

## SPIDERS AND OTHER ARTHROPODS OF CHERNIVTSI POULTRY FARM (UKRAINE) AND THE PRELIMINARY DATA ABOUT BACTERIA INHABITING THEIR EXTERNAL SURFACES

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### ABSTRACT

We inventoried the fauna of synanthropic spiders and their prey occurring in different premises of Chernivtsi poultry farm in 2015 and compared with the data obtained in 2011. *Steatoda castanea* (Clerck, 1757), *Ph. phalangioides* (Fuesslin, 1775), *Ph. ponticus* Thorell, 1875, and *Tegenaria domestica* (Clerck, 1757) formed the dominant nuclei of studied spider assemblages in both years. Spider assemblages of production premises are shown to be more vulnerable in comparison with those in administrative offices, storage rooms, etc. The premises of the last type can be considered as buffer zones to ensure the survival of different spider species and maintenance of normal structure of synanthropic spider assemblages. Spiders on the premises of Chernivtsi poultry farm prey on a wide range of arthropods dominated by Diptera. Nine bacterial species were detected on the external surfaces of studied arthropods, namely *Staphylococcus saprophyticus*, *S. aureus*, *Streptococcus agalactiae*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Proteus mirabilis*, *Escherichia coli*, and *Pseudomonas aeruginosa*. Frequency isolation varied from 10 % (*Pseudomonas aeruginosa*) to 80 % (*Escherichia coli*). The number of bacteria varied from 3.18 log CFU/ml (for *Escherichia coli* isolated from the surface of *Lithobius* sp.) to 5.65 log CFU/ml (for *Pseudomonas aeruginosa* isolated from the surface of *Fannia* sp.). Among the detected bacterial species *S. saprophyticus*, *S. aureus*, *P. aeruginosa*, and *K. pneumoniae* are known to be of high medical importance. Our study reveals limited role of spiders in the dissemination of bacteria. It is caused by the dominance of web-builders which avoid frequent moves in the spider assemblages inhabiting the buildings of the studied poultry farm. Moreover, spiders eliminate from the buildings such important mechanical vectors of potentially virulent bacteria as Diptera, Myriapoda, Coleoptera being predators themselves.

**Keywords:** Araneae, spider assemblages, prey, external bacteria.

## INTRODUCTION

Throughout the history humans have been sharing living spaces with a variety of invited and uninvited guests spanning the tree of life, from large vertebrates (e.g., pets and livestock) to microorganisms (NESCent Working Group., 2015; Madden et al., 2016). Although we know very little about the arthropods we share our homes with apart from major pest groups (Bertone et al., 2016). Over the last years arthropods inhabiting buildings draw an increasing attention. Considering their impact as household pests, disease vectors, generators of allergens, and facilitators of the indoor microbiome, advancing our knowledge of the ecology and evolution of arthropods in homes has major economic and human health implications (Bertone et al., 2016). Only few Arthropoda species can be considered as well studied in terms of their aiding in the transmission of various pathogens. Cockroaches are among them. More than 40 pathogenic and nonpathogenic bacterial species have been isolated from cockroaches, among them are: *Entamoeba histolytica*, *Escherichia coli*, *Klebsiella pneumoniae*, *Mycobacterium leprae*, *Shigella dysenteriae*, and *Salmonella* species, including *S. typhi* and *S. typhimurium*, *Serratia* species, and *Staphylococcus aureus* (Sarwar, 2015).

At the same time, arthropods dominating in houses and other buildings, are represented by true flies (Diptera), spiders (Araneae), beetles (Coleoptera), and wasps and kin (Hymenoptera, especially ants: Formicidae) (Fedoriak, 2010; Bertone et al., 2016). However, they remain insufficiently studied in buildings of different types, including poultry farms. The majority of researches of arthropods from poultry farms are aimed on study chicken ectoparasites – chicken mite (*Dermanyssus gallinae*), northern fowl mite (*Ornithonyssus sylviarum*), chicken body louse (*Menacanthus stramineus*), bedbug (*Cimex lectularius*) (Lancaster & Meisch, 1986; Axtell & Arends, 1990; Sreenivasa Murthy & Panda, 2016). To the best of our knowledge no complex study of free-living arthropods inhabiting poultry farms is available. Nowadays, poultry production has become a major agricultural industry. Meanwhile, the contaminated products of poultry farms pose a health risk to consumers (Esteban et al, 2008; Fotin, Koval, 2013). It is worth mentioning that in Ukraine the cases of poisoning and toxicosis after consuming the poultry products were reported to be caused by pathogenic and conditionally pathogenic microbiota, such as *S. aureus*, *E. coli*, *K. pneumoniae*, *E. agglomerans*, *P. mirabilis*, *Y. enterocolitica*, *C. diversus*, *C. jejuni*, *P. aeruginosa* and their associations (Fotin & Koval, 2013).

