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The incidence and severity of take-all in winter wheat and *Gaeumannomyces graminis* soil inoculum levels in Lithuania

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Abstract

In recent years, because of the constantly changing farming systems and under a limited choice of alternative crops, many farmers have been growing the same crops in the same fields for two or more consecutive years. This practice has resulted in increasing incidence and severity of take-all in winter wheat (*Triticum aestivum* L.) crops. The aim of this study was to evaluate the incidence and severity of take-all in winter wheat and estimate the level of *Gaeumannomyces graminis* var. *tritici* (*Ggt*) and *G. graminis* var. *avenae* (*Gga*) inoculum in the soil in three agro-ecological zones (Western, Middle Lowland and Eastern) of Lithuania. During the 2013–2014 period, take-all incidence in winter wheat varied from 2.0% to 92.0% in 81 fields inspected. The highest take-all incidence and take-all index were identified in the Middle Lowland zone, while the lowest in the Western zone. The inoculum level of *Ggt*/*Gga* in the soil was estimated using the bait method by assessing DNA amounts of pathogens in the roots of wheat plants, grown in the soil samples collected in different agro-ecological zones of Lithuania. The amounts of *Ggt*/*Gga* DNA varied considerably among the sites. Averaged data showed the lowest take-all inoculum level in Eastern zone and the highest in Middle Lowland. The highest amount of *Ggt*/*Gga* DNA was established in the samples collected in Pakruojis and Panevėžys districts. In three samples from Raseiniai, Šiauliai and Alytus districts the quantity of fungal DNA was very small 0.188–0.640 pg of fungal DNA μg^{-1} of plant DNA, and in five samples from Šilutė, Tauragė, Telšiai, Kėdainiai and Panevėžys districts no fungal DNA was detected. In this study, the use of different management and different environmental conditions, also unpredictability of the disease (ability to spread in patches), probably were the main reasons, which had significant impact on the marked variation of take-all incidence and severity in winter wheat crops in Lithuania.

Key words: fungal inoculum, quantification, take-all index, *Triticum aestivum*.

Introduction

Take-all is one of the most important root diseases of winter wheat (*Triticum aestivum* L.) in all cropping areas around the world. The disease is of a particular relevance in the countries, including Lithuania, where the wheat cultivation area has increased and monocropping (crops grown in the same field for two or more consecutive years) is a common practice. Take-all can cause plant death or premature maturation resulting in the appearance of white-heads, which significantly reduce grain yield and quality (Gutteridge et al., 2003). Yield losses as high as 50–60% can be incurred due to the severe epidemics (Shoeny et al., 2001; McMillan et al., 2011). The main causal agent of this disease, soilborne fungus *Gaeumannomyces graminis* var. *tritici* (*Ggt*), is the most economically important pathogen (Hornby et al., 1998). Based on pathogenicity, *G. graminis* species includes three other varieties: *G. graminis* var. *avenae* (*Gga*), *G. graminis* var. *graminis* (*Ggg*) and *G. graminis* var. *maydis* (*Ggm*). The two last mentioned varieties (*Ggg* and *Ggm*) are more closely associated with take-all in rice and maize, respectively, and are weakly dangerous on wheat. *Gga* is a causal agent of take-all in oats, but may affect wheat too (Walker, 1981; Freeman, Ward, 2004).

G. graminis var. *tritici* inoculum can persist for long periods saprophytically in soil on crop debris (Curtin et al., 2008). Two stages of infection are described: primary infection occurs from infected residues on seminal roots, and secondary infection results by mycelial contact from infected roots to susceptible roots (Bailey, Gilligan, 1999). For this reason, the disease is most commonly distributed in circular patches. Take-all is manifested as dark brown to black rotten lesions on the roots (Bockus, Tisserat, 2000). The early infection

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disrupts the water and nutrient flow to the plant stem, which leads to premature maturation. Because of rotted roots, wheat plants with severe infection are easily pulled from the soil (Cook, 2003).

Take-all development and severity depend on the amount of initial inoculum of *G. graminis* var. *tritici* in the soil and environmental conditions. Primarily, this is determined by the field history and by the severity of the disease in the previous crop (Hornby et al., 1998). Severity of take-all is usually low in the first wheat after non-host crops and can be high in the second crops (Werker, Gilligan, 1990; Cromey et al., 2006; Jenkyn et al., 2014). However, the prolonged cereal cultivation in the same field shows partial efficiency in limiting take-all risk; the research shows that usually after the fourth year, in later seasons a take-all decline occurs (Weller et al., 2002; Cook, 2003; 2007; Bailey et al., 2009). Soil type and moisture are very important factors for the spread of take-all. The disease is likely to be more active in the soils with high light silt content, especially in wet seasons (Hornby et al., 1998; Cook, 2003). Control of take-all is complicated, because resistant wheat cultivars are not available and the choice of crop protection products is very limited (Weller et al., 2002; Gutteridge et al., 2003; Kwak, Weller, 2013). Depending on the soil and climate of the location, crop rotation with a break of non-host plants for one or two years is a most effective method in controlling take-all (Cook, 2003; Ramanauskienė et al., 2018).

