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# SCREENING OF HOP BREEDING MATERIAL FOR FIELD RESISTANCE TO DOWNY MILDEW (*PSEUDOPERONOSPORA HUMULI* WILSON) IN THE EARLY STAGES OF PLANT DEVELOPMENT

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**Aim.** To screen the Ukrainian collection of hop breeding material for the level of field resistance to *Pseudoperonospora humuli* at the early stages of the hop plant development and growth, and to identify valuable genotypes for further breeding. **Methods.** The research was conducted in years 2019–2022 in small experimental plots in a field where natural infection of *P. humuli* was present (Zhytomyr district, the Polissia zone, Ukraine). Sixty-five newly created hop genotypes and four standard Ukrainian varieties, Alta, Slovyanka, Zahrava, and Ruslan (as controls), were evaluated for the field resistance against *P. humuli* on base of disease index using a 9-point scale during the initial growth phase of the plant at two stages: in stage I, emergence of sprouts and stage II, shoot growth. **Results.** For the first time a descriptive analysis of field resistance to *P. humuli* of hop plants in two stages of its development and growth was performed for 65 new genotypes from the Ukrainian collection of genetic hop resources and the most resistant ones were selected. The disease development was less intense in stage I than during stage II, which was possibly associated with increased humidity and temperature during the latter stage. No genotype showed immunity (full resistance) to the disease. The four standard varieties used showed moderate susceptibility. Eight genotypes (7667, 8156, 8195, 8367, 8382, 8388, 8604, and 8555) demonstrated high resistance during stage I, while a slightly different set of eight genotypes (7667, 7886, 8156, 8195, 8367, 8438, 8605, and 8555) showed high resistance in stage II. The differences observed across evaluation stages and genotypes were statistically significant ($F=13.4$; $p < 0.001$). **Conclusions.** Evaluation of the Ukrainian collection of hop breeding material for field resistance to *Pseudoperonospora humuli* during early stages of

plant development and growth showed that 25% of the genotypes were classified as resistant, 39% as moderate resistant, 32% as moderate susceptible, and 4% as susceptible. Six genotypes (7667, 8156, 8195, 8367, 8382, and 8555) with the highest total field resistance to *P. humuli* were advised for inclusion into further breeding crossings and investigations for the presence of useful genetic resistance markers.

**Keywords:** *Humulus lupulus*, genotype, damage, primary infection, susceptibility.

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## INTRODUCTION

Hop (*Humulus lupulus* L.) is a dioecious perennial plant of the *Cannabaceae* family (Neve, 1991), which due to its content of unique biochemical compounds in the female inflorescence (cones) is an irreplaceable component of beer production, both traditional, and craft beer, as well as non-alcoholic beverages. During the entire history of cultivation, some hop products were also used in pharmaceutical, food, perfumery, and other industries (Neve, 1991; Bocquet et al., 2018; Bober et al., 2020; Korpelainen & Pietiläinen, 2021; Anderson, 2023; Olšovská et al., 2024).

The analysis of global meteorological models (GMM) demonstrates that weather changes in the key regions of hop cultivation in Europe may have a negative impact on the future realization of the biological potential of the performance of modern varieties. For instance, it was determined that under global warming and a higher number of droughts, there is a considerable risk of reduced hop production, which requires the implementation of urgent adaptive measures (Potopová et al., 2020; Mozny et al., 2023). One of the solutions to this problem may be found in creating new genotypes of hop which should not only meet the market demands of producers and consumers, but also be maximally adjusted to changes in the factors of cultivation environment, and resistance to diseases and pests (Nesvadba et al., 2020; Paguet et al., 2022).

Modern hop breeding is mainly concentrated on taste qualities, aroma, and bitterness, though the agrotechnical traits of varieties are becoming ever more relevant: yield stability, adaptation to climate change, and resistance to pests and diseases (Mongelli et al., 2016, Paguet et al., 2022).

One of the most common and harmful diseases of hops is downy mildew (O'Neal et al., 2015; Trefilová et al., 2022), caused by the oomycete *Pseudoperonospora humuli* [Miyabe et Takahasi] G.W. Wilson. The epiphytotic development of downy mildew in hop plantations (which is annually registered in Ukraine) led to a decrease in yield of hop cones up to 30–50%, if no proper crop protection system was implemented (Venger & Fedorchuk, 2021).

Hop breeding for resistance to *P. humuli* has a long history: it was initiated by Salmon in 1906 within a breeding program of Wye College in the UK, that got an extra impulse after an epiphytotic in 1924 (Darby, 2006). Subsequent outbreaks in Germany led to the launch of a resistance breeding program in Hüll in 1926 (Seigner et al., 2009). Similarly, a breeding program was established at Oregon State University in USA (Corvallis) to ensure economically viable yields under the disease pressure in humid climate in Oregon in 1931 (Darby P, 2006).

A review of the current literature (de Arruda et al., 2024; Purayannur et al., 2021) learns that research on *P. humuli* continues in several directions. These include investigation into the role of secondary metabolites in the infection process, the identification and characterization of resistance markers, (whole) genome mapping, and the elucidation of genetic determinants associated with tolerance, since immunity, till now, has not been observed in hop. Despite these advances, effective breeding strategies continue to rely on robust and reproducible methods for evaluating disease severity under controlled laboratory conditions and in the field. This involves systematic phenotyping and the development of comprehensive datasets documenting disease manifestations, which are essential for identifying resistant genotypes (Gent et al., 2012; Nelson et al., 2015; Shtanko et al., 2018; Čerenak et al., 2019; Feiner et al., 2021; Higgins & Hausbeck, 2021; Trefilová et al., 2022). Henning et al. (2015a) demonstrated that although phenotyping methods vary (such as assessing leaf lesion area under greenhouse conditions or quantifying the proportion of infected seedlings in the field trials), utilizing multiple screening approaches can significantly improve the accuracy and effectiveness of resistance selection in breeding programs.

Hop cultivation is predominantly carried out in humid, temperate regions, which are frequently asso-

ciated with a high incidence of downy mildew (Royle & Kremheller (1981). The disease has two peaks in its development — in spring and in summer. Typical symptoms in the initial stages of fungal development after its dormant period, are the emergence of so-called "spike-like" sprouts (Mitchell et al., 2011), also called "thorns" (Purayannur et al., 2021). In a wet spring, the first symptoms of the disease appear on young leaves and sprouts, resulting in shortening of internodes, deformation, and withering of leaves, that become light green and eventually die. Mature leaves show yellow-brown lesions on the upper surface, and dark gray spots with a purplish hue, on the lower side of the leaf blade. The infection inhibits general plant development, which leads to a considerable decrease in growth intensity and yield. Furthermore, there are additional expenses for fungicide applications (Purayannur et al., 2021; Higgins & Hausbeck, 2021), which may end up to 8 to 10 applications during the growing season (Johnson et al., 2009). Considering modern ecological requirements, including the limitations on the use of chemical pesticides, as applied in the EU member states (Vostřel, 2021), breeding for resistance to the disease became the basis for a healthy hop production in the region (Nesvadba, 2016; Easterling et al., 2018).

Enhancing resistance of hop plants to *P. humuli* requires not only the improvement of the breeding methods, but also strategic study and utilization of the crop's existing genetic diversity. This diversity serves as a foundation for identifying and incorporating resistance traits into new cultivars. Critical steps in this process involves isolating resistant genotypes, identifying associated phenotypic or molecular markers, and integrating these findings into breeding programs and genetic research (Henning et al., 2015a, 2015b).

**The aim of this study** was to evaluate the level of resistance to *P. humuli* within the Ukrainian collection of genetic hop resources specifically during two early stages of plant development (stage I, emergence of sprouts and stage II, shoot growth). These are stages when disease pressure is typically highest. Fungicide application was intentionally withheld to allow for natural infection dynamics. Such timing should enable a more accurate evaluation of disease manifestation to determine statistically significant differences among tested genotypes to identify promising sources of resistance for further use in breeding practice.

