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Non-Sikkim Cucumber Accessions Resistant to Downy Mildew (*Pseudoperonospora cubensis*)

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Abstract: Downy mildew caused by the oomycete *Pseudoperonospora cubensis* is a devastating disease of cucurbits. Cucumis species are attacked by pathotype 3 (clade 2) of the pathogen, while Cucurbita species are attacked by pathotype 6 (clade 1). The Sikkim-type cucumbers PI 197088 and PI 330628 express high levels of resistance against both pathotypes (clades) of the pathogen but no green-fruit cucumber cultivars resistant to the disease are available on the market. Here we report on several non-Sikkim accessions of cucumber that show resistance against downy mildew in four consecutive seasons. Mean % foliage attacked with downy mildew in the susceptible controls Ilan and SMR-18 was 93% and 71%, respectively, as against 0.2% and 1.8% in the Sikkim-type resistant controls PI 197088 and PI 330628, respectively. Twenty-four green fruit accessions were significantly more resistant than the susceptible cucumber controls. Five accessions showed less than 10% infected leaf area with downy mildew as follows: PI 432870—5%, PI 390266—7.5%, PI 418964—8.5%, PI 390258—8.8%, and G12—10%. PI 390258 and PI 390266 were susceptible to race 1 of powdery mildew but resistant to race 2, whereas PI 418964 was resistant to both races. These accessions may be used in breeding programs to accelerate the production of green-fruit, disease-resistant cucumbers.

Keywords: cucurbits; genes for resistance; downy mildew; powdery mildew; PI plant introduction; *Podospheara xanthi*

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1. Introduction

Cucurbit downy mildew (DM), caused by the oomycete *Pseudoperonospora cubensis* (Berk.&Curt.) Rost. is a devastating disease of cucurbits worldwide [1–3]. The pathogen produces chlorotic lesions on the leaves and dark-wall sporangia on their lower leaf surface. The sporangia disseminate by wind or water splashes and cause new infections. Infected leaves turn necrotic, which results in severe crop losses. The current isolates of *P. cubensis* in Israel are more tolerant to heat compared to the isolates of the previous century [4].

P. cubensis is heterothallic, having two opposite mating types, A1 and A2. Isolates belonging to pathotype 3 (attacking cucumber and melon) were all A1, whereas isolates belonging to pathotype 6 (attacking Cucurbita species) were either A1 or A2 [5]. When sporangia of A1 and A2 were mixed and inoculated onto detached leaves of cucumber or melon, oospores were formed in the mesophyll. Oospores inoculated onto detached leaves produced F1 downy mildew lesions, many in *Cucumis sativum*, *Cucumis melo* and *Cucurbita moschata*, very few in *Cucurbita pepo* or *Citrullus lanatus*, and none in *Cucurbita maxima* [6]. Rani et al. (2022) reported the occurrence of oospores in field-grown infected cucumber leaves in Punjab, India [7], and Kikway et al. (2022) reported them in NC, USA [8].

The *P. cubensis* population is composed of two host-adapted genetic clades. Clade 1 is native to North America and infects all cucurbits except cucumber cultivars with the *dm1* gene derived from PI 197087. Clade 2 was introduced to north America in 2004 and preferentially infects cucumber and melon [9,10]. While isolates capable of infecting Cucurbita species are native to north America, isolates incapable of infecting Cucurbita species are native to Israel [11]. A full description of the pathotypes of *P. cubensis* is given in [11]. Races are described in [12].

Two major recent events indicated worldwide changes in the genetic structure of *P. cubensis*: The first was the appearance in 2002 of Clade 1 isolates (pathotype 6, A2 mating type) in Israel [13]. The second was the appearance of Clade 2 isolates in the USA [14] which overcame the *dm1* gene for resistance that was effective against *P. cubensis* for decades. Runge et al. (2011) suggested that Clade 2 originated from Japan and Korea and is indigenous to east Asia [9]. No plausible explanation is yet available for these two resurgence events. One possible explanation is that *P. cubensis* is seed borne [15]. This might have aided its transportation and distribution around the world.

Wallace et al. (2020) reported that Clade 2 isolates were more frequently found in host species including *Cucumis sativus*, *Cucumis melo*, and the wild host *Lagenaria siceraria*, while Clade 1 isolates were more frequently found in *Cucurbita pepo*, *Cucurbita maxima*, *Cucurbita moschata*, *Citrullus lanatus*, *Momordica charantia*, and *Momordica balsamina* [10]. They concluded that the host is the main factor structuring *P. cubensis* populations. Similar observations were made by Cohen et al. (2013), who showed host pathotype preference of Pathotype 3 to Cucumis spp. and of Pathotype 6 to Cucurbita spp. [6]. Keinath (2023) reported on differential responses of Clade 1 and Clade 2 isolates to anti-oomycete fungicides [16]. By using a series of melon cultivars, Lebeda, et al. (2024) showed the occurrence of different races in each pathotype of *P. cubensis* [12].

PI 197087—derived DM resistance is controlled by a single recessive gene (*dm1*) with a classical HR [17–21]. The *dm1*-conferred DM resistance has been widely deployed in commercial cucumber varieties, which have provided effective protection to cucumber production in the USA for over 50 years until 2004, when new DM strain(s) (post-2004 strains) emerged in the cucumber field, rendering *dm1* resistance less effective [14,22,23]. Nevertheless, *dm1* still exhibits moderate resistance to the prevailing post-2004 DM populations in the USA and sufficient resistance in many other countries [24].

Enhanced epidemics of downy mildew occurred after the appearance in 2002 and 2004 of a new genotype of the pathogen in Israel and the USA, respectively. The new genotype in Israel attacked Cucurbita species that have never been attacked before, and that in the USA caused the breakdown of the long-lasting *dm1* recessive gene for resistance derived from *Cucumis sativus* PI 197087 [11].

After the breakdown of the *dm1* gene for resistance, two new Sikkim-type resistant germplasm of cucumber PI 197088 and PI 330628 were soon available to introduce resistance genes in breeding programs; both developed small numbers of HR-type restricted lesions upon leaf inoculation, with limited sporulation of the pathogen. Callose and lignin deposits were associated with such lesions [11,25].

Both PIs have a round fruit and are 15–20 cm in diameter, with rough brown rind (Sikkim type), which are far from the traits required for the market. Crosses made between these PIs and susceptible elite cucumber lines produced susceptible F1 plants, with elongated fruits with brown rind. The F2 population segregated for resistance and fruit type with only about 1/164 plants exhibiting resistance level corresponding to the PI parent, suggesting multiple recessive QTLs associated with resistance [25]. Indeed, OTL analyses revealed multiple SNPs, on various chromosomes, linked with resistance [26–31].

Powdery mildew (PM) caused by the obligatory biotrophic ectoparasite *Podosphaera xanthii* affects cucumber productions worldwide [32]. It has an exceptionally wide host range, infecting species from various plant families [33]. Different races can be distinguished using differential melon lines (*Cucumis melo*) [34]. In melon, *Pm-1* and *Pm-3* are responsible for resistance against race 1, while *Pm-2*, *Pm-4*, and *Pm-6* are responsible for resistance against race 2 [35]. PM-resistant cucumber lines include 'Puerto Rico 37', PI-200815, PI 200818 [36], PI 197087 [37], and Natsufushinari (PI 279465) [38]. Multiple QTLs for resistance to PM were found in PI 197088 [28,39]. Five QTLs were identified on three linkage groups in the $F_{2:3}$ population of the resistant cucumber S06 [40].

