



Spatial variability of inhalable fungal communities in airborne PM_{2.5} across Nanchang, China

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HIGHLIGHTS

- Spatial variability of inhalable fungal communities was investigated.
- Airborne fungal community in forest was diverged from urban and suburban areas.
- Community fluctuation was observed at one site during the short-term period.
- Air pollutants partially contributed to spatial disparity of fungal communities.

GRAPHICAL ABSTRACT



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ABSTRACT

Although fungi are ubiquitous in the atmosphere and have important effect on human health, their spatial variability about diversity and taxonomic composition, remain poorly understood. Considering the differences of environmental conditions, distinct airborne fungal communities were expected in the urban, suburban and forest areas. To test this hypothesis, PM_{2.5} samples were consecutively collected for 14 days across Nanchang, China. The results showed that fungal diversities of samples from forest were higher than that from the other two areas. Even though the airborne fungal communities at one sampling site fluctuated during the short-term period, the compositions in the forest significantly diverged from the other two areas (Anosim and Adonis: $p < 0.01$). Canonical correspondence analysis (CCA) and mantel test ($p < 0.01$) indicated that these disparities among sampling sites were partly drove by air pollutants. High concentrations of air particles (PM_{2.5} and PM₁₀) and gaseous pollutants (NO₂ and CO) associated with human activities were accompanied by high relative abundances of several genera such as *Alternaria*, *Penicillium* and *Coprinellus*. Likewise, Pearson correlation analysis showed that rainfall and relative humidity enhanced the relative abundances of 13 genera like *Malassezia* and *Schizophyllum*. Notably, part of these genera was potential allergens and pathogens to human, and it seemed that there were higher health risks in urban and suburban. This study furthers our understanding of the variation of airborne fungal community in different land-use types and different treatments may be applied to deal with the potential threat of airborne fungi.

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1. Introduction

Atmospheric fine particulate matters (PM_{2.5}, mean aerodynamic diameters $\leq 2.5 \mu\text{m}$) have been proved to be associated with increased

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morbidity and mortality by causing cardiovascular diseases, and shortened life expectancy (Brook et al., 2004; Pope et al., 2009; Wang et al., 2017). To date, abiotic and toxic chemical matters adsorbed on PM_{2.5} have been extensively investigated. However, microorganisms (bacteria, fungi and virus), also represent an important component of PM_{2.5} with concentrations from 10⁴ to 10⁸ cells m⁻³. Moreover, many microbes remain viable and even show metabolic activity despite exposure to UV radiation, low moisture, and extremely oligotrophic conditions (Zhong et al., 2016). When inhaled, the active allergenic or pathogenic fungi can also cause human diseases. Hence, understanding microbial composition and diversity is essential to further reveal the impact of PM_{2.5} on human health and ecosystems.

Though fungi were relatively less abundant than bacteria (Cao et al., 2014), fungi are also ubiquitous in the air and occupy significant proportion of primary biogenic aerosol particles. According to Elbert et al. (2007) and Igarashi et al. (2019), the number concentration of fungal spores emitted into atmosphere varied from 10³ to 10⁵ particles m⁻³, contributing to about 4–13% of the mass concentration of PM_{2.5} (Womiloju et al., 2003). In addition, compared with bacteria, fungal allergen is one of the predominant allergens. Globally, there are at least 3–10% of people sensitive to fungal allergens (Cramer et al., 2006). And fungal spore counts in the exposed environment displayed a strong correlation with allergy and asthma (Cramer et al., 2006; Denning et al., 2006). Previous studies also reported that some atmospheric fungal species such as *Aspergillus flavus*, are identified as both pathogens and allergens (Yamamoto et al., 2012; Cao et al., 2014), which are associated with high mortality in immunocompromised individuals (Lin et al., 2001). Furthermore, Liu et al. (2014) directly demonstrated that etiological fungi *Bjerkandera adusta* isolated from Asian sand dust aerosol could induce allergic lung disease. Therefore, investigating the composition of airborne fungi, in particular allergens and pathogens in PM_{2.5}, has a great health significance.

Most of existing studies about atmospheric microbes have focused on airborne bacteria, while fungi have received less attention. Moreover, in the studies of airborne fungi, traditional culture-based methods have been usually used, which are constrained to identify a small part of culturable airborne fungi and lead to underestimate the diversity of airborne fungi (Haas et al., 2013; Fang et al., 2014; Li et al., 2015). Nowadays, gene-based methods further our understanding of environmental microorganisms, and higher taxonomic diversity has been found compared to traditional and culture-based surveys. Although a few of studies applied next generation sequencing technique based on amplicon to reveal the seasonal variability (Bowers et al., 2013; Du et al., 2018a, 2018b), size distribution (Yamamoto et al., 2012), and haze effect (Yan et al., 2016) on airborne fungal community in recent years, there are still critical gaps in understanding of their spatial variability (Igarashi et al., 2019), which was usually used to explain the disparity of fungal communities in different studies. The airborne fungi mainly originate from soil, plant, water, and animal feces in local environment (Zhai et al., 2018), their diversity and composition are expected to vary in different sampling sites.