Arthropods are known to be potential vectors of human and animal pathogens (including in the premises for livestock and poultry production) and insects were proved to carry a large antibiotic resistant and potentially virulent enterococcal community in confined swine operations (Ahmad et al., 2011). It is important to learn more about arthropods inhabiting premises of poultry farms and associated with them microbiota.

In the study we focused on spider assemblage inhabiting different types of premises of the poultry farm, located in Chernivtsi region, Ukraine. We also analyzed trophic relations between spiders and other arthropods of the mentioned farm and conducted an initial analysis of bacteria inhabiting external surfaces of the most dominant arthropods.

## MATERIALS AND METHODS

Studied arthropods were collected in July-August 2015 in the different premises of the Private Company Chernivtsi poultry farm, located in the village of Valia Kuzmina (48°11'01"N 26°01'06"E), Chernivtsi region, Ukraine. The studied poultry farm specializes in the production of hen eggs. It includes 12 separate premises: 10 houses for poultry, 1 egg storage room, 1 office building. The dimensions of each poultry house are an average 140 m by 20 m with an average area of 2800 m<sup>2</sup>. 6-7 lines of 4-tiered cages are placed in each poultry house. Maximum farm capacity is 500,000 layers.

The arthropods were hand collected exclusively in the premises of the study farm. The amount of the collected spiders was as follows: in the poultry house #1 – 36 specimens, in the poultry house #9 – 69 specimens, in the office building – 40 specimens; the spider prey was collected in the poultry house #1. The majority of arthropods was used to estimate the species composition of both spider assemblages and their prey. For that purpose spiders were

collected and preserved in 70° ethanol; insects were collected from the spider nets into dry tubes with cotton packing.

***The arthropods for the microbiological studies were sampled individually into sterile containers.***

The arthropods were detected at the Department of Ecology and Biomonitoring, Yuriy Fedkovych Chernivtsi National University, Chernivtsi, Ukraine. Certain insects (mostly Diptera) were kindly identified by Victoria Yasinsky (entomologist of Zhytomyr Regional Laboratory Center of Sanitary and Epidemiological Service of Ukraine).

Microbiological studies were carried out at the Scientific Research and Educational Center of Molecular Microbiology and the Immunology of Mucous Membranes (Uzhhorod National University) following the standard protocol (Goldman & Green, 2012; Medical Microbiology..., 2011). Microbiological study of insects was performed with the use of swabs in sterile conditions. The object was placed in a test tube containing 10 ml of sterile buffer solution of sodium chloride (pH = 7.0). Then, the method of serial dilution was used to obtain the suspension where microorganisms titre was  $10^{-4}$  CFU/ml. 100 µl of the suspension was evenly distributed on the surface of the medium with a sterile spatula. For the study we used the following media: Endos agar, Meat peptone agar, Strepto agar and Entero agar (Producer: Bio-Rad, France) in 4 repetitions. Petri dishes with study material were incubated in the thermostat at 37°C for 24 hours in aerobic conditions. The chromogenic selected media Uri-Select 4 (Producer: Bio-Rad, France) was used for isolation of microorganisms in aerobic conditions. All isolated microorganisms were identified by applying of appropriate biochemical test-systems LACHEMA according to the instructions.

***Statistical analysis.***

The structure of dominance of spider assemblages was analysed following Stöcker & Bergmann (1977) with dominance classes such as: 31.7-100 % – eudominant; 10.1-31.6 % – dominant; 3.2-10.0 % – subdominant; 1.1-3.1 % – recedent; less than 1 % – subrecedent.

Results were evaluated by standard techniques using MS Excel to calculate the mean values of the amount of bacteria for each isolate from the studied arthropods. As we examined the single samples of different Arthropoda species we did not attempt to reveal reliable distinctions between the mean values.