Block et al. (2005) screened 977 cucumber accessions from the U.S. National Plant Germplasm System (NPGS) collection for resistance to PM. The twenty most resistant accessions were PIs 418962, 418964, 432860, 432870, 197085, 197088, 605930, 279465, 288238, 390258, 390266), 330628, 426169, 426170, 321006, 321009, and 321011 [41].

Sakata et al. (2006) identified in PI 197088 two and three loci for powdery mildew resistance under 26 °C and 20 °C conditions, respectively, with one major QTL acting under both temperature conditions [39].

Wang et al. (2018) reported that resistances in PI 197088 to downy and powdery mildew pathogens are conferred by 11 (3 with major effect) and 4 (1 with major effect) QTLs, respectively, three of which are co-localized [28].

To identify novel sources of DM resistance, 1300 cucumber cultigens (accessions, breeding lines, and elite cultivars) of the USDA Agriculture Research Service collection were evaluated in multi-year, multi-location experiments. The consistently most resistant genotypes were accessions PI 197088 and PI 605996 (both of Indian origin) and PI 330628 (originating from Pakistan) [42].

New resistance genes were soon derived from PI 197088 and PI 330628. These PIs show unsatisfactory fruit quality and carry multiple QTLs for resistance, none of which is dominant [30].

He et al. (2022) summarized recent findings on the inheritance, molecular markers, and quantitative trait locus mapping of cucumber powdery mildew, downy mildew, and fusarium wilt FM resistance. In addition, several candidate genes, such as PM, DM, and FM resistance genes, with or without functional verification, were reviewed [43].

In their paper on PI 197088, Berg et al., (2020) studied the QTL DM4.1 located on chromosome 4. This QTL was shown to consist of three subQTLs: DM4.1.1 affected pathogen-induced necrosis, DM4.1.2 was shown to have an additive effect on sporulation, and DM4.1.3 had a recessive effect on chlorosis as well as an effect on sporulation [44].

Using genome-wide association analysis (GWAS), Liu et al. (2020) identified 18 DM resistance loci that were distributed on all the seven cucumber chromosomes. Of these loci, only six (dmG1.4, dmG4.1, dmG4.3, dmG5.2, dmG7.1, and dmG7.2) were detected in two experiments and were considered as loci with a stable effect on DM resistance. Further, sixteen out of the eighteen loci colocalized with the QTLs were reported in previous studies, and two loci, dmG2.1 and dmG7.1, were novel [45].

Lebeda et al. (2024) provided comprehensive information on the status of resistance of cucurbits to PMs and the obstacles, gaps and recent progress for six cucurbit genera regarding resistance resources, genetics of resistance, genetic mapping and development of molecular markers, physiology and mechanisms of resistance, developments in *mlo*-mediated resistance, patents, and resistance breeding [33].

In the present study, we evaluated a series of PI entries for their resistance to *P. cubensis* (DM) in four consecutive growth seasons and to *P. xanthi* in one season. All produced non-Sikkim types of fruits. These PIs were listed by Block and Reitsma (2005) as most resistant to *P. xanthi* (PM) in the USA. Seventeen of the twenty most resistant accessions to

PM came from Asian sources, including China, Japan the Philippines, and Taiwan [41]. We first examined their resistance to the Israeli population of powdery mildew and then to downy mildew.

2. Material and Methods

2.1. Plant Material

Seeds of the Sikkim-type PI 197088 and PI 330628 were retrieved from our own collection [25]. Seeds of the other cucumber accessions were obtained from the USDA National Plant Germplasm System "https://www.ars-grin.gov/Collections (accessed on 25.12.2024)". To examine their resistance to powdery mildew (PM), the plants were grown in the soil in a greenhouse (25 × 8 × 7 m) and exposed to natural infection with powdery mildew (Experiment 1, Table 1).

Table 1. Experimental set up for screening resistance against downy mildew and powdery mildew.

Experiment	Year	Disease	Season	Planting Date	Inoculation DM	Scoring Date	Dpi
1	2022	PM	autumn	12.7.2022	Natural	3.10.2022	-
2	2023	DM	spring	14.3.2023	13.4.2023	4.5.2023	21
3	2023	DM + PM	summer	3.7.2023	25.7.2023	15.8.2023	20
4	2023	DM	autumn	18.9.2023	3.10.2023	11.10.2023	8
5	2024	DM	spring	14.3.2024	5.4.2024	25.4.2024	20

In the other four experiments (Table 1) seeds were grown in 7 cm pots in a greenhouse until the 2-leaf stage and thereafter transplanted into polystyrene containers (120 L, 120 × 50 × 20 cm, Polybid, Mishmar Hanegev, Israel) filled with compost: peat (1:10, *v*/*v*), six plants per container. The containers were placed in 50 × 7 × 4 m high net houses (covered with a white plastic net of 50 mesh) located at the Experimental Farm of Bar Ilan University, Ramat Gan, Israel (3204.1519, N, 03450.5853, E).

2.2. Pathogens and Inoculation

Four experiments in high net houses were performed to evaluate the level of resistance of the PI entries to downy mildew during four consecutive seasons: spring, summer and fall of 2023, and spring of 2024 (Table 1). In each season, the plants were artificially inoculated with freshly produced sporangia *P. cubensis* at the 8–10-leaf growth stage. Five isolates of *P. cubensis* were collected from infected cucumber fields in Israel during 2020–2022 and were propagated on detached cucumber leaves in growth chambers at 18 °C as described before [25]. All isolates belonged to pathotype 3 Clade 2, and mating type A1, resistant to mefenoxam. These characteristics were determined as described before [5,6]. Resistance to mefenoxam (MFX) was determined in 2-leaf cucumber plants in growth chambers. Plants were sprayed with MFX of various doses and thereafter inoculated with sporangia of *P. cubensis*. The disease was recorded after a week. Sensitive isolates produced no downy mildew symptoms at 10 ppm (active ingredient), whereas resistant isolates produced symptoms at 1000 ppm.

Plants in the net houses were inoculated with a sporangial mixture of 5 isolates soon after sunset. Two liters of sporangial suspension containing 5×10^3 sporangia per mL were sprayed with a hand sprayer onto the upper leaf surface of the test plants occupying the net house. To ensure successful infection, the inoculated plants were covered with plastic sheets until 8 am of the following morning. The temperature at night ranged between 15 and 22 °C, depending on the season.

2.3. Visual Assessment of Disease

PM development was recorded at the end of the growing season, at fruit maturity. The percentage of leaf area occupied with powdery mildew symptoms was visually assessed in each plant.

