:

No

Damage in the invasive range:

Significant



Current range



INVASION HISTORY*

2002 – North America

2003 – Moscow

2019 – Eastern Europe (Ukraine, Belarus)

Current range



Situation in Russia*:

- A significant expansion of the invasive range.
- The area of established phytosanitary zones for the pest increased in 2025 notably.



*National report on the quarantine phytosanitary state of the territory of the Russian Federation in 2025.

The aims of the study

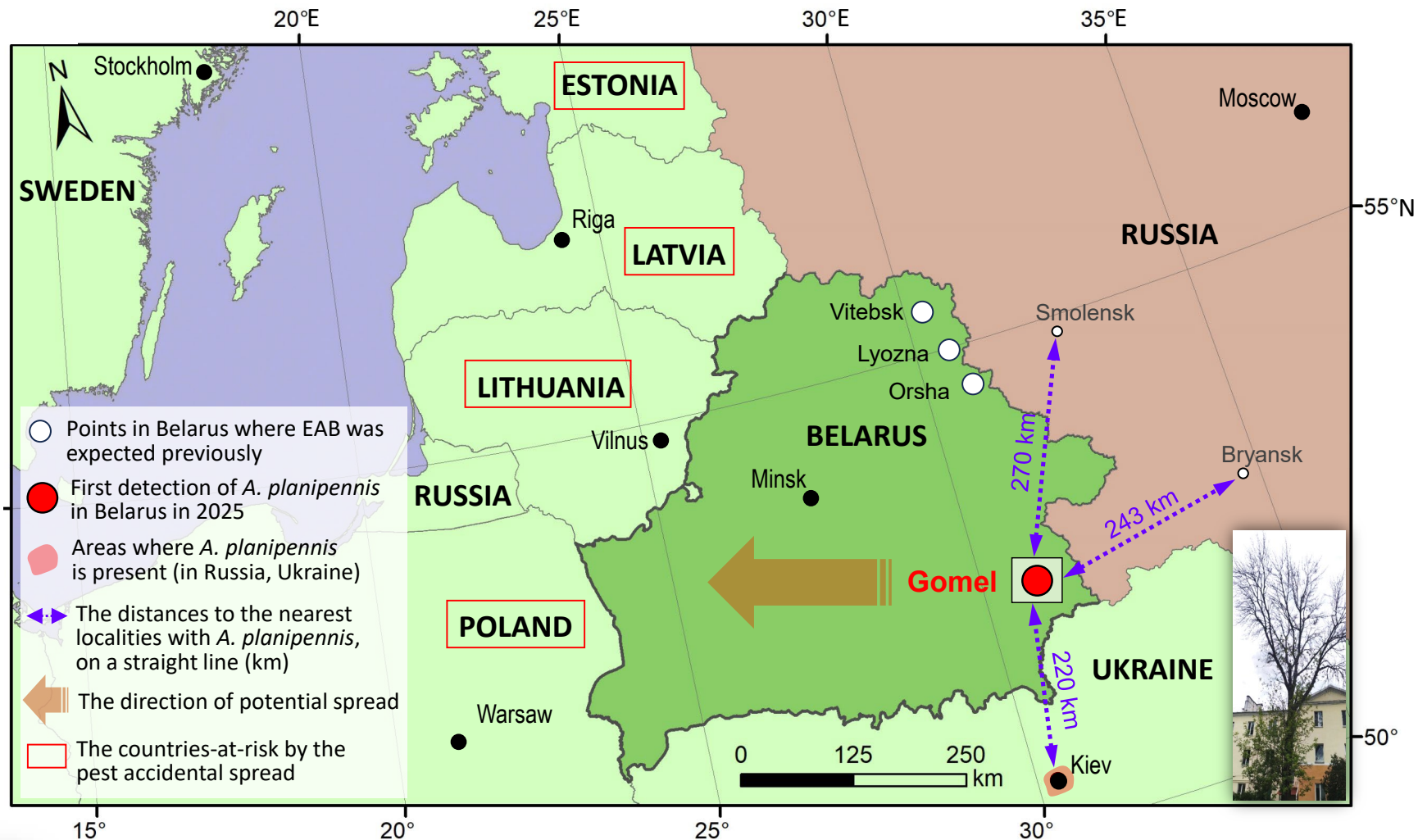


- to verify the western frontier of *A. planipennis* secondary range,
- to clarify the route of the invasion by studying haplotypes of *A. planipennis*.

A. planipennis in Belarus: recorded in 2025



A. planipennis in Belarus: recorded in 2025



- If *A. planipennis* continues spreading in Belarus, it may reach neighboring countries.
- Further spread is mainly due to unintentional transportation rather than natural dispersal.
- Sudden outbreaks in distant locations may happen.

