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> ***[A0]*** For clarity and easy visual distinction, the referee comments are copied here in black preceded by bracketed, italicized numbers (e.g. ***[1.1]***) to itemize individual comments or questions. Authors' responses are offset in blue below each referee statement with matching numbers (e.g. ***[A1.1]***). Page and line numbers refer to online ACPD version.

[1] GENERAL REMARKS The authors have presented extensive details about aerosol composition and concentrations following rain events. The data are interesting and their publication would be a service to the scientific community. The extent of their impact on our understanding of the interaction of land surface covers, bioaerosols and atmospheric processes is not as palpable as the authors claim because some important details are missing in the presentation of the materials and methods and in the results. In the current version of the manuscript, the description of the experimental set-up, in terms of the exact placement of samplers and environmental probes in the forest canopy, is incomplete and makes it difficult to evaluate some of the phenomena observed and how they are related to atmospheric phenomena on a broader scale. Results of the extensive microbial analyses could be presented in more detail to allow the reader to evaluate the validity of the conclusions. The conclusion should be strengthened to better highlight the novel conceptual contributions of this work and how it will boost our understanding of the link between biological ice nucleators and rainfall.

> ***[A1]*** In response to the referee's helpful comments we have strengthened the conclusions, added to the material and methods section by describing methods and sampler placement in significant additional detail, and improved discussion of microbial methods. Specific responses are outlined below.

[2] SPECIFIC REMARKS P 1769-1770 L 26, 1-2: The authors should give more background information to explain the logic of their argument. They state that "however, evidence linking bioaerosols with increases in IN, especially : : : following precipitation, is limited". Why would they expect there to be a link with IN after precipitation? Although this has been observed several times, perhaps it is surprising? A little bit more lead-in information would be useful.

> ***[A2]*** Indeed, observations linking precipitation and IN have been published as have observations linking precipitation and bioaerosol release. Only the Constantinidou et al. (1990) work discussed ice-active bioaerosol during or following rain, however, and this was only for one species of bacteria. Thus, the observations here represent a significant addition to the scientific literature. For clarification the following text has been added:
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> "For example, splash-induced emission of fungal spores during rain has been well documented (e.g. Hirst, 1953; Allitt, 2000). Bigg and Miles (1964) observed a correlation between rainfall and IN concentrations when comparing extensive measurements in Australia, and Constantinidou et al. (1990) observed a downward flux of ice-active *Pseduomonas syringae* bacteria during rain. However, real-time measurements directly linking ambient bioaerosols and ice nuclei have been missing."

[3] P 1770 L 3-4: The authors state "there is an apparent disconnect between concentrations of IN active biological particles commonly found on vegetation and concentrations

in the air above them (Garcia, et al., 2012)". However, Lindemann et al (1982) were able to associate atmospheric bacterial concentrations to those of IN. The technique that they used allowed them to detect 0.001 bacterial cells /L of air. This level of detection was needed because INA bacteria were a very small fraction of the total bacteria and were present at concentrations very near the detection threshold. In the work of Garcia et al, their level of detection for INA bacteria was 0.1 gene copies /L. At 1 gene copy per bacterial cell, this means that they could only detect 0.1 INA bacterial cells /L of air. Hence, in order for them to have detected INA bacteria, the concentrations under their sampling conditions would have needed to be 100 times those observed by Lindemann et al. Hence the "disconnect" that they describe is most likely a problem of sensitivity of detection.

[A3] We think that the referee may have misunderstood what we meant to imply regarding the "apparent disconnection." The goal of the Garcia study was to assess whether the vegetation studied was a potential and significant source of INA bacteria to the atmosphere. Their results showed that INA concentrations were on the order of 10^5-10^7 g^{-1} of vegetation on the ground, while airborne INA bacteria were mostly below the detection limit, which was 0.04 L^{-1}. And so, although the detection limit from the Lindemann et al. (1982) paper that the referee discusses may have been superior to that of Garcia et al. (2012), the point remains that large populations of INA bacteria on the ground do not necessarily equate to large populations in the air above them.

To address the referee's comments, the following text has been added to the main text at P1770, L5:
"For example, Garcia et al. (2012) recently reported that variations in the number concentrations of airborne IN did not correlate with strong variations in the numbers of biological IN on underlying vegetation."