DM development was assessed at various time periods after inoculation, depending on the experiment (Table 1), as the percentage of plant leaf area occupied with downy mildew lesions. In Experiment 3, the number of sporangia per unit leaf area of infected tissue was counted microscopically at 8 dpi as follows: two infected leaves were detached from each of 6 plants per entry and placed on wet filter paper in 20 cm dishes in growth chambers at 20 °C for 24 h. Leaves were then cut into two halves and photographed, with upper and thereafter lower surface uppermost. Five 12 mm leaf discs were punched out from each leaf, placed in 10 mL of 10% ethanol, and stirred for 2 min. The number of sporangia was counted with the aid of a cytometer (Sigma Aldrich, St. Louis, MO, USA).

2.4. Data Analysis

All experiments were performed with six or more plants per entry. Tukey's HSD test was employed to determine if the mean percentage of disease scores, or sporangial counts per square cm of leaf area, of the different accessions were significantly different at $\alpha = 0.05$.

3. Results

Twenty-five accessions of cucumber *Cucumis sativus* L. were reported resistant to powdery mildew (PM) in the USA [41,42]. They were evaluated for resistance to powdery mildew (PM) in one season, and to downy mildew (DM) in four consecutive seasons. Data on the five experimental set ups are given in Table 1. The origin and fruit characters of the accessions are given in Table 2 and their appearance in Figure 1.

Table 2. Origin of *Cucumis sativus* accessions and morphology of their mature fruits.

Accession	Origin	Length (cm)	Diameter (cm)	Shape	Rind Structure	Rind Color	Spikes
G12	Unknown	50	6	curved	smooth	yellow	Yes
PI 197085	India	13	15	round	netted	brown	No
PI 197088	India	16	16	round	netted	brown	No
PI 288238	Egypt (Japan)	41	10	straight	smooth	yellow	No
PI 321006	Taiwan	35	10	straight	smooth	green	Yes
PI 321009	Taiwan	37	10	straight	smooth	yellow	No
PI 321011	Taiwan	39	11	straight	smooth	yellow-green stripes	Yes
PI 330628	Pakistan	11	11	Round	netted	brown	No
PI 385967	Kenya	23	7	straight	smooth	green	Yes
PI 390258	Japan	39	9	straight	smooth	yellow	No
PI 390266	Japan	75	9	curved	smooth	yellow-green stripes	Yes
PI 390268	Japan	47	6	straight	smooth	yellow	No
PI 418962	China	43	9	curved	smooth	yellow-green stripes	Yes
PI 418964	China	62	5	curved	smooth	yellow-green stripes	Yes
PI 426169	Philippines	23	9	straight	smooth	brown	Yes
PI 426170	Philippines	27	9	straight	netted	brown	Yes
PI 432860	China	39	5	curved	smooth	yellow	Yes
PI 432870	China	43	8	curved	smooth	yellow	Yes
PI 432875	China	43	4	curved	smooth	green	Yes
PI 451975	Japan	52	5	curved	smooth	green	No
PI 531313	Hungary	21	8	straight	smooth	yellow	No
PI 605930	India	20	9	straight	smooth	green	Yes
PI 605996	India	22	9	straight	smooth	yellow	No
PI 606015	India	21	8	straight	netted	brown	Yes
SMR-18	USA	17	8	straight	smooth	yellow	Yes

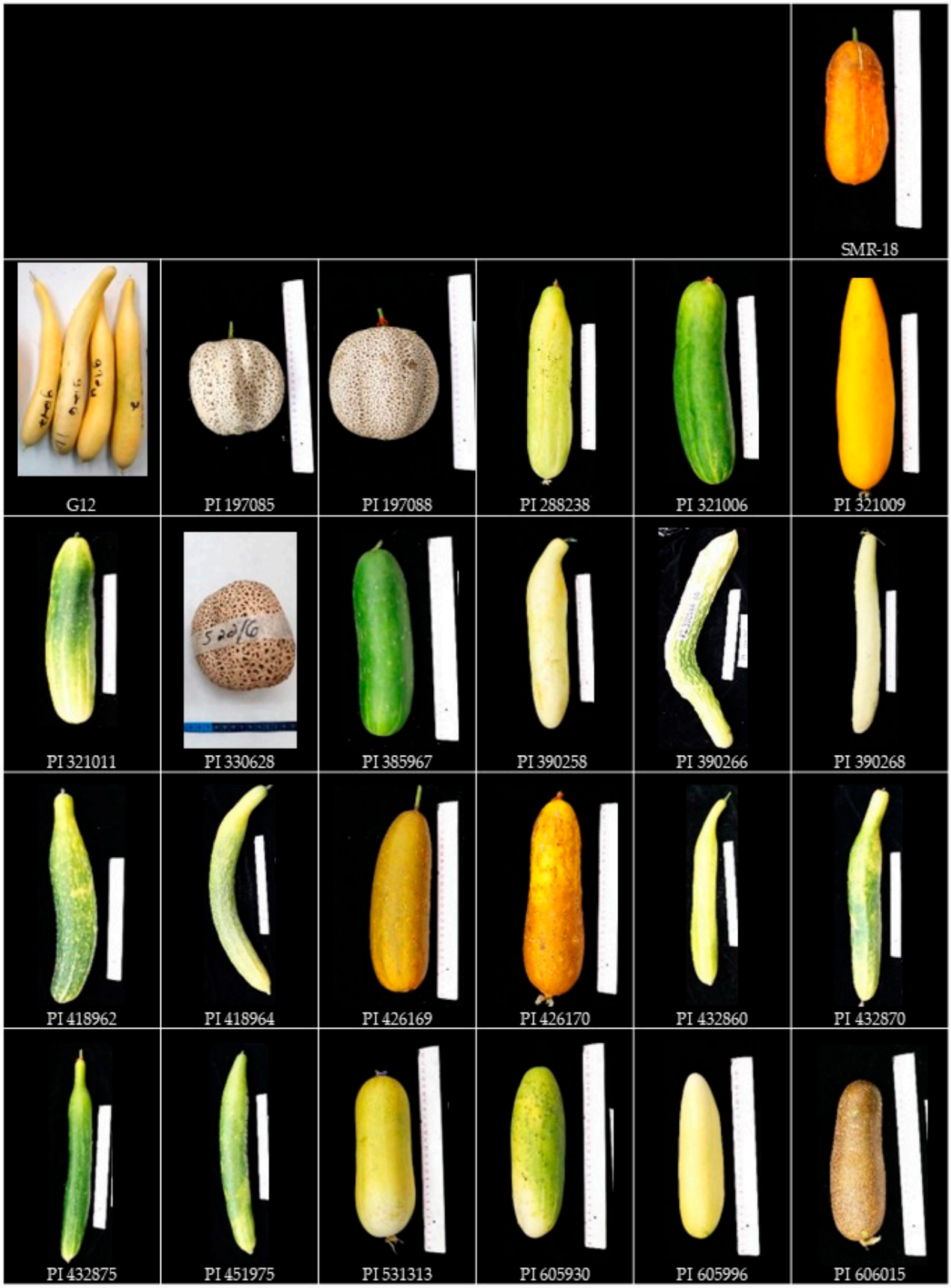


Figure 1. Fruit shape of Cucumis sativus accessions used in this study. Bar = 26.5 cm.