The aim of this study was to evaluate the incidence and severity of take-all in winter wheat crops and estimate the combined level of *G. graminis* var. *tritici* and *G. graminis* var. *avenae* inoculum in the soil in different agro-ecological zones of Lithuania.

Materials and methods

Field sites and sampling. In 2013 and 2014, winter wheat (*Triticum aestivum* L.) plant and soil samples were collected from the commercial fields in three agro-ecological zones of Lithuania. The fields were chosen randomly, and during two years a total of 81 samples from 29 districts (23 samples from Western, 47 samples from Middle Lowland and 11 samples from Eastern zones) were taken. The plant sampling was done at milk-ripening stage. Growth stages were defined according to the BBCH scale (Witzenberger et al., 1989). Approximately 20 plants from 5 places (in total 100 stems) were dug randomly from a field. The plant samples were analysed visually and take-all incidence and severity were determined (Fig. 1). From five spots of each field, 5.5 cm diameter × 10 cm deep soil cores were randomly collected for estimation of inoculum level of *Gaeumannomyces graminis* var. *tritici* and *G. graminis* var. *avenae*.

Disease assessment. The roots of 100 plants collected from the field were analysed for take-all severity, assessed as the percentage of affected root area.

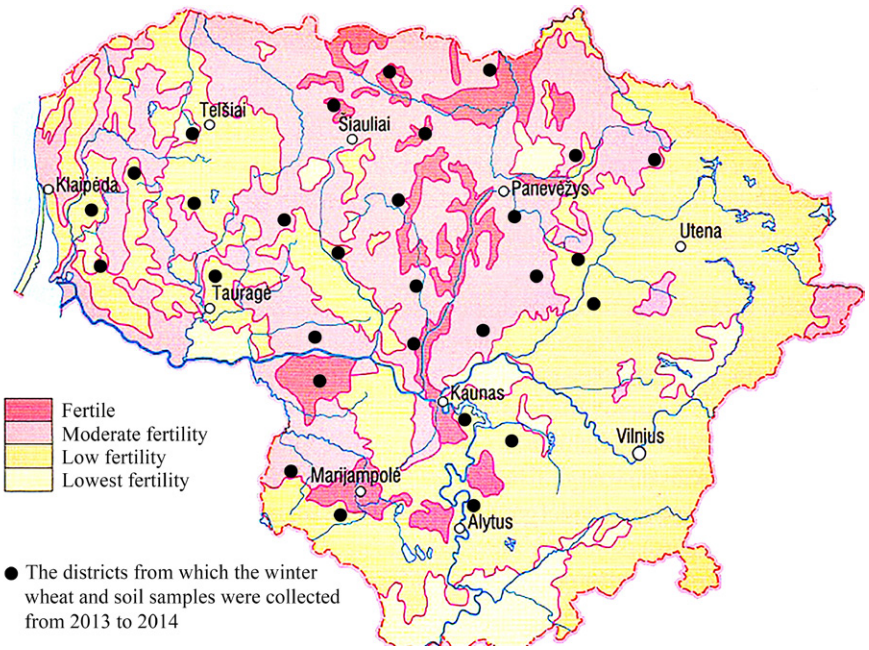

Figure 1. Sampling sites and fertility of Lithuanian soils

Assessments were done according to Bithell et al. (2012) using the 0 to 4 scale, where 0 – no disease, 1 – 1–10% of root system affected, 2 – 11–30% of root system affected, 3 – 31–60% of root system affected, 4 – 61–100% of root system affected. The number of plants in each sample was used to calculate the take-all index (TAI):

$$TAI = (0N1 + 10N2 + 30N3 + 60N4 + 100N5) / T,$$

where N is the number of plants in each of the five infection categories, T – the total number of assessed plants. The incidence of take-all was calculated as the percentage of infected plants in each sample.

Inoculum in the soil. The level of inoculum of take-all in the soil was estimated using the bait method (Gutteridge, Hornby, 2003). Five plastic cups, 7.5 cm in diameter and 11 cm in height, containing drainage holes were filled with soil samples from each field. Prior to that, 1 cm of coarse sand was placed on the bottom of each cup. Breeding varieties for resistance to take-all is the most promising way to protect cereals, but no effective resistance has been achieved yet (Gutteridge et al., 2003; Yang et al., 2011), therefore we arbitrarily chose a Lithuanian winter wheat cultivar ‘Kovas DS’.

Ten non-treated grains were placed on the soil surface and covered with clay beads. The cups were watered and placed in a controlled growth chamber at 12°C in a 16/8 day/night regime. The cups were watered twice a week. After six weeks, plants were pulled from the soil. The roots were washed and homogenized in liquid nitrogen. Homogenized samples were stored in 2-ml micro centrifuge tubes at −20°C for DNA extraction.

DNA extraction and real-time polymerase chain reaction (RT-PCR). G. graminis var. *tritici* and *G. graminis* var. *avenae* DNA extraction from winter wheat roots was carried out on composite samples. DNA was extracted using a commercial genomic DNA purification kit (Thermo Fisher Scientific Baltics, Lithuania) according to the manufacturer's instructions. The DNA extraction was done in two replicates from one homogenized sample.