[4] P 1770, Materials and Methods. ***[4.1]*** In this section of the manuscript (including the relevant information from the supplemental materials section) I cannot find information to allow me to understand the position of the sampling devices relative to the plant canopy. They state that the work was conducted in the Manitou Experimental Forest. ***[4.2]*** How tall is the canopy and what is the leaf-area index (roughly)? ***[4.3]*** Is there an important understory? ***[4.4]*** When rainfall is measured, is this the amount of rain observed on the ground inside the canopy or elsewhere? ***[4.5]*** Likewise, in what part of the canopy was leaf wetness measured, and how did they account for the variability within the canopy? ***[4.6a]*** The authors state that inlets of samplers were placed at 4 m above the ground and in the supplemental materials they state that they are at 1 – 4 m above the ground. Given that they used the calculation of Lindemann et al for flux, then I suppose that the 1 m samples were used to calculate the difference in particle concentrations at the 2 heights. ***[4.6b]*** I don't think that the assumptions of this calculation are met for measurements within a canopy. The gradient method that they used for flux measurements has an important assumption of fetch that I think could not be met under a canopy (generally you need very large open fields with no obstacles to meet the assumption of fetch). ***[4.6c]*** The authors seem to be suggesting that the measured flux is linked to emission from the canopy, but can the measurements they made be extrapolated to what is happening above the canopy? ***[4.7]*** In light of these remarks, Figure 5 is confusing and maybe even misleading because it does not necessarily illustrate what they have measured.

[A4.1] A new figure (Fig. 1) has been added to the manuscript that details the location of inlets and samplers.

[A4.2-A4.3] The following text has been added to address the referee's comment regarding canopy height, leaf-area index, and understory:

"The forest canopy at the site is sparse and highly variable. Clusters of ponderosa pine trees approximately 10-20 m in height are separated by large open spaces of grass and forb understory. Grasses are generally ~20 cm tall, with seed shocks occasionally reaching as high as 1 m. The leaf area index (LAI) is also highly variable and was estimated to be a mean of approximately 1.9 (DiGangi et al., 2011), with trees covering ~60% of the site." (Inserted at P1770, L25).

[A4.4] The following text was added to the main text at P1771, L6:

"Rainfall was measured in a clearing between tree clusters (Fig. 1) with a minimum of a 45^{o} sky view present at the precipitation monitoring sites. Therefore, summer precipitation measurements were not affected by the tree overstory. Additional under-canopy precipitation measurements were collected at the site but were not discussed in this manuscript. Those measurements suggest that canopy interception within tree clusters is approximately 30% of the open area precipitation when aggregated over the entire warm season."

[A4.5] The following text was added at P1771, L11:

"The LWS was deployed approximately 1 m above ground in a clearing next to the precipitation measurement sensor (Fig. 1)."

[A4.6a] Estimates of bioparticle flux were taken from the WIBS instrument operated from an automated vertical profiling system running between 3 m and 22 m above ground. These details were included in the online Supplement, but have been moved to the main text.

[A4.6b] The vertical profile was split into several sections, and a flux was calculated from the gradient between these sections for data associated with each of the different clusters. This analysis provided a large range of flux values immediately after rain events. While this wide range implied the values are imprecise, the order-of-magnitude estimate was significant to share with the community. As such, we have framed the stated range as a rough estimate rather than a canonical calculation.

K-theory, or the flux-gradient method, is generally inadequate in dense forest canopies for use in estimating fluxes from profile measurements, particularly where counter gradients in heat flux occur in the trunk space and in thermally stratified conditions. Specifically, Monin and Obukhov Similarity (MOS) theory (Monin and Obukhov, 1954) for wind and temperature do not hold, because the Manitou Experimental Forest is not very dense. To correctly estimate a net flux would require a more sophisticated inverse modeling approach (e.g. Siqueira et al., 2000), which we cannot provide. However, recent measurements, Zhang et al. (2010), suggest that ϕ_m flux profiles can be described by the local Richardson number, R_i, which increases linearly with ϕ_m in the canopy with height, provided there is no counter gradient in sensible heat flux. The in-canopy derived momentum flux profile (measured by the sonic anemometer profile) is used to derive this in association with the WIBS concentration profile. The estimates listed here could be as uncertain as the aerobiology approach adopted in climate models Sesartic et al. (2012), Jacobson & Streets (2009), but probably better due to the inclusion of local momentum flux measurements.

