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# Twenty years of elucidating diversity and function of cloudborne microorganisms: from lab studies to biotechnological applications

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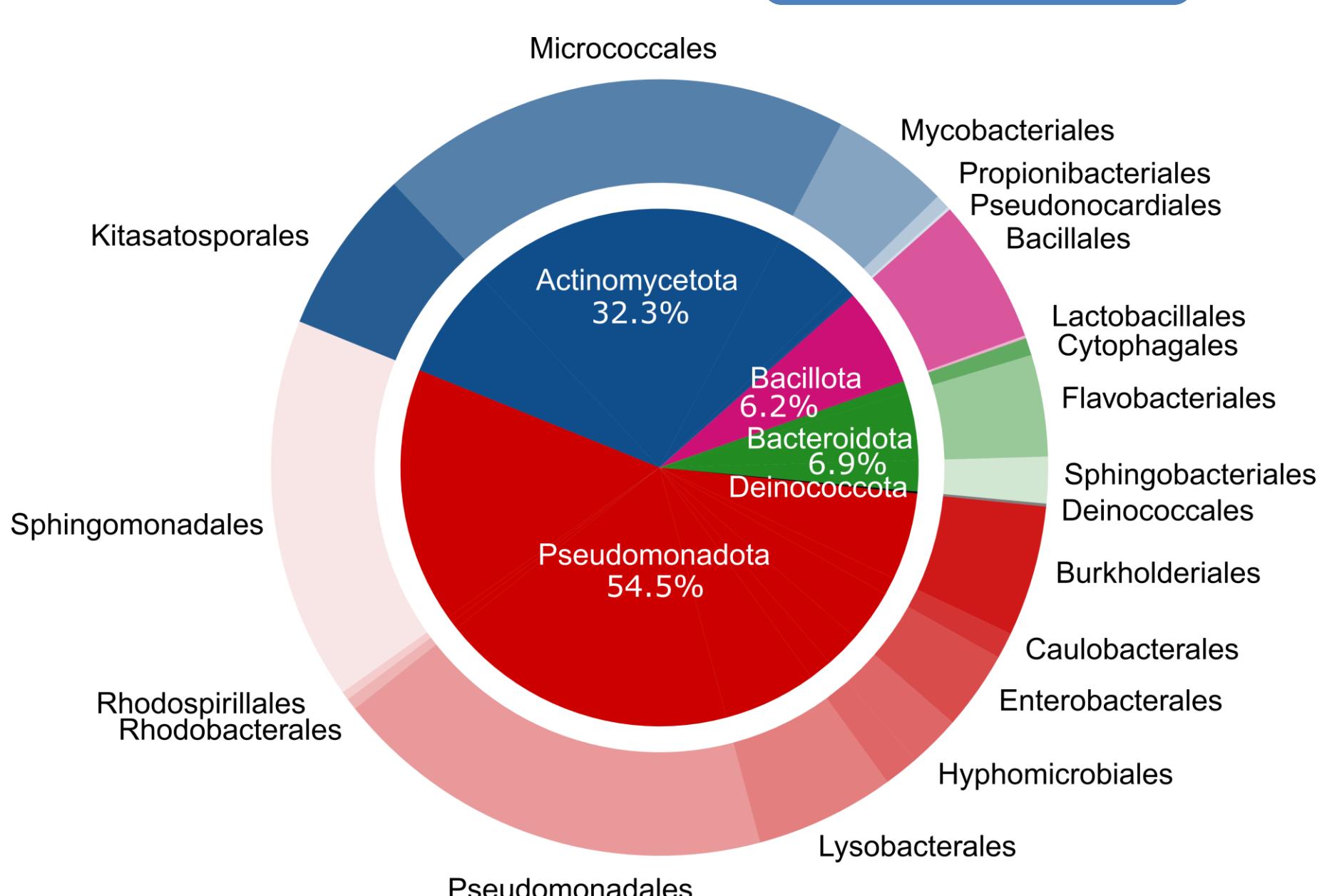
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## Microbial diversity in the ICCF cloudborne culture collection