Involvement of researchers and volunteers

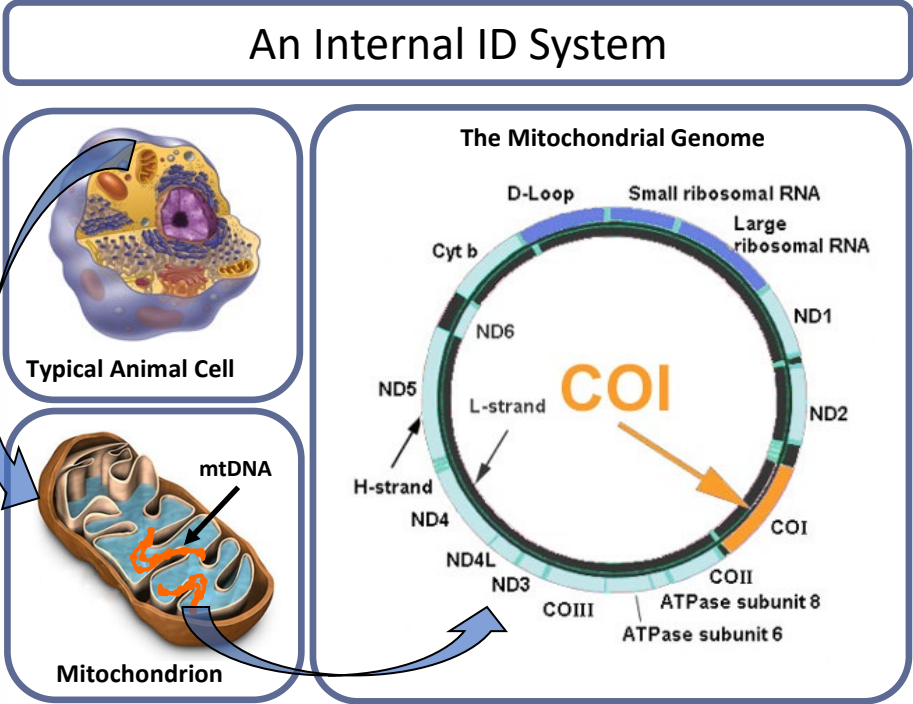
Collecting samples of *A. planipennis* for the phylogeographic study (in collaboration with the EPPO Network of experts working on surveillance, monitoring, and control of the Emerald ash borer, *Agrilus planipennis*)



DNA barcoding



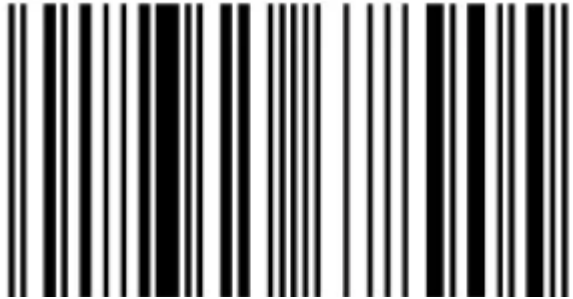
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Molecular genetics

BOLD SYSTEMS

Natalia Kirichenko

Back to Main Console

Back to Data Console

Record List

Options

Publication

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Sequence Analysis

Aggregate Data

Distribution Map

Image Library

Checklist Hit List Report

Checklist Progress Report

Checklist Disagreement Report

BOLD Main Menu

Project & Dataset Search
Code Record Search

Record List - EABRU

Specimens

285

Specimens

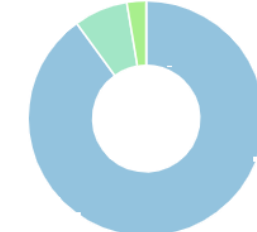
- 📍 GPS: 190 / 190
- 🌍 Country: 190 / 190
- 🖼️ Images: 190 / 190
- 📊 Barcode Compliant: 0 / 190

Sequences

0


Sequences

Taxonomy



Common class: Insecta

- Coleoptera (order): 171
- Lepidoptera (order): 14
- Diptera (order): 5



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500 records per page

	Identification	Specimen Page	Sequence Page	Extra Info	BIN	Record Flags	Legend	Tag
All						📍 🖼️ 📄 📊 * ✖️ 🚫		
✓	Agrilus planipennis	NK2531	EABRU001-24			📍 1 0		
✓	Agrilus planipennis	NK2532	EABRU002-24			📍 1 0		
✓	Agrilus planipennis	NK2533	EABRU003-24			📍 1 0		
✓	Agrilus planipennis	NK2534	EABRU004-24			📍 1 0		
✓	Agrilus planipennis	NK2535	EABRU005-24			📍 1 0		
✓	Agrilus planipennis	NK2536	EABRU006-24			📍 1 0		
✓	Agrilus planipennis	NK2537	EABRU007-24			📍 1 0		
✓	Agrilus planipennis	NK2538	EABRU008-24			📍 1 0		
✓	Agrilus planipennis	NK2539	EABRU009-24			📍 1 0		
✓	Agrilus planipennis	NK2540	EABRU010-24			📍 1 0		
✓	Agrilus planipennis	NK2541	EABRU011-24			📍 1 0		
✓	Agrilus planipennis	NK2542	EABRU012-24			📍 1 0		

Molecular genetics

Specimens used for DNA barcoding (285 sequences)



A phylogenetic trees

Will be published soon.

Take home messages



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- The **phylogeography of *A. planipennis*** was studied across its current range in Eurasia based on 180 COI mtDNA sequences, among which **six haplotypes were revealed**, with **one dominant haplotype (H1)** widely distributed throughout the pest's invasive range.
- The phylogenetics and phylogeographic patterns suggest that the **species' range expansion in Russia was due to the bridgehead effect** – establishment of non-native populations from those already established in the neighbor regions, rather than from native range.
- ***A. planipennis*** is now present **in Belarus**. Based on the genetic data, the pest came from the **neighboring Russian territories** and **Moscow Region** (a long-distance jump).
- From Belarus, ***A. planipennis*** **can soon reach** neighboring **Baltic countries** and **Poland**.
- Further long-distance dispersal is expected to result primarily from **unintentional human-mediated transportation** rather than natural spread.

Thank you
to all colleagues
who provided specimens!



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Thank you for attention!



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Contact us if you have any questions: Natalia Kirichenko (nkirichenko@yahoo.com)
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