Abstract: We investigated fungal communities colonising black cherry stumps. We tested the hypothesis that black cherry stumps of greater diameter should be characterised by more diverse fungal communities than stumps of smaller diameter. The material for analyses came from Podanin Forest District. DNA was extracted using a Plant Genomic DNA purification kit. The results were subjected to bioinformatic analysis and statistical analysis. The OTU sequences were compared using the BLAST algorithm with reference sequences from the UNITE database. In total, 8192 raw sequences were obtained from samples of black cherry stumps applying the Illumina sequencing technique. The results of the statistical analysis indicate a trend towards increased diversity in bigger black cherry stumps. The dominant share of fungi associated with wood decomposition indicates the progressing process of decomposition in stumps. Identification of the role and functions of the individual components of fungal communities colonising stumps may provide insight into the overall ecology of these organisms and provide a basis for improved plant protection, with a view to limiting the occurrence of black cherries in the future in undesirable locations outside their natural range.

Keywords: Prunus serotina, Illumina System, saprotrophs, invasive species

1 Introduction

Dynamic development of the black cherry (Prunus serotina) population has been observed in monocultures of Scots pine (Pinus sylvestris L.), plantations of black pine (P. nigra Arn.) and European larch (Larix decidua Mill.) [1], fresh mixed coniferous forest, fresh mixed forest and fresh forest stands [2, 3]. When appearing on a mass scale in the shrub layer, black cherry hinders regeneration, growth and development of native tree species such as oak or pine, which lose in the competition e.g. for light [1]. For these reasons remedial action is being undertaken to limit the occurrence of black cherry. The methods used to control invasive species are frequently based on experience, rather than on the results of research [4]. Attempts to control black cherry based on methods which are not supported by the results of reliable evidence-based research may be inappropriate, and in the longer term a mistaken strategy, comparable in severity to the original intended introduction of that species [1].

One of the factors leading to the classification of a species as invasive is the lack of organisms that are antagonistic to it in the newly colonised environment [3]. Our current knowledge concerning antagonistic organisms, particularly fungi, in relation to the black cherry is far from satisfactory. In Poland very few studies have been published on the mycological pathogens of this host plant species or more broadly the genus Prunus [5, 6, 4]. The most numerous publications concern Chondrostereum purpureum (Pers.), which in Western Europe is used in the biological control of undesirable deciduous species, including the black cherry [7-9]. Observations in the Kampinos National Park provided information on the occurrence of macrofungi on decomposing black cherry wood [10, 4].

However, there are no reports on communities of microfungi colonising black cherry wood. In view of the above it was decided to investigate fungal communities...
colonising black cherry stumps. Herein, we tested the hypothesis that black cherry stumps of greater diameter should be characterised by more diverse and more numerous fungal communities than stumps of smaller diameter (i). It was also assumed that: the saprotrophs will dominate in the fungal communities of black cherry (ii), the Illumina system will identify the majority of fungi at the level of genus or species (iii), and the month of felling will have an influence on the fungal communities (iv).

2 Materials and Methods

The material for analyses consisted of 15 black cherry stumps of maximum 5 cm diameter outside bark (sample K1) and 15 stumps that were over 5 cm in diameter outside bark (sample K2), left after the trees had been felled in March, April and May in the Podanin Forest District (19°28’00”E 52°04’00”N, the Margonin Forest Division, compartment 342a) (with 5 stumps in each month). The dominant forest site type was fresh mixed forest (LMśw), growing on a rusty brown soil (RDbr). From the selected stumps 2 cm discs were cut, which were then spot drilled using a SPARKY BUR 15E cordless impact drill with a 2 mm bit. The material collection procedure was performed according to [11]. Samples of pulvurised wood were ground in a mortar frozen to –70°C. DNA was extracted using a Plant Genomic DNA purification kit (A&A Biotechnology). The amplification reaction was run in a thermocycler and included initial denaturation (94°C 5 min); 35 cycles of denaturation (94°C 30 s), annealing (56°C 30 s) and elongation (72°C 30 s); and final elongation (72°C 5 min). The reaction mixture was composed of 2.5 µl DNA, 0.2 µl each primer, 10.6 µl deionised water and 12.5 µl 2X PCR MIX (Genomed S.A. Warszawa).

The most common fungi in small stumps (K1) included *Pleurophoma osticolor* (25.46%), *Mycena megaspora* (5.49%), *Trichosporon stacteae* (3.26%), *Penicillium citreonigrum* (2.93%), *Yarrowia lipolytica* (2.06%), *P. lapidum* (2.35%), *Blastobotrys* sp. (2.02%), and *Candida fructis* (1.98%). However, in larger stumps (K2) the most common fungi were *Proliferodiscus* sp. (3.73%), *Laetiporus sulphureus* (3.73%), *Tumularia* sp. (2.24%), *Curvibasidium polymorph* (1.84%), *Curvibasidium cygneicollum* (1.61%), *C. mycetangii* (1.42%), *Biotia sphaeroidizax* (1.37%), *Rhizoscyphus* sp. (1.32%), *Fellozyma inositophila* (1.23%), *Hamamotopho lignophila* (1.04%) (Tab. 2).