Real-time PCR was carried out in 20 µl of reaction mixture comprising 10 µl Maxima™ SYBR Green qPCR Master Mix (Thermo Fisher Scientific Baltics), 2.5 µl tested DNA, 6.9 µl nuclease-free water and 0.3 µl of each forward and reverse primer. DNA of *G. graminis* var. *tritici* plus *avenae* (*tritici/avenae*) was quantified using specific combined primers Ggtritici/avenaeF and Ggtritici/avenaeR (Bithell et al., 2012). Primers Hor1F/Hor2R were used for the detection of plant DNA and for normalisation of the reactions (Table 1).

A five-fold dilution series with *G. graminis* var. *avenae* (*Gga*) DNA isolated from pure cultures obtained from the VTT Technical Research Centre of Finland Culture Collection and with plant DNA extracted from winter wheat were used for individual standard curves. The reactions were calculated as pg of fungal DNA per µg of plant DNA (Nicolaisen et al., 2009). PCR was performed in three replications with a 7900HT Fast Sequence Detection System (Applied Biosystems, USA). Procedure regime was modified by Liu et al. (2013) and following cycling regime 95°C for 10 min (95°C for 15 s and 60°C for 35 s) were used.

Table 1. Specific primers and their sequences

Target	Primer	Sequence (5'-3')
G. graminis var. *tritici/avenae*	GgtriticiavenaeF	AACTCCAACCCCTGTGACCA
	GgtriticiavenaeR	CGCTGCGTTCTTCATCGATGCC
Plant EF1α	Hor1F	TCTCTGGGTTTGAGGGTGAC
	Hor2R	GGCCCTTGTACCAGTCAAGGT

Statistical analysis. Data of take-all incidence and take-all index were analysed using the software *SAS*, version 9.4 (SAS Institute Inc., USA) and presented as mean and standard errors of the means. PROC CORR procedure was used for Person's correlation test between disease infection indicators (take-all incidence and take-all index), cultivation areas and amounts of fungal DNA.

Results

The incidence and severity of take-all in Lithuania. The fields were chosen arbitrarily and the results of the present study represent the overall take-all occurrence in Lithuania. Over the 2013–2014 period, the presence of take-all was identified in 95.0% of the total 81 winter wheat fields inspected. Depending on the location, environmental and cultivation conditions the disease incidence in winter wheat fields varied from 2.0% to 92.0% (Table 2). Of all the tested fields, in four of them symptoms of take-all were not identified.

Table 2. The disease incidence and take-all index (TAI) (%) in winter wheat, 2013 and 2014

District	Incidence	TAI	Incidence	TAI
1	2	3	4	5
		Western zone		
Kelmė	10.0	1.60	na	na
Klaipėda	38.0	7.40	12.0	1.20
Plungė	34.0	5.00	4.0	0.40
Raseiniai	28.0	9.40	2.0	0.20
Šilalė	68.0	21.60	na	na
Šilutė	0	0	4.0	0.40
Tauragė	4.0	0.40	14.0	2.40
Telšiai	12.0	1.20	12.0	1.20
Mean	24.3 ± 9.41	5.83 ± 3.41	8.0 ± 2.13	0.90 ± 0.34
		Middle Lowland zone		
Jonava	44.0	4.40	6.0	0.60
Joniškis	na	na	36.0	14.40
Jurbarkas	na	na	8.0	0.80
Kaišiadorys	82.0	24.80	na	na
Kaunas	na	na	0	0
Kėdainiai	38.0	11.80	38.0	13.60
Kupiškis	na	na	0	0
Marijampolė	60.0	15.60	24.0	7.00
Pakruojis	6.0	0.60	6.0	0.60
Panevėžys	64.0	17.20	80.0	14.00
Pasvalys	46.0	15.40	92.0	20.40
Prienai	70.7	8.67	20.0	2.00
Radviliškis	12.0	1.20	32.0	5.80

Table 2 continued

1	2	3	4	5
Šakiai	34.0	4.60	12.0	1.20
Šiauliai	4.0	0.40	24.0	2.40
Vilkaviškis	100.0	29.20	0	0
Mean	46.7 ± 8.73	11.16 ± 2.76	25.2 ± 9.68	5.49 ± 4.57
Eastern zone				
Alytus	42.0	7.40	na	na
Anykščiai	na	na	8.0	0.80
Rokiškis	na	na	12.0	1.20
Ukmergė	58.0	11.80	26.0	7.60
Širvintos	na	na	10.0	1.00
Mean	50.0 ± 8.00	9.60 ± 2.20	14.0 ± 4.08	2.65 ± 1.65
Mean in Lithuania	40.3 ± 9.41	8.96 ± 3.41	15.7 ± 3.43	3.01 ± 1.52
Min	4.0	0.40	2.0	0.20
Max	82.0	29.20	92.0	20.40

Min – the lowest, Max – the highest take-all incidence and TAI; ± – standard error of the mean, na – not assessed

A comparison of data from different agro-ecological zones of Lithuania indicated that the highest take-all incidence and take-all index were in the Middle Lowland zone and the lowest in the Western zone. The highest (29.20%) TAI was established in the Middle Lowland zone, while the lowest (0.20%) TAI was determined in the Western zone.

