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Prevalence and genotypic distribution of high-risk human papilloma virus in Gomel region: Screening results of 11,382 women over 2018–2023

Volha P. Lohinava¹✉, Natalia I. Shevchenko¹, Alla V. Voropayeva¹, Elena L. Gasich²

¹ Republican Scientific and Practical Centre of Radiation Medicine and Human Ecology, 290 Ilyich Street, Gomel 246040, Republic of Belarus

² Research Institute of Hygiene, Toxicology, Epidemiology, Virology and Microbiology of the Republican Centre for Hygiene, Epidemiology and Public Health, 23 Filimonov Street, Minsk 220114, Republic of Belarus

✉ Volha P. Lohinava; loginovaolga81@mail.ru

ABSTRACT

INTRODUCTION. High-risk human papillomavirus (hrHPV) is a proven aetiological factor in prevalence of cervical cancer. Screening with HPV genotyping in women and identifying significant regional virus genotypes is vital for implementation of HPV immunisation programmes. **AIM.** This study aimed to examine the prevalence, spectrum, and regional characteristics of hrHPV in women from different districts of Gomel region in 2018–2023, prior to the mass vaccination programme in the Republic of Belarus.

MATERIALS AND METHODS. A total of 11,382 women from Gomel region and the city of Gomel aged 18 to 79 years were examined in 2018–2023. Biomaterial samples (endocervical scrapings) were taken from each study participant for subsequent molecular genetic analysis using polymerase chain reaction.

RESULTS. A total of 14 different HPV genotypes have been detected. The incidence of hrHPV was 9% in the overall population and 9.7% in women of reproductive age. High hrHPV incidence was noted in women of early reproductive age: group of 18–24 years – 18.8% (95% CI 16.8–20.9), 25–29 years – 12.1% (95% CI 10.3–14.1), and 30–34 years – 9.2% (95% CI 7.8–10.7). A single HPV genotype was detected most frequently (78.6%); a combination of two HPV genotypes was detected in 86 patients (14.5%); ≥3 genotypes – in 41 patients (6.9%). The most common genotypes were 16 (52.2%), 18 (15.1%), 51 (18.9%), 56 (9.8%), and 31 (9.7%) HPV. Groups α9 (16 and 31 genotypes), α7 (18 genotype), α5 (51 genotype), and α6 (56 genotype) most frequently caused hrHPV infection in women. A change has been found in the structure of dominant hrHPV genotypes in Gomel region over the past 10 years.

CONCLUSION. A high hrHPV prevalence has been established among women of reproductive age in Gomel region. Data on HPV genomic diversity in the region are essential for molecular epidemiological surveillance and will help assess the effectiveness of the Republican HPV immunisation programme launched in 2025.

Keywords: human papillomavirus; genotype; genomics; uterine cervical neoplasms; women; PCR; HPV; prevalence; immunization programs; immunisation programmes; early diagnosis of cancer

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Распространенность и генотипическая характеристика вируса папилломы человека высокого канцерогенного риска в Гомельской области: результаты скрининга 11382 женщин за 2018–2023 гг.

О.П. Логинава^{1,✉}, Н.И. Шевченко¹, А.В. Воропаева¹, Е.Л. Гасич²

¹ Государственное учреждение «Республиканский научно-практический центр радиационной медицины и экологии человека», ул. Ильича, д. 290, г. Гомель, 246040, Республика Беларусь

² Научно-исследовательский институт гигиены, токсикологии, эпидемиологии, вирусологии и микробиологии государственного учреждения «Республиканский центр гигиены, эпидемиологии и общественного здоровья», ул. Филимонова, д. 23, г. Минск, 220114, Республика Беларусь

✉ Логинава Ольга Павловна; loginovaolga81@mail.ru

РЕЗЮМЕ

ВВЕДЕНИЕ. Вирус папилломы человека (ВПЧ) высокого канцерогенного риска (ВПЧ ВКР) является доказанным этиологическим фактором развития рака шейки матки. Проведение скрининга с генотипированием ВПЧ среди женщин и выявлением значимых для региона генотипов вируса важно для реализации программ вакцинации против ВПЧ.

ЦЕЛЬ. Изучить распространенность, спектр и региональные особенности ВПЧ ВКР у женщин из разных районов Гомельской области за 2018–2023 гг. до начала кампании массовой вакцинопрофилактики в Республике Беларусь.

МАТЕРИАЛЫ И МЕТОДЫ. За 2018–2023 гг. обследовано 11382 женщины из Гомельской области и г. Гомеля в возрасте от 18 до 79 лет. У каждой участницы исследования забирались образцы биоматериала (соскобы из цервикального канала шейки матки) для последующего молекулярно-генетического анализа методом полимеразной цепной реакции.