3.1. Experiment 1: Powdery Mildw 2022

In the first season (summer 2022), plants growing in soil in a greenhouse at BIU farm until fruit maturity were exposed to natural infection with powdery mildew from air-borne conidia. At the end of the season (83 days after planting), SMR-18 (susceptible control) showed 100% leaf area infected with powdery mildew, whereas melon Ein Dor showed no symptoms (fully resistant), suggesting that race 1 of *Podospheara xanthi* (formerly *Sphaerotheca xanthi*) prevailed in the greenhouse [35]. Three accessions were fully resistant to race 1, PI 197088, PI 426169 and PI 432870, and two accessions, PI 418964 and PI 426170, were resistant (below 10% infected leaf area) (Figure 2). No downy mildew developed in the greenhouse due to the lack of adequate moisture on the foliage.

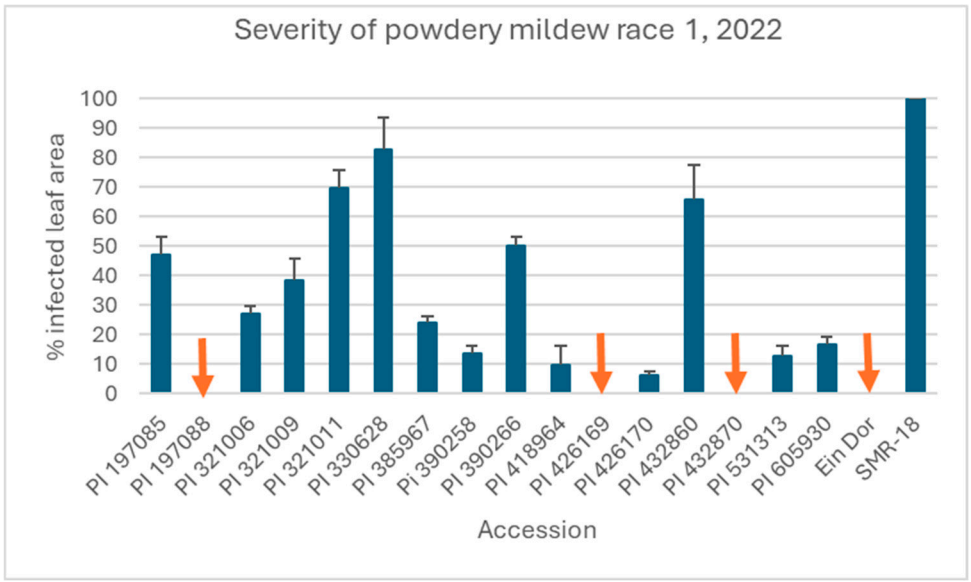
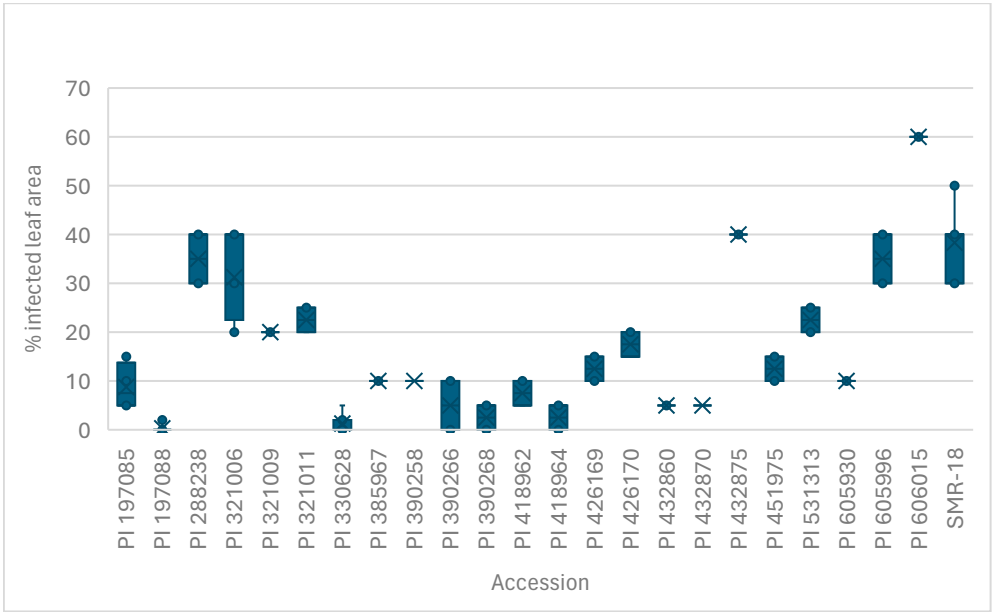


Figure 2. Severity of powdery mildew (*Sphaerotheca xanthi* Race 1) in mature *Cucumis sativus* accessions under greenhouse conditions in Israel. Red arrows indicate fully resistant accessions.

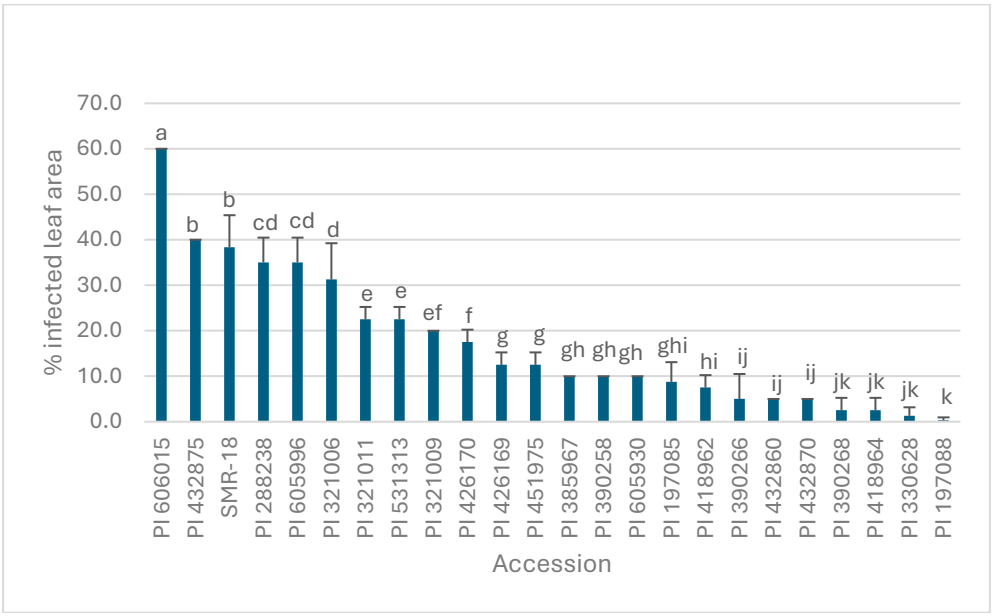
3.2. Experiment 2: Downy Mildew Spring 2023

Screenings for DM resistance were conducted in four experiments in the spring, summer and autumn of 2023 and spring 2024 (Table 1). In all seasons, the cucumber plants were artificially inoculated with the DM pathogen *P. cubensis* (pathotype 3) and were exposed to natural infection with the PM pathogen *P. xanthi* until fruit maturity. The commercial lines SMR-18 and and/or Ilan served as susceptible controls, while PI 197088 and PI 330628 served as resistant controls [25].