To test the hypothesis, we conducted the experiment in spring when the relative abundances of fungi peaked (Bowers et al., 2013). PM_{2.5} samples were consecutively collected from urban, suburban, and forest areas across Nanchang (China) for two weeks, and fungal communities were analyzed by high throughput DNA sequencing. The obtained data allowed us to investigate the diversity and composition of airborne fungi in PM_{2.5}, and then obtained the disparity among three sampling sites.

2. Materials and methods

2.1. Sampling sites

PM_{2.5} samples were collected on the rooftops of three buildings in Nanchang, one inside Jiangxi Province Center for Disease Control and

Prevention (U: urban area, 28.68°N, 115.94°E), another one inside East China University of Technology (S: suburban area, 28.72°N, 115.82°E), and the last one located in Meiling mountain (F: forest, 28.75°N, 115.71°E) (Fig. 1). U, S and F were arranged from east to west and S was located 13 km and 11 km apart from U and F, respectively.

2.2. Collection of sampling and environmental data

From April 30, 2019 to May 13, 2019, a two-week continuous sampling was performed by a high-volume sampler (KC-1000, Qingdao Laoshan Electric Inc., China) equipped with PM_{2.5} fractionating inlet. Daily PM_{2.5} samples (23.5 h, from 5:00 pm to 4:30 pm the next day) were collected onto quartz filter membranes (8 in × 10 in. at a flow rate of 1.05 m³ min⁻¹. Prior to sampling, all membrane filters were sterilized at 450 °C for 4 h in a Muffle furnace. In total, 42 PM_{2.5} samples were collected during the campaign and all samples were stored at -20 °C until analysis. Samples from the three sites were labeled as U1-U14, S1-S14 and F1-F14 according to the sampling day, respectively.

Corresponding air quality data (SO₂, NO₂, O₃, CO, PM_{2.5} and PM₁₀) were obtained from the environmental monitoring station nearest to each sampling site. Meteorological data (temperature (T), relative humidity (RH), wind speed (WS) and precipitation) were downloaded from the Global Weather and Climate Information Network (<http://www.weatherandclimate.info/>). All data were integrated based on sampling time.

2.3. DNA extraction and sequencing

One-eighth filter membrane was cut and ground to powder in ceramic mortar, which was then transferred to bead solution tube provided by QIAGEN Dneasy PowerSoil Kit (USA). Bacterial DNA was further extracted according to manufacturer's protocols. The internal transcribed spacer region (ITS2) was amplified by PCR using primers ITS3_KYO2 (GATGAAGAACGYAGYRAA) and ITS4 (TCCTCCGCTTATG TATGC) (Toju et al., 2012). The amplicons were extracted from 2% agarose gels and purified using the Axyprep DNA Gel extraction kit (Axygen Biosciences, Union City, CA, USA). Then the purified amplicons were pooled in equimolar and paired-end sequenced on an Illumina platform in GENE DENOVO Co., Ltd. (Guangzhou, China).

2.4. Sequence data analysis

After sequencing, reads containing more than 10% of unknown nucleotides and less than 50% of bases with quality Q-value >20, were removed. Paired and clean reads were merged as raw tags which were then filtered by QIIME (version 1.9.1) to obtain clean tags. The effective tags were then clustered into operational taxonomic units (OTUs) of ≥97% similarity using UPARSE pipeline (Edgar, 2013). The OTU sequences were classified into fungi by a naive Bayesian model using RDP classifier based on ITS2 database (Ankenbrand et al., 2015). Chao1, Ace, Evenness, Simpson and Shannon indexes were calculated in QIIME, where Chao1 and ACE indicated the richness (OTU number) of fungal community while Simpson and Shannon comprehensively reflected the diversity including richness and evenness. The non-metric multi-dimensional scaling (NMDS) analysis based on the Bray-Curtis distance, was performed to visualize the difference of fungal communities at three sampling sites. The disparity in OTU composition for samples collected in three sites was also tested by similarity analyses (Adonis and Anosim). *t*-Test and Kruskal-Wallis H test were applied to identify the significantly different genera among groups. Canonical correspondence analysis (CCA) and mantel test were applied to estimate the relationship between air quality and genus community, while Pearson's correlation was used to link meteorological conditions with specific genera.