## RESULTS

In summer 2015, we collected a total of 145 spider specimens representing 9 genera of which 13 were identifiable to the species level. They belong to 8 families with Pholcidae and Theridiidae being the most common. The detected species and genera are listed below alphabetically according to the families following the World Spider Catalog (2017): Agelenidae: *Tegenaria domestica* (Clerck, 1757); Clubionidae: *Clubiona lutescens* Westring, 1851; Dictynidae: *Dictyna uncinata* Thorell, 1856; Dysderidae: *Dysdera* sp.; Lycosidae: *Pardosa agrestis* (Westring, 1861); Pholcidae: *Pholcus alticeps* Spassky, 1932, *Ph. opilionoides* (Schrank, 1781), *Ph. phalangioides* (Fuesslin, 1775), *Ph. ponticus* Thorell, 1875; Pisauridae: *Pisaura mirabilis* (Clerck, 1757), *Pisaura novicia* (L. Koch, 1878); Theridiidae: *Parasteatoda tepidariorum* (C. L. Koch, 1841), *Steatoda castanea* (Clerck, 1757), *S. triangulosa* (Walck., 1802). The majority of the species were presented by singular individuals only.

Table 1 provides the comparison of our recent data on the most abundant species with the published previously (Fedoriak et al., 2011). In summer 2011, we collected 184 spider specimens representing 15 species belonging to 10 families in the premises of the same poultry farm (Fedoriak et al., 2011).

Among the detected from the studied premises spider species (20 species in total) only 7 were collected both in 2015 and 2011: *T. domestica*, *Ph. alticeps*, *Ph. phalangioides*, *Ph. ponticus*, *P. tepidariorum*, *S. castanea*, and *S. triangulosa*. They are recorded from various cities of Ukraine (Fedoriak, 2010; Fedoriak et al., 2012; Fedoriak & Moskaliuk, 2013) and Europe (Helsdingen, 2017) and are considered to be eusynanthropic. All the mentioned species are sit-and-wait predators and use webs to catch the prey. Thus, they do not move often from patch to patch. As it was showed by Vollrath (1985), web-building spider species avoided frequent moves, thus their role in the dissemination of bacteria is notably limited.

Table 1. The most abundant spider species from Chernivtsi poultry farm collected in 2015 and 2011. Numbers show the amount of collected specimens (ind.) and relative abundance of species (%).

Taxa	Recent data (collected in 2015)		Published data (Fedoriak et al., 2011)	
	ind.	%	ind.	%
Agelenidae				
<i>Tegenaria domestica</i> (Clerck, 1757)	11	7.59	25	13.59
Pholcidae				
<i>Pholcus alticeps</i> Spassky, 1932	2	1.38	6	3.26
<i>Ph. phalangioides</i> (Fuesslin, 1775)	35	24.14	27	14.67
<i>Ph. ponticus</i> Thorell, 1875	34	23.44	20	10.87
Theridiidae				
<i>Parasteatoda tepidariorum</i> (C. L. Koch, 1841)	4	2.76	7	3.80
<i>Steatoda castanea</i> (Clerck, 1757)	48	33.10	70	38.04
<i>S. triangulosa</i> (Walck., 1802)	2	1.38	5	2.72

Considering importance of the structure of dominance both for estimation of animal assemblages state and revealing the future tendencies (Fedoriak, 2010), we analyzed the structure of dominance of spider assemblages inhabiting the premises of Chernivtsi poultry farm in 2011 and 2015 following Stöcker & Bergmann (1977).

In 2015, *S. castanea* (33.10%) remained the eudominant species, dominant species were *Ph. phalangioides* (24.14%), *Ph. ponticus* (23.44%), subdominant – *T. domestica* (7.59 %); recedent – *P. tepidariorum* (2.76%), *Ph. alticeps* (1.38%), *S. triangulosa* (1.38 %). The other species belonged to subrecedent class.

In 2011, *S. castanea* was an eudominant species of studied assemblages presenting 38 % of all the collected specimens; dominant species were *Ph. phalangioides* (14.67%), *T. domestica* (13.59 %), and *Ph. ponticus* (10.87%); subdominant – *P. tepidariorum* (3.80 %), *Ph. alticeps* (3.26%); recedent – *S. triangulosa* (2.72%). The other species belonged to subrecedent class.