РЕЗУЛЬТАТЫ. Всего было обнаружено 14 разных генотипов ВПЧ. Частота встречаемости ВПЧ ВКР составила 9% в общей популяции женщин и 9,7% у женщин репродуктивного возраста. Высокая частота встречаемости ВПЧ ВКР отмечена у женщин раннего репродуктивного возраста в группе 18–24 года – 18,8% (95% ДИ 16,8–20,9), 25–29 лет – 12,1% (95% ДИ 10,3–14,1), 30–34 года – 9,2% (95% ДИ 7,8–10,7). Один генотип ВПЧ был обнаружен с частотой 78,6%, сочетание двух генотипов ВПЧ – 14,5%, три и более генотипов – 6,9%. Наиболее распространены ВПЧ 16 (52,2%), 18 (15,1%), 51 (18,9%), 56 (9,8%) и 31 (9,7%) генотипов. Вклад в инфицирование женщин ВПЧ ВКР вносят группы $\alpha 9$ (16 и 31 генотипы), $\alpha 7$ (18 генотип), $\alpha 5$ (51 генотип) и $\alpha 6$ (56 генотип). Выявлено изменение структуры доминирующих генотипов ВПЧ ВКР за последние 10 лет в Гомельской области.

ВЫВОДЫ. Установлена высокая распространенность ВПЧ ВКР среди женщин репродуктивного возраста в Гомельском регионе. Данные о геномном разнообразии ВПЧ в регионе имеют большое значение для молекулярно-эпидемиологического надзора и помогут оценить эффективность программы вакцинации против ВПЧ-инфекции в Республике Беларусь, которая стартовала в 2025 г.

Ключевые слова: вирус папилломы человека; генотип; геномика; новообразования шейки матки; женщины; ПЦР; ВПЧ; распространенность; программы иммунизации; раннее выявление рака

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INTRODUCTION

Human papillomavirus (HPV) is one of the main viral pathogens of the reproductive tract. High-risk HPV (hrHPV) is a proven aetiological factor of cervical intraepithelial neoplasia (CIN) and cervical cancer [1, 2]. International Agency for Research on Cancer classifies HPV subtypes according to their oncogenic potential as follows: carcinogenic HPV subtypes (group 1); probable carcinogenic HPV subtypes (group 2A); possibly carcinogenic HPV subtypes (group 2B); low-risk HPV subtypes (group 3), and subtypes not classified according to their oncogenic potential. HPV genotype 16 has the highest carcinogenic potential; HPV genotypes 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59 are classified as carcinogenic to humans; HPV genotype 68 is probably carcinogenic. HPV 26, 30, 34, 53, 66, 67, 69, 70, 73, 82, 85, and 97 genotypes are possibly carcinogenic; HPV 6, 11, 42, 43, and 44 genotypes have a low carcinogenic risk [3–6]. In addition, there is a classification based on differences in HPV genomes and phylogenetic topology. It distinguishes $\alpha 5$ (26, 51, 69 and 82 genotypes), $\alpha 6$ (30, 53, 56 and 66 genotypes), $\alpha 7$ (19, 39, 45 and 59 genotypes), $\alpha 9$ (16, 31, 33, 35, 52 and 58 genotypes), $\alpha 11$ (34 and 73 genotypes), $\alpha 13$ (54 genotype), and $\alpha 3$ (61 genotype) [7].

The prevalence and spectrum of various HPV genotypes varies across countries and even within a country, with 70% of all CC cases worldwide associated with HPV genotypes 16 and 18 [8, 9]. A relationship has been shown between the detection rate and spectrum of HPV genotypes and factors such as age, sexual behaviour, as well as socioeconomic profile of the study population [10, 11]. For example, HPV genotypes 16, 18, 45, 31, and 33¹ are prevalent in the European region. In Asian countries, genotypes 52 and 58 are second most

common after HPV genotypes 16 and 18, prevailing over genotypes 31 and 45 [9, 12]. These differences may affect both effectiveness of the vaccination programs and the need to adjust screening programs given spreading new virus variants. Therefore, it is relevant to enhance regional screening among women of reproductive age with HPV genotyping for detection of the most significant genotypes, taking into account age groups. These data will facilitate effectiveness assessment of the regional HPV screening and vaccination programmes included in the National Immunisation Schedule of the Republic of Belarus in January 1, 2025, and provide for vaccination of HIV-positive girls and women aged 11 to 50 years not previously vaccinated against HPV infection².