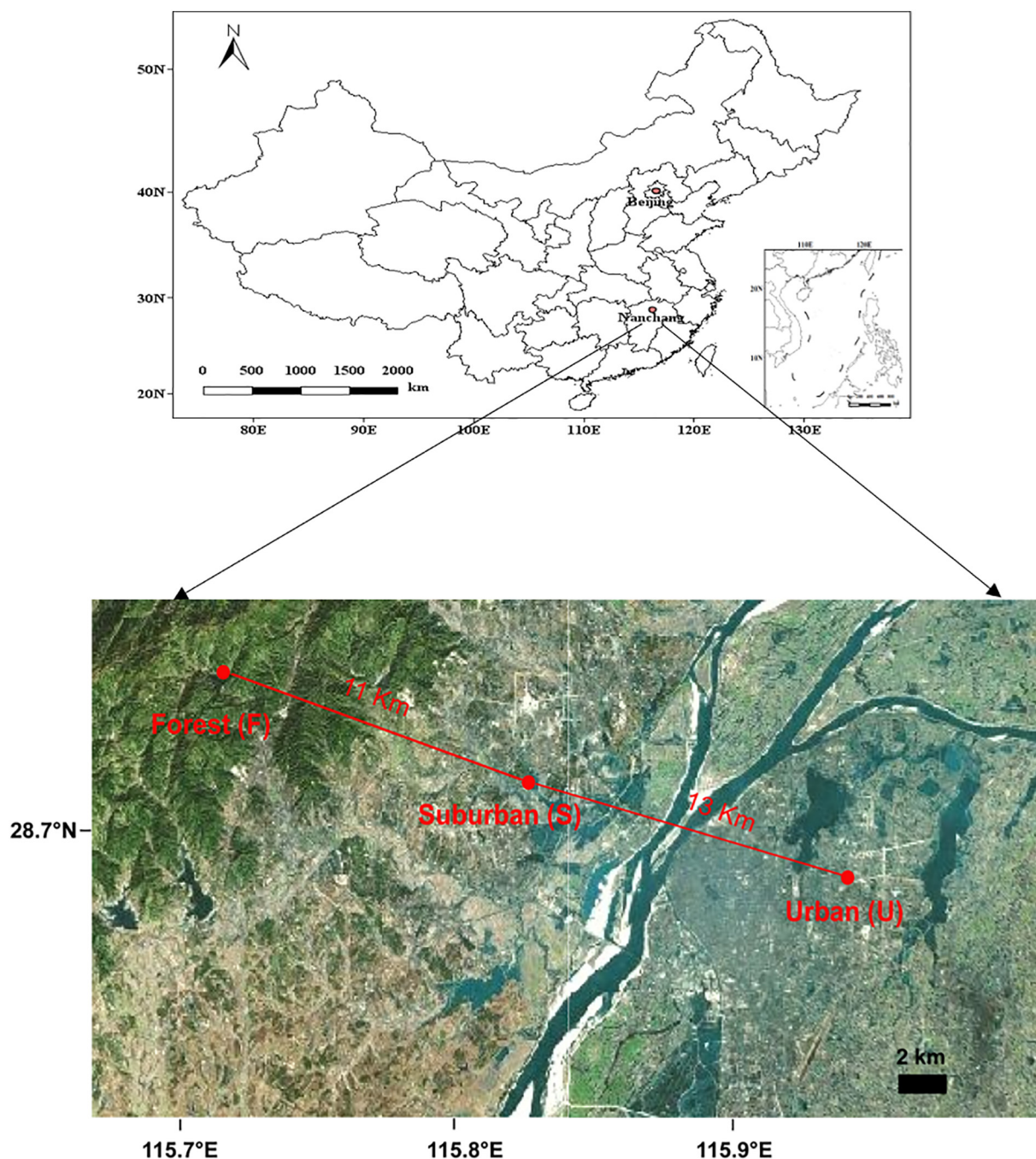


Fig. 1. Sampling sites of $PM_{2.5}$ in Nanchang. U, S, and F were short for Urban, Suburban, and Forest. And the numbers indicated the straight-line distance between two sites.

3. Results and discussion

3.1. Air quality and meteorological characteristics during sampling period

The highest concentrations of $PM_{2.5}$ and PM_{10} were observed in urban site, followed by suburban site and then forest site (Table S1). NO_2 and CO concentrations were comparable between urban and suburban sites, significantly higher than forest site. However, SO_2 in suburban site was similar with forest site, obviously lower than urban site. These results suggested that there were more human disturbances such as traffic and industry in urban and suburban areas, and the level of air pollution was sorted by urban > suburban > forest. In addition, during the sampling period, the air condition was relatively stagnant

with wind speed $1.4 \pm 0.3 \text{ m s}^{-1}$. However, it rained 4.2 mm and 31.4 mm on April 29 and May 12, respectively, and several other days like May 4–7 and May 11 light rained ($\leq 1 \text{ mm}$), resulting in the shift of relative humidity from 56.8% to 92.4%.

3.2. Richness and diversity of fungal communities in Nanchang

Similar with bacteria, fungi are with high diversity in air particulate matter (Fröhlich-Nowoisky et al., 2009; Cao et al., 2014; Igarashi et al., 2019). In the present study, a total of 3,983,353 clean tags of the fungal ITS gene sequences were obtained after quality filtering, clustered into 302–988 OTUs for each sample with Simpson index from 0.79 to 0.97 (Table S2). This was similar to other sequence-based surveys in Mainz

Table 1
Comparison of species richness and diversity of fungal community in PM_{2.5} at different sites.