Thus, the dominant nucleus (the number of all the eudominant, dominant and subdominant species) of Chernivtsi poultry farm indoor spider assemblages undertook minor changes: *S. castanea* remains in the status of eudominant species, *Ph. phalangioides* i *Ph. ponticus* – in the status of dominant species. *T. domestica* in 2011 belonged to dominant species, while in 2015 – to subdominant. *P. tepidariorum* i *Ph. alticeps* did not belong to the dominant nucleus in 2015. Significant changes were observed in the lower classes of dominance. Only *S. triangulosa* remained recedent. All the subrecedent species were collected either in 2011 or 2015 which suggests their accidental occurrence in studied premises.

We obtained important information on spider assemblages of the studied farm collecting spiders in the same production premises – poultry house № 9 both in 2011 and 2015. Obtaining such material poses difficulties due to the peculiarities of production processes.

In 2011, in the poultry house № 9 of Chernivtsi poultry farm the dominant species were *Ph. ponticus* (29.23%), *S. castanea* (27.69%); subdominant – *T. domestica* (10.77%), *Larinioides* sp. (7.69%), and *Drassyllus* sp. (6.15%). The rest of the species belonged to lower classes of dominance.

In 2015, *Ph. ponticus* (46.87%) was detected as an eudominant species in the poultry house № 9; *T. domestica* (18.75%) was dominant; *S. castanea* (9.38%) decreased its relative abundance significantly and was referred to as subdominant species together with *Drassyllus* sp. (6.25%), *Ph. alticeps* (6.25%), *Parasteatoda* sp. (9.38%). Therefore, spider assemblages of production premises that undergo regular mechanical and chemical treatments are more vulnerable. Thus, administrative offices, storage rooms, etc. can be considered as buffer zones to ensure the survival of different spider species and maintenance of normal structure of synanthropic spider assemblage of Chernivtsi poultry farm.

Within the study period of 2015 we also collected 88 individuals of arthropods which were eaten by the spiders inhabiting different premises of Chernivtsi poultry farm. We detected insects (Insecta), crustaceans (Crustacea), millipedes (Myriapoda), and arachnids (Arachnida) among the spider prey. The highest relative abundance was recorded for Diptera (flies, mosquitoes, *Psychoda*, Syrphidae etc.) (46.59%), Coleoptera (10.22 %), Isopoda (9.09%), and Lepidoptera (7.95 %) (Tab. 2).

Table 2. Relative abundance of spider prey from the premises of Chernivtsi poultry farm.

Subphylum/Class	Order	ind.	%
Malacostraca	Isopoda	8	9.09
Arachnida	Araneae	6	6.82
Myriapoda	Lithobiomorpha	4	4.55
	Julida	6	6.82
Insecta	Orthoptera	1	1.14
	Coleoptera	9	10.22
	Lepidoptera	7	7.95
	Hymenoptera	5	5.68
	Diptera	41	46.59
	Dermaptera	1	1.14
Total		88	100

Diptera being the most abundant among the spider prey were represented mostly by the flies *Musca domestica* L., *Fannia canicularis* L., *Calliphora uralensis* Will. and mosquitoes *Culicidae* sp. Beetles were represented mostly by Carabidae spp. and Curculionidae sp.; Isopoda – by wood lice (Oniscidae sp.).

Spiders constituted 6.82 % among the prey, which illustrated the high level of cannibalism. Ants and one specimen of honey bee *Apis mellifera* L. were detected among Hymenoptera. Pincher bug *Forficula auricularia* L. turned out to be the sole representative of Dermaptera. Among the listed above arthropods which we recorded for the studied poultry farm, mostly flies and some representatives of Coleoptera are well known to play an important role in mechanical transmission of pathogens for serious diseases (Axtell & Arends, 1990; Sarwar, 2015). We chose ten individual samples of representatives of the most common spider prey and spiders themselves and sampled them into sterile containers for further microbiological study. We allocated 38 isolates from the external surfaces of mentioned arthropods (Tab. 3-4).

Table 3. Bacteria enumeration (log CFU/ml) of external surfaces of selected arthropods from the premises of Chernivtsi poultry farm after 24 hours incubation at 37°C.