[A4.6c] Regarding extrapolation to aerosol dynamics above the canopy, we cannot comment with certainty about what happens to the aerosols after they are emitted from the canopy. As the referee points out, we do not make the appropriate measurements for above-canopy flux estimates. It should be noted that the uppermost measurements of the aerosol profile were above the top of the canopy, allowing assertions to be made about flux between in and out of the canopy. Positive flux values

mean that aerosols, by definition, that are emitted from the canopy do not then re-enter. As such, one might expect the aerosols to be transported away from the local area.

In response to the referee's comment about flux calculations, we have added the following text for clarification (P1771, L26):

"Measurements within the canopy provide an upper limit for the role of biological IN in the region above the canopy."

[A4.7] Finally, Figure 5 has been moved to the Supplement in response to the possible confusion it could bring into the main text.

[5] If the work had been conducted over a low canopy of an annual crop, for example, then the results would be relatively easy to interpret in light of experimental design. But for the work as reported here, there is likely to be a very important impact of canopy heterogeneity – both vertically and horizontally – on the measurements. When rain hits the canopy top, much of it is likely to "dribble" down through the canopy after the initial splashing, collecting particles as it successively comes into contact with leaves. As pine leaves are very fine and hydrophobic, rain drops are likely to roll right off. Secondly, there is often considerable litter in the understory, and when drops fall on the litter, splashing of the abundant associated microflora will occur. Rainsplash movement of spores within canopies can be very heterogeneous even for relatively short canopies. Furthermore there have been considerable studies in this area, mostly concerning the dissemination of plant pathogens. A few examples include: Paul et al 2004. Rain Splash Dispersal of Gibberella zeae Within Wheat Canopies in Ohio. Phytopathology 94:1342-1349. or, the very detailed chapter by Huber, Madded and Fitt on Rain-splash and spore dispersal: a physical perspective, Chapter 17 in Jone D.G (ed.) The Epidemiology of Plant Diseases, 1998 Kluwer Academic Publishers

[A5] There is no doubt that the processes involved in rain splash dispersal of bioparticles are complex. We do not intend to suggest the precise mechanisms by which the observed particles were emitted, and thus spend relatively little time on our proposed hypotheses within the manuscript. The scope and conclusions of the manuscript are rather to show the larger scale observations regarding the relationship between bioparticles, ice nuclei, and rain. And, as pointed out by the referee, there is very well established literature showing rain splash as an important emission mechanism for many types of spores and bacteria. In the submitted manuscript we had cited two of these (at P1776, L18). We have added the citations suggested by the referee as well as several others for a total of ten citations detailing previous work related to rain splash dispersal of bioparticles. As a part of this change we have added the following text:

"The process of rain splash emission has been well documented and is the most likely source of bioparticles observed, and several theories have been suggested to explain the micro-scale dynamics involved (Hirst and Stedman, 1963; Leach, 1976;Allitt, 2000)."

[6.1] Hence, a considerable improvement to this manuscript could be made by the addition of a figure that indicates precisely where in the plant canopy the measurements were made. This figure could then indicate the scenario of the processes of rainfall impaction and emission at the scale at which they were measured. It would add to the pertinence of statements such as that in the Results and Discussion section concerning the origin of the bioparticles observed after rainfall. ***[6.2]*** For example, on pp 1776-1776, lines 28-29 and lines 1-7, the authors mention that bioparticles could have been emitted from wetted surfaces near the measurement location. What does "near" mean? The forces of agitation and wetting due to rainfall are known to release some spores on the scale of

centimeters. Are the measurements made within centimeters of these sources, and if not then what trajectories and forces explain their abundance near the sampling inlets? (I am not casting doubt; I am just asking for clarification.)

[A6.1] In response to the referee's first comment above we have added a new Figure 1, which shows the relative locations of samplers and inlets. In addition we have added clarifying text to the materials section that numbers each inlet in relation to the added figure, and the text now outlines the specific heights from which each inlet sampled air.

[A6.2] The referee also asked for clarification of the proximity of the sampling point to the emission point. We don't have measurements that detail the dynamics involved in the processes that moved particles from the surfaces from which they were likely emitted to heights at which we were able to sample them, and we don't claim to present a hypothesis on this process. The point here is to say that, at the heights of our samplers (~a few meters) the concentrations of bioparticles and IN followed the trends we discussed. Ultimately, the goal is not necessarily to understand the dynamics a few centimeters from leaves, but to understand the overall air mass at "ground level" which could be lofted upward.