Take-all inoculum level in the soil. Inoculum level of *G. graminis* var. *tritici* plus *G. graminis* var. *avenae* (*Ggt/Gga)* in the soil was estimated using the bait method by assessing DNA amounts of pathogens in plant roots, grown in the soil samples from different agro-ecological zones of Lithuania. The lowest concentrations of pathogens were established in Eastern zone, while the highest concentrations were determined in Middle Lowland zone (Table 3).

Table 3. The amounts of *Gaeumannomyces graminis* var. *tritici* plus *avenae* (*Ggt*/*Gga*) (pg of fungal DNA per µg of plant DNA) in the soil described by mean values and 95% confidence interval, 2013 and 2014 (bait method)

District	*Ggt*/*Gga* DNA (pg of fungal DNA μg^{-1} of plant DNA)		
	2013	2014	total amount of 2013 and 2014
1	2	3	4
Eastern zone			
Alytus	1794.35	0.642	1794.99
Anykščiai	na	442.67	442.67
Rokiškis	na	9.66	9.66
Ukmergė	4476.07	1838.21	6314.28
Širvintos	na	3767.33	3767.33
Mean	3135.21 ± 2626.4	1211.70 ± 1414.0	2465.76 ± 2278.8
Amount	6270.42	6058.51	12328.93
Middle Lowland zone			
Jonava	1084.94	54.68	1139.62
Joniškis	na	157.33	157.33
Jurbarkas	na	223.92	223.92
Kaišiadorys	1857.41	na	1857.41
Kaunas	850.25	4519.02	5369.27
Kėdainiai	820.94	0	820.94
Kupiškis	na	252.35	252.35
Marijampolė	1734.86	517.32	2252.18
Pakruojis	9117.16	8.68	9125.84
Panevėžys	5158.63	0	5158.63
Pasvalys	2703.21	1221.82	3925.04
Prienai	122.09	137.82	259.90
Radviliškis	67.36	593.93	661.29
Šakiai	421.70	179.04	600.74
Šiauliai	694.21	0.19	694.40
Vilkaviškis	37.34	1496.32	1533.66
Mean	1897.70 ± 1402.4	624.16 ± 1106.2	2127.03 ± 1239.0
Amount	24670.11	9362.41	34032.52
Western zone			
Kelmė	587.23	na	587.23
Klaipėda	2095.06	120.61	2215.67
Plungė	4914.32	721.16	5635.47
Raseiniai	1335.03	0.57	1335.60
Šilalė	1731.88	na	1731.88

Table 3 continued

1	2	3	4
Šilutė	735.77	0	735.77
Tauragė	507.26	0	507.26
Telšiai	14179.09	0	14179.09
Mean	3260.71 ± 3211.0	140.39 ± 308.7	3366.00 ± 3238.0
Amount	26085.64	842.34	26927.98
Mean in Lithuania	2479.40 ± 1685.0	625.51 ± 169.1	2527.22 ± 1159.0
Amount in Lithuania	57026.17	14723.77	73289.42
Min	37.34	0.19	9.66
Max	9117.16	4519.02	14179.09

Min – the lowest, Max – the highest amount of *Ggt*/*Gga* DNA; ± – 95% confidence interval; na – not assessed

Quantification of the biomass of *Ggt*/*Gga* DNA showed that for each agro-ecological zone there is a large variation between samples, reflected by the 95% confidence interval. Of the total 81 samples investigated the highest amounts of *Ggt*/*Gga* DNA was established in the samples collected in Pakruojis and Panevėžys districts, while the lowest in Rokiškis district. In three samples from Raseiniai, Šiauliai and Alytus districts the quantity of fungal DNA was very small – 0.188–0.642 pg of fungal DNA μg^{-1} of plant DNA, and in five samples from Šilutė, Tauragė, Telšiai, Kėdainiai and Panevėžys districts no fungal DNA was detected.

The data averaged over two years showed the highest incidence and severity of the disease in Middle Lowland zone; however, the highest amounts of *Ggt*/*Gga* DNA were established in the samples from Western zone (Fig. 2).