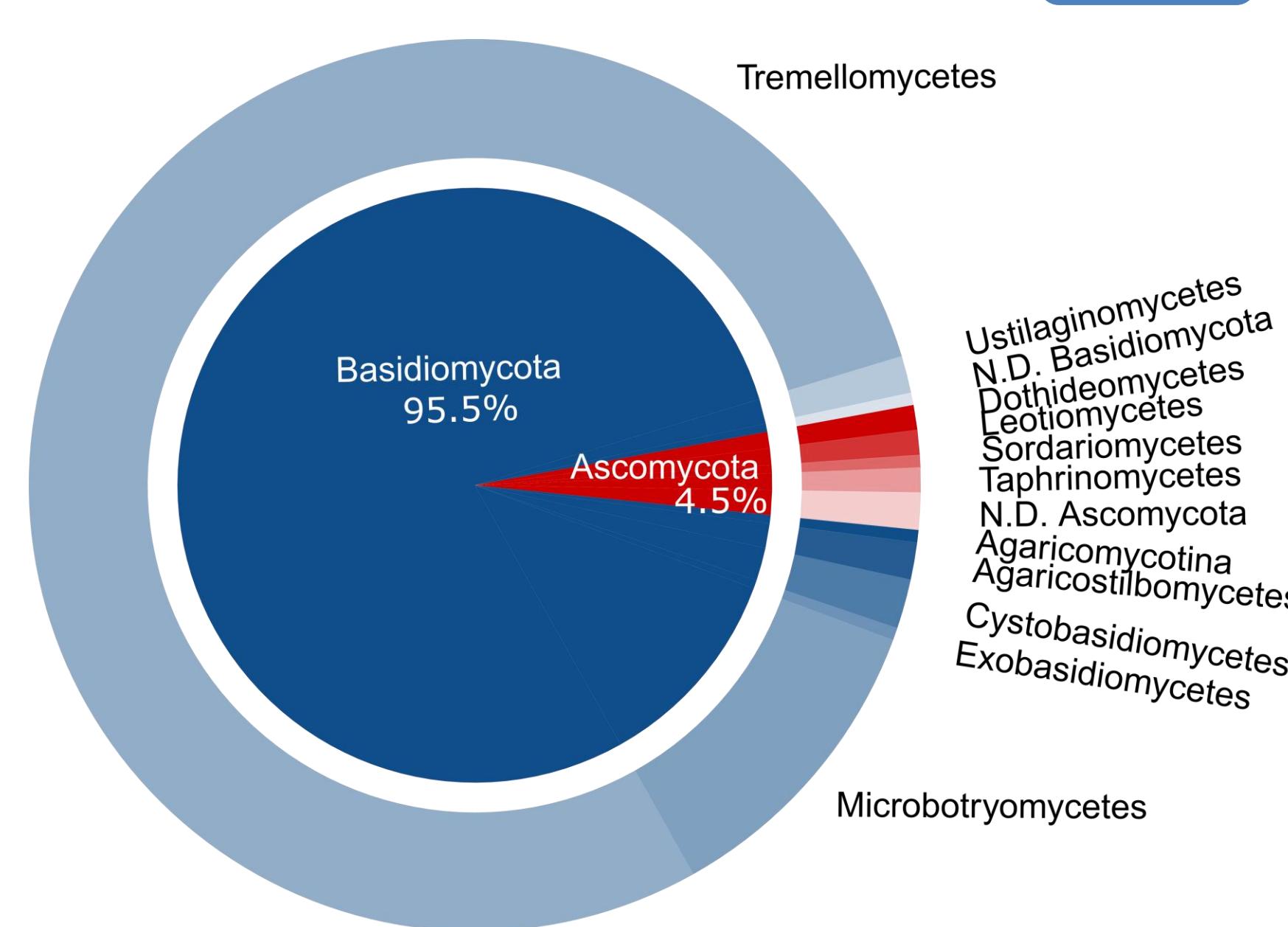
- 827 bacterial strains and 223 fungal strains were isolated from cloud water sampled at the top of the puy de Dôme (Auvergne) or the Maïdo (Reunion island, Indian ocean) mountains to form a unique culture collection