[7] P 1171 last line: In the sentence, "Fluorescent particles (Nf) detected by the UV-APS and WIBS can be regarded as a lower limit for the abundance of primary biological aerosol particles", two things are unclear. Does "can be regarded as" really mean "are" (in fact are)? If so, please say it directly. Secondly, if this is the lower limit for abundance, it would be useful if the authors indicated precisely what this meant in terms of the number of particles /m3, for example.

[A7] The terminology has been changed from "can be regarded as" to "represent" to clarify this point. The degree to which these numbers are a lower limit is not well understood, but was addressed to a certain extent by Huffman et al. (2012), as cited in the text.

[8] P1773, paragraph beginning on line 6: There is no mention of detection limits for microorganisms in this work. In particular, for DNA analyses, how many "copies" (cells, spores) of a given microorganism need to be present in one m3 of air in order to be detected with these techniques?

[A8] Amplification of DNA was performed via the PCR method, which is generally very efficient for amplifying the DNA of biological organisms. In theory even minute amounts, e.g. one molecule DNA per organism, are sufficient for the identification of PBAP (e.g. Després et al., 2007). Thus, as little as one DNA molecule of the organism in question deposited onto the sample can be detected if PCR settings have been optimized. However, primer pair sensitivity can vary and some primer pairs may need more than one molecule to initiate amplification. Additionally, DNA can be lost during the extraction process, and this loss can vary as a function of experimental procedure (e.g. between extraction kits). Although optimal sampling, extraction and amplification scenarios have been tested previously, specific detection limits have not been rigorously studied.

For clarification, the following text was added:
"Although PCR can theoretically lead to detection of as few as an individual molecule of DNA within a sample, actual results may be less efficient. Extraction and amplification scenarios have been tested previously (Fröhlich-Nowoisky et al., 2009; 2012), but specific fungal and bacterial DNA detection limits have are not yet available."

[9] P 1773, paragraph beginning on line 23: Other information is necessary to be able to

interpret the results and compare with other works. ***[9.1]*** For bacterial and fungal cultures, how long were the cultures incubated? In the case of bacterial cultures, was the incubation time sufficient to get the cells past the exponential phase of growth? ***[9.2]*** A second very important piece of information that is needed concerns the densities of the suspensions tested in each well. For bacteria in particular, this would allow comparison with other reports concerning the number of ice nuclei/cell. This would also allow the authors to compare the activity in the strains they characterized here: does a negative reaction at -6_C, for example, for one strain have the same weight as a negative reaction for another strain (in light of the fact that they might have been tested at different cell concentrations). ***[9.3]*** Finally, what was considered as a positive result? Was a single well frozen at a given temperature sufficient to be considered positive?

[A9.1] Some of this information had been discussed in the online supplement, but we have moved it to the main text for clarification. The following text, for example, was moved to the main text into what was Section 2.3 P 1773/L25 (now Section 2.5.3):

"Fungal and bacterial colonies were picked and cultured … and incubated at 16 °C for 13-40 days (first test) and 62-82 days (second test)."

And among additional information moved from the supplement:

"Ice active isolates were then cultured on DPY agar and incubated at 16 ^{o}C for ~ 3-7 days and tested again for ice nucleation activity."

[A9.2] The concentration density of bacteria or fungal material in suspension was not measured. Additionally, the bacteria colonies were not picked intentionally, because the experimental procedure had been optimized for fungal analysis. The referee's comments are interesting, but will require follow-up in an additional experiment. To clarify this point we have added the following text at the beginning of Section 2.5.3:

"The intention was to pick select fungal colonies from the culturing media, but several bacterial colonies were picked unintentionally as well."

[A9.3] This information has now been added to the manuscript in Section 2.5.3:

"Isolates were considered as positive if they showed ice nucleation activity in all tests."

[10] P1775, L 8-16: Here the authors mention that precipitation leads to increases in the concentration of coarse aerosol particles not embedded in rain droplets. It would have been interesting to know if these phenomena and the types of particles liberated are specifically linked to rainfall per se or rather to the mechanical agitation caused by rainfall. Interesting future experiments could involve supplemental mechanical agitation during certain rainfall events and during certain dry periods. Can the authors speculate about this based on existing literature concerning the role of mechanical forces in the concentration of particulate matter in aerosols?

[A10] As the referee points out, indeed it would have been interesting to know the direct source of the bioparticles observed during and after rainfall, and this work certainly opens additional question that will be interesting to explore in future experiments. We refrained from speculating on hypothetical possibilities we had no means of measuring, but rather decided to cite additional previous work on bioparticles associated with rain.