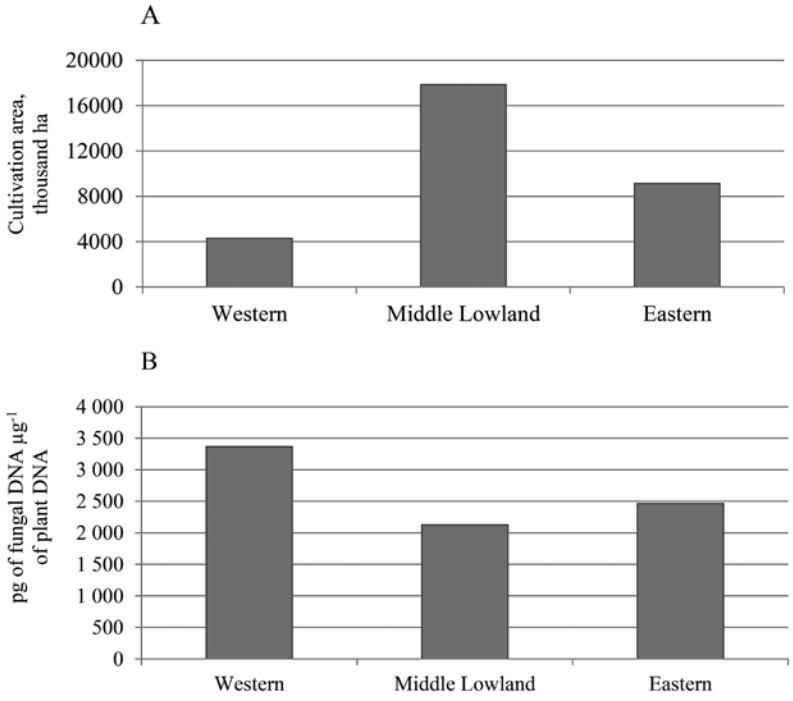

Figure 2. Average of winter wheat cultivation area (A) and amounts of *Gaeumannomyces graminis* var. *tritici/avenae* DNA (B) in different agroecological zones of Lithuania, 2013 and 2014

Correlation analysis. Pearson's correlation test showed moderately significant relationships between grown areas of winter wheat in Lithuania and take-all inoculum level in the soil (measured by estimating the amounts of *G. graminis* var. *tritici/avenae* DNA in the roots of winter wheat) and disease severity (Table 4). Correlation analysis demonstrated a weak correlation between take-all incidence and cultivation area. However, take-all incidence and severity did not correlate with the amounts of *G. graminis* var. *tritici/avenae* DNA.

Table 4. Pearson correlation coefficients

Variable	Correlation coefficient	
	cultivation area	*G. graminis* var. *tritici/avenae* DNA
Gaeumannomyces graminis var. *tritici/avenae* DNA	0.566*	–
Take-all index (TAI)	0.565*	0.190
Take-all incidence	0.473	0.175

* – significance of correlation coefficients at the < 0.05

Discussion

Different growing technologies, including reduced soil tillage and continuous wheat sowing, have become more popular in recent years (Bankina et al., 2015). Most often farmers do not necessarily use rotation and repeatedly grow wheat in the same field for at least 2–3 years, which strongly affects the amount of *Ggt* inoculum in the soil. Previous research on *Ggt* inoculum has focused on the possibility of infecting other crops, inoculum transfer in a break year, the survival of inoculum in field after harvesting and effects of environmental conditions and different length of break crops on *Ggt* inoculum in the soil (Gutteridge, Hornby, 2003; Gutteridge et al., 2006; 2007; Bithell et al., 2009). Take-all control is complicated, because the disease occurs in patches; the severity of the disease can significantly differ in different parts of the same field. Also the progression of disease epidemics in winter wheat is significantly influenced by the number of interacting factors (Hornby et al., 1998; Freeman, Ward, 2004; Bailey et al., 2005; Ennaifar et al., 2007). In this study, the cropping histories of inspected fields were not known, and it is likely that growing technologies, environmental and weather conditions differed between field sites. Therefore, the results in this paper show the overall prevalence of take-all in Lithuania.

Previous research has shown that high soil moisture levels are related to higher severity of take-all (Cook, 2003; Pillinger et al., 2005; Smiley, 2009). Cook (1981) indicated that for take-all to spread it needs a field with high water potential largely for the pathogens to grow and infect the plants in the 25 cm layer of the soil. The findings of this research indicated that the highest take-all severity was in the Middle Lowland zone and the lowest in the Western zone. Surprisingly, our findings slightly contradict the main aspects of the epidemiology of the disease. According to the mean annual amount of precipitation in our country (http://old.meteo.lt/english/climate_precipitation.php), the greatest amount of precipitation falls annually in the Western zone and the lowest in the Middle Lowland. In Lithuania, the largest production areas of winter wheat with the highest productivity are concentrated in the Middle Lowland zone (Statistics Department of Lithuania, https://osp.stat.gov.lt/statistiniu-rodikliu-analize#/), and it is normal that this important risk factor caused stronger development of the disease in this zone.

Soil type is a great risk factor; on lighter and low-mineral soils take-all can be very severe in wet seasons (Hornby et al., 1998). The most fertile soils in our country are in the Middle Lowland zone, and the least fertile soils are in the sandy Eastern zone (Motuzas et al., 2009) (Fig. 1). The study involving 81 fields showed differences of take-all incidence and severity between agro-ecological zones. The highest disease incidence and severity were in the Middle Lowland zone with most fertile soils and the largest production areas of winter wheat in Lithuania, while the lowest in Western zone of our country. Our study showed that the application of intensive growing technologies with continuous wheat sowing and rotations with limited break crops, which are often at greater risk of the disease damage, resulted in higher disease occurrence in the Middle Lowland zone.

Sowing date, tillage type and sequences of the rotations are important risk factors that influence the amounts of take-all and rates of epidemic development. The mentioned factors differed between the sites and were responsible for a strong variation in take-all severity in Lithuania. Series of studies showed negative influence of early sowing on the increase in take-all severity, especially when early sowing prevails in monocultures (Jenkyn et al., 1992). Research has proven that winter wheat sown with a delay left less inoculum of *Ggt* in the soil than sown early, because conditions for infection were less favourable and less inoculum of pathogens survived to infect plants (Hornby et al., 1998).