Samples	OTU	Chao	ACE	Evenness*	Shannon*	Simpson*
Urban	488 (107)	816 (200)	832 (205)	0.56 (0.07)	4.95 (0.69)	0.89 (0.05)
Suburban	527 (177)	856 (301)	870 (324)	0.58 (0.09)	5.21 (0.92)	0.90 (0.05)
Forest	540 (147)	851 (237)	874 (276)	0.63 (0.05)	5.67 (0.57)	0.93 (0.03)

* Indicated that there was significant difference among three sampling sites ($p < 0.05$).

(Fröhlich-Nowoisky et al., 2009), New Heaven (Yamamoto et al., 2012) and Beijing (Yan et al., 2016; Du et al., 2018a, 2018b). Furthermore, except Chao, all of the richness (OTU, ACE) and diversity (Evenness, Shannon, and Simpson) indexes for three sampling sites followed the pattern: urban area < suburban area < forest area (Table 1), which was contrast with the level of air pollution (Table S1). However, *t*-test showed that no obvious effect of sampling site on richness ($p > 0.05$) but diversity ($p < 0.05$). Partially, it was similar with the result of Bowers et al. (2011) who also found land-use type (forest, agricultural, suburban) had no effect on bacterial richness. Overall, this result suggested that sampling site affected the diversity of airborne fungal community.

3.3. Fungal community structure in PM_{2.5} in Nanchang

Ascomycota and Basidiomycota were the predominant airborne fungi in sequence-based studies, and displayed global pattern (Fröhlich-Nowoisky et al., 2009; Yamamoto et al., 2012; Yan et al., 2016; Du et al., 2018a, 2018b). Similarly, in this study, Ascomycota and Basidiomycota were the absolutely dominant phyla across all samples with total relative abundance more than 99% (Fig. 2(a)). In general, Ascomycota (mean 90.04%) was more abundant than Basidiomycota (mean 9.74%). This result was attributed to the features of these two phyla, where the ascospores of Ascomycota were generally smaller

than 2.5 μm and thus easily aerosolized while most of the basidiospores of Basidiomycota were large than 5 μm and a small part was less than 2.5 μm (Ingold, 1995; Fröhlich-Nowoisky et al., 2009; Moore et al., 2011).

Consistent with previous studies conducted in Mainz (Fröhlich-Nowoisky et al., 2009) and Beijing (Du et al., 2018b), *Dothideomycetes* (46.90%), *Sordariomycetes* (20.09%), *Eurotiomycetes* (11.59%), *Leotiomycetes* (9.55%) were the most abundant classes in the phylum Ascomycota (Fig. 2(b)). And mushroom-forming class *Agaricomycetes* (9.11%) was dominant in the phylum Basidiomycota. At the genus level, more than 75% sequences were classified to genera, and about 50% sequences were categorized to the genera *Ascochyta*, *Alternaria*, *Nigrospora*, and *Aspergillus* (the relative abundances > 5%). Among these genera, although pathogenic and saprotrophic *Ascochyta* from plant was first reported in airborne PM_{2.5}, its teleomorph *Mycosphaerella* (Moussart et al., 1998), the same as the other three genera, were commonly detected as dominant genera in atmosphere (Yan et al., 2016; Du et al., 2018a, 2018b).

3.4. Spatial variability of fungal communities

Airborne fungi are mainly derived from the aerosolization and dispersal of fungi inhabiting in soil, water, plant, and animal fur and feces (Zhai et al., 2018), so it supposed that local environment would shift