[11] P1776 L 5-6. Here the authors make a statement about the diameter of the particles related to the data presented in Fig 1e (Da) collected with the UV-APS. In the legend in Figure 2 they again refer to particle diameter, measured with the same equipment,

but this time they call it aerodynamic diameter. This is confusing because for bioparticles in particular the correlation between these two parameters (physical diameter and aerodynamic diameter) is very poor (Reponen, T., et. al. 2001. Aerodynamic versus physical size of spores: Measurement and implication for respiratory deposition. Grana 40, 119-125). I think that the UV-APS device measures physical size of particles. If this is the case the authors should make this clear and avoid using the term aerodynamic diameter.

[A11] In this instance, the referee misunderstands the measurement parameter being discussed. The UV-APS stands for ultraviolet aerodynamic particle sizer and only provides particle size as an aerodynamic diameter (D_a), not as a physical diameter.

[12] P 1777 L 4-5: Here the authors state "suggesting a net upward flux of fluorescent bioparticle emission after rainfall (50-500 /m/s)". As mentioned above, it is crucial to know the spatial pertinence of this estimate; where was flux estimated and is this estimate representative of conditions that can be extrapolated above the canopy? It would also be useful to see details about the flux calculations. They present the range of values, but it would be interesting to see if in fact net flux after rainfall is always upward and how variable are the measurements among all the replicates.

[A12] Please see author responses ***[A4]*** above. Additionally, aerosol gradient fluxes were calculated using the WIBS4 located on the chemistry tower. We had intended this to be clear from text in the supplementary material. However, we have clarified this point by adding the following text to Section 2.3:

"The three minute WIBS4 descent profile data was split into several sections with height, and the gradient flux calculated between each of these sections."

We assumed that the canopy concentration profile was homogeneous throughout the forest and so this estimate represents a net vertical flux. The referee is asking for the "flux footprint". This can be calculated using the appropriate Gaussian footprint model. The footprint will, of course, vary significantly with atmospheric stability and height. Again, in order to avoid both introduction of more uncertainty and over-interpretation of uncertainty estimates, we made the assumption of spatial homogeneity when generalizing flux estimates to the wider forest.

We made an attempt to convey these fluxes while not encouraging their over interpretation by characterizing them as such a wide range of values, i.e. 50-500 m^{-2} s^{-1}. We feel that expressing variability between events in the paper would be overly verbose and would convey a lower level of uncertainty than the analysis currently provides.

[13] P 1777, paragraph beginning on line 8. In this paragraph the authors indicate that the identified microorganisms comprise a number of plant pathogens and human allergens. Identification of bacteria was based on sequencing the gene for 16S rRNA. To attribute a species name to the bacterium that is at the origin of the DNA, the authors most likely compared the sequence to the NCBI data base (this is not described in the methods). Likewise for fungi. These comparisons are associated with a probability of similarity to sequences deposited in the data base. It is a common phenomenon that sequences can be equally affiliated to several species. Likewise, many sequences often do not find a significant match at the species level. In any case, the information garnered from this approach only indicates the probability that the sequence resembles something deposited in the NCBI data base (and most of what is deposited represents soil habitats). This is why the details are very important here. How close were the

matches to the putative plant pathogens and human allergens? And did they match at the species level or the genus level? A list of matches and their probabilities (at least of list of the specific matches that correspond to well-known plant pathogens and human allergens) would better substantiate their claim.

[A13] In response to the referee's comments we have added significantly more detail in Section 2.5.2, as detailed below (bold, italicized text added):

"Optimized methods of DNA extraction, amplification, and sequence analysis of the internal transcribed spacer (ITS) regions ***of genes*** were used to determine fungal diversity from the high-volume air filter samples (Fröhlich-Nowoisky et al., 2009; 2012). The primer pair ITS4Oo and ITS5 (Nikolcheva and Bärlocher, 2004) was used for amplification of *Peronosporomycetes* (formerly *Oomycota*). Also specific for this study, the ITS regions from fungal lysates, obtained from the cultivation experiments of Andersen impactor samples, were amplified with the primer pair ITS4 and ITS5 (White et al., 1990; Fröhlich-Nowoisky et al., 2009; 2012). The obtained PCR products were sequenced using the primer ITS5 and sequence analysis was performed as described previously (Fröhlich-Nowoisky et al., 2009; 2012). ***Summarized fungal sequences were compared with known sequences using the Basic Local Alignment Search Tool (BLAST) at the National Center for Biotechnology (NCBI) and identified to the lowest taxonomic rank common to the top BLAST hits after chimeric sequences had been removed. Subsequently sequences that produced the same BLAST results were pairwise aligned using the program BioEdit (version 7.1.3) and the similarity calculated using the PAM250 Matrix. Sequences were grouped into operational taxonomic units (OTU) when their similarity was > 97%.*** The sequences from the obtained operational taxonomic units have been deposited in the GenBank database under following accession numbers: JX135610 - JX136661 (fungi, and JQ976038 - JQ976273 (*Peronosporomycetes*).