## MATERIAL AND METHODS

The evaluation was conducted over a 4 years (seasons) period, from 2019 to 2022, in fields of the experimental hop plantation of the Polissia Institute of Agriculture (PIA), the NAAS, Zhytomyr, Ukraine. The climate of the area is moderate continental with warm, relatively wet summers, and mild winters. The average perennial temperature of the coldest month (January) is minus 6°C, and that of the warmest month (July) +19°C. The sum of positive air temperatures (above 10°C) is 2,400–2,500°C. The amount of precipitation in the period of active vegetation is 300–350 mm. The plantation is in the zone of medium humidification (with a hydrothermal coefficient of 0.9–1.1), on turf-medium podzolic low-humus soil, which was formed on glacial sandy depositions (humus — 0.6–1.2%, humus horizon thickness from 12 to 20 cm, soil acidity — 5.2–5.6). The evaluation of weather indices was done using the data of the Zhytomyr meteorological station, in particular, it involved precipitation amount (mm), the average daily air temperature ($T_{mean}$, °C), the average temperature ($T_{mean\,2019–2022}$, °C), relative humidity (RH, %) and average relative air humidity ($RH_{mean\,2019–2022}$, %) during the initial stages of hop plant development.

**Plant material.** The plant material used for the study consisted of four standard varieties and 65 genotypes of the hop breeding collection. These genotypes were obtained via complex crossings representing generations $F_2$–$F_6$. While the collection was formed between 2010 and 2018, it is also including breeding forms derived from earlier experiments initiated in 1998 using various parental genetic materials, including the Ukrainian varieties Alta, Ksanta, Ruslan, Slov'ianka and Zahrava (UKR); the European varieties Perle, Hallertau Magnum (DEU), Saaz (CZE) and Bullion (GBR); as well as moderately resistant male genotypes, as determined by multi-year field observation under natural infection pressure. These male genotypes included $F_2$ progeny from the crossing of the varieties Ksanta and Ruslan, and $F_{3–4}$ progenies from the crossing of the variety Bullion with a wild form collected in the Transcarpathian region in 1984, noted for field tolerance to *P. humuli* (M.Y. Zahrafova, personal communication).

According to previous breeding phenological descriptions, based on observations recorded in hybrid nurseries and other trial plots, the genotypes were classified into maturity groups. The duration of the growing season (GSD) was determined as the number

of days from seedling emergence to full technical maturity of cones and documented in the corresponding institutional reeding reports. The classification included: early maturity (EM), with a growing season duration of 115–120 days, medium maturity (MM), 121–128 days and medium late maturity (MLM), 129–134 days and late maturity (LM), more than 135 days.

The most commonly grown modern Ukrainian hop varieties Alta (early), Slov'ianka, Zahrava (medium), Ruslan (medium late) were used as control varieties, with their officially documented resistance levels taken from the national varietal passport data (State Register of Plant Varieties Suitable for Dissemination in Ukraine (https://minagro.gov.ua/file-storage/reyestr-sortiv-roslin and atlas of Ukrainian hop varieties (Protsenko et al., 2017)). Each variety and genotype in the breeding nursery were represented by three plants.

The evaluation of plant damage caused by the fungus *P. humuli* was performed by visual inspection of individual plants belonging to the different genotypes and varieties (three plants per variety or genotype). The methodology was based on the procedure for assessing breeding hop forms (Methodology UIPVE, 2016; Shtanko et al., 2020, and Purayannur et al., 2021). The evaluation was carried out in two distinct growth stages: Stage I (emergence of sprouts), from April 15 till April 30 and Stage II (shoot growth), from May 1 to May 15.

For Stage I (where primary infection by the fungus takes place), the degree of infection was determined using the 9-point scale:

1 = very weak infection, presence of 1–2 spike-like sprouts (ss) (*Fig. 1, a*);

2–3 = weak infection, 3–5 ss (*Fig. 1, a*) ;

4–5 = medium infection, 6–10 ss (*Fig. 1, b*);

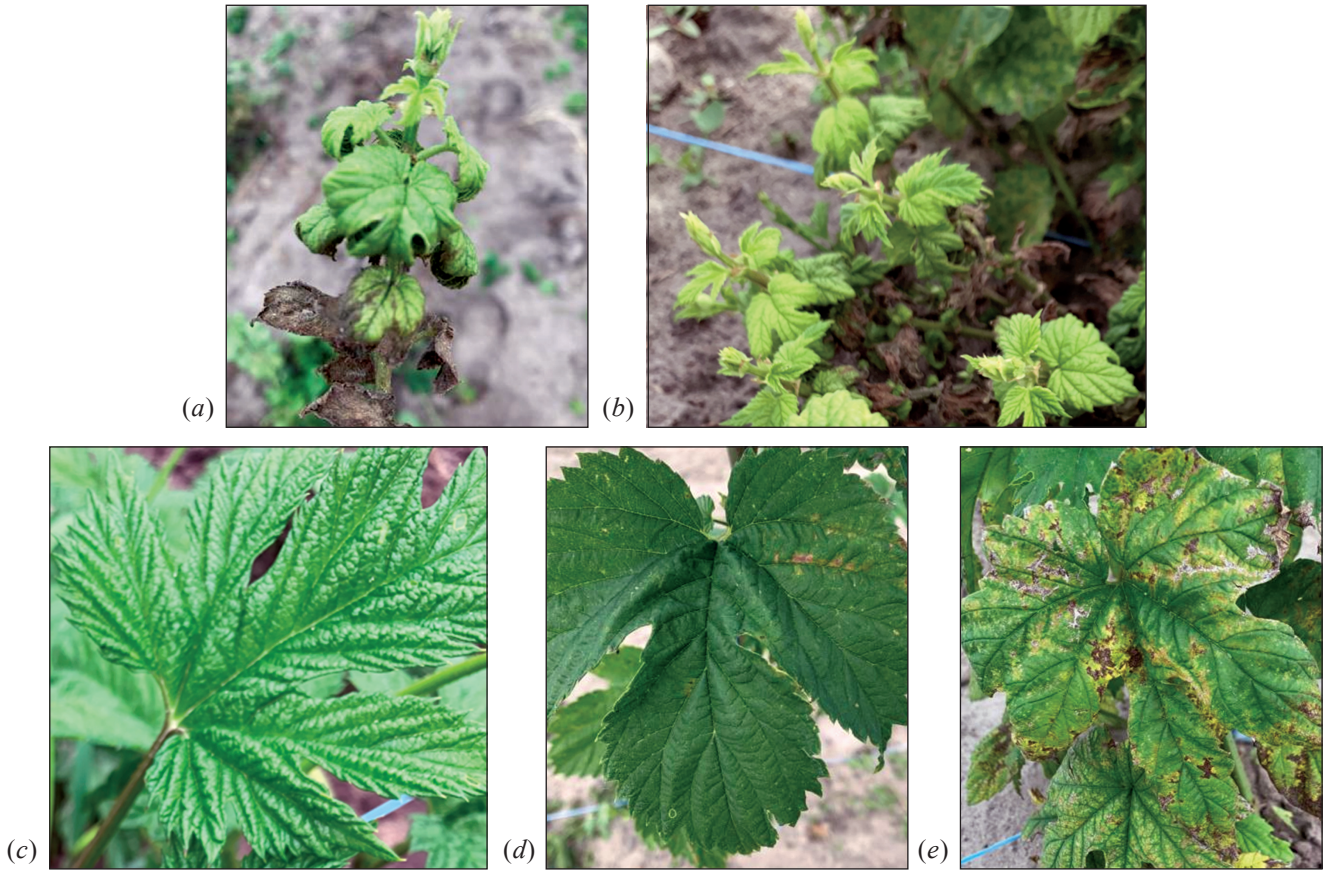



**Fig. 1.** Symptoms of *P. humuli* on hop plants during the early stages of development and growth, used in the evaluation according to a nine-point scale for Stage I (emergence of sprouts) and Stage II (shoot growth). (*a*) Rare primary "spike-like" sprouts (1 point, Stage I), (*b*) Formation of a considerable number of "spike-like" sprouts (4–5 points, Stage I); (*c*) Absence of leaf infection (Stage II); (*d*) Very weak and weak leaf infection (2–3 points, Stage II); (*e*) Medium leaf infection (4–5 points, stage II). (*photos I. Shtanko*)

6–7 = strong infection, 11–15 ss;

8–9 = very strong infection, most sprouts are deformed.