Tillage type influences the spatial structure of the diseases and might have an effect on prevalence of take-all. Ploughing can bury the infected residues, whilst tillage breaks up the infected plant residues which are more quickly degraded by other soil microorganisms (Wilkinston et al., 1985). Gosme et al. (2007) also have found a significant effect of soil management. Studies have shown higher take-all level in the plots with conservation tillage than in ploughed ones. Because the pathogens do not survive well in the soils without their hosts, it is very important to carefully plan crop rotation, which is one of the economically viable cultural take-all control methods (Cook, 2003; Jenkyn et al., 2014). Take-all severity is generally lower in wheat crops grown after non-host break crops. In the study conducted in Lithuania the take-all incidence and index clearly varied depending on the rotations. Out of the three winter wheat rotations, the lowest take-all incidence and severity were identified in the crop rotation, where winter wheat had been sown after oil seed rape, compared to winter wheat monoculture and second winter wheat (Ramanauskienė et al., 2018).

The amount of *Ggt* inoculum in the soil at the time of sowing greatly influences the primary infection of take-all in winter wheat. Primarily this is determined by the cropping history, the level of the disease in previous crop and inoculum decay time (Hornby et al., 1998). As expected, the *Ggt*/*Gga* inoculum level in the soil varied between the locations. The correlation analysis demonstrated that winter wheat cultivation area had influence on take-all severity and inoculum level in the soil. Because in this study the cropping histories of the inspected fields were not known, it is difficult to account for the main reasons for these differences. Therefore, the results in this paper show the overall amount of *Ggt*/*Gga* inoculum level in Lithuania.

Conclusions

1. Different site factors, also unpredictability of the disease (ability to spread in patches) are likely to be responsible for the marked variation of take-all prevalence in winter wheat crops. The presence of the disease was identified in 95.0% of the 81 winter wheat fields inspected. Depending on the site, the disease incidence varied from 2.0% to 92.0%.

2. The highest take-all prevalence was detected in the Middle Lowland zone of Lithuania, where the largest production areas of winter wheat are concentrated.

3. A Pearson's correlation test showed very weak relationships between the take-all inoculum level in the soil and the disease severity. The lowest take-all index (TAI) but the highest amounts of *Gaeumannomyces graminis* var. *tritici* plus *avenae* (*Ggt/Gga*) DNA were established in the Western zone.