DM scores collected in the spring of 2023 are shown in Figure 3A,B. PI 197088 PI and 330628 were highly resistant (0.2 and 1.3% infected leaf area, respectively) as against 38.3.% in SMR-18. Five accessions were moderately resistant (7.5–10% infected leaf area) and five other accessions were resistant (2.5–5% infected leaf area). No powdery mildew appeared in the spring experiment.



(**A**)



(**B**)

Figure 3. Severity of downy mildew in accessions of *Cucumis sativus* in Israel under high net house conditions in spring 2023. (**A**) Box plot showing severity of DM in numerical order. (**B**) Bar plot showing severity of DM in severity order. Different letters on bars indicate a significant difference between means at $\alpha = 0.05$ (HDS Tukey's test). X marks average, horizontal line is the median line.

3.3. Experiment 3: Powdery and Downy Mildew Summer 2023

Both downy and powdery mildews developed in the following summer season (Figure 4). Seventy and forty percent of the leaf area of the susceptible controls Ilan and SMR-18 were occupied with lesions of DM. Six accessions showed resistance to DM (0–4% infected leaf area). PI 197088 showed zero infection (Figure 4A,B). PI 330628 was not included in this experiment. The severity of powdery mildew is shown in Figure 4C,D. The occurrence of powdery mildew on melon Ein Dor suggested that race 2 of *P. xanthi* prevailed in the net house [35]. SMR-18 and Ilan plants showed 30 and 50% infected leaf area with powdery mildew, respectively. Among all the accessions evaluated, six were fully resistant and seven were moderately resistant to PM (Figure 4C,D). PI 197088, PI 418964,

and PI 390258 showed complete resistance both in Block's study [41] and our study. For other accessions, the results of Block were as follows: PI 451975—24% S, 12% I, 64% R; PI 432860—8% S, 27% I, 65% R; and PI 385967—13% S, 2% I, 85% R. However, in our study they all were fully resistant.

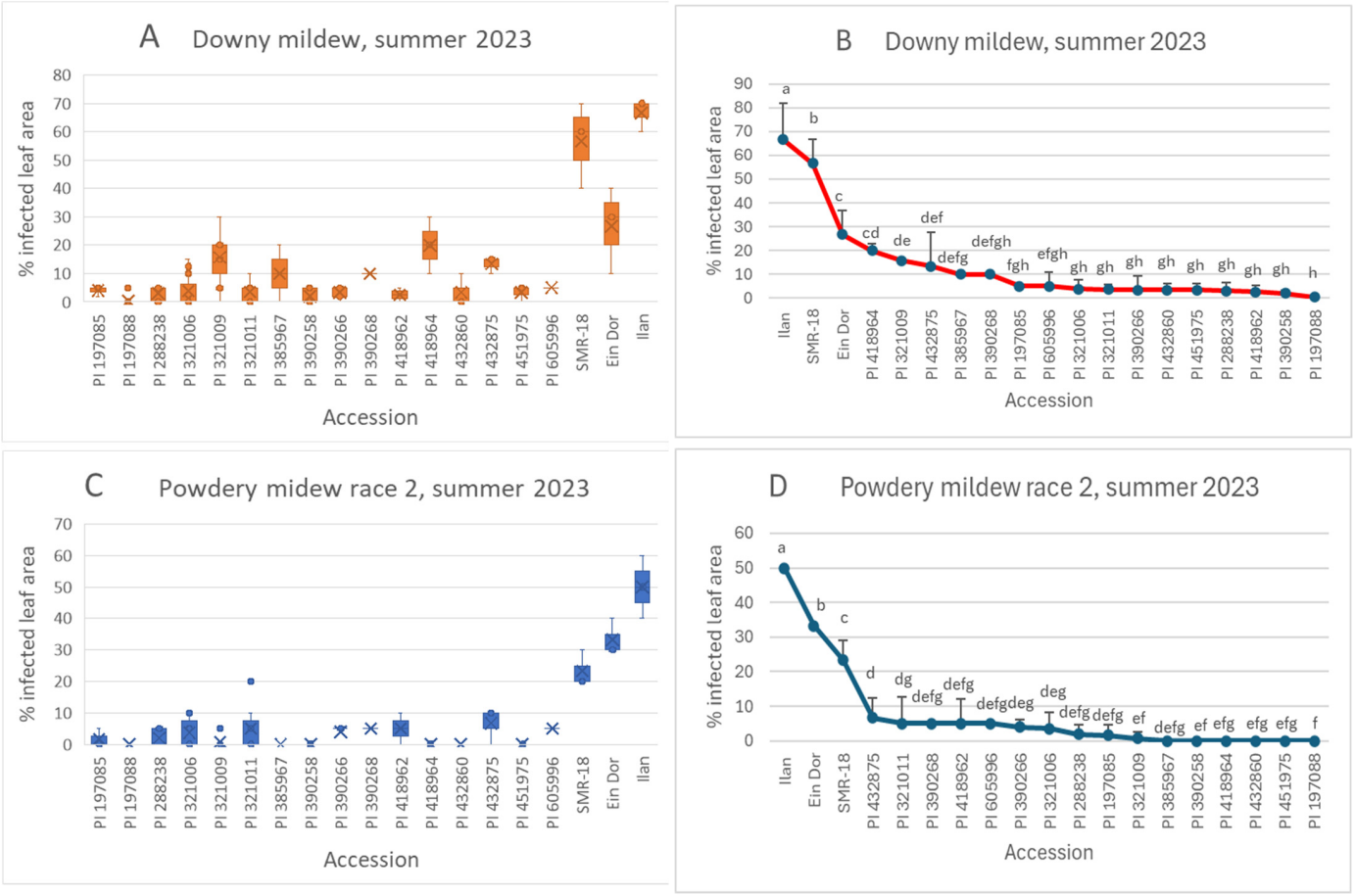


Figure 4. Co-epidemics of downy mildew (*Pseudoperonospora cubensis* Pathotype 3) (**A**,**B**), and powdery mildew (*Sphaerotheca xanthi* race 2) (**C**,**D**), on mature plants of cucumber accessions. Data in panels (**A**,**C**) are arranged in ascending order of the PI numbers. Data in (**B**,**D**) are arranged in ascending order of disease severity. Different letters on bars indicate a significant difference between means at $\alpha = 0.05$ (HDS Tukey's test).

3.4. Experiment 4: Downy Mildew, Autumn 2023

In the following autumn season, DM scores were taken at 7 dpi (Figure 5A,B) and sporulation of *P. cubensis* in detached leaves was measured at 8 dpi (Figure 5C,D). In the control SMR-18, 86.6% of the leaf area was occupied with DM lesions as against significantly lower scores of 0–36.6% in the other accessions. Six accessions showed below 10% infected leaf area, with PI 197088 and PI 330628 being the most resistant entries. In detached leaves, about 100×10^3 sporangia/cm^2 were produced on SMR-18, as against about $0.1–1 \times 10^3$ sporangia/cm^2 in eight accessions and about $2–9 \times 10^3$ sporangia/cm^2 in four other accessions (Figure 5C,D). The appearance of the disease on the detached leaves at 8 dpi is shown in Figure 6. No powdery mildew appeared until fruit maturity in this experiment.