3 Results

In total, 8192 raw sequences were obtained from 18 samples of black cherry stumps applying the Illumina sequencing technique. This number includes sequences of culturable fungi (6652 = 81.20%), non-culturable fungi (540 = 6.59%) and organisms with no reference sequence in the database (1001 = 12.21%). The stumps were colonised by 363 taxa. Cultured fungi of small stumps (K1): Ascomycota, Basidiomycota, Glomeromycota and Zygomycota were represented by 1134 (55.06%), 286 (11.8%), 6 (0.25%) and 6 (0.25%) taxa, respectively, comprising 85.15% of all taxa detected. In turn, cultured fungi from big stumps (K2), i.e. Ascomycota, Basidiomycota, Glomeromycota and Zygomycota, were represented by 3245 (56.25%), 1265 (21.93%), 1 (0.02%) and 28 (0.49%) taxa, respectively. Non-culturable organisms were represented by 310 taxa in samples K1 and 335 in samples K2.

### Table 1

|                      | Spring K1 | Spring K2 |
|----------------------|-----------|-----------|
| D-Mg index           | 13.9807   | 34.1791   |
| Shannon’s diversity index H | 2.4793 | 3.5573   |
| Shannon’s evenness index E | 0.5275 | 0.6248   |
| Simpson’s diversity index | 0.14   | 0.0731   |
| Berger-Parker Dominance index | 0.1258 | 0.16     |

Margalef’s index (DMg), Shannon’s diversity index (H’) and Simpson’s diversity index (D) indicate a trend towards increased diversity in bigger black cherry stumps (K2) (Table 1). Similarly, the dominance of single taxa in communities in larger stumps (K2) resulted in low values for Shannon’s evenness index (E) and high values for Berger–Parker’s dominance index (d).

The most common fungi in small stumps (K1) included *Pleurophoma osticolor* (25.46%), *Mycena megaspora* (5.49%), *Trichosporon stacteae* (3.26%), *Penicillium citreonigrum* (2.93%), *Yarrowia lipolytica* (2.06%), *P. lapidum* (2.35%), *Blastobotrys* sp. (2.02%), and *Candida fructis* (1.98%). However, in larger stumps (K2) the most common fungi were *Proliferodiscus* sp. (14.75%), *Laetiporus sulphureus* (3.73%), *Tumularia* sp. (2.24%), *Curvibasidium polymorph* (1.84%), *Curvibasidium cygneicollum* (1.61%), *C. mycetangii* (1.42%), *Biotia sphaeroidizax* (1.37%), *Rhizoscyphus* sp. (1.32%), *Fellozyma inositophila* (1.23%), *Hamamotopho lignophila* (1.04%) (Tab. 2).

The fungi found on both small and large stumps were *Beauveria pseudobassiana*, *Chalarara* sp., *Ciborinia candolleana*, *Dictyochara minutata*, *Infundichalara minuta*, *Jattaea ribicola*, *Lachnellula calyciformis*, *Penicillium*...
bialowiezense, P. citreonigrum, P. lapidosum, P. raphiae, Phialocephala compacta, Pleurophoma ossicola, Proliferodiscus sp., Sordariomycetes sp., Tumularia sp., Agaricomycetes sp., Microstroma album, Mycena megaspora, Vishniacozyma victoriae, Rozellomycota sp., and Umbelopsis isabellina.

4 Discussion

Greater diversity of fungal species in the community was observed for black cherry stumps exceeding 5 cm in diameter. In both cases the fungal community was dominated by fungi from the Phylum Ascomycota, with their share slightly exceeding 55% in the analysed communities, as confirmed by earlier reports concerning deciduous trees [14, 15]. These results indicate that the dominance of Ascomycota in the fungal community associated with dead wood is also related to the degree of its decomposition, i.e. the earlier the decomposition stage of wood, the greater the share of Ascomycota in the community [16-20]. The analysed stumps were classified into wood decomposition class 1 and samples were collected 1 year after the black cherries were removed from the stand, thus the recorded results confirm earlier reports. Fungi belonging to the Phylum Ascomycota cause slow wood decomposition, which is limited only to surface decay in periods of increased humidity. However, alternating drought and wet periods promote deeper penetration of the mycelium and lead to extended wood decomposition [21]. In turn, in the analysed community the share of taxa belonging to the Phylum Basidiomycota was almost 2-fold greater in the community of black cherry stumps with diameters exceeding 5 cm than in black cherry stumps with diameters not exceeding 5 cm. A lesser share was recorded for taxa belonging to the Phylum Basidiomycota. Similar results were also reported by van der Wall et al. 2015 [22] and Kwaśna et al. 2016 [15].