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References

1. Bailey D. J., Gilligan C. A. 1999. Dynamics of primary and secondary infection in take-all epidemics. Phytopathology, 89: 84–91. https://doi.org/10.1094/PHYTO.1999.89.1.84
2. Bailey D. J., Paveley N., Pillinger C., Foulkes J., Spink J., Gilligan C. A. 2005. Epidemiology and chemical control of take-all on seminal and adventitious roots of wheat. Phytopathology, 95: 65–68. https://doi.org/10.1094/PHYTO-95-0062
3. Bailey D. J., Paveley N., Spink J., Lucas P., Gilligan C. A. 2009. Epidemiological analysis of take-all decline in winter wheat. Phytopathology, 99: 861–868. https://doi.org/10.1094/PHYTO-99-7-0861
4. Bankina B., Ruža A., Paura L., Priekule I. 2015. The effects of soil tillage and crop protection on the development of winter wheat leaf diseases. Zemdirbyste-Agriculture, 102 (1): 67–72. https://doi.org/10.13080/z-a.2015.102.008
5. Bithell S. L., Mclachlan A. R. G., Hide C. C. l., Mckay A., Cromey M. G. 2009. Changes of post-harvest levels of *Gaeumannomyces graminis* var. *tritici* inoculum in wheat fields. Australasian Plant Pathology, 38: 277–283. https://doi.org/10.1071/AP09003
6. Bithell S. L., Mckay A., Butler R. C., Ophel-Keller K., Ophel-Keller H., Hartley D., Cromey M. G. 2012. Predicting take-all severity in second-year wheat using soil DNA concentrations of *Gaeumannomyces graminis* var. *tritici* determined with qPCR. Plant Disease, 96: 443–451. https://doi.org/10.1094/PDIS-05-11-0445
7. Bockus W. W., Tisserat N. A. 2000. Take-all root rot. The Plant Health Instructor. https://doi.org/10.1094/PHI-I-2000-1020-01
8. Cook J. R. 1981. The effect of soil reaction and physical conditions. Asher M. J. C., Shipton P. J. (eds). Biology and control of take-all. Academic Press, p. 343–352.
9. Cook J. R. 2003. Take-all of wheat. Review. Physiological and Molecular Plant Pathology, 62: 73–86. https://doi.org/10.1016/S0885-5765(03)00042-0
10. Cook J. R. 2007. Take-all decline: model system in the science of biological control and clue to the success of intensive cropping. Vincent C. et al. (eds). Biological control: a global perspective. CAB International, chapter 44, p. 399–414. https://doi.org/10.1079/9781845932657.0399
11. Cromey M. G., Parkes R. A., Fraser P. M. 2006. Factors associated with stem base and root diseases of New Zealand wheat and barley crops. Australasian Plant Pathology, 35: 1–10. https://doi.org/10.1071/AP06032
12. Curtin D., Francis G. S., McCallum F. M. 2008. Decomposition rate of cereal straw as affected by soil placement. Australasian Journal of Soil Research, 46: 152–160. https://doi.org/10.1071/SR07085
13. Ennaifar S., Makowski D., Meynard J. N., Lucas P. 2007. Evaluation of models to predict take-all incidence in winter wheat as a function of cropping practices, soil and climate. European Journal of Plant Pathology, 118: 127–143. https://doi.org/10.1007/s10658-007-9119-7
14. Freeman J., Ward E. 2004. *Gaeumannomyces graminis*, the take-all fungus and its relatives. Molecular Plant Pathology, 5: 235–252. https://doi.org/10.1111/j.1364-3703.2004.00226.x
15. Gosme M., Willosquet L., Lucas P. 2007. Size, shape and intensity of aggregation of take-all disease during natural epidemics in second wheat crops. Plant Pathology, 56: 87–96. https://doi.org/10.1111/j.1365-3059.2006.01503.x
16. Gutteridge R. J., Hornby D. 2003. Effects of sowing data and volunteers on the infectivity of soil infested with *Gaeumannomyces graminis* var. *tritici* and on take-all disease in successive crops of winter wheat. Annals of Applied Biology, 143: 272–282. https://doi.org/10.1111/j.1744-7348.2003.tb00295.x
17. Gutteridge R. J., Bateman G. L., Todd A. D. 2003. Variation in the effects of take-all disease on grain yield and quality of winter cereals in field experiments. Pest Management Sciences, 59: 215–224. https://doi.org/10.1002/ps.574
18. Gutteridge R. J., Jenkyn J. F., Bateman G. L. 2006. Effects of different cultivated or weed grasses, grown as pure stands or in combination with wheat, on take-all and its suppression in subsequent wheat crops. Plant Pathology, 55: 696–704. https://doi.org/10.1111/j.1365-3059.2006.01405.x
19. Gutteridge R. J., Jenkyn J. F., Bateman G. L. 2007. The potential of non-pathogenic *Gaeumannomyces* spp., occurring naturally or introduced into wheat crops or preceding crops, for controlling take-all in wheat. Annals of Applied Biology, 150: 53–64. https://doi.org/10.1111/j.1744-7348.2006.00107.x
20. Hornby D., Bateman G. L., Guitteridge R. J., Lucas P., Osbourn A. E., Ward E., Yarham D. J. 1998. Take-all disease of cereals: a regional perspective. CAB International, 384 p.
21. Jenkyn J. F., Gutteridge R. J., Todd A. D. 1992. Effects of sowing winter barley on different dates in autumn on the severity of take-all (*Gaeumannomyces graminis* var. *tritici*) in those and the subsequent crops. Journal of Agricultural Science, 119: 19–25. https://doi.org/10.1017/S0021859600071501
22. Jenkyn J. F., Gutteridge R. J., White R. P. 2014. Effects of break crops, and of wheat volunteers growing in break crops or in set-aside or conservation covers, all following crops of winter wheat, on the development of take-all (*Gaeumannomyces graminis* var. *tritici*) in succeeding crops of winter wheat. Annals of Applied Biology, 165: 340–363. https://doi.org/10.1111/aab.12139
23. Kwak Y.-S., Weller D. M. 2013. Take-all of wheat and natural disease suppression: a review. The Plant Pathology Journal, 29: 125–135. https://doi.org/10.5423/PPJ.SI.07.2012.0112
24. Liu X., Yang L., Zhou X., Zhou M., Lu Y., Ma L., Ma H., Zhang Z. 2013. Transgenic wheat expressing *Thinopyrum intermedium* MYB transcription factor TiMYB2R-1 shows enhanced resistance to the take-all disease. Journal of Experimental Botany, 64: 2243–2253. https://doi.org/10.1093/jxb/ert084
25. McMillan V. E., Hammond-Kosack K. E., Guiteridge R. J. 2011. Evidence that wheat cultivars differ in their ability to build up inoculum of the take-all fungus *Gaeumannomyces graminis* var. *tritici*, under a first wheat crop. Plant Pathology, 60: 200–206. https://doi.org/10.1111/j.1365-3059.2010.02375.x
26. Motuzas A. J., Buivydaitė V. V., Vaisvalavičius R., Šleinys R. A. 2009. Dirvotyra, 286–290 p. (in Lithuanian).
27. Nicolaisen M., Supronienė S., Nielsen L. K., Lazzaro I., Spliid N. H., Justesen A. F. 2009. Real-time PCR for quantification of individual *Fusarium* species in cereals. Journal of Microbiological Methods, 76 (3): 234–240. https://doi.org/10.1016/j.mimet.2008.10.016