For the determination of bacterial diversity from high-volume aerosol filter samples DNA was extracted as described by Després et al. (2007). The 16S ribosomal gene was first amplified for taxonomic identification with primer pairs 9/27f and 1492r (Weisburg et al., 1991) with PCR conditions given by Després et al. (2007), and then cloned and sequenced. The same primer pair was used for the bacterial lysates obtained from Andersen sampler culture plates. For the bacterial sequences OTUs were identified using the Mothur software package (Schloss et al., 2009) and chimeric sequences excluded (using the Bellerophon program (Huber et al., 2004). Representative sequences of the OTUs were aligned using the multiple sequence comparison by log expectation (MUSCLE) package (Edgar, 2004) and thereafter manually checked. Sequence identification was based on phylogenetic analysis. Representative sequences were included as well as type-species of various bacterial groups. Phylogenetic trees were based on a neighbor-joining algorithm based on Jukes Cantor corrected distances within the Phylip package (Felsenstein, 2005). Bacterial sequences are deposited in the GenBank database under the following accession numbers: JX228219-JX228862.

Although PCR can theoretically lead to detection of as few as an individual molecule of DNA within a sample, actual results may be less efficient. Extraction and amplification scenarios have been tested previously (Fröhlich-Nowoisky et al., 2009; 2012), but specific fungal and bacterial DNA detection limits have are not yet available."

Also, to clarify the general point of the referee we also modified the discussion text discussed (P1777/L16) by the referee here (bold, italicized text added):

"The identified groups of microorganisms comprise a number of plant pathogens and human allergens (mildew, smut and rust fungi, molds, *Enterobacteraceae, Pseudomonadaceae)*, ***though not***

all species within these groups exhibit pathogenic or allergenic properties. These findings provide a *possible* rationale for reported enhancements of asthma and other respiratory diseases during rain showers (Taylor and Jonsson, 2004; Dales et al., 2012). ***Follow-up studies will be necessary to investigate the possible relationships and mechanisms on a species level.***"

[14] Overall, the data concerning microbial characterization have been presented in too little detail. The authors present these data to support important points about the processes underlying increases in IN abundance after rain. They went through a lot of work to obtain them. So it is unfortunate that more detail is not presented. It is also unfortunate that they make a cursory presentation of the results that corroborate their underlying hypotheses without allowing the reader to evaluate the strength of their conclusions. Out of curiosity, I recovered some the sequences for bacteria that they deposited in GenBank and Blasted them against the NCBI data base to see what types of bacteria they might have encountered. The sequences that I looked at corresponded to soil-associated bacteria such Streptomyces and Arthrobacter. This made me wonder if the relative abundances of soil bacteria were considerably less after rain than during dry periods. It would be very useful if the authors presented a more detailed analysis, perhaps by pooling the data for events after rainfall and those during dry periods and then presenting the relative frequencies of the different groups of micro-organisms encountered.

[A14] Please see author response ***[A13]*** above. Additionally, the detailed data for fungi and bacteria will be published in separate manuscripts, as fully unraveling the inter-sample variability on species level and detailed comparison of species associated with different ecosystems goes beyond the scope of this study.

In general this manuscript presented an overview of the observations that biological particles and IN increased during and after rainfall. The focus is to bring the observations to the community of atmospheric scientists. While more detailed microbiological detail would be interesting to a small subset of the readers here, these data will be more appropriate in a follow-up to a journal with a deeper biological focus. As an example of the importance of this, Referee #3 requested that we *decrease* the amount of microbiological detail that we give in the manuscript, because it is already "difficult to read" for a non-biologist. As a result we have chosen not to radically expand the detail in these sections, beyond what we have now added to Section 2.5.2.