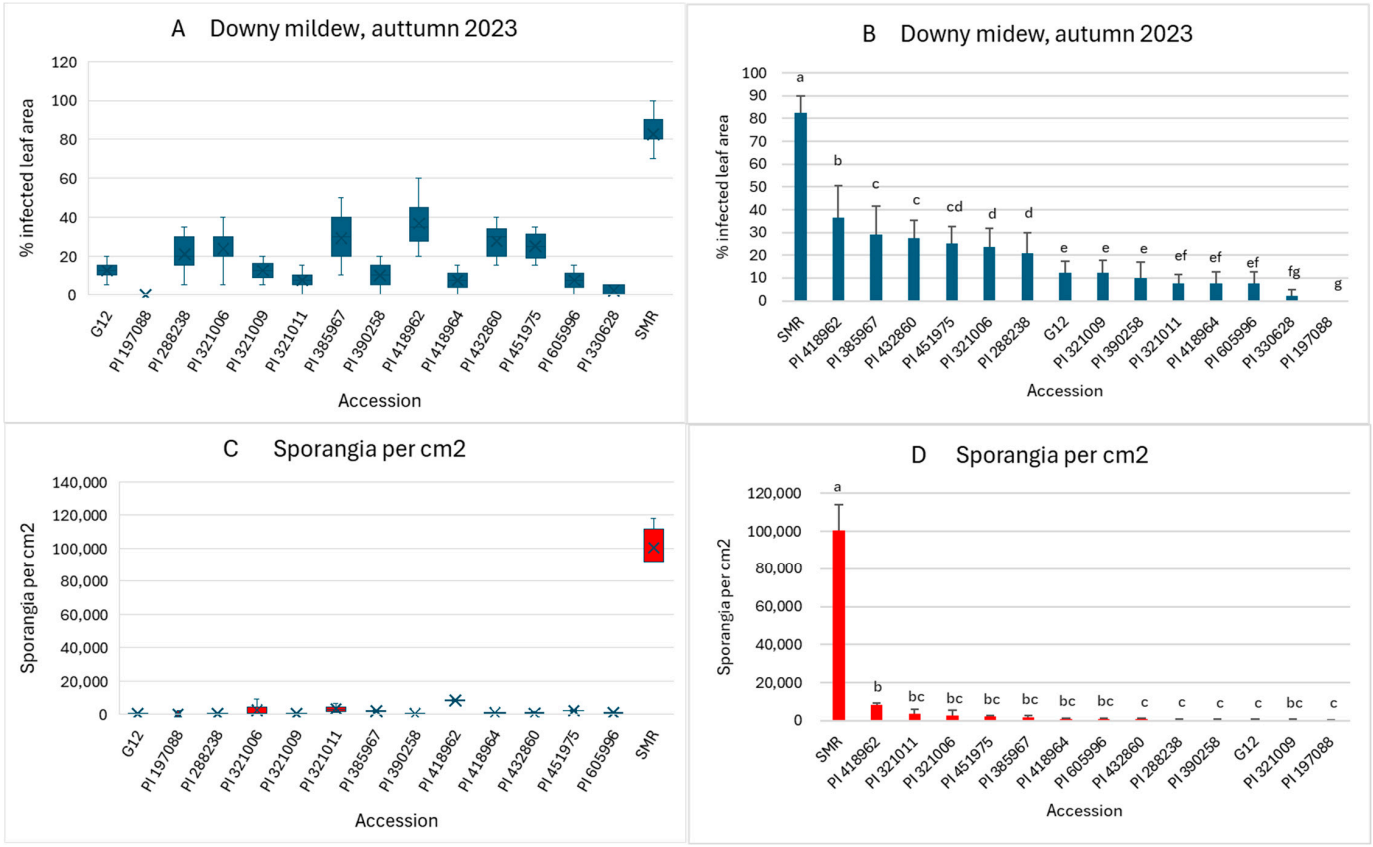


Figure 5. Severity of downy mildew on accessions of *Cucumis sativus* in Israel under high greenhouse conditions in autumn 2023. (**A**) Box plot showing severity of DM in numerical order. (**B**) Bar plot showing severity of DM in severity order. (**C**) Box plot showing sporangia/cm^2 in numerical order. (**D**) Bar plot showing sporangia/cm^2 in quantity order. Different letters on bars indicate a significant difference between means at $\alpha = 0.05$ (HDS Tukey's test).