### Bacteria



TOP10 genera	# isolates
<i>Pseudomonas</i>	143
<i>Sphingomonas</i>	129
<i>Streptomyces</i>	57
<i>Rhodococcus</i>	36
<i>Stenotrophomonas</i>	34
<i>Clavibacter</i>	28
<i>Curtobacterium</i>	28
<i>Bacillus</i>	26
<i>Microbacterium</i>	25
<i>Frigoribacterium</i>	20

### Fungi



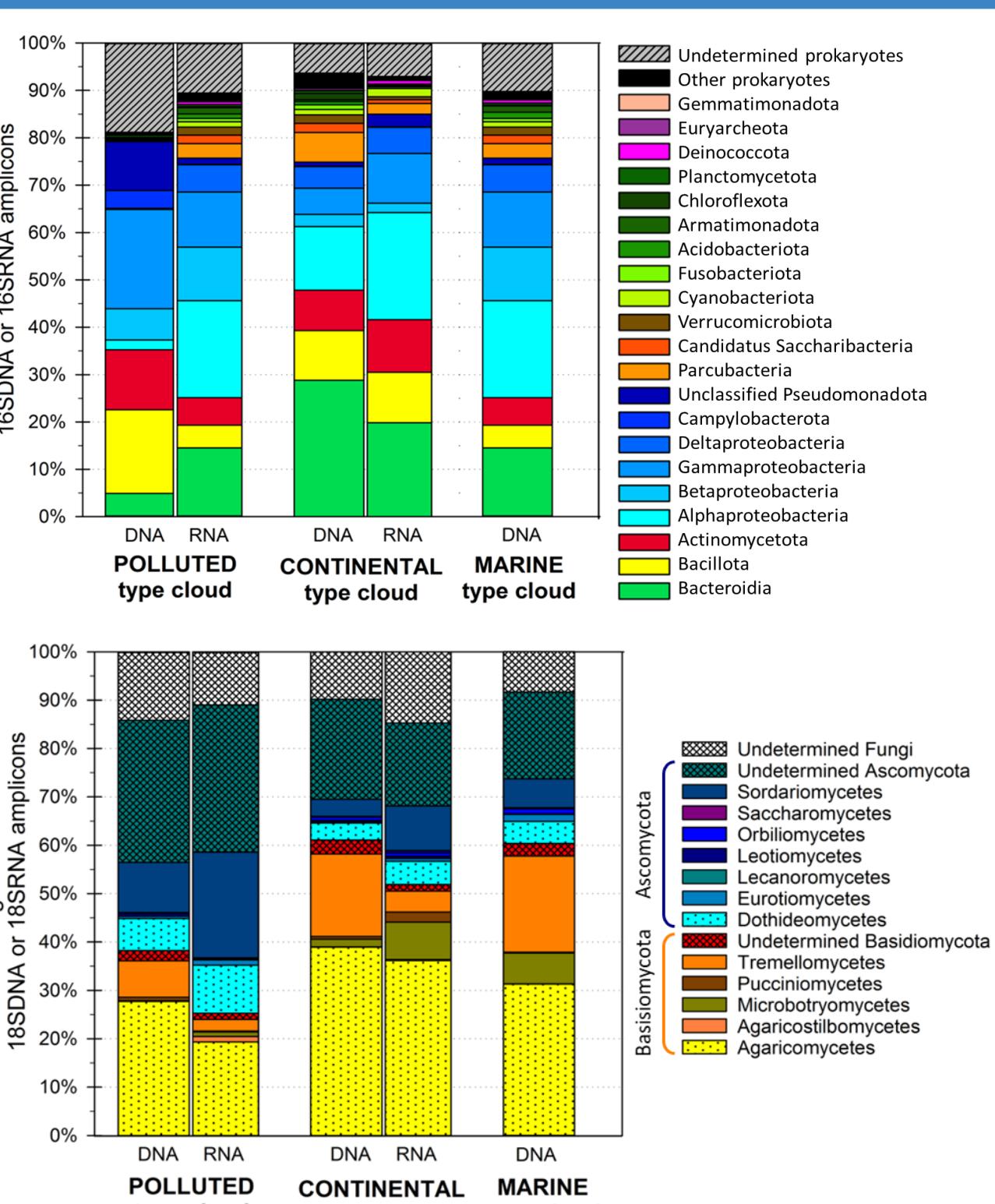
TOP6 genera	# isolates
<i>Dioszegia</i>	87
<i>Itersonilia</i>	34
<i>Udeniomyces</i>	17
<i>Vishniacozyma</i>	13
<i>Sporobolomyces</i>	11
<i>Cryptococcus</i>	8