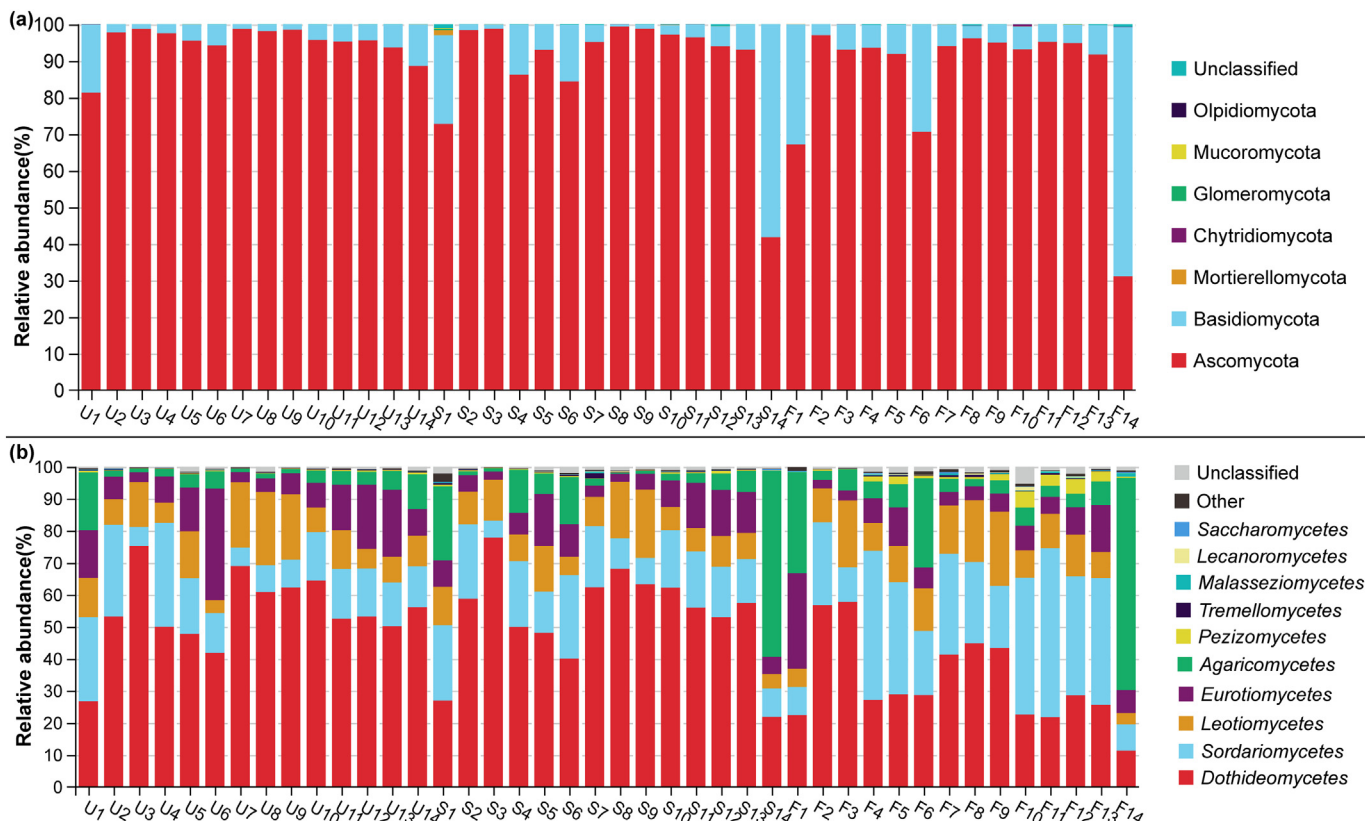


Fig. 2. Phylogenetic classification of airborne fungal communities at the phylum (a) and class (b) levels for all samples.

the fungal composition and led to the spatial variability. In the present study, the results of NMDS based on bray-curtis distance and similarity test (Anosim and Adonis: U vs S, $p > 0.05$; U/S vs F, $p < 0.01$) at the OTU level showed that fungal communities in urban and suburban areas were similar and both of them were diverged from that in forest, independent of their geographical distance (Figs. 1 and 3). Similar pattern was also observed for the result of CCA at the genus level (Fig. S1). It seemed that human activities had effects on fungal communities in atmosphere. Wang et al. (2010) also found that visitors had significant influence on bacterial distribution in the Mogao Grottoes. A simple explanation might be that human activities were conducive to the aerosolization of environmental microbes.

In comparison, the preponderant class *Dothideomycetes* (54.52% and 53.26%) in urban and suburban samples, were obviously higher than that in forest samples (32.93%), as a contrast to the other dominant class *Sordariomycetes* (urban, 15.56%; suburban, 15.87%; forest, 28.84%) ($p < 0.05$) (Fig. 2(b)). Previous studies also showed that the abundance of *Dothideomycetes* in Mountain Tai (37.3%) (Xu et al., 2017), was lower than that in Beijing's urban (>70%) and suburban areas (52.88%) (Du et al., 2018a, 2018b). Furthermore, among 43 genera with relative abundances higher than 1%, 4 genera including *Ascochyta*, *Alternaria*, *Torula*, and *Coprinellus* were abundantly enriched in urban and suburban samples, while 12 genera such as *Fomitopsis*, *Arthrimum*, *Phlebia*, *Erysiphe*, and *Malassezia* were the opposite (Fig. 4). However, it was worth noting that fungal communities within one sampling site were not stable but fluctuant, especially on rainy days (Fig. 2). For example, the relative abundance of phylum Basidiomycota changed with up to 14, 51, and 20 times in urban, suburban, and forest sites, respectively. It was similar to the result of Bertolini et al. (2013) who found airborne bacterial communities showed large temporal variability, even between consecutive days. The fluctuation may result in no obvious change of fungal compositions in urban and suburban areas.

3.5. Relationship between environmental factors and fungal community

In previous studies, some crucial air pollutants have showed potential influences on fungal community composition such as O_3 (Adhikari et al., 2006), NO_2 , $PM_{2.5}$, PM_{10} , SO_2 , and CO (Haas et al., 2013; Yan et al., 2016). Herein mantel test ($p < 0.01$) and CCA analysis with 72.52% explanation (CCA1 and CCA2) of genus variability, confirmed that these air pollutants had significant effects on variability of fungal composition, especially NO_2 and PM_{10} (Fig. S1). Pearson correlation further showed the genera in group A including *Alternaria*, *Penicillium*, *Aspergillus*, *Torula*, and *Coprinellus* were positively correlated with air quality (Fig. 5). Although gaseous pollutants were usually considered to be toxic to microorganisms (Abdel Hameed et al., 2012), it depended

on concentration and transformation. For example, atmospheric microorganisms will be killed under high O_3 , while low O_3 had no evident effect on atmospheric microorganisms or even positively with genera such as *Alternaria* (Grinn-Gofroñ et al., 2011), consistent with this study. In addition, these air pollutants may enhance secondary chemical process and then provide adsorbing sites or nutrients for airborne fungi. In fact, most of these pollutants (NO_2 , SO_2 , CO) were directly released by human activities such as industry, traffic, and agriculture. Thus, spatial variability of airborne fungal community could be partially explained by human activities.