Pleurophoma ossicola was the taxon found most frequently on black cherry stumps of lesser diameter (over 25%), although it was also recorded to some extent on larger stumps (0.23%). It was found in a stand with Scots pine in Germany [23]. The literature lacks data on the function of this fungus in the community. The rotting bonnet fungus (Mycena megaspora) was one of the most abundant species recorded in the fungal community of black cherry stumps (K1, 5.49%), as well as a species common for both analysed variants (K1 and K2). Fungi belonging to that genus are most frequently classified as saprotrophs, except for M. citricolor (Ber. & Curt.). Fungi from the genus Mycena are commonly found on dead wood of coniferous trees and angiosperms, on decomposing stems and branches, on the bark of living trees, in soil, and less frequently on decomposing ferns, grasses or other herbaceous plants and mosses [24].

In the fungal community of black cherry stumps of over 5 cm in diameter (K2) the most abundant taxon was Proliferodiscus, which was a common taxon for both analysed black cherry communities. Fungi from that genus play an important role in the decomposition of various organic substances, including dead wood, branches and leaf litter. An example is provided by P. pulveraceus, a new species in Poland discovered in 2008, which is found on dead hornbeam wood [25].

Beauveria pseudobassiana was a common species in both analysed communities; nevertheless, its share was below 1%. This genus includes B. bassiana and B. brongniartii, used in biological control of harmful insects [26]. The genus Chalara was also found to be a common taxon for both communities, comprising pathogens such as Ch. fraxinea causing ash die-back [27,28]. Other taxa recorded in both communities were Ciborinia candolleana, Dictyochaeta, and Infundichalara minuta, which is classified as a saprotrophic species [29-31]. Lchnellula calyciformis was another species common in both communities; as a saprotroph it colonises knots, snags, dead branches and twigs, and, less commonly, living trees [32]. Other species common for both communities of black cherry stumps include Penicillium bialowiezense, which so far has been isolated from forest soil (in Poland), as well as P. raphiae found in soil [33]. In both cases Microstroma album was identified, which is classified as an obligate parasite of Quercus [34].

The available literature still lacks reports thoroughly detailing communities of fungi colonising black cherry stumps. Information on fungi on roots of that species and studies of Macromycetes colonising black cherry wood have been published by Kwaśna et al. 2008 [35]. Similarly, as reported by Kwaśna et al. 2008 [35], in the current study of the community of fungi colonising black cherry stumps species from the genus Mycena were recorded, e.g. M. cinerella, M. galericulata, M. megaspora and M. sanguinolenta. In the fungal community colonising stumps exceeding 5 cm, similarly to the study by Kwaśna et al. 2008 [35], we found a small group of fungi from the genus Fusarium and a single species F. cyanostomum, as well as Humicola spp. Sporothrix dimorphospora. In stumps of less than 5 cm in diameter a fungal species from the genus Trichoderma was identified: T. asperellum. In wood of stumps of all black cherry trees, fungi from the genus Penicillum were identified, although this community differed from that reported in black cherry roots. In black
cherry stumps the following Penicillium fungi were found: *P. angulare*, *P. bialowiezense*, *P. citreonigrum*, *P. kongii*, *P. lanosum*, *P. lapidosum*, *P. miczynskii*, *P. raphiae* and *P. viticola*. Identification of fungal communities in black cherry roots and stumps was not consistent due to the differences in the analysed material and the methods applied to identify the respective communities. In the Kampinos National Park in the wood of black cherries subjected to mechanical analysis, control showed the presence of *Nectria cinnabarina* (Tode) Fr. anamorph [4], whereas in our study a share of the mesenterica wood of larger black cherry stumps, as well as cm. share in wood of stumps with diameters larger than 5 cm, and *M. haematopus* (Pers.) P. Kumm; *Peniophora cinerea* (Pers.) Cooke; *Phaeotremella pseudofoliacea* Rea and *Stereum rugosum* [4], which we identified in the wood of larger stumps. *Stereum rugosum* was only recorded in approximately 2% of trees, but accounted for approximately 7% of trees which were colonised by fungi. This species is mainly saprotrophic in character. Locally it causes bark necroses or cankers on stems of deciduous trees [36]. In the Kampinos National Park *Laetiporus sulphureus* has been reported on logs, branches and trees of the black cherry [4], while in this study it had a 3.76% share in wood of stumps with diameters larger than 5 cm. *Stereum hirsutum* was identified in this study in the wood of larger black cherry stumps, as well as *Tremella mesenterica* Rez [4], whereas in our study a share of the genus *Tremella* was identified in this community.

5 Conclusion

The results of the above-mentioned study are consistent with our hypothesis that larger black cherry stumps should be characterised by a more diverse fungal species composition both qualitatively and quantitatively. Taking into account this study’s results, it seems justified to undertake further studies on the species *Pleurophoma ossicola*, whose share in black cherry stumps with diameters of maximum 5 cm exceeded 25%, while its ecology and function in the forest environment have not been thoroughly identified to date.