The aim of the work is to study the prevalence, spectrum, and regional HPV profile in women from different districts of the Gomel Region in 2018–2023, prior to start of the mass vaccination campaign in the Republic of Belarus.

MATERIALS AND METHODS

Study design. A total of 11,382 women participated in the study. 11,146 women (86.3% of reproductive age) were residents of four districts in the Gomel region: Khoyniki ($n=2,800$), Chachersk ($n=1,640$), Vetka ($n=1,912$), and Dobrush ($n=4,794$). The average age of the study participants examined in 2018–2021 was 38 ± 10^3 (from 18 to 79). The study also included 236 women (of them 90.7% of reproductive age) examined in 2022–2023 in Gomel city and the region.

Signed informed consents to participate in the study were obtained from all study participants.

Biospecimens. Endocervical swabs were collected by obstetricians and gynecologists in regional women's healthcare centres and delivered to the

¹ <https://hpvcentre.net/statistics/reports/XWX.pdf>

² Постановление Министерства здравоохранения Республики Беларусь от 01.07.2024 № 111. https://minzdrav.gov.by/upload/lcfiles/постановление_МЗ_2024_111.pdf

³ Mean $\pm$ standard deviation.

laboratory for PCR-based molecular genetic analysis. Initially, samples from all patients were examined for HPV 16, 18, and other genotypes using Abbott RealTime High Risk (HR) HPV kit (Abbott, USA), recommended for screening by the WHO. After detection of other HPV genotypes, a confirmatory analysis of samples ($n=593$) was performed to detect the specific HPV genotype using a AmpliSens® HPV high carcinogenic risk genotype-FL kit (Central Research Institute of Epidemiology of Rospotrebnadzor surveillance, Russia).

Statistical data processing. The age of the study participants is presented as mean $\pm$ standard deviation ($M \pm SD$). Detection frequency of HPV genotypes is presented as a percentage with calculated 95% confidence intervals (CI). The Chi-square test was used to analyse contingency tables; if the statistical hypothesis was rejected when using the Chi-square test, Fisher's exact test was applied. To analyse ordered categorical data, the Cochran-Armitage test was used in case the second variable was binary; the linear-by-linear association test was used in the case of two variables with ordered categories. Calculations were performed using R statistical software v.4.1 (R Core Team, 2023) and Microsoft Excel 10. The results were considered statistically significant at $p < 0.05$.

RESULTS AND DISCUSSION

According to the data obtained, high-risk HPV DNA was detected in 9.0% of the samples

(1,022/11,382), the detection rate of high-risk HPV being 9.7% (952/9,831) among women of reproductive age, which is consistent with global data. HPV prevalence among women with normal cytology is approximately 11–12% worldwide [13], while, according to D.A. Obeid et al., the highest rates are observed in the Northeast Africa (21%) [9]; in Eastern Europe (21.4%), and Latin America (16%), HPV prevalence is approximately 11.7% (95% CI 11.6–11.7) in healthy women over 30 years of age [13]. In some countries, HPV prevalence can range from 2 to 42% [14, 15].

The spectrum of HPV genotypes and their detection rates were comparable all over the region (Table 1): high-risk HPV occurrence varied from 8.1 (Dobrush district) to 9.3% (Chachersk district). In all districts, HPV genotype 16 was predominant (2.2%), ranging from 2.0% (Vetka district) to 2.9% (Chachersk district); HPV genotype 18 – from 0.4% (Khoyniki district) to 0.7% (Chachersk district). Combinations of several HPV genotypes were detected in almost all districts with a frequency of 0.1 to 0.4%. Other HPV genotypes were most frequently detected in Vetka (5.7%) and less frequently in Dobrush (4.9%) district.

In view of the women living in different parts of Gomel region and the absence of statistically significant ($p=0.523$) differences in the occurrence of high-risk HPV, the results obtained were extrapolated to the entire region (Fig. 1, Table 1).

Table 1. Distribution of high-risk human papilloma virus (hrHPV) genotypes in Gomel region districts, 2018–2021

Таблица 1. Распределение генотипов вируса папилломы человека высокого канцерогенного риска (ВПЧ ВКР) в районах Гомельской области (2018–2021 гг.)