Arthropoda sample	Bacteria species	Number of bacteria log CFU/ml
<i>Musca domestica</i> L.	<i>Staphylococcus saprophyticus</i>	4.31
	<i>Streptococcus agalactiae</i>	4.26
	<i>Enterococcus faecalis</i>	4.09
<i>Fannia</i> sp.	<i>Escherichia coli</i>	4.18
	<i>Enterobacter cloacae</i>	4.18
	<i>Staphylococcus saprophyticus</i>	5.57
	<i>Pseudomonas aeruginosa</i>	5.65
Carabidae sp.	<i>Staphylococcus saprophyticus</i>	4.11
	<i>Klebsiella pneumoniae</i>	4.65
	<i>Streptococcus agalactiae</i>	4.19
	<i>Enterobacter cloacae</i>	4.50
<i>Calliphora</i> sp.	<i>Proteus mirabilis</i>	4.80
	<i>Escherichia coli</i>	4.05
	<i>Streptococcus agalactiae</i>	4.22
	<i>Enterococcus faecalis</i>	3.72
Julida sp.	<i>Staphylococcus saprophyticus</i>	5.05
	<i>Escherichia coli</i>	3.78
	<i>Streptococcus agalactiae</i>	4.19
	<i>Enterococcus faecalis</i>	4.92
Syrphidae sp.	<i>Klebsiella pneumoniae</i>	5.13

	<i>Escherichia coli</i>	3.83
	<i>Enterococcus faecalis</i>	3.68
<i>Lithobius</i> sp.	<i>Staphylococcus saprophyticus</i>	3.91
	<i>Escherichia coli</i>	3.18
	<i>Proteus mirabilis</i>	4.13
	<i>Enterobacter cloacae</i>	4.06
	<i>Staphylococcus aureus</i>	4.63
	<i>Escherichia coli</i>	3.93
Oniscidae sp.	<i>Streptococcus agalactiae</i>	4.11
	<i>Enterococcus faecalis</i>	4.08
	<i>Staphylococcus aureus</i>	4.74
<i>Pholcus ponticus</i> Thor.	<i>Escherichia coli</i>	4.40
	<i>Streptococcus agalactiae</i>	3.89
	<i>Proteus mirabilis</i>	4.56
	<i>Staphylococcus aureus</i>	5.61
<i>Psychoda</i> sp.	<i>Escherichia coli</i>	3.94

All the studied arthropods were proved to host bacteria, represented by 9 species within 8 genera, viz., *Staphylococcus* (2 species), *Streptococcus*, *Enterococcus*, *Klebsiella*, *Enterobacter*, *Proteus*, and *Escherichia*, *Pseudomonas* on the external surfaces. Among them *S. saprophyticus*, *S. aureus*, *P. aeruginosa*, and *K. pneumoniae* are considered to be of high medical importance (Stover et al., 2000; Livermore, 2002; Baxtrom et al., 2006; Fotin & Koval, 2013; Holt et al., 2015; Sarwar, 2015; Tong et al., 2015; Rioua et al., 2016).

The number of bacteria varied from 3.18 log CFU/ml (for *Escherichia coli* isolated from the surface of *Lithobius* sp.) to 5.65 log CFU/ml (for *Pseudomonas aeruginosa* isolated from the surface of *Fannia* sp.). The number of staphylococci was relatively high (3.91-5.61 log CFU/ml). Among the detected bacteria the frequency isolation of pathogenic bacteria was the lowest: 10% for *Pseudomonas aeruginosa* and 20 % for *Klebsiella pneumoniae*. The most common species on the external surfaces of the studied arthropods was *Escherichia coli* (frequency isolation 80 %) (Tab. 4).

Table 4. Bacteria from the external surfaces of selected arthropods inhabiting premises of Chernivtsi poultry farm.  
 “+” - the species was isolated, “-” - the species was not isolated.