Saprotrophs and pathogens, both termed facultative parasites, that are primarily found in the analysed black cherry stumps include *Proliferodiscus* sp., *Laetiporus sulphureus*, *Mycena megaspora*, *Trichosporon otae*, *Yarrowia lipolytica*, *Tumularia* and *Curvibasidium cygneicollum*. The dominant share of fungi associated with wood decomposition indicates the progressing process of decomposition in stumps; however, the rate of black cherry wood decomposition by the above-mentioned taxa has not been determined. In the fungal community of black cherry stumps we did not find any economically important pathogens associated with tree root systems, for example genera such as *Armillaria* and *Heterobasidion*. Using the criterion of a 1% share in the community, we recorded the presence of a mycorrhizal fungus *Rhizoscyphus* sp. associated with the family Ericaceae. Moreover, we also identified fungi which to date have been considered to have no economic importance in the forest economy.

The applied sequencing method based on the Illumina System made it possible to identify most fungi (nearly 90%) to the genus or species levels. Classification of fungi was more effective than in studies based on 454 sequencing, in which 40% sequences were unidentified even at the genus level [19,20]. This confirms the efficacy of the applied method for determining and defining the composition of fungal communities.

The analysis of the quantitative and qualitative composition undertaken in our study on fungal communities colonising black cherry stumps is in line with basic research on this species. Identification of the role and functions of the individual components of fungal communities colonising stumps may provide some insight into the overall ecology of these organisms and provide a basis for improved plant protection and control, with a view to limiting the occurrence of black cherries in the future in undesirable locations outside their natural range. Our study is an introduction into an analysis of variability in the structure of the above-mentioned community.

