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COMPARATIVE ROLE OF OPEN-FIELD AND GREENHOUSE AGROCENOSIS IN THE FORMATION OF THE DIASPIDIDAE (HEMIPTERA: COCCOMORPHA) FAUNA

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The family Diaspididae comprises 422 genera and 2,722 species worldwide and is considered an important object of international phytosanitary control due to its high invasive potential and broad polyphagy [1]. In recent years, the import of ornamental plant seedlings into Uzbekistan has been increasing rapidly; however, the scale insect fauna of the region has traditionally been studied mainly in open-field environments, such as orchards, parks, and public gardens. As a result, the role of greenhouse agrocenoses as a potential “gateway” for the introduction and a reservoir of coccoids has remained largely unassessed.

This study is devoted to the first comparative analysis of the results of open-field and greenhouse surveys conducted using a standardized methodology in Andijan Region during 2022–2025, with the aim of distinguishing the autochthonous and introduced components of the regional Diaspididae fauna.

The study was conducted during 2022–2025 in fruit and ornamental gardens and public green spaces (open-field sites) across 14 districts and cities of Andijan Region,

as well as in seven commercial greenhouses located in five districts. Specimens were collected from infested twigs and leaves using entomological needles and fine brushes and were fixed in 70% ethanol; specimens intended for molecular analysis were preserved in 96% ethanol. Permanent microscopic slides were prepared according to the methodology of Kosztarab and Kozár (1988) [2] and examined using an A15.2601-T-T light microscope (Beijing, China) at magnifications of 40×, 100×, and 400×. Species were identified based on pygidial morphology, including the L1–L3 lobes, macroducts, gland spines, and perivulvar disc pores. Zoogeographical grouping was performed based on data from the ScaleNet database [1]. The specimens are deposited in the entomological collection of Andijan State University.

A total of 11 species belonging to eight genera were recorded in open-field conditions. In terms of species richness, *Lepidosaphes* Shimer, 1868 (3 species; 27.3%) and *Diaspidiotus* Berlese, 1896 (2 species; 18.2%) were the leading genera, while the remaining six genera—*Prodiaspis*, *Unaspis*, *Chionaspis*, *Aulacaspis*, *Parlatoria*, and *Salicicola*—were each represented by a single species (9.1%). Based on the 456 specimens collected, however, the pattern of dominance differed, with *Diaspidiotus salicis* (Lupo, 1953) and *Parlatoria oleae* (Colvée, 1880) being the most widely distributed species [7].

Under greenhouse conditions, six coccoid species belonging to three families were identified, of which *Chionaspis salicis* (Linnaeus, 1758) and *Chrysomphalus dictyospermi* (Morgan, 1889) belonged to the family Diaspididae [3]. In February 2025, *Pseudaulacaspis cockerelli* (Cooley, 1897) was recorded for the first time in Uzbekistan from *Phoenix roebelenii* cultivated in a greenhouse in Andijan city. At the same time, the genus *Pseudaulacaspis* was also recorded from Uzbekistan for the first time. Of the 20 plants examined, 10 were infested, with a mean population density of 20 individuals/cm² (range: 12–28) [5].

A comparative analysis of the two environments revealed the following pattern (Fig. 1.).

Fig. 1. Comparative characterization of the open-field and greenhouse Diaspididae complexes (Andijan region, 2022–2025). Summary: open field shows higher species diversity with seasonal cycles, greenhouse has fewer species but year-round activity.

While the open-field complex is composed predominantly of autochthonous elements of the Irano-Turanian subregion, including *Lepidosaphes turanica*, *Diaspidiotus elaeagni*, and *Salicicola archangelskyae*, the greenhouse complex consists mainly of allochthonous species of tropical and subtropical origin with a broad polyphagous feeding range. The zoogeographical analysis of the regional coccoid fauna further confirms this pattern [4].

An important finding is that *Pseudaulacaspis cockerelli* was not recorded during open-field monitoring conducted in 2022–2024 [2], indicating that the species has not yet spread into the natural environment and is currently restricted to protected cultivation. At the same time, the detection of *Diaspidiotus ostreaeformis* on *Salix integra*, with a density of 15–20 scale covers per 10-cm twig, indicates that the autochthonous complex has not yet been fully inventoried [6].

When all available data are considered together, the 11 species recorded in open-field conditions, supplemented by *Diaspidiotus ostreaeformis* and the greenhouse-detected species *Chrysomphalus dictyospermi* and *Pseudaulacaspis cockerelli*, bring the number of currently known Diaspididae species in the region to 14. The third species recorded in the greenhouse, *Chionaspis salicis*, was not counted again because it was already included in the open-field species list. Its occurrence in both environments indicates that autochthonous species are capable of adapting to and persisting under protected cultivation conditions.

Considering the proximity of the study area to the border with Kyrgyzstan (approximately 30 km), the risk of transboundary spread of species introduced through greenhouses is considered realistic.

The Diaspididae fauna of Andijan Region is ecologically divided into two complexes with limited overlap: an Irano-Turanian autochthonous core associated with open-field habitats and an allochthonous complex of tropical origin associated with greenhouse environments.

Greenhouses serve as gateways for the introduction and stable reservoirs of new scale insect species in the region; the first record of *Pseudaulacaspis cockerelli* provides direct evidence of this process.

In addition to open-field habitats, phytosanitary monitoring should include the regular inspection of nurseries and greenhouses, as well as imported planting material.

The increase in the known regional Diaspididae species list from 11 to 14 within a short period highlights the need to continue faunistic inventories, including the integration of morphological analysis with molecular identification.

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