For Stage II (where leaf infection by the fungus takes place), the degree of infection was determined using another 9-point scale, based on the percentage of infected leaf surface (*Fig. 1, c, d, e*):

1 = rare brown spots;

2–3 = brown spots cover 1–5% of the surface of leaves;

4–5 = 6–10%;

6–7 = 11–50%;

8–9 = >50%.

The evaluation of the infection was conducted under natural disease pressure without any additional inoculation. During the assessment periods, plants in the test plots were not treated with pesticides. Following the completion of these assessments, to prevent further disease development and spread, the plots were treated with Ridomil Gold MZ 68 WG (metalaxyl-M + mancozeb) at a rate 2.5 kg/ha. Subsequently, other pesticides registered for use in Ukraine were applied according to the standard crop protection schedule.

The disease index (DI, %) was calculated for each genotype using the formula according to Chester (1950), also see Willocquet et al (2023):

$$DI = [\sum(N_x \times b_x) \times 100]/(N_t \times K),$$

where:

DI — disease index, %;

$\sum(N_x \times b_x)$ — the sum of the products of the number of plants ($N_x$) and the corresponding infection score ($b_x$);

$N_t$ — total number of plants evaluated;

K — maximum possible score on the assessment scale.

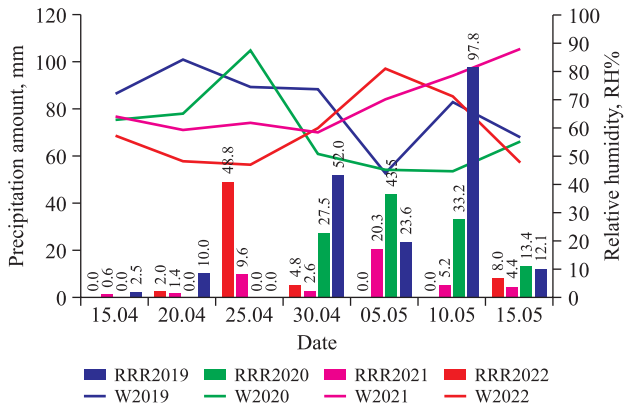
The samples with DI from 0% to 20% were considered resistant (R); from 21% to 30%, moderately resistant (MR); from 31% to 40%, moderately susceptible (MS); from 41 to 50%, susceptible (S); over 51%, very susceptible (VS).

**Statistics.** To evaluate differences in the expression of the studied traits between genotypes and groups of genotypes based on DI, the following basic statistical parameters were used: mean DI value, standard deviation (Sd), and pairwise comparisons between mean DI values using t-test. The F-statistics from ANOVA was used to test the null hypothesis of no significant differences between variants. All statistical analyses were conducted in MS Excel and/or ANOVA.

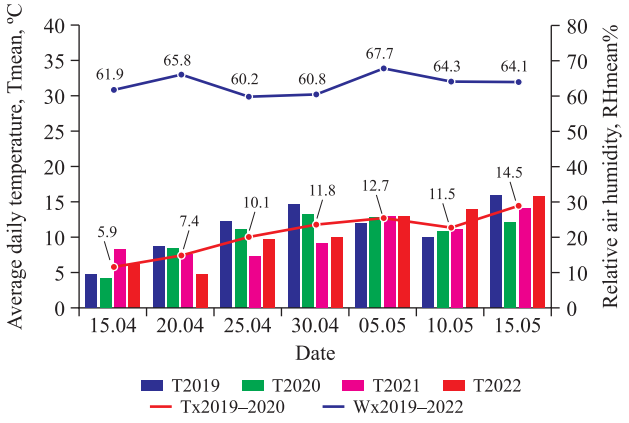
## RESULTS

In the initial infection stages, variations in disease development were found to be closely associated with weather parameters, such as relative humidity, precipitation amount, and air temperature. To quantify the influence of these factors, mean values of weather indices were calculated for five-day intervals within the period from April 15 to May 15 (*Fig. 2, A and B*).

During the first stage of evaluation in the four years studied, the relative humidity remained at a level,




*A*)




*B*)

**Fig. 2.** The dynamics of: (*A*) — precipitation (mm) and relative humidity (RH, %); (*B*) — average daily temperature (T, °C), average temperature ($T_{mean\,2019–2022}$, °C) and average relative humidity ($RH_{mean\,2019–2022}$, %) in the initial stages of hop plant development (15.04–15.05), 2019–2022

sufficient for the prevalence of *P. humuli* (≈65%). It is known that the most significant infections occur when wetness is coincident with high humidity and relatively warm nights (Gent & Ocamb, 2009). These conditions were especially fulfilled in Stage II. A summary of the results is presented in *Table I* and detailed below.

**Stage I:** *Emergence of sprouts*. During this stage, the degree of infection across all genotypes and varieties ranged from 1 to 5 points. Throughout the four-year study no genotype showed complete resistance (immunity) to the disease; but some of them (namely 7667, 8195, 8156, 8367, 8555) did not show any visual symptoms in some years. The average disease

**Table 1.** Results of resistance to *Pseudoperonospora humuli* evaluation of 65 newly bred hop genotypes and four standard varieties as controls in the initial phase of plant development (Stage I — emergence of sprouts, April 15–30, and Stage II — shoot growth, May 1–15) in the years 2019–2022