[15] P 1778, paragraph beginning on line 9: Here the authors describe increases in the abundance of ice nucleators active at temperatures warmer than -15_C and the concomitant increases in particle sizes that are suggestive of biological particles. In parallel, they have isolated fungi and bacteria that are ice nucleation active in laboratory tests. ***[15.1]*** This is precisely where it would be useful to know the rates of ice nucleation activity per biomass of the microorganisms. This information is critical for the authors to claim that these micro-organisms were present in the atmosphere at sufficient concentrations so that they could have contributed to the observed increases in ice nucleation activity. Toward the end of this paragraph the authors state: "Overall, the DNA analyses of aerosol samples collected during rain events showed higher diversity and frequency of occurrence for bacteria and fungi from groups that comprise IN active species (Pseudomondaaceae; Sordariomycetes). Identification of both Pseudomonas sp. and Sordariomycetes directly from IN samples collected using the CFDC during rain shows conclusively that the biological particles were indeed active as ice nuclei." ***[15.2]*** It should be noted that most bacterial species in the very large Pseudomonadaceae

family ARE NOT ice nucleation active. INA is limited to strains of a few species within this family. Likewise for the over 10000 species in the Sordanomycetes: only one or 2 are INA. Even among the species of Pseudomonas, only a few are INA. The recent work of Joly et al (2013. Ice nucleation activity of bacteria isolated from cloud water. Atmos. Environ. (in press)) revealed that in clouds only about 10% of the fluorescent pseudomonads isolated from clouds had measureable INA. So the statement made by the authors is not well-supported by their generalizations. It would be better to indicate the specific species that contributed directly to this increase in INA and the rates (concentrations) at which they were present in the air.

[A15.1] The referee asked for detail about the ice nucleation activity per biomass of the microorganisms. This information is not readily available but is planned for future experiments.

[A15.2] It is true that ice activity cannot be determined at the species level, because only certain strains are IN active. This is why we discuss results from the high-volume and Andersen samplers at the family level. For example, the following text was copied from the manuscript discussion:

"Overall, the DNA analyses of aerosol samples collected during rain events showed higher diversity and frequency of occurrence for bacteria and fungi from groups that comprise IN active species (*Pseudomondaaceae; Sordariomycetes*)."

In contrast to this, DNA analyses of samples collected from behind the CFDC directly measure particles that acted as IN within the instrument, and thus no assumptions are necessary. Particles that formed ice crystals were collected onto a grid and analyzed with respect to their relative abundance and type. So in this case, the statement as previously written is still defensible:

"Identification of both *Pseudomonas sp.* and *Sordariomycetes* directly from IN samples collected using the CFDC during rain shows conclusively that the biological particles were indeed active as ice nuclei."

The genetic data was collected and preliminary results presented to support the results gained by the UV-APS data to show an increase in IN abundance after rain. Please also see response ***[A14]***. For the specific comment given by the referee, no soil samples were taken at the sampling site to be able to compare their composition and abundance before and after rain.

[16] P 1779, Conclusions. The first statement is accurate in light of the results of the work presented here. But, an added detail would be useful. To the phrase "bursts of bioparticle emission and massive enhancement of atmospheric bioaerosol concentrations", it would be useful to delimit this increase in terms of space. Where is the massive enhancement occurring? Is it above the canopy or within the canopy in the forest system studied?

[A16] We added text clarifying that the bursts were observed within the canopy. The first sentence of the conclusions now read (bold, italicized text added):

"Our observations indicate that rainfall can trigger intense bursts of bioparticle emission ***within the forest canopy*** and massive enhancements of atmospheric bioaerosol concentrations by an order of magnitude or more …"

[17] The second statement is something that has not been demonstrated here (in terms of spread and reproduction), but it is something that is well-known in the field of plant pathology, for example. In this light, it does not seem pertinent that it is a conclusion of this study.

[A17] Several citations were added to clarify that the observation of microorganism dispersal was not uniquely observed by our experiments:

"… (e.g. Hirst and Stedman, 1963; Fitt et al., 1989; Constantinidou et al., 1990; Paul et al., 2004)."

[18] Figure 5: This figure does not really add anything to the manuscript. It contains well known information (pathogen spread, for example) and also does not present any specific details that have not been presented in other figures in other publications about the interaction of bioaerosols with landscapes and the atmosphere.

[A18] Figure 5 has been moved to the Supplement (now Fig. S1) in response to the referee's suggestion.

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