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| No. | Taxon                                                      | K1  | K2  |
|-----|-----------------------------------------------------------|-----|-----|
|     | **Fungi**                                                 |     |     |
|     | **Ascomycota**                                            |     |     |
|  1  | *Absconditella* sp.                                       | 0.000 | 0.017 |
|  2  | *Acephala apllanata* Grünig & T.N. Sieber                | 0.124 | 0.000 |
|  3  | *Alatospora* sp.                                         | 0.000 | 0.017 |
|  4  | *Arachnopeziza* sp.                                      | 0.000 | 0.312 |
|  5  | *Articulospora* sp.                                      | 0.000 | 0.017 |
|  6  | *Ascomycota*                                              | 12.629 | 15.999 |
|  7  | *Barssia maroccana* G. Moreno, Manjón, Carlavilla & P. Alvarado | 0.124 | 0.000 |
|  8  | *Beauveria pseudobassiana* S.A. Rehner & Humber          | 0.083 | 0.104 |
|  9  | *Biatora sphaeroidiza* Printzen & Holien                 | 0.000 | 1.369 |
| 10  | *Bionectriaceae*                                          | 0.000 | 0.017 |
| 11  | *Blastobotrys* sp.                                        | 2.022 | 0.000 |
| 12  | *Cadophora luteo-olivacea* (J.F.H. Beyma) T.C. Harr. & McNew | 0.000 | 0.087 |
| 13  | *Calicopsis beckhausii* (Körb.) Garrido-Ben. & Pérez-Ort. | 0.000 | 0.052 |
| 14  | *Candida fructus* (Nakase) S.A. Mey. & Yarrow + *C. mycetangii* Kurtzman + *Candida* sp. | 1.981 | 1.487 |
| 15  | *Capronia pilosella* (P. Karst.) E. Müll., Petrini, P.J. Fisher, Samuels & Rossman + *C. pulcherrima* (Munk) E. Müll., Petrini, P.J. Fisher, Samuels & Rossman + *Capronia* sp. | 0.000 | 0.087 |
| 16  | *Cephalosporium* sp.                                      | 0.000 | 0.017 |
| 17  | *Cephalothecaceae*                                        | 0.083 | 0.503 |
| 18  | *Chaetomium* sp.                                          | 0.000 | 0.017 |
| 19  | *Chaetothyriales*                                         | 0.000 | 0.589 |
| 20  | *Chalaras* sp.                                            | 0.041 | 0.017 |
| 21  | *Chloridium* sp.                                          | 0.124 | 0.000 |
| 22  | *Ciborinia candolleana* (Lév.) Whetzel                    | 0.041 | 0.017 |
| 23  | *Ciliophora* sp.                                          | 0.124 | 0.000 |
| 24  | *Cladophialophora arxii* Tintelnat + *Cladophialophora* sp. | 0.000 | 0.364 |
| 25  | *Claussenomycetes*                                        | 0.000 | 0.017 |
| 26  | *Collophora* sp.                                          | 0.000 | 0.104 |
| 27  | *Colpoma quercinum* (Pers.) Wallr.                        | 0.000 | 0.017 |
| 28  | *Coniochaeta* sp.                                         | 0.000 | 0.121 |
| 29  | *Crociereas epicalamia* (Fuckel) Raitv. & Kutorga + *Crociereas* sp. | 0.206 | 0.017 |
| 30  | *Cyphellophora reptans* (de Hoog) Réblová & Unter.        | 0.000 | 0.191 |
| 31  | *Dermateaceae*                                             | 0.206 | 0.052 |
| 32  | *Desertella* sp.                                           | 0.000 | 0.156 |
| 33  | *Diaporthe helicis* Niessl                                | 0.000 | 0.035 |
| 34  | *Dictyochaeta* sp.                                        | 0.165 | 0.017 |
| 35  | *Discosia pseudoartocreas* Crous & Damm                    | 0.000 | 0.069 |
| 36  | *Discostroma* sp.                                         | 0.000 | 0.069 |
| No. | Taxon                                                                 | K1 % | K2 % |
|-----|----------------------------------------------------------------------|------|------|
| 37  | *Exophiala* bergeri Haase & de Hoog *+ E. castellanii* lwatsu, Nishim. & Miyaji *+ E. psychrophila* O.A. Pedersen & Langvard *+ E. sideris* Seyedm. & de Hoog *+ Exophiala* sp. | 0.000 | 1.005 |
| 38  | *Fusarium* cyanostomum (Sacc. & Flageolet) O'Donnell & Geiser *+ Fusarium* sp. | 0.000 | 1.004 |
| 39  | *Fusicladium* cordae Koukol                                                  | 0.000 | 0.017 |
| 40  | *Geomyces* auratus Traen                                               | 0.000 | 0.035 |
| 41  | *Helotiaceae*                                                          | 0.000 | 0.624 |
| 42  | *Helotiales*                                                            | 1.197 | 0.312 |
| 43  | *Herpotrichiellaceae* sp.                                                | 0.041 | 2.704 |
| 44  | *Humicola* sp.                                                          | 0.000 | 0.416 |
| 45  | *Hyalorbilia* inflatula (P. Karst.) Baral & G. Marson                  | 0.000 | 0.017 |
| 46  | *Hydnotrya* tulasnei (Berk.) Berk. & Broome                           | 0.041 | 0.000 |
| 47  | *Hyphodiscus* hyneniophilus (P. Karst.) Baral                           | 0.000 | 0.052 |
| 48  | *Hypocreales*                                                           | 0.165 | 0.537 |
| 49  | *Infundichalara* minuta Koukol                                          | 0.000 | 0.052 |
| 50  | *Lachnellula* calyciformis (Batsch) Dharne                              | 0.413 | 0.156 |
| 51  | *Lecanora* sp.                                                         | 0.000 | 0.017 |
| 52  | *Lecanorales*                                                           | 0.000 | 0.035 |