| No | Genotype (clone) number/ variety name | Maturity* | Infection *P. humuli*, score | | | Disease index (DI)**± Sd), % | | | Resistance level*** (for the entire evaluation period) |
|---|---|---|---|---|---|---|---|---|---|
| | | | Stage I | Stage II | Infection range during the evaluation period | Stage I | Stage II | Average for the entire evaluation period | |
| 1 | Alta | E | 1–4 | 2–5 | 1–5 | 28.5±17.1 | 41.3±13.8 | 34.9±16.0 | MS |
| 2 | 7683 | E | 2–4 | 2–5 | 2–5 | 35.8±10.5 | 35.8±16.5 | 35.8±12.8 | MS |
| 3 | 7843 | E | 2–3 | 2–4 | 2–4 | 27.5±6.4 | 33.0±9.0 | 30.3±7.8 | MS |
| 4 | 8556 | E | 2–5 | 3–5 | 2–5 | 35.8±13.8 | 44.0±9.0 | 39.9±11.7 | MS |
| 5 | Slov'ianka | MM | 2–4 | 3–4 | 2–4 | 33.0±9.0 | 38.5±6.4 | 35.8±7.8 | MS |
| 6 | Zahrava | MM | 2–4 | 3–4 | 2–4 | 24.8±5.5 | 41.3±5.5 | 33.0±10.2 | MS |
| 7 | 7667 | MM | 1–2 | 1–3 | 1–3 | 7.5±9.8 | 15.8±14.3 | 11.6±12.2 | HR |
| 8 | 7756 | MM | 1–3 | 2–3 | 1–3 | 22.0±15.6 | 30.3±5.5 | 26.1±11.7 | MR |
| 9 | 7886 | MM | 1–3 | 1–3 | 1–3 | 13.8±16.5 | 17.5±18.0 | 15.6±16.1 | HR |
| 10 | 7987 | MM | 2–4 | 2–4 | 2–4 | 33.0±12.7 | 35.8±10.5 | 34.4±10.9 | MS |
| 11 | 8058 | MM | 1–4 | 2–4 | 1–4 | 21.3±20.4 | 33.0±9.0 | 27.1±15.9 | MR |
| 12 | 8179 | MM | 2–3 | 2–4 | 2–4 | 27.5±6.4 | 35.8±10.5 | 31.6±9.2 | MS |
| 13 | 8182 | MM | 1–3 | 1–4 | 1–4 | 13.8±16.5 | 28.5±17.1 | 21.1±17.5 | MR |
| 14 | 8195 | MM | 1–3 | 1–3 | 1–3 | 9.3±15.9 | 18.5±16.7 | 13.9±15.9 | HR |
| 15 | 8219 | MM | 2–5 | 3–5 | 2–5 | 41.3±13.8 | 46.8±10.5 | 44.0±11.8 | S |
| 16 | 8230 | MM | 2–4 | 3–4 | 2–4 | 33.0±9.0 | 41.3±5.5 | 37.1±8.2 | MS |
| 17 | 8271 | MM | 3–4 | 3–4 | 3–4 | 38.5±6.4 | 41.3±5.5 | 39.9±5.7 | MS |
| 18 | 8273 | MM | 2–4 | 2–4 | 2–4 | 33.0±9.0 | 33.0±9.0 | 33.0±8.3 | MS |
| 19 | 8310 | MM | 1–3 | 1–4 | 1–4 | 22.0±15.6 | 28.5±17.1 | 25.3±15.5 | MR |
| 20 | 8321 | MM | 2–3 | 3 | 2–3 | 27.5±6.4 | 33.0±0 | 30.3±5.1 | MS |
| 21 | 8323 | MM | 2–3 | 2–4 | 2–4 | 27.5±6.4 | 33.0±9.0 | 30.3±7.8 | MS |
| 22 | 8356 | MM | 2–4 | 3–4 | 2–4 | 30.3±10.5 | 38.5±6.4 | 34.4±9.2 | MS |
| 23 | 8364 | MM | 1–3 | 2–3 | 1–3 | 18.5±16.7 | 27.5±6.4 | 23.0±12.7 | MR |
| 24 | 8373 | MM | 1–3 | 1–3 | 1–3 | 19.3±13.8 | 23.0±13.7 | 21.1±12.9 | MR |
| 25 | 8429 | MM | 2–4 | 1–3 | 1–3 | 33.0±9.0 | 25.8±14.5 | 29.4±11.8 | MR |
| 26 | 8462 | MM | 1–3 | 2–4 | 1–4 | 14.8±15.5 | 33.0±9.0 | 23.9±15.2 | MR |
| 27 | 8489 | MM | 1–3 | 2–4 | 1–4 | 14.8±15.5 | 33.0±9.0 | 23.9±15.2 | MR |
| 28 | 8599 | MM | 1–3 | 1–3 | 1–3 | 19.3±13.8 | 23.0±13.7 | 21.1±12.9 | MR |
| 29 | Ruslan | ML | 2–4 | 3–4 | 2–4 | 33.0±9.0 | 38.5±6.4 | 35.8±7.8 | MS |
| 30 | 7734a | ML | 2–3 | 3–4 | 2–4 | 27.5±6.4 | 35.8±5.5 | 31.6±7.0 | MS |
| 31 | 7858 | ML | 1–3 | 1–3 | 1–3 | 20.3±21.6 | 22.0±15.6 | 21.1±17.5 | MR |
| 32 | 7879 | ML | 1–3 | 1–3 | 1–3 | 22.0±15.6 | 24.8±16.5 | 23.4±14.9 | MR |

*End of the Table 1*

| No | Genotype (clone) number/ variety name | Maturity* | Infection *P. humuli*, score | | | Disease index (DI)**± Sd), % | | | Resistance level*** (for the entire evaluation period) |
|---|---|---|---|---|---|---|---|---|---|
| | | | Stage I | Stage II | Infection range during the evaluation period | Stage I | Stage II | Average for the entire evaluation period | |
| 33 | 8156 | ML | 1–2 | 1–3 | 1–3 | 6.5±10.5 | 15.8±14.3 | 11.1±12.6 | HR |
| 34 | 8157 | ML | 1–3 | 1–3 | 1–3 | 10.3±15.3 | 22.0±15.6 | 16.1±15.6 | HR |
| 35 | 8168 | ML | 1–3 | 2–3 | 1–3 | 23.0±13.7 | 30.3±5.5 | 26.6±10.4 | MR |
| 36 | 8223 | ML | 3–4 | 3–5 | 3–5 | 38.5±6.4 | 44.0±9.0 | 41.3±7.8 | S |
| 37 | 8244 | ML | 1–3 | 2–3 | 1–3 | 22.0±15.6 | 30.3±5.5 | 26.1±11.7 | MR |
| 38 | 8258 | ML | 1–3 | 2–3 | 1–3 | 11.3±14.5 | 24.8±5.5 | 18.0±12.5 | HR |
| 39 | 8351 | ML | 1–3 | 1–3 | 1–3 | 11.3±14.5 | 20.3±12.0 | 15.8±13.2 | HR |
| 40 | 8352 | ML | 2–3 | 3–4 | 2–4 | 24.8±5.5 | 35.8±5.5 | 30.3±7.8 | MS |
| 41 | 8367 | ML | 1–2 | 1–3 | 1–3 | 7.5±9.8 | 14.8±15.5 | 11.1±12.6 | HR |
| 42 | 8368 | ML | 1–3 | 1–3 | 1–3 | 16.5±19.1 | 22.0±15.6 | 19.3±16.4 | HR |
| 43 | 8375 | ML | 1–2 | 2–3 | 1–3 | 12.0±11.7 | 27.5±6.4 | 19.8±12.0 | HR |
| 44 | 8376 | ML | 2–4 | 1–4 | 1–4 | 33.0±12.7 | 23.0±24.3 | 28.0±18.7 | MR |
| 45 | 8382 | ML | 1–2 | 1–3 | 1–3 | 7.5±9.8 | 20.3±12.0 | 13.9±12.2 | HR |
| 46 | 8388 | ML | 1–3 | 1–3 | 1–3 | 9.3±15.9 | 23.0±13.7 | 16.1±15.6 | HR |
| 47 | 8424 | ML | 2–3 | 1–3 | 1–3 | 30.3±5.5 | 25.8±14.5 | 28.0±10.4 | MR |
| 48 | 8438 | ML | 1–2 | 1–3 | 1–3 | 11.0±12.7 | 19.3±13.8 | 15.1±13.1 | HR |
| 49 | 8442 | ML | 1–4 | 1–4 | 1–4 | 28.5±19.3 | 31.3±18.9 | 29.9±17.8 | MR |
| 50 | 8452 | ML | 1–4 | 2–4 | 1–4 | 28.5±17.1 | 35.8±10.5 | 32.1±13.7 | MS |
| 51 | 8485 | ML | 1–3 | 2–3 | 1–3 | 23.0±13.7 | 30.3±5.5 | 26.6±10.4 | MR |
| 52 | 8501 | ML | 1–3 | 1–3 | 1–3 | 19.3±13.8 | 23.0±13.7 | 21.1±12.9 | MR |
| 53 | 8503 | ML | 1–2 | 1–3 | 1–3 | 12.0±11.7 | 24.8±10.5 | 18.4±12.3 | HR |
| 54 | 8537 | ML | 1–2 | 2–3 | 1–3 | 13.0±10.4 | 27.5±6.4 | 20.3±11.1 | MR |
| 55 | 8539 | ML | 2–3 | 2–3 | 2–3 | 27.5±6.4 | 27.5±6.4 | 27.5±5.9 | MR |
| 56 | 8549 | ML | 2–5 | 1–3 | 1–5 | 41.3±13.8 | 25.8±14.5 | 33.5±15.5 | MS |
| 57 | 8557 | ML | 2–5 | 4–6 | 2–6 | 41.3±13.8 | 52.5±11.0 | 46.9±13.0 | S |
| 58 | 8577 | ML | 1–3 | 4–6 | 1–6 | 19.3±13.8 | 55.3±9.4 | 37.3±22.1 | MS |
| 59 | 8594 | ML | 2–3 | 2–4 | 2–4 | 27.5±6.4 | 33.0±9.0 | 30.3±7.8 | MS |
| 60 | 8601 | ML | 1–4 | 2–3 | 1–4 | 28.5±17.1 | 30.3±5.5 | 29.4±11.8 | MR |
| 61 | 8603 | ML | 2–3 | 2–4 | 2–4 | 24.8±5.5 | 35.8±10.5 | 30.3±9.8 | MS |
| 62 | 8604 | ML | 1–2 | 2–4 | 1–4 | 6.5±10.5 | 33.0±9.0 | 19.8±16.8 | HR |
| 63 | 8605 | ML | 1–3 | 1–3 | 1–3 | 18.5±16.7 | 15.8±14.3 | 17.1±14.5 | HR |
| 64 | 8606 | ML | 1–3 | 2–3 | 1–3 | 18.5±16.7 | 27.5±6.4 | 23.0±12.7 | MR |
| 65 | 8161 | LM | 1–3 | 2–4 | 1–4 | 17.5±18.0 | 30.3±10.5 | 23.9±15.2 | MR |
| 66 | 8167 | LM | 1–3 | 1–4 | 1–4 | 17.5±18.0 | 25.8±17.1 | 21.6±16.8 | MR |
| 67 | 8451 | LM | 1–3 | 2–4 | 1–4 | 17.5±18.0 | 35.8±10.5 | 26.6±16.8 | MR |
| 68 | 8528 | LM | 1–3 | 2–4 | 1–4 | 23.0±13.7 | 35.8±10.5 | 29.4±13.2 | MR |
| 69 | 8555 | LM | 1–2 | 1–3 | 1–3 | 6.5±10.5 | 19.3±13.8 | 12.9±13.3 | HR |
| | Xn ± SE | | | | | 22.4±12.6 | 30.2±10.8 | 26.3±12.5 | |