## Metabarcoding of total and active communities

- Cloud water is a rich environment with > 28 000 OTU<sub>97%</sub> for bacteria and > 2600 OTU<sub>95%</sub> for fungi
- Pseudomonadota and Bacteroidota phyla dominate total prokaryotic community while Ascomycota and Basidiomycota dominate fungi community
- Active orders (based on 16S or 18S rRNA) comprise Sphingomonadales, Rhodospirillales, Hyphomicrobiales, Burkholderiales and Pseudomonadales for prokaryotes

Updated from Amato et al., PlosOne (2017) doi.org/10.1371/journal.pone.0182869



## Cloud water, a source of undescribed species

- ~ 1% of bacterial isolates share < 97% of identity with the closest type strain rDNA 16S sequence
- ~ 4% of yeast isolates share < 97% of identity with the closest type strain rDNA 18S sequence and ~3% have < 95% of similarity with their closest neighbor
- Cloud water is poorly explored for its biodiversity and potentially contains new species never described before**

Strain identifier	Most probable affiliation	Maximal percentage identity (16S/18S rDNA)
MAIDO-R6b-21	Micrococcaceae bacterium	96.7%
PDD-58b-27	<i>Flavobacterium</i> sp.	96.0%
PDD-23b-17	<i>Hymenobacter</i> sp.	96.6%
PDD-54b-11	<i>Hymenobacteraceae</i> bacterium	96.3%
PDD-69b-30	Burkholderiales bacterium	96.5%
PDD-70b-11	Burkholderiales bacterium	96.7%
PDD-26b-32	<i>Leotiomycetes</i> yeast	96.9%
PDD-23b-2	<i>Sordariomyceta</i> yeast	93.9%
PDD-77b-8	<i>Agaricomycotina</i> yeast	93.8%
PDD-33b-4	<i>Microbotryomycetes</i> yeast	95.6%
PDD-26b-29	<i>Pucciniomycotina</i> yeast	93.5%
PDD-24b-25	<i>Itersonilia</i> sp.	93.5%
PDD-26b-11	<i>Tremellomycetes</i> yeast	94.7%
PDD-77b-14	<i>Tremellomycetes</i> yeast	92.2%