HPV genotypes Генотипы ВПЧ	District, n (%) / Район, n (%)				
	Dobrush Добрушский	Chachersk Чечерский	Khoyniki Хойникский	Vetka Ветковский	Total Всего
16	99 (2.1)	48 (2.9)	61 (2.2)	39 (2.0)	247 (2.2)
18	25 (0.5)	11 (0.7)	10 (0.4)	12 (0.6)	58 (0.5)
16, 18	6 (0.1)	2 (0.1)	1 (0.04)	0	9 (0.1)
16 and others / и другие	14 (0.3)	4 (0.2)	9 (0.3)	8 (0.4)	35 (0.3)
18 and others / и другие	6 (0.1)	0	5 (0.2)	4 (0.2)	15 (0.1)
16, 18 and others / и другие	2 (0.04)	0	3 (0.1)	1 (0.1)	6 (0.1)
Others / Другие	236 (4.9)	88 (5.4)	152 (5.4)	109 (5.7)	585 (5.3)
Total / Всего	388 (8.1)	153 (9.3)	241 (8.6)	173 (9.0)	955 (8.6)
Number of women examined / Число обследованных женщин	4794	1640	2800	1912	11146

The table is prepared by the authors using their own data / Таблица составлена авторами по собственным данным

Table 2. Detection frequency of high-risk human papilloma virus (hrHPV) among women of different age groups**Таблица 2.** Частота обнаружения вируса папилломы человека высокого канцерогенного риска (ВПЧ ВКР) у женщин в разных возрастных группах

Groups Группы	Age group, n (%) / Возрастная группа, n (%)						
	18–24	25–29	30–34	35–39	40–44	45–49	≥50
All women ^a Все женщины ^а	1432 (12.8)	1219 (10.9)	1593 (14.3)	1670 (15)	1830 (16.4)	1870 (16.8)	1532 (13.7)
Women, HPV detected ^b Женщины с обнаруженным ВПЧ ^б	269 (18.8)	147 (12.1)	146 (9.2)	121 (7.2)	107 (5.8)	102 (5.5)	63 (4.1)
95% CI / ДИ	16.8–20.9	4.1–10.3	7.8–10.7	6.1–8.6	4.8–7.0	4.5–6.6	3.2–5.3

The table is prepared by the authors using their own data / Таблица составлена авторами по собственным данным

Note. HPV, human papillomavirus; HPV detected, human papillomavirus detected by polymerase-chain reaction; CI, confidence interval.
Примечание. ВПЧ – вирус папилломы человека; обнаруженный ВПЧ – вирус папилломы человека обнаружен методом полимеразной цепной реакции; ДИ – доверительный интервал.

^a n=11146.^b n=955.

Prevalence analysis of high-risk HPV in different age groups demonstrated the highest frequency of 18.8% (95% CI 16.8–20.9) in 18–24 years women. In the groups of 25–29 years and 30–34 years, high-risk HPV was detected with a frequency of 12.1% (95% CI 10.3–14.1) and 9.2% (95% CI 7.8–10.7), respectively (Table 2). The data obtained are explained by high sexual activity of young women, which significantly increases the risk of HPV infection. Similar data were reported by N. Berza et al. [15]. They showed that the maximum prevalence of HPV in Europe is observed in women younger than 30 years.

A decrease in the incidence of high-risk HPV was found in women of late reproductive age (40–49 years) and ≥50 years – 5.5% (95% CI 4.5–6.6) and 4.1% (95% CI 3.2–5.3), respectively (Table 2). Consequently, the incidence of high-risk HPV infection in women of early reproductive age is significantly higher and shows the need to include them in the high-risk group of HPV-associated precancerous lesion of the cervix. In addition, the results of this study are important for researching epidemiology of HPV infection as a public health disease. For example, the negative impact of HPV infection on the economic and demographic components was predicted in case of a woman's death or loss of fertility [16]. Genotyping 593 samples allowed us to assess the contribution of individual HPV genotypes and/or their combinations to the formation of the genotypic structure, as well as to evaluate representation of the HPV genotypes in the Gomel region. It was found that the most common HPV genotypes in the Gomel region during the study period were HPV genotypes 16, 18, 51, 56, and 31

(Fig. 2). The frequencies of HPV genotypes 52, 33, 45, 66, 58, 39, 59, 35, and 68 were then distributed in descending order.

The landscape of the main HPV genotypes in the Gomel region over the past 15 years has varied significantly. V.N. Belyakovskiy et al. [17] studied the distribution of HPV genotypes in a group of women with cervical cancer in the Gomel region in 2000–2005 and found that the incidence of HPV genotype 16 was 64.7±3.3% ($p<0.05$). The authors indicated that HPV genotype 58 was detected more often in cervical cancer compared to the other 11 HPV genotypes, and the differences in relation to HPV genotypes 45, 31, 39, 59, 66 were significant ($p<0.05$) [17].