Where: * Maturity: early maturity (EM), medium maturity (MM), medium-late maturity (MLM), late maturity (LM); ** disease index (DI), % ± standard deviation (Sd); *** Resistance/susceptibility level: highly resistant (HR), moderately resistant (MR), moderately susceptible (MS), susceptible (S).

index for *P. humuli* (DI±Sd) among 65 new genotypes and 4 varieties was 22.4±12.6% at this stage. The distribution of the resistance frequency based on DI (Fig. 3) showed that 28 of the genotypes were highly resistant (or 41%), 20 moderately resistant (29%), 18 moderately susceptible (26%), and 3 were susceptible (4%).

Eight genotypes, namely no. 7667, 8195, 8156, 8367, 8382, 8388, 8604 and 8555 exhibited the lowest DI in the first stage, not exceeding 10%. Genotypes 8219, 8549, and 8557 were determined as susceptible (DI>40%). The standard varieties Alta and Zahrava were moderately resistant (DI 20–30%), whereas Slov'ianka and Ruslan were moderately susceptible (DI 30-40%).

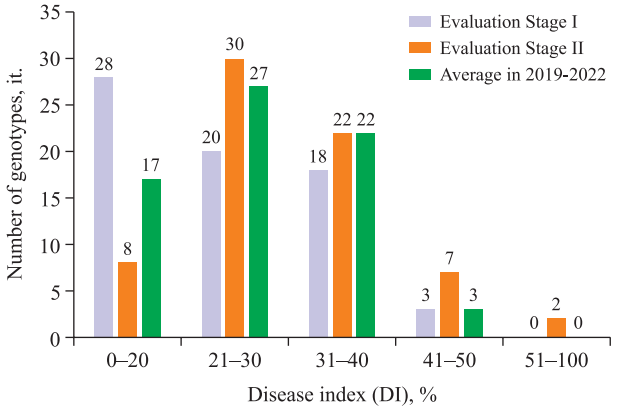



**Fig. 3.** The distribution of the resistance levels to *P. humuli* based on the disease index (DI) in hop genotypes during the initial growth stages

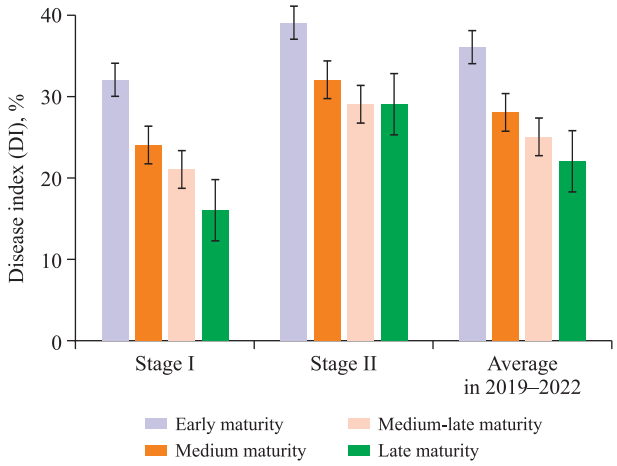



**Fig. 4.** Results of evaluation of resistance of 65 hop genotypes to *P. humuli* in the initial stages of plant development and growth by the average disease indices (DI, %) for different groups of maturity

**Stage II:** *Shoot growth*. During this period, the disease impact intensified, as reflected by higher infection scores and an increased disease index. The average DI in this stage was 30.2±10.8%, which is 1.3 times higher in Stage I. The distribution of resistance/susceptibility also shifted (*Fig. 3*): 8 genotypes were highly resistant (12%), 30 moderately resistant (43%), 22 moderately susceptible (32%), 7 susceptible (10%), and 2 very susceptible (3%). The genotypes 7667, 7886, 8156, 8195, 8367, 8438, 8605, and 8555 were classified as highly resistant, whereas genotypes 8557 and 8577 were very susceptible. In this stage the standard varieties Alta and Zahrava were moderately susceptible, while Slov'ianka and Ruslan demonstrated moderate resistance, which contradicted the results from Stage 1.

Across 2019–2022 and the two stages of evaluation, the overall mean disease index (DI±Sd) was 26.3±12.5%. Based on DI, 25% of genotypes were highly resistant, 39% moderately resistant, 32% moderately susceptible, and 4% susceptible (*Fig. 3*). All standard varieties were classified as moderate susceptible. The lowest DI value was registered for the genotypes 7667, 8156, 8195, 8367, 8382, and 8555, which are bitter hop forms, whose pedigree include the high-resin varieties Hallertau Magnum (7667), Ruslan (8156 and 8195), or Ksanta (8367, 8382, and 8555).

ANOVA analysis indicated significant differences in DI values between the evaluation stages I and II and across years 2019-2022 ($F = 13.4$, $p < 0.001$). A paired-samples t-test confirmed a higher DI in Stage II ((M2± Sd = 30.2±8.7) compared with Stage I ((M1± Sd = 22.4±9.6), $t(68) = 8.7$, $p < 0.001$.

The assessment of resistance by plant maturity group (*Fig. 4*) showed that early-maturing genotypes were the most affected by *P. humuli*. For this group, DI values averaged 31.9% in Stage I, 38.5% in Stage II, and 35.2% across the entire evaluation period. Medium- and medium-late-maturity groups were generally more resistant, with DI values of 24.1% and 21.0% in Stage I, 31.5% and 28.6% in Stage II, and 27.8% and 24.8% respectively, over the entire period. The lowest infection levels were recorded in late-maturing genotypes. Notably, this group exhibited the highest increase in DI values between Stages I and II (+79.3%), whereas early maturity genotypes showed only a 20.7% increase.

Medium-maturing genotypes 7667, 8195, 8555, as well as medium-late genotypes 8156, 8382, and

8367, demonstrated the highest resistance to *P. humuli*, making them promising candidates for use in further breeding programs.

## DISCUSSION

*Pseudoperonospora humuli* is known to overwinter as mycelium in the hop perennial root system and crown (Kitner et al., 2021). High relative humidity, elevated soil moisture, and rising spring temperatures favor the early infection of buds and young shoots (Gent et al., 2012; Venger et al., 2021, Trefilová et al., 2022; Olatoye et al., 2023). We confirmed these findings and observed that especially in the initial infection stage, variations in disease development were closely associated with these parameters. Profuse sporulation occurs on infected tissues and sporangia, which are subsequently dispersed by air currents. Under favourable conditions, these sporangia germinate to release biflagellate zoospores that infect healthy tissue, thereby continuing the infection cycle. Though oospores are produced in infected tissues, their role in the infection cycle is not yet defined (Royle & Thomas, 1971; Johnson et al., 2009; Purayannur et al., 2021).