28. Pillinger C., Paveley N., Foulkes M. J., Spink J. 2005. Explaining variation in the effects of take-all (*Gaeumannomycesgraminis* var. *tritici*) on nitrogen and water uptake by winter wheat. Plant Pathology, 54: 491–501. https://doi.org/10.1111/j.1365-3059.2005.01229.x
29. Ramanauskienė J., Semaškienė R., Jonavičienė A., Ronis A. 2018. The effect of crop rotation and fungicide seed treatment on take-all in winter cereals in Lithuania. Crop Protection, 110: 14–20. https://doi.org/10.1016/j.cropro.2018.03.011
30. Shoeny A., Jeuffroy M. H., Lucas P. 2001. Influence of take-all epidemics on winter wheat yield formation and yield loss. Phytopathology, 91: 694–701. https://doi.org/10.1094/PHYTO.2001.91.7.694
31. Smiley R. W. 2009. Water and temperature parameters associated with winter wheat diseases caused by soilborne pathogens. Plant Pathology, 93: 73–80.
32. Walker J. L. 1981. Taxonomy of the take-all fungi and related genera and species. Asher M. J. C., Shipton P. J. (eds). Biology of take-all. Academic Press, p. 15–74.
33. Weller D. M., Raaijmakers J. M., Gardener B. B. M., Thomashow L. S. 2002. Microbial populations responsible for specific soil suppressiveness to plant pathogens. Annual Review of Phytopathology, 40: 309–348. https://doi.org/10.1146/annurev.phyto.40.030402.110010
34. Werker A. R., Gilligan C. A. 1990. Analysis of the effects of selected agronomic factors on the dynamics of the take-all disease of wheat in field plots. Plant Pathology, 39: 161–177. https://doi.org/10.1111/j.1365-3059.1990.tb02487.x
35. Wilkinston H. T., Cook R. J., Alldredge J. R. 1985. Relation of inoculum size and concentration to infection of wheat roots by *Gaeumannomyces graminis* var. *tritici.* Phytopathology, 75: 98–103. https://doi.org/10.1094/Phyto-75-98
36. Witzenberger A., Hack H., Van den Boom T. 1989. Erläuterungen zum BBCH-Dezimal-Code für die Entwicklungsstadien des Getreides – mit Abbildungen. Gesunde Pflanzen, 41: 384–388 (in German).
37. Yang M., Mavrodi D. V., Mavrodi O. V., Bonsall R. F., Parejko J. A., Paulitz T. C., Thomashow L. S., Yang H. T., Welle D. M., Guo J. H. 2011. Biological control of take-all by fluorescent *Pseudomonas* spp. from Chinese wheat fields. Phytopathology, 101: 1481–1491. https://doi.org/10.1094/PHYTO-04-11-0096

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Javaklupės išplitimas bei intensyvumas žieminiuose kviečiuose ir *Gaeumannomyces graminis* infekcijos lygis Lietuvos dirvožemiuose

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Santrauka

Pastaraisiais metais dėl nuolat kintančių žemdirbystės sistemų taikymo ir riboto alternatyvių kultūrų pasirinkimo daugelis ūkininkų tuos pačius augalus tame pačiame lauke dažnai augina dvejus ar daugiau metų iš eilės. Tai turi didelę įtaką javaklupės plitimo rizikai žieminių kviečių pasėliuose. Tyrimo tikslas – įvertinti javaklupės išplitimą ir intensyvumą žieminių kviečių pasėliuose ir nustatyti ligos sukėlėjų *Gaeumannomyces graminis* var. *tritici* (*Ggt*) ir *G. graminis* var. *avenae* (*Gga*) infekcijos lygį skirtingų Lietuvos agroekologinių zonų dirvožemiuose. Tyrimo laikotarpiu buvo ištirta 81 žieminių kviečių pasėlis. Priklausomai nuo tyrimo metų ir vietovės, javaklupės išplitimas pasėliuose įvairavo nuo 2,0 iki 92,0 %. Tyrimo duomenimis, javaklupė žieminius kviečius smarkiausiai pažeidė Vidurio žemumos zonoje, o ligos mažiausias intensyvumas nustatytas Vakarų zonoje. *Ggt*/*Gga* infekcijos lygis dirvožemyje buvo nustatytas taikant jauko metodą ir įvertinus patogenų DNR kiekį žieminių kviečių šaknelėse, išaugintose skirtingų Lietuvos agroekologinių zonų dirvožemių mėginiuose. *Ggt*/*Gga* DNR kiekis smarkiai varijavo tarp vietovių. Vidutiniais duomenimis, mažesnis javaklupės infekcijos lygis nustatytas Rytų zonoje, didesnis – Vidurio žemumos zonoje. Didžiausi *Ggt*/*Gga* DNR kiekiai nustatyti Pakruojo ir Panevėžio rajonuose. Trijuose dirvožemio mėginiuose, kurie buvo paimti Raseinių, Šiaulių ir Alytaus rajonuose, nustatyti labai maži kiekiai (tik 0,188–0,640 pg grybo DNR μg^{-1} augalo DNR) patogenų DNR, o penkiuose tirtuose dirvožemio mėginiuose iš Šilutės, Tauragės, Telšių, Kėdainių ir Panevėžio rajonų *Ggt*/*Gga* DNR neaptikta. Nustatyta kad, skirtingų javų auginimo technologijų taikymas ir nevienodos šalies oro bei aplinkos sąlygos, taip pat ligos gebėjimas plisti židiniais, sunkinantis javaklupės kontrolę, tikėtina, buvo pagrindinė priežastis, kuri turėjo esminės įtakos smarkiam javaklupės išplitimo ir intensyvumo varijavimui žieminių kviečių pasėliuose.

Reikšminiai žodžiai: grybo infekcija, javaklupės intensyvumo indeksas, kiekybinis įvertinimas, *Triticum aestivum*.