A.N. Volchenko has described the spectrum and frequency of the main HPV genotypes in the general population of women in the Gomel region over 2009–2010 [18]. It was shown that the frequency of HPV genotype 16 was 29.4% (95% CI 20.8–38.0) (first place), HPV genotype 56 – 15.9% (95% CI 6.5–25.3) (second place), and HPV genotype 31 – 14.3% (95% CI 4.8–23.8) (third place); the remaining HPV genotypes were distributed in the descending order: 51, 52, 33, 39, 58, 45, 18, 35, and 59. HPV genotype 18 is one of the main oncogenic genotypes, ranked tenth by frequency – 9.9% (95% CI 0.1–19.7) [18]. To assess the stability of the genetic landscape over the past 10–15 years, a comparison was made between the spectrum and frequency of various HPV genotypes in the Gomel region for 2009–2010 (study by A.N. Volchenko [18]) and the data of the present study for 2018–2021 (Table 3). Since the data of V.N. Belyakovskiy et al. [17] were obtained only for a group of patients with cervical

cancer, they were not included in the analysis. It was found that in the general population, infection with 16 ($p<0.001$) and 18 ($p=0.034$) HPV genotypes significantly increased. Thus, in 2018–2021, the frequency of HPV genotype 16 increased by 20.7% (95% CI 14.3–27.1), and HPV genotype 18 by 4.9% (95% CI 0.5–9.4) compared with 2009–2010.

In 2018–2021, HPV genotype 16 still occupied the first place, but its frequency increased to 50.1%. HPV genotype 18 occupied the second place (14.8%); HPV genotype 51 occupied the third place (10.6%), although in comparison with the data by A.N. Volchenko [18], the frequency decreased by 3.4% (95% CI –8...–1.2). HPV of the phylogenetic group $\alpha 9$, 56 and 31 genotypes, occupied fourth and fifth places with 9.1% and 8.9%, respectively. Notably, the frequency of infection with HPV genotypes 56 and 31 also significantly decreased in comparison with 2009–2010. Therefore, phylogenetic groups $\alpha 9>\alpha 7>\alpha 5$ mainly contribute to high-risk HPV infection in women in the Gomel region.

Co-infection with several high-risk HPV genotypes is known to significantly increase the risk of developing cervical pathology [19]. L. Wu et al. [20] demonstrated a significant increase in the likelihood of developing CIN with simultaneous infection with HPV genotypes 16 and 18. According to

our data, both monogenotypes and combinations of different HPV genotypes were found (Table 4). Single HPV genotype was detected with the highest frequency (78.6%), four genotypes were found in 6 patients (1%). A combination of two HPV genotypes was detected in 86 patients (14.5%), and ≥ 3 genotypes were found in 41 patients (6.9%).

According to the PCR results, a statistically significant difference in the detection frequency of HPV monogenotypes belonged to the age groups of 25–29 years (87.9%), 30–34 years (82.1%), and 35–39 years (84.8%) (Table 5). One HPV genotype was most often featured for women of early reproductive age. Infection with two and three HPV genotypes was more common for women aged 40–44 years (20.8 and 7.5%, respectively, $p=0.005$) and 18–24 years (18.5 and 6.9%, respectively, $p=0.005$). More than four HPV genotypes were detected in women aged 18–24 and 30–34 years, 5.3 and 3.6%, respectively. Combination of multiple HPV genotypes was not observed in women of late reproductive age. A linear-linear association test showed that the changes in the number of genotypes were directional, indicating a decrease in the number of cases of multiple genotypes detected with increasing patient age ($p=0.005$).



The figure is prepared by the authors / Рисунок подготовлен авторами

Fig. 1. Map of Gomel region: districts where the screening took place are in dark yellow color.

Рис. 1. Карта Гомельской области: районы, в которых проводилось скрининговое исследование, выделены темно-желтым цветом.

Thus, the highest frequency of both HPV monogenotypes and their combinations is found in women of reproductive age. This should be taken into account at routine screening of possible early precancerous cervical conditions associated with HPV-specific cervical cancer.

Structure and frequency analysis of HPV infection in women examined in Gomel city and the region revealed HPV-specific cervical cancer in 67 of 236 women (28.4%) and in 60 of 214 (28.0%) women of reproductive age (Table 6).

Regarding the incidence of HPV monogenotypes or their combinations, it was demonstrated that HPV genotype 16, combination of HPV genotype 16 with other HPV genotypes, and other HPV genotypes were detected with the highest frequency both in the general population and in women of reproductive age. Notably, 55.3% of women of reproductive age (Gomel city and Gomel district) were infected with a single HPV genotype (Table 7). Two and ≥ 3 HPV genotypes were detected in 16.4 and 28.4% of all cases examined.