Severe outbreaks of downy mildew may result in total yield loss, which highlights the importance of implementing preventive and control measures against the pathogen. These can include sanitary pruning of the primary shoots (called "primary spikes" when infected, owing their resemblance to wheat spikes), conducting systematic disease monitoring (Richardson & Gent, 2023) as well as timely fungicide applications (Purayannur et al., 2021). The other cultural practices that can reduce inoculum and modify the microclimate of yards include removal of excess foliage, and grubbing of heavily diseased plants (Purayannur et al., 2021). Thus, breeding for resistance to *P. humuli* remains a key priority in modern hop breeding programs, although known sources of resistance are rare, genetically narrow, and quantitatively inherited. Thus, varieties for which a very low level of infection registered are considered as moderately resistant (Henning et al., 2015a). Breeding progress is hampered by hop perennial growth, inbreeding depression, and the need to maintain brewing quality traits, which are often associated with susceptibility (Woods & Gent, 2016). An important achievement in this direction is the development and registration of the resistant male hop germplasm USDA 21087M, which opens up new opportunities for obtaining resistant hop varieties (Henning et al., 2018). Further progress in this area requires more precise identification of resistance sources, developing robust molecular markers, and application of genomic selection tools (Henning et al., 2015a and b; Čerenak et al. 2019; Feiner et al., 2021).

Breeding efforts in hop-producing countries lead to a number of cultivars with a reasonable level of resistance. Assessment of 110 commercial hop cultivars in the USA demonstrated that the highest level of vigor and resistance to shoot infection are associated with cultivars originating from Europe, rather than with the cultivars from the United States, Japan, and Australia/New Zealand (Woods & Gent, 2016). A number of European cultivars are involved in the Ukrainian hop breeding program, such as moderately resistant varieties Perle, Hall. Magnum (DEU), moderately susceptible variety Saaz (CZE), as well as the susceptible variety Bullion (GBR) (O'Neal et al., 2015). Together with the moderately resistant Ukrainian varieties Alta, Ksanta, Ruslan, Slov'ianka, and Zahrava (UKR), they were used by us in a complex crossing to obtain new genotypes with the desired traits and better adaptation to local cultivation conditions.

The aim of our research was to evaluate the level of resistance to *P. humuli* of new genotypes within the Ukrainian collection of genetic hop resources under characteristic weather conditions in the Polissia zone during the second half of April till half of May. Over the four years of observation, the highest disease severity in this period was recorded in early-maturing genotypes. This trend may be related to the earlier bud break and more rapid shoot growth in these plants, which potentially exposes them to infection during periods favorable for pathogen development. In medium-late and late-maturity genotypes, lower infection levels coincided with periods of reduced humidity and increasing air temperature, conditions which are less conducive to pathogen spread and developement. However, it remains difficult to fully distinguish whether the observed differences in disease severity were driven predominantly by weather factors, intrinsic genetic resistance or susceptibility, or (an interaction of) both. Further controlled studies are required to clarify the relative contribution of these factors.

An earlier study demonstrated that leaf infection by *P. humuli* can occur at temperatures as low as 5°C, if wetness is maintained for 24 hr or more, leading to localized leaf spots (Royle, 1973). Systemic shoot

infection develops under similar conditions, but requires a 3–6 hr period of wetness within a temperature range of 8–23°C (Royle, 1970). Rain-induced wetness is particularly important for severe infection (Royle, 1973), with the highest disease severity observed when prolonged wetness coincides with high humidity and relatively warm night temperatures (Johnson & Skotland, 1985; Gent & Ocamb, 2009). Our observation during Stage I demonstrated clear differences in susceptibility of early emerging shoots of hop plants to *P. humuli* infection. While at the onset of Stage II — with temperatures of approximately 10–15°C and relative humidity of 60–67%, environmental conditions coincided with a pronounced increase in infection severity. Across all genotypes, the disease index rose on average by 47% compared to Stage I. This increase is likely associated with both favorable weather conditions for pathogen development and the progressive expansion of infected leaf area as the canopy developed. However, the specific contribution of leaf area enlargement to the observed increase in disease severity was not quantified in this study.

Overall evaluation of genotypes based on average DI values enabled the identification of 17 new genotypes (25%) as highly resistant. Among these, medium-maturity genotypes 7667, 8195, 8555, as well as medium-late maturity genotypes 8156, 8382, and 8367, representing bitter hop forms with highly resinous varieties in their pedigree, showed the most stable resistance to *P. humuli*. These genotypes can therefore be considered promising sources of resistance and are of significant interest for future hop breeding programs.

Our follow up investigations will focus on clarifying the genetic basis of resistance through detailed pedigree analysis, the identification of specific morphological traits associated with reduced susceptibility, and the use and/or development of markers (Driskill M et al., 2022, Havill J et al., 2023) to facilitate resistance evaluation at different stage of plant development. Such work will contribute to more efficient breeding strategies aimed at combining durable resistance to downy mildew with high brewing quality.

## CONCLUSIONS

In 2019-2022, our hop breeding collection was screened, and the level of field resistance to *Pseudoperonospora humuli* was determined in the initial stages of plant development and growth for 65 new genotypes, created using moderately resistant Ukrainian and foreign varieties, as compared to standard moderately susceptible varieties Alta, Zahrava, Slov'ianka, and Ruslan. A visual two-stage evaluation of symptom development in the initial phases of hop plant growth and development, which occur in late April and early May, respectively, was performed under the prevalent weather conditions in the Polissia province.

According to average values of the disease index (DI), 17 genotypes (25%) were found to be highly resistant, but not immune.

Medium maturity, highly resinous genotypes 7667, 8156, 8195, 8367, 8382, and 8555, created using varieties Hallertau Magnum (DE), Ruslan, and Ksanta (UKR) were found to be highly resistant, with a DI index not higher than 15% and low variability of this index.

The genotypes of the early maturity group were generally less resistant/more susceptible than the medium and late ones. The medium maturity and late genotypes had a lower DI, probably also due to weather changes. In the phase of emergence of sprouts, the disease development was less severe than during the shoot growth phase for genotypes of all the maturity groups.

The following highly resistant hybrid genotypes 7667, 8156, 8195, 8555, 8382 and 8367 are recommended for further use in hop breeding, and the investigation of their genetic, hereditary traits and morphological specificities, including those of resistance to downy mildew, will be the purpose of further studies.

**Adherence to ethical principles.** This article is not associated with any studies using humans and animals as study objects.

**Conflict of interests.** The authors deny any conflict of interests.

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development of agrosphere in Polissia", 2021–2025 "Scientific foundations for enhancing the adaptability of hop genotypes (*Humulus lupulus* L.) under the variability of climate factors of Polissia zone using breeding-genetic and biotechnological methods".

## REFERENCES


Anderson K (2023) The emergence of lower-alcohol beverages: The case of beer. *Journal of Wine Economics, 18*(1):66–86. https:// doi.org/10.1017/jwe.2023.8

Bober A, Liashenko M, Protsenko L, Slobodyanyuk N, Matseiko L, Yashchuk N, Gunko S, Mushtruk M (2020) Biochemical composition of the hops and quality of the finished beer. *Potravinarstvo Slovak Journal of Food Sciences, 14*:307–317. https://doi.org/10.5219/1311.