Meteorological parameters were relatively constant during a short-time span, and usually not considered as influence factors (Bowers et al., 2011). However, as mentioned in Section 3.4, dramatic fluctuations of fungal and bacterial compositions in the same site were frequently observed (Fierer et al., 2008; Bertolini et al., 2013; Igarashi et al., 2019). In this study, when integrating data based on sampling time, Pearson correlation analysis showed that temperature and wind speed, in particular relative humidity and rainfall, had significant correlation with abundances of some genera (Fig. 5). The genera *Alternaria*

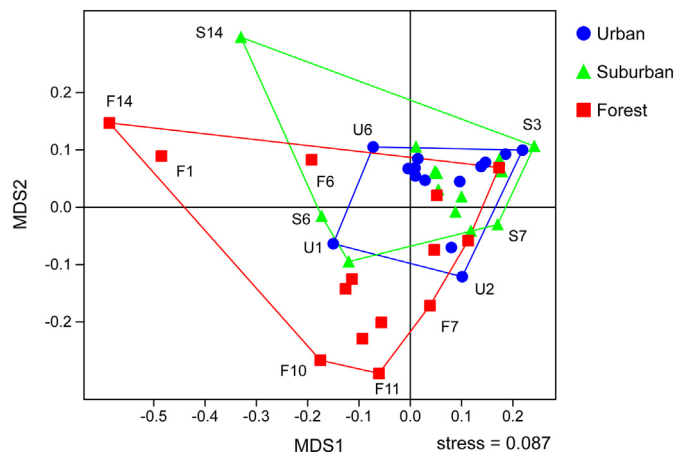


Fig. 3. NMDS based on bray-Curtis distance at the OTU level (stress = 0.087). Samples from the same site were connected to distinguish from other sites.

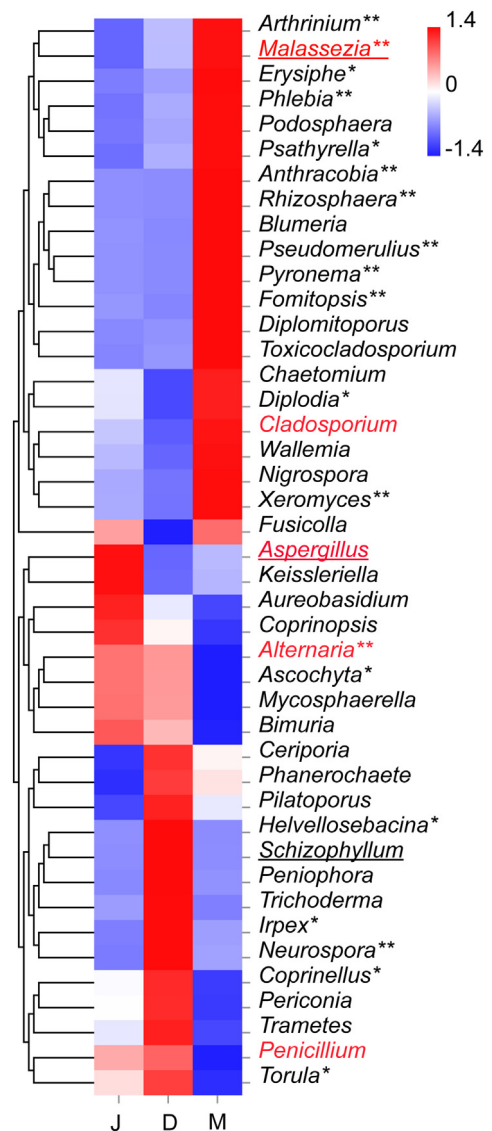


Fig. 4. Heatmap based on relative abundances of dominant fungal genera (>1%). The genera containing known allergens (in red) and pathogens (underlined) were listed. And the genera with significant difference among three sampling sites were marked in * ($p < 0.05$) and ** ($p < 0.01$).