The highest occurrence (87.5%) of one HPV genotype was observed in the age group of 30–34 years (Table 8). The combination of two HPV genotypes was found in 42.9% of women aged 18–24 years. Three HPV genotypes with the same frequency of 14.3% were detected in the age groups of 18–24 years, 35–39 years, and ≥ 50 years. Four or more HPV genotypes prevailed in the groups of 35–39 years (28.6%), 40–44 years (30.8%), and ≥ 50 years (28.6%). According to the data published [21], the combination of HPV 16 and 31 genotypes more

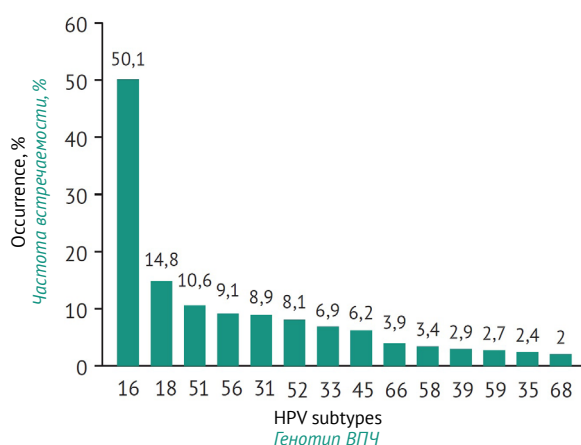
often leads to persistent HPV infection and longer periods of viral elimination [21], and is also associated with severe lesions [22]. In a meta-analysis by A.F. Rositch et al. [23], a high tendency for persistence was demonstrated in a combination of HPV genotypes 16, 31, 33, and 52.

A combination of HPV genotypes 16 and 31, 16 and 33, 16 and 56, and 16 and 51 was observed in some patients from Gomel city and the region; isolates were found to contain HPV genotype 16 in combination with several other genotypes, for example, 31, 33, 56, and 51 simultaneously. Taking into account the data by A.F. Rositch et al. [23], it can be assumed that long-term persistence of the virus in these patients will be an independent risk factor for the development of precancerous condition and cervical cancer.

Ranking HPV genotypes by prevalence showed that of the 45.4% of all cases, HPV genotype 16 accounts for 17%, 51 for 7.8%, 58 for 7.8%, 68 for 7.1%, and 52 for 5.7%. The detected HPV genotypes can be distributed by frequency as follows: 16>51=58>68>52>18=39=56=82>31=66=53=31>33>45=59. Therefore, HPV genotypes 16, 51, and 58 were prevalent in women from Gomel city and the region.

The detected HPV genotypes, taking into account the phylogenetic classification, can be distributed as follows: in four districts of the Gomel region, the HPV groups $\alpha 9$, $\alpha 7$, $\alpha 6$, and $\alpha 5$ were dominant, while in Gomel city and the region, the $\alpha 9$ (39.7%) and $\alpha 7$ (22.7%) groups were dominant, which, according to IARC, have the greatest carcinogenic potential (Fig. S1, published on the journal website⁴). In the districts of the Gomel region, $\alpha 9$ group (79.8%) was represented by HPV 16 (50.1%), 31 (8.9%), 33 (6.9%), 35 (2.4%), 52 (8.1%), and 58 (3.4%) genotypes, $\alpha 7$ group (28.6%) – HPV 18 (14.8%), 39 (2.9%), 45 (6.2%), 59 (2.7%), 68 (2%) genotypes, $\alpha 6$ group (13%) – HPV 56 (9.1%) and 66 (3.9%) genotypes, and $\alpha 5$ group (10.6%) – HPV 51 genotype. In Gomel city, phylogenetic groups $\alpha 6$ (13.6%) and $\alpha 5$ (12.8%) were found with decreasing frequency. $\alpha 9$ group included HPV genotypes 16 (17%), 31 (4.3%), 33 (3.5%), 35 (1.4%), 52 (5.7%), and 58 (7.8%); $\alpha 7$ group included HPV genotypes 18 (5%), 39 (5%), 45 (2.8%), 59 (2.8%), and 68 (7.1%); $\alpha 6$ group included HPV genotypes 53 (4.3%), 56 (5%), and 66 (4.3%); and $\alpha 5$ group included HPV genotypes 51 (7.8%) and 82 (5%).

A vaccination programme against HPV for girls aged 11 years and older is to be introduced in the Republic of Belarus in 2025; the programme is



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Fig. 2. Occurrence of carcinogenic human papillomavirus (HPV) genotypes in Gomel region ($n=593$).

Рис. 2. Частота встречаемости онкогенных генотипов вируса папилломы человека (ВПЧ) в Гомельской области ($n=593$).