Bocquet L, Sahpaz S, Hilbert J, Rambaud C, Rivière C (2018) *Humulus lupulus* L., a very popular beer ingredient and medicinal plant: Overview of its phytochemistry, its bioactivity, and its biotechnology. *Phytochemistry Reviews, 17*:1047–1090. https://doi.org/10.1007/s11101-018-9584-y

Čerenak A, Kolenc Z, Sehur P, Whittock S, Koutoulis A, Beatson R, Buck E, Javornik B, Škof S, Jakše J (2019) New male specific markers for hop and application in breeding program. *Sci Rep, 9*:14223 https://doi.org/10.1038/s41598-019-50400-z

Chester KS (1950) Plant disease losses: their appraisal and interpretation. *Plant dis. rep, suppl. 193*:190–362. https://doi.org/10.5962/bhl.title.86198

Darby P (2006). The history of hop breeding and development. *Journal of the Brewery History Society, 121*:94–111. https://www.breweryhistory.com/journal/archive/121/bh-121-094.htm

de Arruda MM, Soares FdS, Lima MT, Doracenzi EL, Costa PB, Oliveira DN, Fonsêca TKdS, de Jesus Junior WC, Santos ARd (2024) Bibliographic analysis of scientific research on downy mildew (*Pseudoperonospora humuli*) in hops (*Humulus lupulus* L.). *Agriculture, 14*(5):714. https://doi.org/10.3390/agriculture14050714

Driskill M, Pardee K, Hummer KE, Zurn JD, Amundsen K, Wiles A, et al. (2022) Two fingerprinting sets for *Humulus lupulus* based on KASP and microsatellite markers. *PLoSONE, 17*(4):e0257746.https://doi.org/10.1371/journal.

Easterling K, Pitra N, Jones R, Lopes L, Aquino J, Zhang D, Matthews P, Bass H (2018) 3D molecular cytology of hop (*Humulus lupulus*) meiotic chromosomes reveals non-disomic pairing and segregation, aneuploidy, and genomic structural variation. *Frontiers in Plant Science, 9*:1–13. https://doi.org/10.3389/fpls.2018.01501.

Feiner A, Pitra N, Matthews P, Pillen K, Wessiohann LA, Riewe D (2021) Downy mildew resistance is genetically mediated by prophylactic production of phenylpropanoids in hop. *Plant, Cell & Environment, 44*(1):323–338. https://doi.org/10.1111/pce.13906

Gent DH, Ocamb CM (2009) Predicting infection risk of hop by *Pseudoperonospora humuli*. *Phytopathology, 99*(10):1190–8. https://doi.org/10.1094/PHYTO-99-10-1190

Gent DH, Farnsworth JL, Johnson DA (2012) Spatial analysis and incidence–density relationships for downy mildew on hop. *Plant Pathology, 61*:37–47. https://doi.org/10.1111/j.1365-3059.2011.02491.x

Havill J, Richardson B, Rohwer C, Gent D, Henning J, Muehlbauer G (2023) Identification of quantitative trait loci associated with R1-mediated resistance to powdery mildew and sex determination in hop (*Humulus lupulus* L.). *Theor Appl Genet, 136*:154. https://doi.org/10.1007/s00122-023-04399-7

Henning JA, Coggins J, Peterson M (2015a) Simple SNP-based minimal marker genotyping for *Humulus lupulus* L. Identification and variety validation. *BMC Res Notes, 8*:542. https://doi.org/10.1186/s13104-015-1492-2

Henning JA, Gent DH, Twomey M, Townsend MS, Pitra N, Matthews P (2015b) Precision QTL mapping of downy mildew resistance in Hop (*Humulus lupulus* L.). *Euphytica, 202*(3):487–498. DOI: 10.1007/s10681-015-1356-9

Henning JA, Gent DH, Townsend MS, Haunold A (2018). Registration of downy mildew-resistant male hop germplasm USDA 21087M. *Journal of Plant Registrations, 12*:379–381. https://doi.org/10.3198/jpr2017.09.0067crg

Higgins D, Hausbeck M (2021) Susceptibility of hop cultivars and rootstock to downy mildew caused by *Pseudoperonospora humuli*. *HortScience, 56*(5):543–550. https://doi.org/10.21273/HORTSCI15580-20

Johnson DA & Skotland CB (1985) Effects of temperature and relative humidity on sporangium production of *Pseudoperonospora humuli* on hop. *Phytopathology, 75*(2):127–129. https://www.apsnet.org/publications/phytopathology/backissues/Documents/1985Articles/Phyto75n02_127.pdf

Johnson DA, Engelhard B, Gent DH (2009) Downy Mildew. In W. Mahaffee, S. J. Pethybridge, & D. H. Gent (Eds.), Compendium of Hop Diseases and Pests (pp. 18–22). St. Paul, Minnesota: The American Phytopathological Society. https://my.apsnet.org/APSStore/ProductDetail.aspx?WebsiteKey=2661527A-8D44-496C-A730-8CFEB6239BE7&iProductCode=43764

Kitner M, Runge F, Lebeda A et al. (2021) *Pseudoperonospora humuli* might be an introduced species in Central Europe with low genetic diversity but high distribution potential. *Eur J Plant Pathol, 159*:903–915. https://doi.org/10.1007/s10658-021-02214-x

Korpelainen H, Pietiläinen M (2021) Hop (*Humulus lupulus* L.): Traditional and present use, and future po-

tential. *Econ Bot, 75*:302–322. https://doi.org/10.1007/s12231-021-09528-1.

Methodology UIPVE (2016) Methodolgy for conducting an examination of varieties of industrial and fodder crops for suitability for distribution in Ukraine. UIPVE (2016). 35–41. https://sops.gov.ua/uploads/page/5a5f41539f40a.pdf

Mitchell MN, Ocamb CM, Grünwald NJ, Mancino LE, Gent DH (2011) Genetic and pathogenic relatedness of Pseudoperonospora cubensis and *P. humuli*. *Phytopathology, 101*(7):805–18. doi: 10.1094/PHYTO-10-10-0270. PMID: 21405990.

Mongelli A, Rodolfi M, Ganino T, et al. (2016) Italian hop germplasm: Characterization of wild *Humulus lupulus* L. genotypes from Northern Italy by means of phytochemical, morphological traits and multivariate data analysis. *Ind Crops Prod, 70*:16–27. https://doi.org/10.1016/j.indcrop.2015.02.036

Mozny M, Trnka M, Vlach V, Zalud Z, Cejka T, Hajkova L, Potopova V, Semenov MA, Semeradova, D, Büntgen U (2023) Climate-induced decline in the quality and quantity of European hops calls for immediate adaptation measures. *Nature Communications, 14*(1):6028. https://doi.org/10.1038/s41467-023-41474-5.

Nelson ME, Gent DH, Grove GG (2015) Meta-analysis reveals a critical period for management of powdery mildew on hop cones. *Plant Dis, 99*:632–640. https://doi.org/10.1094/PDIS-04-14-0396-RE

Nesvadba V (2016) Breeding process aimed at dwarf hops. *Kvasny Prumysl, 62*(6):166–172. https://doi.org/10.18832/kp2016022.

Nesvadba V, Charvátová J, Trnková S (2020) Breeding of flavour hops in the Czech Republic. *Kvasny prumysl, 66*(6):366–371. https://doi.org/10.18832/kp2019.66.366.

Neve R (1991) Fungal diseases. In: Hops. Springer, Dordrecht. 137–173. https://doi.org/10.1007/978-94-011-3106-3_7

Olšovská J, Straková L, Nesvadba V, Vrzal T, Přikryl J (2024) The comparison and brewing value of Saaz hop pedigree. *Beverages, 10*:101. https://doi.org/10.20944/preprints202408.0856.v1.

O'Neal SD, Walsh DB, and Gent DH, eds. (2015) Field Guide for Integrated Pest Management in Hops. 3rd ed. Pullman, WA: U.S. Hop Industry Plant Protection Committee. https://www.canr.msu.edu/uploads/234/71503/hop_field_guide_third_edition.pdf

Olatoye M, Wiseman M, Gent D, Henning J, Altendorf K (2023) Genetic characterization of downy mildew resistance from the hop (*Humulus lupulus* L.) line USDA 64035M. *Crop Science, 63*:1082–1091. https://doi.org/10.1002/csc2.20880.