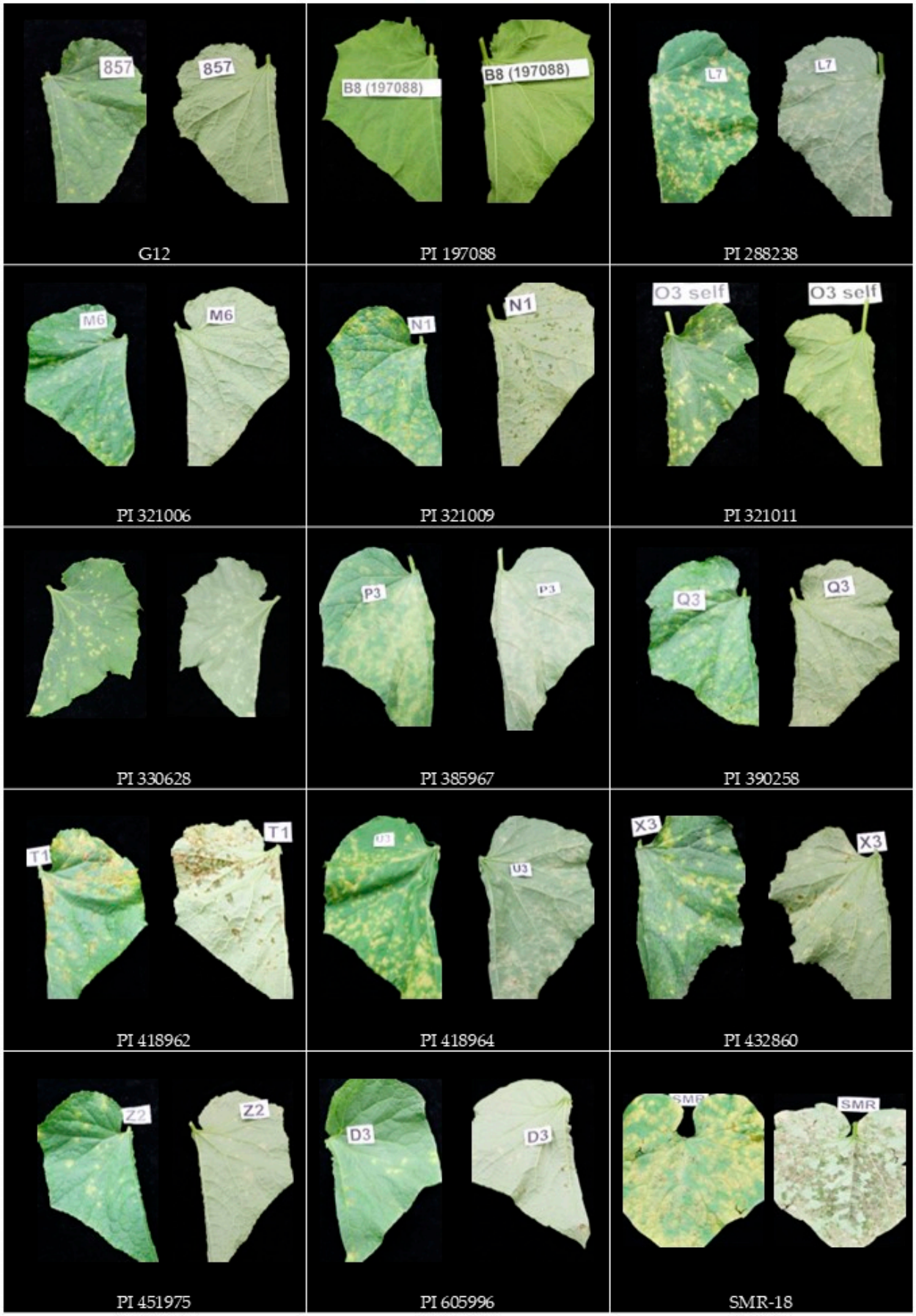


Figure 6. Downy mildew symptoms on upper leaf surface and sporulation of *P. cubensis* on lower leaf surface of cucumber.

3.5. Experiment 5: Downy Mildew Spring 2024

The fifth experiment was performed in the spring of 2024 (Figure 7A,B). Disease severity (% infected leaf area) in the susceptible controls Ilan and SMR-18 reached 97 and 86%, respectively, as against significantly lower scores of 0–60% infected leaf area in the other accessions. Eleven accessions showed less than 10% infected leaf area while five accessions showed 0–5% infected leaf area. PI 197085 and PI 197088 showed no symptoms. No powdery mildew was observed on the plants until fruit maturity.

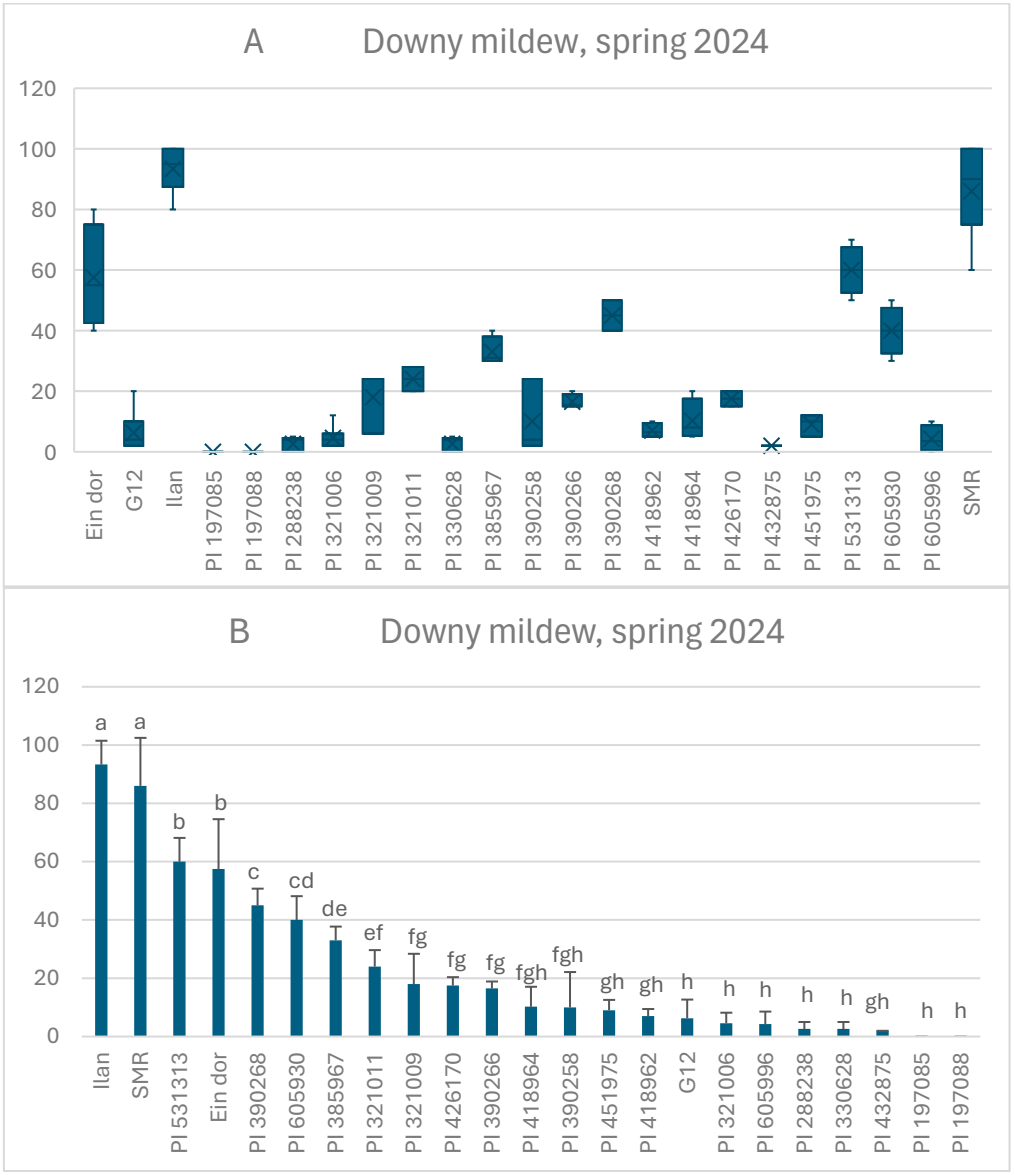


Figure 7. Severity of downy mildew on accessions of *Cucumis sativus* in Israel under high greenhouse conditions in spring 2024. (**A**) Box plot showing severity of DM in numerical order. (**B**) Bar plot showing severity of DM in severity order. Different letters on bars indicate a significant difference between means at $\alpha = 0.05$ (HDS Tukey's test).

3.6. Mean of Four Downy Mildew Experiments

The mean data of the four DM experiments are given in Figure 8. The most resistant accessions were PI 197088 and PI 330628. Twenty-four other wild accessions of cucumber showed significantly less disease compared to the susceptible controls Ilan or SMR-18 as well as the melon Ein Dor. Five accessions were scored at 5.71–10% infected leaf area, and three accessions were scored lower with 0.2–5% infected leaf area. Among the eight

accessions, five were non-Sikkim types: G12, PI 390258, PI 418964, PI 390266, and PI 432870.