⁴ <https://doi.org/10.30895/2221-996X-2025-25-3-332-342-fig-s1>

Table 3. Comparison of the spectrum and prevalence of various high-risk human papillomavirus (hrHPV) genotypes of the female population in Gomel region for 2009–2010 and 2018–2021

Таблица 3. Сравнение спектра и частоты встречаемости разных генотипов вируса папилломы человека высокого канцерогенного риска (ВПЧ ВКР) в популяции женщин Гомельской области в 2009–2010 и 2018–2021 гг.

HPV genotype Генотип ВПЧ	Research / Исследование 2009–2010, n=364	Research / Исследование 2018–2021, n=593	Changes in proportions Изменения в пропорциях	p-value p-значение
	n (%)	n (%)	% (95% CI/ДИ)	
16	107 (29.4)	297 (50.1)	20.7 (14.3–27.1)	<0.001
18	36 (9.9)	88 (14.8)	4.9 (0.5–9.4)	0.034
31	52 (14.3)	53 (8.9)	–5.3 (–9.8...–0.9)	0.014
33	44 (12.1)	41 (6.9)	–5.2 (–9.3...–1)	0.009
35	32 (8.8)	14 (2.4)	–6.4 (–9.8...–3.1)	<0.001
39	41 (11.3)	17 (2.9)	–8.4 (–12.1...–4.7)	<0.001
45	37 (10.2)	37 (6.2)	–3.9 (–7.8... 0)	0.037
51	51 (14)	63 (10.6)	–3.4 (–8... 1.2)	0.142
52	51 (14)	48 (8.1)	–5.9 (–10.3...–1.5)	0.005
56	58 (15.9)	54 (9.1)	–6.8 (–11.5...–2.2)	0.002
58	38 (10.4)	20 (3.4)	–7.1 (–10.7...–3.4)	<0.001
59	23 (6.3)	16 (2.7)	–3.6 (–6.7...–0.6)	0.01
66	Not determined Не определялся	23 (3.9)	Нет No	Нет No
68	Not determined Не определялся	12 (2.0)	Нет No	Нет No

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Note. HPV, human papillomavirus; CI, confidence interval.

Примечание. ВПЧ – вирус папилломы человека; ДИ – доверительный интервал.

included in the national immunisation schedule⁵. Its success is predicted in the prevention of pre-cancerous conditions in the Gomel region. According to WHO recommendations, vaccination against papillomavirus should be included in the national calendars of all the countries worldwide⁶. Recent studies have discussed the issue that bi- and quadrivalent vaccines provide protection against infection and precancerous conditions caused by HPV of related genotypes (31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68) that are not included in the vaccines, that is, cross-immunity is formed [24, 25]. However, the cross-protection of bi- and quadrivalent vaccines is partial and weakens over time, which must be taken into account when carrying out specific prevention [25].

Our data for the Gomel region fully reflect HPV prevalence and genotypic landscape in the re-

Table 4. Distribution of detection frequency of mono- and multiple human papillomavirus (HPV) genotypes

Таблица 4. Распределение частоты обнаружения моногенотипов и множественных генотипов вируса папилломы человека (ВПЧ)

Number of HPV genotypes Число генотипов ВПЧ	n (%)
1	466 (78.6)
2	86 (14.5)
3	28 (4.7)
4	6 (1.0)
≥5	7 (1.2)
Total / Всего	593 (100)

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⁵ Постановление Министерства здравоохранения Республики Беларусь от 01.07.2024 № 111. https://minzdrav.gov.by/upload/lcfiles/постановление_МЗ_2024_111.pdf

⁶ [https://www.who.int/news/item/11-04-2022-one-dose-human-papillomavirus-\(hpv\)-vaccine-offers-solid-protection-against-cervical-cancer](https://www.who.int/news/item/11-04-2022-one-dose-human-papillomavirus-(hpv)-vaccine-offers-solid-protection-against-cervical-cancer)

Table 5. Frequency distribution of mono- and multiple human papillomavirus (HPV) genotypes in different age groups
Таблица 5. Распределение частоты встречаемости моногенотипов и множественных генотипов вируса папилломы человека (ВПЧ) в разных возрастных группах

Number of HPV genotypes ^a Число генотипов ВПЧ ^a	Age group, n (%) / Возрастная группа, n (%)					
	18–24	25–29	30–34	35–39	40–44	45–49
1	69.3	87.9	82.1	84.8	71.7	77
2	18.5	9.1	13.1	12.1	20.8	16.4
3	6.9	3	1.2	3	7.5	6.6
≥4	5.3	0	3.6	0	0	0
n	189	99	84	66	53	61

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^a n=593.