Arthropoda sample	<i>Staphylococcus saprophyticus</i>	<i>Streptococcus agalactiae</i>	<i>Staphylococcus aureus</i>	<i>Enterococcus faecalis</i>	<i>Klebsiella pneumoniae</i>	<i>Enterobacter cloacae</i>	<i>Proteus mirabilis</i>	<i>Escherichia coli</i>	<i>Pseudomonas aeruginosa</i>
<i>Musca domestica</i> L.	+	+	-	+	-	-	-	-	-
<i>Fannia</i> sp.	+	-	-	-	-	+	-	+	+
Carabidae sp.	+	+	-	-	+	+	-	-	-
<i>Calliphora</i> sp.	-	+	-	+	-	-	+	+	-
Julida sp.	+	+	-	+	-	-	-	+	-
Syrphidae sp.	-	-	-	+	+	-	-	+	-
<i>Lithobius</i> sp.	+	-	-	-	-	+	+	+	-
Oniscidae sp.	-	+	+	+	-	-	-	+	-
<i>Pholcus ponticus</i> Thor.	-	+	+	-	-	-	+	+	-
<i>Psychoda</i> sp.	-	-	+	-	-	-	-	+	-
Frequency isolation	50%	60%	30%	50%	20%	30%	30%	80%	10%

We isolated *Enterococcus faecalis* from the surfaces of the arthropods of various taxa (frequency isolation 50 %). This bacterium was reported by Ahmad et al. (2011) as the most common among the enterococci from the digestive tracts of house flies and cockroaches from the commercial swine farms in the USA. The authors of the study conclude that house flies and German cockroaches in the confined swine production environment are likely to serve as vectors and/or reservoirs of antibiotic resistant and potentially virulent enterococci and consequently may play an important role in animal and public health (Ahmad et al., 2011).

We isolated *Klebsiella pneumoniae* from the surfaces of both Carabidae and Syrphidae representatives. *K. pneumoniae* is now recognized as an urgent threat to human health because of the emergence of multidrug-resistant strains associated with hospital outbreaks and hypervirulent strains associated with severe community-acquired infections (Holt et al., 2015).

We found *Pseudomonas aeruginosa* to inhabit the surfaces of fly *Fannia* sp. in a large amount (5.65 log CFU/ml). The view is that *P. aeruginosa* is a ubiquitous environmental bacterium that is one of the top three causes of opportunistic human infections (Stover et al., 2000). It is considered to be a problematic pathogen due to the combination of the following: the species' inherent resistance to many drug classes; its ability to acquire resistance via mutations to all relevant treatments; its high and increasing rates of resistance in different localities; and its frequent role in serious infections (Livermore, 2002; Rioua et al., 2016).

We isolated *Staphylococcus aureus* from the surfaces of the arthropods of three taxa, including spiders. *S. aureus* is an important opportunistic pathogen and persistently colonizes about 20% of the human population (Foster et al., 2014) and it is considered to be a major human pathogen that causes a wide range of clinical infections (Tong et al., 2015).

Ten percent of the sampled arthropods were contaminated with two bacteria species, 20 % – with three species, and 70 % – with four bacteria species (Tab. 4). Four bacteria species we found to inhabit the external surfaces of flies (*Fannia* sp. and *Calliphora* sp.), beetle, myriapoda and spider. According to the recent publications, flies are known to transmit numerous diseases to humans. For example, the house fly, which is a common and cosmopolitan species, can carry the pathogens for dysentery (*Shigella dysenteriae*), typhoid fever (*Eberthella typhosa*) and cholera (*Vibrio comma*) on their feet and mouth parts. House flies may also spread rickettsiae of Q fever (*Coxiella burnetii*); viruses of polio, coxsackie and infectious hepatitis; bacteria such as cholera (*Vibrio cholerae*), anthrax, *Campylobacter*, *Shigella*, *Salmonella*, *Escherichia coli*, *Staphylococcus aureus* (Sarwar, 2015). Our samples of flies – *Musca domestica* L. and *Fannia* sp. – were contaminated with three and four bacteria species correspondingly, including such pathogenic for humans and animals bacteria as *Staphylococcus saprophyticus* and *Pseudomonas aeruginosa* (Tab. 4).

Spiders are the second after flies abundant group of arthropods inhabiting buildings (Bertone et al., 2016). The studied sample of *Pholcus ponticus* was contaminated with four bacteria species including such pathogen as *Staphylococcus aureus*. *Staphylococcus aureus* was not previously recorded to be found both in external and internal bacterial community of the spiders even in the studies which were focused on the mentioned bacteria species (Baxtrom et al., 2006; Gaver-Wainwright et al., 2011).