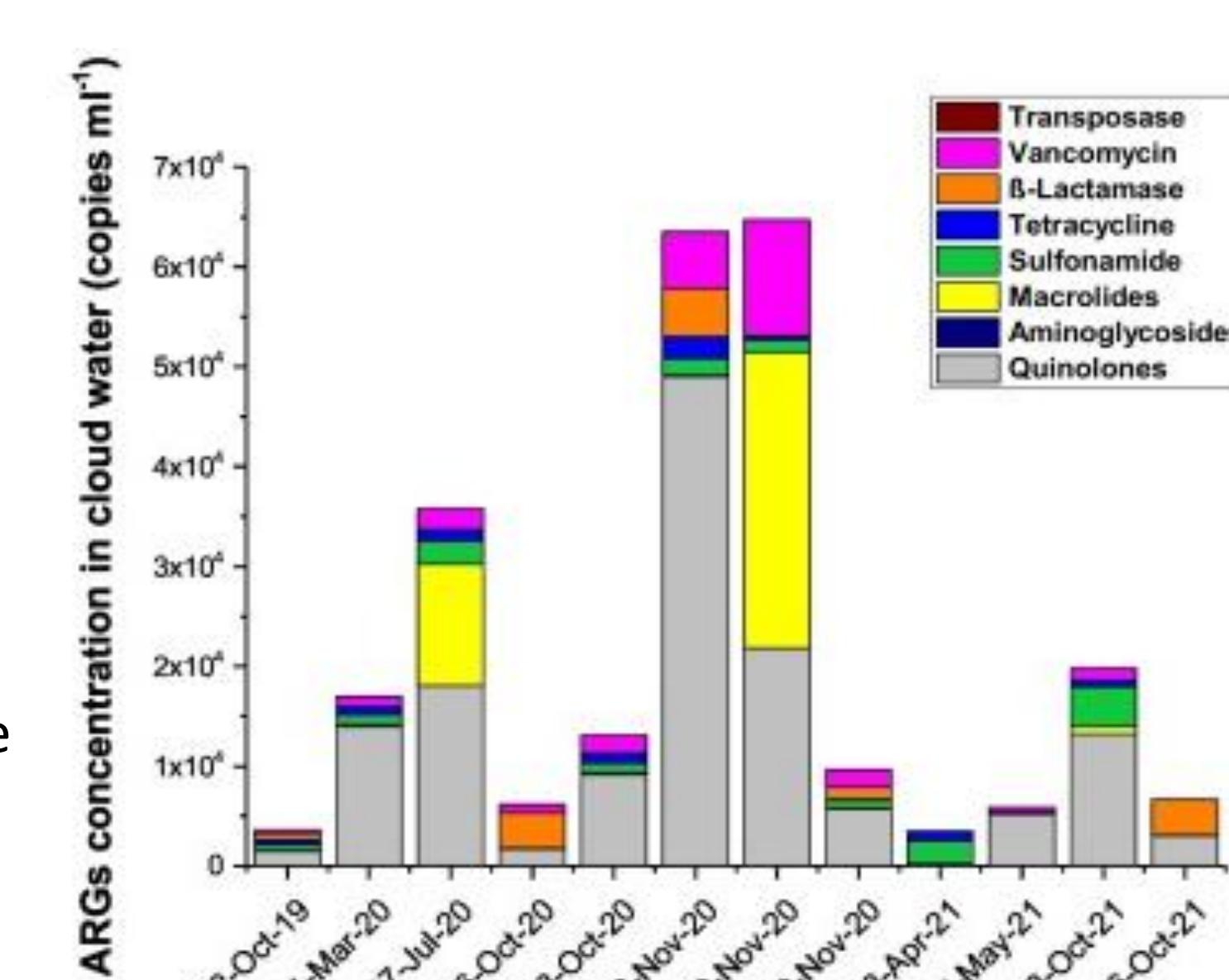
Unpublished data - BlastN against nr/nt nucleotide collection - 2021



## Ice nucleating bacteria, possible rainmakers

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- Biological particles participate in ice nucleation at high temperature in cloud water sampled at the puy de Dôme mountain
  - 7 bacterial strains of our cloud collection belonging to *Pseudomonas* and *Xanthomonas* genera were identified as ice nucleation active at near 0°C temperatures. They are among the most active identified to date
  - Bacteria could contribute to cloud evolution by triggering precipitation at temperatures close to 0°C**

Adapted from Joly et al., Atm Env (2013), doi.org/10.1016/j.atmosenv.2013.01.027 and Joly et al., ACP (2014), doi:10.5194/acp-14-8185-2014



Rossi et al., STOTEN (2023), doi.org/10.1016/j.scitotenv.2022.161264



## Surfactant-producing microorganisms to facilitate droplet formation

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- Surfactants in the atmosphere may facilitate the formation of cloud droplets by reducing water surface tension
  - ~41% of strains isolated from cloud water are active producers of biosurfactants, 7 % are extremely active

Adapted from Renard et al. ACP (2016), doi:10.5194/acp-16-12347-2016



## Towards biotechnological applications

- 
- Biocontrol agents for vegetal cultures?**  
Promotion of plant growth?
  - Production of therapeutic molecules?**
  - Production of enzymes to recycle and reuse industrial wastes?**
  - Production of food or cosmetic additives?**
  - New species from cloud water may also represent a source of new activities for emerging biotechnological purposes**



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