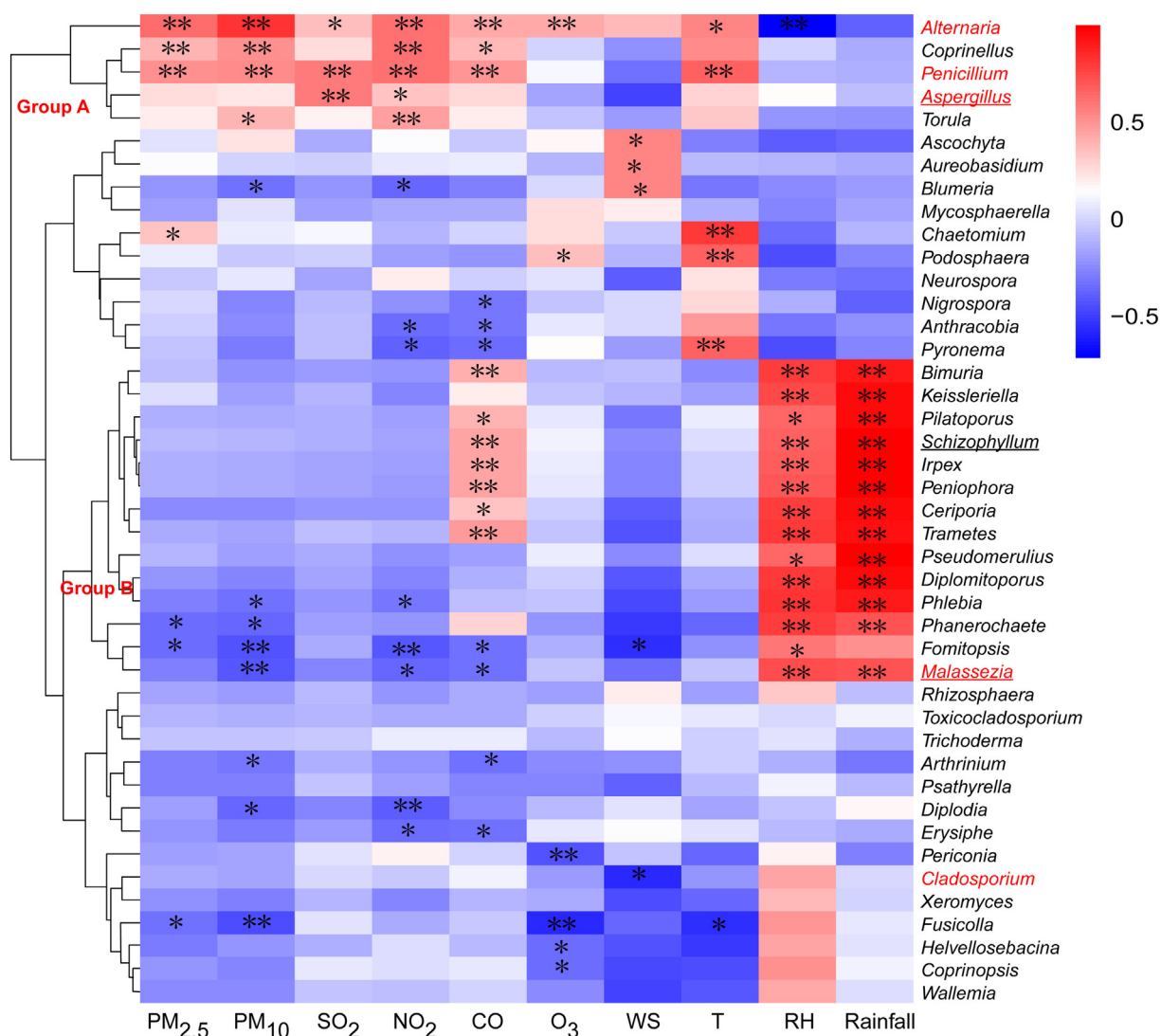


Fig. 5. Heatmap of the genera with relative abundance >1% based on Pearson's correlation coefficients between relative abundances and environmental factors. * and ** indicated the significance with $p < 0.05$ and $p < 0.01$, respectively.

and *Penicillium* were positively with temperature, and *Cladosporium* was negatively related with wind speed, consistent with the result of Grinn-Gofroń et al. (2011). Moreover, among the 43 genera with relative abundance >1% in each sample, 13 genera in group B such as *Phlebia* (average 0.54%), *Irpex* (0.33%), *Bimuria* (0.22%), *Malassezia* (0.11%), and *Schizophyllum* (0.11%), were strongly correlated with the relative humidity and rainfall with $r > 0.9$. Hence, meteorological conditions, rainfall in particular, also shaped the fungal variability during short-term sampling period.

3.6. Implications for human health

One important purpose in studies of airborne fungi should be their influence to human health. In this study, five fungal genera were identified to be human allergens in Nanchang, including genera *Alternaria*, *Aspergillus*, *Cladosporium*, *Penicillium*, and *Malassezia* (Simon-Nobbe et al., 2008). The genus *Alternaria* was reported to produce a wide of mycotoxins and cause children's asthma (Halonen et al., 1997). Also, *Aspergillus* and *Malassezia* were opportunistic human pathogens to cause airway or lung infections (Niernan et al., 2005). Another pathogenic genus *Schizophyllum* (0.11%), as one exception of the class *Agaricomycetes* which generally do not contain known allergens and

pathogens (Kern and Uecker, 1986), was also found in this study. Higher total abundance of these genera in urban (25.74%) and suburban (21.21%) areas than forest areas (14.77%), implied more potential threat to human health in urban and suburban areas. Nevertheless, because not all fungi belonging to these genera are allergens and pathogens, and some fungal allergens and pathogens have not been explored and documented, these results need further studies to be confirmed. Moreover, their actual pathogenicity in local environment should be confirmed by next isolation and simulation experiments.