No sufficient information on spider microbiome is available. Few studies have highlighted noteworthy interactions between spiders and associated microbes. For example, colony-wide epizootic mycoses in the African social spider *Stegodyphus dumicola* was observed by Henschel (1998). Intracellular endosymbiotic bacteria (e.g., *Rickettsia* and *Wolbachia*) were shown to influence population sex ratios, dispersal, and post-copulatory behavior of spiders (Goodacre et al., 2009; Gunnarsson et al., 2009; Vanthournout et al., 2011). Vanthournout and Hendrickx (2015) recently applied a combination of cloning assay, DGE profiling and high-throughput sequencing on multiple individuals of dwarf spider *Oedothorax gibbosus* which allowed to detect such bacterial endosymbionts as *Wolbachia*, *Rickettsia*, *Cardinium*, and *Rhabdochlamydia*. Keiser et al. (2016) showed cuticular bacteria to appear detrimental to the African social spider *Stegodyphus dumicola* in mixed but not monoculture exposure. *Bacillus thuringiensis* caused increased mortality when injected into the hemolymph of spiders. No bacterial monocultures increased mortality when applied topically. However, a bacterial cocktail of cuticular bacteria caused weight loss and mortality when applied topically, yet did not detectably alter spider behaviour (Keiser et al., 2016). The authors urge that follow-up studies should test these host–microbe interactions across different social contexts to determine the role that microbes play in colony performance.

A few studies on microbial assemblages associated with spiders are focused on the medical importance of spiders as vectors of potentially human pathogenic bacteria. Baxtrom et al. (2006) showed that common house spiders (Pholcidae, Theridiidae, Lycosidae, Salticidae and others) are unlikely to be a source of methicillin-resistant *Staphylococcus aureus* (MRSA). Of about 100 spiders collected, none was found to carry *Staphylococcus aureus* or

MRSA. Relatively low numbers of microbial flora were isolated, and only a single isolate with pathogenic potential in humans (*Aeromonas* spp.) was recorded to be found both in external and internal bacterial community of the spiders (Baxtrom et al., 2006).

The bacterial diversity of spider *Tegenaria agrestis* was surveyed using a polymerase chain reaction-based assay to determine whether the spider carries any pathogenic bacteria and to determine the ability of the spiders to transfer MRSA. 10 genera of ubiquitous bacteria were found on the exterior surface of the spiders. None of the spiders exposed to MRSA transferred this pathogen (Gaver-Wainwright et al., 2011). Another spider species *Tegenaria saeva* was not found to be a vector or reservoir of community associated methicillin-resistant *Staphylococcus aureus* (Lee, 2010).

Single spider species were studied for the presence of pathogenic bacteria associated with their venom and fangs (Silvestre et al., 2005; Mascarelli et al., 2013).

Therefore, spider microbiome still remains unexplored today. We discovered spiders themselves and their prey in production premises of poultry industry to be contaminated with the wide scope of bacteria, including pathogenic for humans and animals bacteria (*Staphylococcus aureus*, *Staphylococcus saprophyticus*, and *Pseudomonas aeruginosa*). As insects can move freely between animal waste and food they are involved in dissemination of bacteria. According to our recent research, the dominating spider species are web-builders and they cannot play significant role in the spread of bacteria. Moreover, preying on other arthropods spiders eliminate them from the buildings.

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## CONCLUSION

- ✓ Thirteen spider species are recorded from the material, collected in 2015 in the premises of Chernivtsi poultry farm. The dominant nuclei of studied spider assemblages gathered collectively from all the inventoried premises viz., production, storage and administrative buildings remain stable compared with 2011 and include *Steatoda castanea*, *Pholcus phalangioides*, *Pholcus ponticus*, and *Tegenaria domestica*. Spider assemblages of production premises are shown to be more vulnerable in comparison with non-production premises. The latter can be considered as buffer zones to ensure the survival of different spider species and maintenance of the structure of synanthropic spider assemblage.
- ✓ Spiders in the premises of Chernivtsi poultry farm prey on a wide range of arthropods. The representatives of 10 orders of Arthropoda, dominated by Diptera, were detected.
- ✓ In total, 9 species of pathogenic and conditionally pathogenic bacteria, viz., *Staphylococcus saprophyticus*, *Staphylococcus aureus*, *Streptococcus agalactiae*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Proteus mirabilis*, *Escherichia coli*, and *Pseudomonas aeruginosa* were detected on the external surfaces of studied arthropods.

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