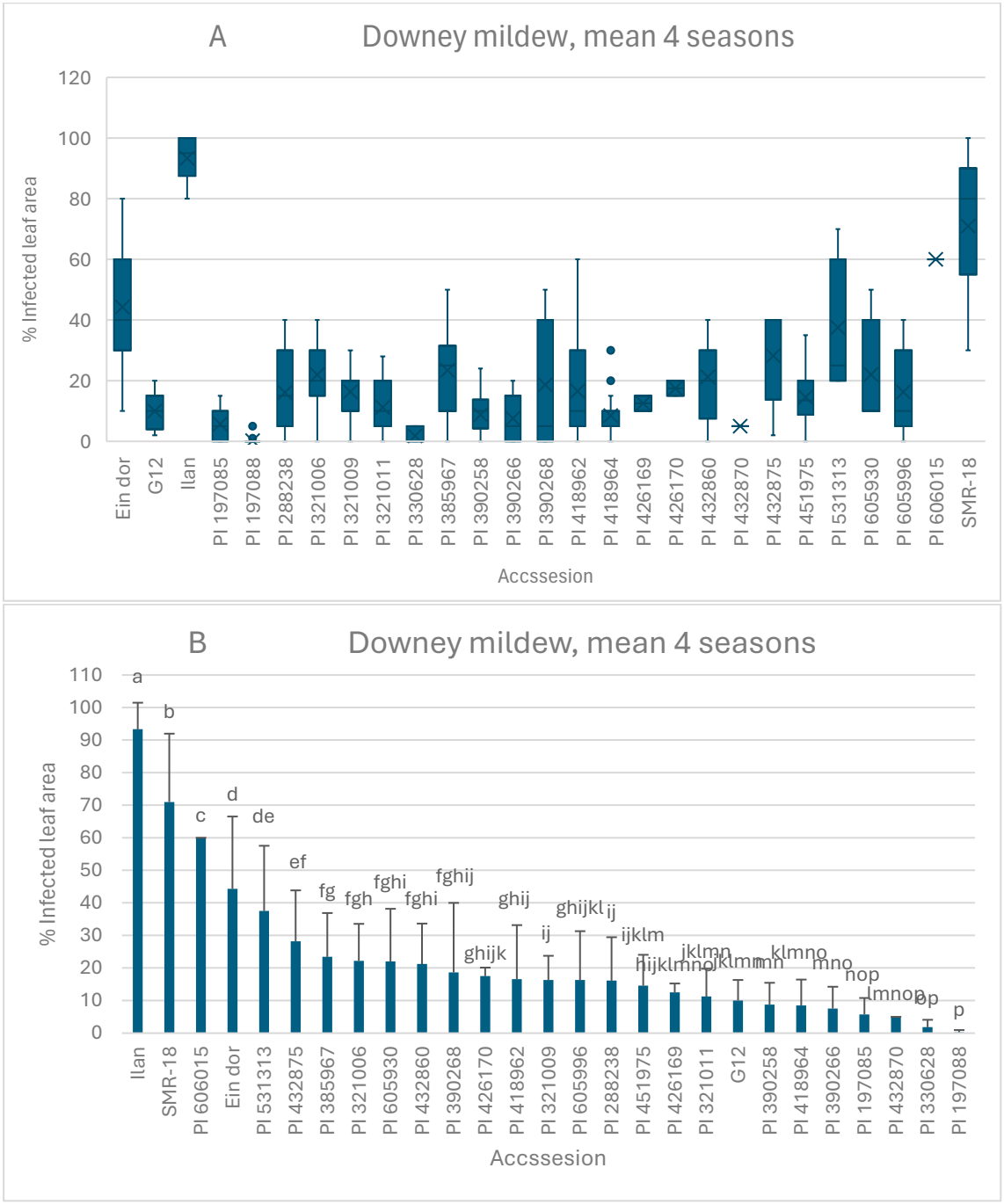


Figure 8. Mean of downy mildew severity on accessions of *Cucumis sativus* in Israel under high greenhouse conditions during four seasons. (**A**) Box plot showing severity of DM in numerical order. (**B**) Bar plot showing severity of DM in severity order. Different letters on bars indicate a significant difference between means at $\alpha = 0.05$ (HDS Tukey's test).

4. Discussion

The aim of this study was to discover non-Sikkim cucumber accessions resistant to downy mildew incited by *Pseudoperonospora cubensis*. Sikkim-type accessions PI 197088 and PI 330628 are highly resistant cucumbers. They carry multiple QTLs for resistance against both PM and DM [27,28,30,31,44,46–48]. Unfortunately, they both bear Sikkim fruits (Figure 1). Such fruits are unacceptable in most markets. When Sikkim-type cucumbers are used in breeding programs, multiple backcross generations are required to restore the

green fruit quality of the recurrent parent. Our study aimed to find resistant green-type cucumber accessions that may be used in breeding programs with a probably reduced number of recurrent backcrosses.

We, therefore, included in our screening non-Sikkim cucumber types which were reported by others to be resistant to powdery mildew caused by *Podosphaera xanthi* or downy mildew caused by *Pseudoperonospora cubensis* [25,41,42,49–52]. We examined twenty-six accessions, including PI 197088 and PI 330628 as resistant controls, in five growing seasons (Experiments). In all seasons, plants were artificially inoculated at an early stage with sporangia of *P. cubensis* and exposed to natural infestation with powdery mildew until fruit maturity. Resistance levels were determined by visual scoring of the percent of leaf area occupied by lesions of downy mildew and powdery mildew. In one season, we took measures of the sporulation of *P. cubensis* on the inoculated plants. In two seasons, natural infection with powdery mildew occurred.

Although the results were variable among seasons, they consistently confirmed that PI 197088 and PI 330628 were the most resistant accessions across all seasons. They exhibited slight infection or no symptoms. When symptoms occurred, the sporulation of *P. cubensis* was negligible, thus confirming our previous observations [25]. Yet, when PM did appear in the greenhouse or net house, PI 330628 was susceptible, thus contradicting the results published in the USA [41].

All our tested accessions showed significantly reduced mean DM scores relative to the two susceptible controls SMR-18 and Ilan. While the susceptible controls showed a mean infected leaf area in all seasons of 71–93%, some accessions had means less than 5%, others of less than 10%, and still others less than 20%.

The following accessions performed best in our experiments and might serve as parents in breeding programs: PI 432870 from China, 5% DM, resistant to PM race 1, moderate fruit length, with spikes. PI 390266 from Japan, 7.5% DM, resistant to PM race 2, very long fruit with spikes. PI 418964 from China, 8.5% DM, resistant to race 1 and race 2 of PM, long fruit with stripes and spikes. PI 390258 from Japan, 8.8% DM, resistant to PM race 2, moderate fruit length, straight and smooth. PI 197087 (the source of *dm1*) was not evaluated in our study.

Contrary to other studies that found high resistance against PM in PI 197088, a study conducted in India found that PI 197088 was susceptible [49]. This response might be related to differences in the prevailing races or even prevailing PM pathogens in India [33]. Metwally et al. (2015) found that PI 197088 was moderately resistant to DM in Egypt, while it was reported resistant in the USA and Israel [51]. PI 197085 was still resistant in the USA [42,50,52].

Some accessions were resistant to both PM and DM in both USA and Israel. One accession PI 432870 was found to be resistant to DM in both locations (but not in India), while some others were moderately resistant in all locations.

Taken together, this study provides data on the resistance to DM of non-Sikkim-type accessions of cucumber, some of which may be used in breeding programs to accelerate the production of green-fruit DM-resistant cucumber cultivars.

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