| 53  | *Lecanoromycetes*                                                      | 0.000 | 0.329 |
| 54  | *Lecophagus* sp.                                                       | 0.000 | 0.347 |
| 55  | *Leotiomycetes*                                                        | 0.083 | 0.988 |
| 56  | *Lepraria* elobata* Tønsberg                                            | 0.000 | 0.069 |
| 57  | *Leptodontidium* trabinellum (P. Karst.) Baral, Platas & R. Galán       | 0.000 | 0.329 |
| 58  | *Lophium* arboricola (Buczacki) Madrid & Gené                           | 0.000 | 0.052 |
| 59  | *Metapochonia* bulbillosa (W. Gams & Malla) Kepler, S.A. Rehner & Humber | 0.000 | 0.087 |
| 60  | *Mollisia* cinerea (Batsch) P. Karst.                                   | 0.000 | 0.017 |
| 61  | *Nectriaceae*                                                          | 0.000 | 0.035 |
| 62  | *Neofabraea* sp.                                                       | 0.000 | 0.052 |
| 63  | *Oldiodendron* majus G.L. Barron                                       | 0.000 | 0.017 |
| 64  | *Onygenaceae*                                                          | 0.000 | 0.052 |
| No. | Taxon                                                                 | K1       | K2       |
|-----|-----------------------------------------------------------------------|----------|----------|
| 75. | *Ophiostoma tsotsi* Grobbel., Z.W. De Beer & M.J. Wingf. si          | 0.000    | 0.069    |
| 76. | Ophiostomataceae                                                      | 0.000    | 0.087    |
| 77. | *Orbilia apriliis* Velen. + *O. aristata* (Velen.) Velen.             | 0.000    | 0.156    |
| 78. | Orbiliomyctes sp.                                                     | 0.000    | 0.052    |
| 79. | *Otidea subterranea* Healy & M.E. Sm.                                | 0.000    | 0.069    |
| 80. | *Pannaria athonophylla* (Stirt.) Elvebakk & D.J. Galloway            | 0.000    | 0.087    |
| 81. | *Parmelia subdivaricata* Asahina                                      | 0.000    | 0.017    |
| 82. | *Penicillium angulare* S.W. Peterson, E.M. Bayer & Wicklow + *P. bialowiezense* K.W. Zaleski + *P. citreonigrum* Dierckx + *P. kongii* L. Wang + *P. lanosum* Westling + *P. lapidosum* Raper & Fennell + *P. miczynskii* K.W. Zaleski + *P. raphiae* Houbraken, Frisvad & Samson + *P. viticola* Nonaka & Masuma | 5.365    | 1.144    |
| 83. | *Pezicula sporulosa* Verkley                                         | 0.000    | 0.191    |
| 84. | *Phacidium grevilleae* Crous & M.J. Wingf.                            | 0.000    | 0.173    |
| 85. | *Phaeomollisia piceae* T.N. Sieber & Grünig                          | 0.000    | 0.035    |
| 86. | *Phaeomoniella* sp.                                                  | 0.000    | 0.017    |
| 87. | *P. compacta* Kowalski & Kehr + *P. glacialis* Grünig & T.N. Sieber + *P. scopiformis* Kowalski & Kehr + *Phialocephala* sp. | 0.330    | 0.572    |
| 88. | *Picoa juniperi* Vittad.                                             | 0.000    | 0.676    |
| 89. | *Pleurophoma ossicola* Crous, Krawczynski & H.-G. Wagner             | 25.464   | 0.225    |
| 90. | *Proliferodiscus* sp.                                                | 0.413    | 14.751   |
| 91. | Pseudeurotiaceae                                                     | 0.000    | 0.035    |
| 92. | *Pseudogymnoascus verrucosus* A.V. Rice & Currah                     | 0.000    | 0.451    |
| 93. | *Rhizoscyphus* sp.                                                   | 0.000    | 1.317    |
| 94. | Saccharomycetales                                                    | 0.000    | 0.260    |
| 95. | *Sarea resinae* (Fr.) Kuntze                                        | 0.000    | 0.069    |
| 96. | *Sarocladium strictum* (W. Gams) Summerb.                           | 0.000    | 0.711    |
| 97. | Sordariales                                                           | 0.000    | 0.017    |
| 98. | *Sordariomyctes* sp.                                                 | 0.083    | 0.416    |
| 99. | *Sporothrix dimorphosphora* (Roxon & S.C. Jong) Madrid, Gené, Cano & Guarro | 0.000    | 0.208    |
| 100.| *Stachybotrys* sp.                                                   | 0.000    | 0.260    |
| 101.| *Talaromyces amestolkiae* N. Yilmaz, Houbraken, Frisvad & Samson + *T. verruculosus* (Peyronel) Samson, N. Yilmaz, Frisvad & Seifert + *T. wortmannii* C.R. Benj. | 0.165    | 0.070    |
| 102.| *Taphrina confusa* (G.F. Atk.) Giesenh.                              | 0.000    | 0.035    |
| 103.| *Tolypocladium* sp.                                                  | 0.000    | 0.087    |
| 104.| *Trichoderma asperellum* Samuels, Lieckf. & Nirenberg                | 0.371    | 0.000    |
| 105.| *Tridentaria implicans* Drechsler                                    | 0.000    | 0.035    |
| 106.| Trimmatostroma cordae N.D. Sharma & S.R. Singh                       | 0.000    | 0.017    |
| 107.| *Truncatella restionacearum* S.J. Lee & Crous                        | 0.000    | 0.087    |
| 108.| Truncatella sp.                                                       | 0.083    | 2.236    |
| 109.| Valsaceae                                                             | 0.041    | 0.347    |
| 110.| *Venturia hystrioides* (Dugan, R.G. Roberts & Hanlin) Crous & U. Braun +Venturia sp. | 0.000    | 0.168    |
The effect of size of black cherry stumps on the composition of fungal communities colonising stumps