Paguet AS, Siah A, Lefèvre G, et al. (2022) Agronomic, genetic and chemical tools for hop cultivation and breeding. *Phytochem Rev. 21*:667–708. https://doi.org/10.1007/s11101-022-09813-4.

Potopová V, Lhotka O, Možný M, Musiolková M (2021) Vulnerability of hop-yields due to compound drought and heat events over European key-hop regions. *Int. J. Climatol. 41*:E2136–E2158 https:// doi.org/10.1002/joc.6836.

Purayannur S, Gent DH, Miles TD, Radišek S, Quesada-Ocampo LM (2021) The hop downy mildew pathogen *Pseudoperonospora humuli*. *Mol Plant Pathol. 22*: 755–768. https://doi.org/10.1111/mpp.13063.

Protsenko L, Rudyk R, Lyashenko M, Shtanko I, Tsybulsky V, Chernenko O, Grynyuk T, Vlasenko A (2017) Atlas of Ukrainian hop varieties. Institute of Agriculture of Polissya NAAS. Publishing House O.O. Yevenok, 2017. 78 p. https://isgpnaan.org/upload/Catalogue%20of%20%20Ukrainian%20Hop%20Varieties.pdf

Richardson BJ, Gent DH (2023) Impact of infection timing and autumnal fungicide applications on perennation of *Pseudoperonospora humuli* and severity of hop downy mildew. *Plant Disease, 107*(11):3430–3436. https://doi.org/10.1094/PDIS-02-23-0268-RE

Royle DJ (1970) Infection periods in relation to the natural development of hop downy mildew (*Pseudoperonospora humuli*). *Annals of Applied Biology, 66*:281–291. https://doi.org/10.1111/j.1744-7348.1970.tb06435.x

Royle DJ, & Thomas GG (1971) The influence of stomatal opening on the infection of hop leaves by *Pseudoperonospora humuli*. *Physiological Plant Pathology, 1*(3):329–343. https://doi.org/10.1016/0048-4059(71)90053-1

Royle DJ (1973) Quantitative relationships between infection by the hop downy mildew pathogen, *Pseudoperonospora humuli*, and weather and inoculum factors. *Annals of Applied Biology, 73*:19–30. https://doi.org/10.1111/j.1744-7348.1973.tb01305.x

Royle DJ, Kremheller, HT (1981) Downy mildew of the hop. In D. M. Spencer (Ed.), The downy mildews (pp. 395–419). Academic Press. ISBN: 012656860X

Seigner E, Lutz A, Oberhollenzer K, et al. (2009) Breeding of hop varieties for the future. *Acta Hortic, 848*: 49–58. https://doi.org/10.17660/ActaHortic.2009.848.4

Shtanko I, Venger O, Shpakevich L, Fedorchuk N, Saykin M (2018) Determination of the resistance of genotypes of the breeding nursery to the main biotic pathogens of hops. *Agricultural Production in Polissia, 11*: 75–79. http://nbuv.gov.ua/UJRN/avpol_2018_11_17

Shtanko I, Venger O, Dzyadovich O, Fedorchuk N (2020) Selection and genetic basis for the creation, evaluation, and use of new hop genotypes resistant to biotic environmental factors with valuable characteristics for brewing, pharmaceutical, and other industries: scientific and methodological recommendations. Zhytomyr: PP. Ruta. 36 pp. https://isgpnaan.org/upload/nauk_-

metodichni-rekomendatsii-zavdannya-0116U004654.pdf (in Ukrainian).

Trefilová M, Nesvadba V, Charvátová J (2022) Evaluation of resistance to *Pseudoperonospora humuli* and of the content of alpha acids and hop oils in hops of selected genetic resources of hop *Humulus lupulus* L. *Czech J. Genet. Plant Breed*. https://doi.org/10.17221/70/2021-CJGPB

Venger O, Fedorchuk N (2021) Protection of hop against the primary infection with false powdery mildew. *Bulletin of Agricultural Science Vol. 99*(10). https://doi.org/10.31073/agrovisnyk202110-04.

Venger OV, Kliuchevych MM, Stoliar SH, Strygun OO, Vygera SM, Shtanko IP, Honcharenko OM (2021) Fungicidal and growth-stimulating effect of microbial preparations on hop plants yield. *Ukrainian Journal of Ecology, 11*(2):40–46. https://doi.org/10.15421/2021_74

Vostřel J (2021) New possibilities of environmentally safe hop protection against pests and diseases with the help of botanical pesticides, basic substances and bio-fungicides. *Acta Horticulturae, 1328*:103–108. https://doi.org/10.17660/ActaHortic.2021.1328.14.

Willocquet L, Savary S, Singh KP (2023) Revisiting the use of disease index and of disease scores in plant pathology. *Indian Phytopathology, 76*:909–914. https://doi.org/10.1007/s42360-023-00663-4

Woods JL, Gent DH (2016) Susceptibility of hop cultivars to downy mildew: associations with chemical characteristics and region of origin. *Plant Health Progress, 17*(1):42–48. https://doi.org/10.1094/PHP-RS-15-0044

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## СКРИНІНГ СЕЛЕКЦІЙНОГО МАТЕРІАЛУ ХМЕЛЮ НА ПОЛЬОВУ СТІЙКІСТЬ ДО НЕСПРАВЖНЬОЇ БОРОШНИСТОЇ РОСИ (*PSEUDOPERONOSPORA HUMULI* WILSON) НА РАННІХ СТАДІЯХ РОЗВИТКУ РОСЛИН

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**Мета.** Провести скринінг української колекції селекційного матеріалу хмелю з визначенням рівня польової стійкості до *Pseudoperonospora humuli* на ранніх стадіях розвитку та росту хмелю, а також виявити цінні генотипи для подальшої селекції. **Методи.** Дослідження проводилося у 2019–2022 роках на дослідних ділянках (м. Житомир, Полісся, Україна) на фоні природної інфекції *P. humuli*. Шістдесят п'ять новостворених генотипів хмелю та чотири стандартні українські сорти Альта, Слов'янка, Заграва та Руслан були оцінені за стійкістю до *P. humuli* на основі індексу захворювання за 9-бальною шкалою впродовж початкових фаз росту рослин на двох етапах: поява сходів (І етап) та ріст пагонів (ІІ етап). **Результати.** Вперше було проведено описовий аналіз польової стійкості хмелю до *P. humuli* на двох етапах його розвитку та росту для 65 нових генотипів з української колекції селекційного матеріалу хмелю та відібрано найстійкіші з них. Розвиток хвороби був менш інтенсивним на етапі І, ніж на етапі ІІ, що, ймовірно, було пов'язано з підвищенням вологості та температури на другому етапі. Жоден генотип не проявив імунітету (повної стійкості) до хвороби. Чотири стандартні сорти, що використовувалися, показали помірну сприйнятливість. Вісім генотипів (7667, 8156, 8195, 8367, 8382, 8388, 8604 та 8555) продемонстрували високу стійкість на стадії І, тоді як дещо інший набір з восьми генотипів (7667, 7886, 8156, 8195, 8367, 8438, 8605 та 8555) продемонстрував високу стійкість на стадії ІІ. Відмінності за ознакою стійкості на різних стадіях оцінки та між генотипами були статистично значущими ($F=13,4$; $p < 0.001$). **Висновки.** Оцінка української колекції селекційного матеріалу хмелю за рівнем польової стійкості до *Pseudoperonospora humuli* на ранніх стадіях розвитку та росту рослин показала, що 25% генотипів було класифіковано як стійкі, 39% — як помірно стійкі, 32% — як помірно сприйнятливі та 4% — як сприйнятливі. Шість генотипів (7667, 8156, 8195, 8367, 8382 та 8555) з найвищою загальною польовою стійкістю до *P. humuli* було рекомендовано включити до подальшого селекційного вивчення та досліджень з визначення генетичних маркерів стійкості.

**Ключові слова:** *Humulus lupulus*, генотип, пошкодження, первинна інфекція, сприйнятливість.