Table 6. Distribution of high-risk human papillomavirus (hrHPV) genotypes in Gomel and Gomel district for 2022–2023
Таблица 6. Распределение генотипов вируса папилломы человека высокого канцерогенного риска (ВПЧ ВКР) в г. Гомеле и Гомельском районе в 2022–2023 гг.

HPV genotypes Генотипы ВПЧ	All women ^a Все женщины ^a n (%)	Women of reproductive age ^b Женщины репродуктивного возраста ^b n (%)
16	9 (3.8)	9 (4.2)
18	1 (0.4)	0
16, 18	1 (0.4)	1 (0.5)
16 and others / и другие	13 (5.5)	13 (6)
18 and others / и другие	3 (1.3)	2 (0.9)
16, 18 and others / и другие	1 (0.4)	1 (0.5)
Others / Другие	39 (16.5)	34 (15.9)
Total / Всего	67 (28.4)	60 (28)

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^a n=236.

^b n=214.

Table 7. Distribution of detection frequency of mono- and multiple human papillomavirus (HPV) genotypes in Gomel and Gomel district
Таблица 7. Распределение частоты обнаружения моногенотипов и множественных генотипов вируса папилломы человека (ВПЧ) в г. Гомеле и Гомельском районе

Number of HPV genotypes Число генотипов ВПЧ	n (%)
1	37 (55.3)
2	11 (16.4)
3	7 (10.4)
4	5 (7.5)
≥5	7 (10.4)
Total / Всего	67 (100)

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gion as a whole, as well as the distribution of HPV genotypes across different age groups. These data also serve as a component of the HPV-associated disease prevention strategy. In the future, this will enable us to assess the impact of the vaccination program on HPV prevalence in the region.

CONCLUSIONS

1. The incidence of high-risk HPV in the Gomel region was 9% in women in the general population and 9.7% in women of reproductive age. More cases of high-risk HPV were observed in women of early reproductive age: 18–24 years – 18.8% (95% CI 16.8–20.9); 25–29 years – 12.1% (95% CI 10.3–14.1); 30–34 years – 9.2% (95% CI 7.8–10.7). The incidence of high-risk HPV decreased in women of late reproductive age and older than 50 years.

2. Currently, the most common HPV genotypes in the Gomel region are genotypes 16 (52.2%), 18 (15.1%), 51 (18.9%), 56 (9.8%), and 31 (9.7%).

Table 8. Frequency distribution of multiple human papillomavirus (HPV) genotypes in different age groups of patients in Gomel and Gomel district

Таблица 8. Частота распределения множественных генотипов вируса папилломы человека (ВПЧ) в разных возрастных группах пациенток в г. Гомеле и Гомельском районе

Number of HPV genotypes ^b Число генотипов ВПЧ ^б	Age group, n (%) / Возрастная группа, n (%)						
	18–24	25–29	30–34	35–39	40–44	45–49	≥50
1	28.5	66.7	87.5	57.1	30.8	77.8	42.8
2	42.9	22.2	0	0	30.8	11.1	14.3
3	14.3	0	12.5	14.3	7.6	11.1	14.3
≥4	14.3	11.1	0	28.6	30.8	0	28.6
n	7	9	8	14	13	9	7

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^a n=141 HPV genotypes detected in 67 patients / генотип ВПЧ, обнаруженный у 67 пациенток.

The dominant phylogenetic groups are α9 (HPV genotypes 16 and 31), α7 (genotype 18), α5 (genotype 51), and α6 (genotype 56), classified as group 1 (the highest carcinogenic potential), according to IARC classification. A comparative analysis revealed changes in the structure of the dominant HPV genotypes in the Gomel region over the past 10 years.

3. No statistically significant regional differences in the landscape and prevalence of HPV genotypes were found across the four districts of the Gomel region and Gomel city. Taking into account different locations of the districts covered by HPV screening, the results obtained can be extrapolated to the region as a whole.

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Authors / Об авторах

Volha P. Lohinava / Логинова Ольга Павловна

ORCID: <https://orcid.org/0000-0001-7189-3799>

Natalia I. Shevchenko, Cand. Sci. (Biol.), Assoc. Prof. / Шевченко Наталья Ивановна, канд. биол. наук, доц.

ORCID: <https://orcid.org/0000-0003-0579-6215>

Alla V. Voropayeva, Cand. Sci. (Biol.), Assoc. Prof. / Воропаева Алла Викторовна, канд. биол. наук, доц.

ORCID: <https://orcid.org/0000-0003-0213-2421>

Elena L. Gasich, Dr. Sci. (Biol.), Assoc. Prof. / Гасич Елена Леонидовна, д-р биол. наук, доц.

ORCID: <https://orcid.org/0000-0002-3662-3045>

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