4. Conclusions

The spatial variability of airborne fungal communities were investigated in this study. Compared with urban and suburban areas, higher fungal diversity (Shannon index: 5.67) was observed in forest. Although *Ascomycota* and *Basidiomycota* were the predominant phyla at three sampling sites, airborne fungal communities at other taxa levels were significantly different. The spatial variability was attributed to the air pollutants (particles and gaseous pollutants) released by human activities and meteorological conditions. We found that one group of dominant genera such as *Alternaria* and *Penicillium* were positively influenced by air quality, while another group of genera like *Malassezia*

and *Schizophyllum* were obviously related with rainfall and relative humidity. Additionally, this study suggested that inhalable PM_{2.5} in urban and suburban areas may pose more threats to human health due to higher relative abundances of potential allergens and pathogens. These results provide a basic understanding about the response of fungal community to land-use types and the effect of rainfall on dominant genera. However, the pathogenicity of potential allergens and pathogens in the air needs further confirmation.

CRediT authorship contribution statement

Yuanyuan Pan: Investigation, Formal analysis, Writing - original draft. **Li Luo:** Writing - review & editing. **Hongwei Xiao:** Writing - review & editing. **Renguo Zhu:** Investigation. **Huayun Xiao:** Methodology, Writing - review & editing, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.scitotenv.2020.141171>.

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Supplemental materials of

**Spatial variability of inhalable fungal communities in airborne PM_{2.5} across
Nanchang, China**

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Table S1 Parameters of air quality at three sampling sites.

Samples	PM _{2.5}	PM ₁₀	NO ₂	SO ₂	CO	O ₃
Urban	37.53 (12.35)	86.19 (38.96)	28.66 (14.02)	13.60 (8.51)	0.85 (0.27)	74.06 (20.10)
Suburban	27.67 (11.59)	79.99 (33.07)	29.94 (12.53)	5.32 (4.63)	0.74 (0.45)	82.26 (35.19)
Forest	22.88 (9.21)	36.42 (14.63)	8.17 (2.78)	6.23 (2.39)	0.38 (0.07)	76.32 (18.97)

Table S2 Fungal diversity and richness for all samples

Group	OTU	Chao	ACE	Shannon	Simpson	Evenness
U1	386	537	508	5.53	0.95	0.65
U2	311	456	462	4.96	0.92	0.60
U3	390	785	892	3.60	0.79	0.42
U4	391	586	594	5.01	0.91	0.59
U5	682	1051	1063	5.86	0.94	0.62
U6	649	1104	1149	5.32	0.89	0.57
U7	377	618	647	3.86	0.80	0.45
U8	498	866	850	4.41	0.85	0.49
U9	481	896	944	4.29	0.85	0.48
U10	504	1014	941	4.72	0.86	0.53
U11	535	848	881	5.35	0.92	0.59
U12	535	843	899	5.31	0.92	0.58
U13	546	984	981	5.31	0.92	0.58
U14	543	833	835	5.81	0.93	0.64
S1	302	402	380	5.79	0.96	0.70
S2	422	549	573	5.02	0.90	0.58
S3	391	912	958	3.49	0.80	0.41
S4	575	1023	1049	5.15	0.91	0.57
S5	763	1387	1424	5.69	0.93	0.59
S6	988	1463	1516	7.29	0.98	0.73
S7	334	501	471	4.65	0.86	0.55
S8	419	684	674	4.27	0.84	0.48
S9	514	883	872	4.18	0.83	0.47
S10	578	869	965	5.22	0.90	0.57
S11	513	774	810	5.33	0.92	0.59
S12	519	800	806	5.46	0.93	0.60
S13	566	995	1004	5.29	0.91	0.58
S14	489	744	675	6.14	0.96	0.68
F1	326	407	413	5.03	0.90	0.60
F2	574	964	930	5.32	0.91	0.58
F3	545	965	1103	4.37	0.84	0.49
F4	444	652	591	6.05	0.96	0.68
F5	621	795	816	6.43	0.97	0.69
F6	959	1478	1613	6.64	0.96	0.67
F7	434	742	745	5.53	0.94	0.63
F8	551	827	869	5.62	0.93	0.62
F9	562	836	845	5.44	0.91	0.60
F10	545	789	840	5.98	0.96	0.66
F11	563	1060	1076	5.76	0.95	0.64
F12	526	822	863	6.10	0.96	0.68
F13	537	804	821	5.70	0.95	0.63
F14	368	778	709	5.48	0.94	0.64

Fig. S1 Biplot of the air quality and airborne fungal genus-level community using canonical correspondence analysis (CCA), showing the explanation of air quality to the variation of fungal community. Air quality parameters are showed by arrows. The relative length represents the positive importance in influencing community, and the angle between the arrow and axis represents the contribution on this axis. 72.52% of the variability is explained by the two axes.