| No. | Taxon                                                                 | K1  | K2  |
|-----|----------------------------------------------------------------------|-----|-----|
|     |                                                                      | %   | %   |
| 111 | Venturiaceae                                                         | 0.000 | 0.035 |
| 112 | Venturiales                                                          | 0.000 | 0.069 |
| 113 | *Xenopolyscytalum pinea* Crous                                       | 0.000 | 0.017 |
| 114 | Xylariaceae                                                          | 0.083 | 0.000 |
| 115 | *Yamadazyma mexicana* (M. Miranda, Holzschu, Phaff & Starmer) Billon-Grand | 0.000 | 0.052 |
| 116 | *Yarrowia lipolytica* (Wick., Kurtzman & Herman) Van der Walt & Arx | 2.064 | 0.000 |
|     | **Frequency of Ascomycota**                                         | 55.056 | 56.249 |

**Basidiomycota**

1. Agaricaceae                        | 0.083 | 0.035 |
2. Agaricales                         | 0.165 | 0.052 |
3. *Agaricomycetes* sp.               | 0.041 | 0.017 |
4. Agaricostilbales                   | 0.000 | 0.017 |
5. *Amanita parciolvata* (Peck) E.-J. Gilbert | 0.000 | 0.017 |
6. Auriculariales                      | 0.041 | 0.000 |
7. Basidiomycota                      | 0.537 | 1.161 |
8. *Bullera* sp.                      | 0.000 | 0.017 |
9. *Bulleromyces albus* Boekhout & Â. Fonseca | 0.000 | 0.017 |
10. Cantharellales                    | 0.083 | 0.000 |
11. *Chionosphaera cuniculicola* R. Kirschner, Begerow & Oberw. | 0.000 | 0.017 |
12. Chrysozymaceae                    | 0.000 | 0.017 |
13. *Clitopilus hobsonii* (Berk.) P.D. Orton | 0.000 | 0.052 |
14. *Colacogloea philyla* (Van der Walt, Klift & D.B. Scott) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000 | 0.087 |
15. Colacogloea                        | 0.000 | 0.052 |
16. *Corticium confine* Bourdor & Galzin | 0.000 | 0.017 |
17. *Cryptococcus pseudolongus* M. Takash., Sugita, Shinoda & Nakase + C. psychrotolerans V. de García, Zalar, Brizzi, Gunde-Cim. & Van Broock + *Cryptococcus* sp. | 0.041 | 0.671 |
18. *Cuniculitrema polymorpha* R. Kirschner & J.P. Samp. | 0.000 | 1.837 |
19. *Curvibasidium cygneicollum* J.P. Samp. | 0.000 | 1.612 |
20. Cystobasidiomycetes                | 0.000 | 0.069 |
21. *Cystobasidium piniocola* (F.Y. Bai, L.D. Guo & J.H. Zhao) Yurkov, Kachalkin, H.M. Daniel, M. Groenew., Libkind, V. de Garcia, Zalar, Gouliamova, Boekhout & Begerow | 0.000 | 0.537 |
22. Cystofilobasidiales                | 0.000 | 0.173 |
23. *Cystofilobasidium infirmominiatrum* (Fell, I.L. Hunter & Tallman) Hamam., Sugiy. & Komag. +C. macerans J.P. Samp. | 0.000 | 0.069 |
24. *Dacrymyces chrysospermus* Berk. & M.A. Curtis | 0.000 | 0.485 |
25. *Dioszegia fristingensis* Â. Fonseca, J. Inácio & J.P. Samp. | 0.000 | 0.017 |
26. Erythrobasidiales                  | 0.000 | 0.069 |
27. *Erythrobasidium* sp.              | 0.000 | 0.052 |
28. *Exobasidium arescens* Nannf. + *E. maculosum* M.T. Brewer + *Exobasidium* sp. | 0.000 | 0.624 |
| No. | Taxon                                                                 | K1     | K2     |
|-----|----------------------------------------------------------------------|--------|--------|
| 29  | *Fellomyces horovitziae* Spaaij, G. Weber & Oberw. + *F. mexicanus* Lopandić, O. Molnár & Prillinger + *Fellomyces* sp. | 0.000  | 0.069  |
| 30  | *Fellozyma inositophila* (Nakase & M. Suzuki) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 1.231  |
| 31  | *Fibulobasidium murrhardtense* J.P. Samp., Gadano, M. Weiss & R. Bauer | 0.000  | 0.035  |
| 32  | *Fibobasidium stepposum* (Golubev & J.P. Samp.) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 0.087  |
| 33  | *Genolevuria amylolytica* (Á. Fonseca, J. Inácio & Spenc.-Mart.) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 0.017  |
| 34  | *Hamamatoa lignophila* (I. Dill, C. Ramírez & A.E. González) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 1.040  |
| 35  | *Hydnaceae*                                                        | 0.083  | 0.000  |
| 36  | *Hygrophoraceae*                                                   | 0.083  | 0.017  |
| 37  | *Hymenochaetales*                                                  | 0.124  | 0.000  |
| 38  | *Inocybe* sp.                                                      | 0.000  | 0.884  |
| 39  | *Itersonilia pannonica* (Niwata, Tornai-Leh., T. Deák & Nakase) Xin Zhan Liu, F.Y. Bai, J.Z. Groenew. & Boekhout | 0.000  | 0.156  |
| 40  | *Kockovaella machilophila* Cañ.-Gib., M. Takash., Sugita & Nakase    | 0.000  | 0.676  |
| 41  | *Kondoa aeria* Â. Fonseca, J.P. Samp. & Fell                       | 0.000  | 0.017  |
| 42  | *Kriegeria eriophori* Bres. 1891                                    | 0.000  | 0.156  |
| 43  | *Kurtzmanomyces*                                                   | 0.000  | 0.035  |
| 44  | *Kwoniella pini* (Golubev & I. Pfeiff.) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 0.139  |
| 45  | *Laetiporus sulphureus* (Bull.) Murrill                             | 0.000  | 3.727  |
| 46  | *Leucosporidiales*                                                  | 0.000  | 0.017  |
| 47  | *Leucosporidiella creatinivora* (Golubev) J.P. Samp.                | 0.000  | 0.139  |
| 48  | *Leucosporidium drummii* Yurkov, A.M. Schäfer & Begerow + *L. fasciculatum* Babeva & Lisichk. +0.000 | 0.000  | 0.416  |
| 49  | *Leucosporidium* sp.                                               | 0.000  | 0.121  |
| 50  | *Luellia recondita* (H.S. Jacks.) K.H. Larss. & Hjortstam           | 0.000  | 0.371  |
| 51  | *Malassezia restricta* E. Guého, J. Guillot & Midgley               | 0.000  | 0.000  |
| 52  | *Mastigobasidium intermedium* Golubev                                | 0.000  | 0.017  |
| 53  | *Microbotryomycetes*                                                | 0.000  | 0.485  |
| 54  | *Microsporumycies pini* (C.H. Pohl, M.S. Smit & Albertyn) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 0.104  |
| 55  | *Microstroma album* (Desm.) Sacc.                                   | 0.330  | 0.087  |
| 56  | *Mrakia frigida* (Fell, Statzell, I.L. Hunter & Phaff) Y. Yamada & Komag. | 0.000  | 0.017  |
| 57  | *Mycozira cinerea* (P. Karst.) P. Karst. + *M. galericulata* (Scop.) Gray + *M. megaspora* Kauffman + 6.108 *M. sanguinolenta* (Alb. & Schwein.) P. Kumm. | 0.000  | 0.156  |
| 58  | *Oberwinklearzyza yarrowii* (Á. Fonseca & Uden) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 0.017  |
| 59  | *Papiliotrema pernicioso* (Golubev, Gadano, J.P. Samp. & N.W. Golubev) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout | 0.000  | 0.121  |
| 60  | *Peniophora pini* (Schleich. ex DC.) Boidin                        | 0.000  | 0.017  |
| 61  | *Phaeotremella skinneri* (Phaff & Carmo Souza) Yurkov & Boekhout,   | 0.000  | 0.017  |
| 62  | *Rhodotorula glutinis* (Fresen.) F.C. Harrison + *R. nothofagi* C. Ramírez & A.E. González + *Rhodotorula* sp. | 0.000  | 0.329  |
| 63  | *Schizophyllum* sp.                                                 | 0.041  | 0.017  |
## The effect of size of black cherry stumps on the composition of fungal communities colonising stumps

### Table of Fungal Taxa

| No. | Taxon                                                                 | K1 % | K2 % |
|-----|----------------------------------------------------------------------|------|------|
| 64  | *Septobasidium broussonetiae* C.X. Lu, L. Guo & J.G. Wei + *S. pallidum* Couch ex L.D. Gómez & Henk | 0.000 | 0.130 |
| 65  | *Slooffia tsugae* (Phaff & Carmo Souza) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000 | 0.035 |
| 66  | Sporidiobolales                                                        | 0.000 | 0.156 |
| 67  | *Stereum hirsutum* (Willd.) Pers. + *S. rugosum* Pers.                | 0.000 | 0.034 |
| 68  | *Tausonia pullulans* (Lindner) Xin Zhan Liu, F.Y. Bai, J.Z. Groenew. & Boekhout | 0.000 | 0.624 |
| 69  | Thelephorales                                                          | 0.000 | 0.035 |
| 70  | *Tremella globispora* D.A. Reid + *T. indecorata* Sommerf. + *Tremella* sp. | 0.000 | 0.416 |
| 71  | Tremellales                                                            | 0.000 | 0.659 |
| 72  | Tremellomyces                                                          | 0.000 | 1.179 |
| 73  | *Trichosporon otae* Sugita, Takshima & Kikuchi                        | 3.260 | 0.000 |
| 74  | *Tulasnella* sp.                                                       | 0.330 | 0.000 |
| 75  | *Vishniacozyma carrancens* (Verona & Luchetti) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout + *V. victoriae* (M.J. Montes, Belloch, Galiana, M.D. Garcia, C. Andréés, S. Ferrer, Torr.-Rodr. & J. Guinea) Xin Zhan Liu, F.Y. Bai, M. Groenew. & Boekhout | 0.083 | 0.208 |
| 76  | *Vonarxula javanica* (Arx & Weijman) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000 | 0.087 |
| 77  | *Yunzhangia auriculariae* (Nakase) Q.M. Wang, F.Y. Bai, M. Groenew. & Boekhout | 0.000 | 0.017 |

### Frequency of Basidiomycota

- **Zygomycota**
  1. *Mortierella hyalina* (Harz) W. Gams | 0.247627
  2. *Umbelopsis isabellina* (Oudem.) W. Gams | 0.247627

### Others

#### Plantae

1. Anthophyta | 0 | 0.034668
2. Chlorophyta | 0.288898 | 1.716069
3. Plantae | 0.123813 | 0.225342

#### Protista

1. Cercozoa sp. | 0.165085 | 0.554689

### Frequency of Others

1. No sequence in the database UNITE | 19.27363 | 12.98319
2. Non-cultivable fungi | 12.79406 | 5.806899
3. Number of isolates | 100 | 100
4. Number of fungi isolates | 80.14858 | 84.48605