Impact of COVID-19 Pandemic on Pharmaceutical Industry Microflora Diversity

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1 ABSTRACT

"Speed" is the most frequently cited reason as to why organizations have implemented COVID-19-related changes. The pandemic posed unique challenges globally, including the need to release pharmaceutical products faster. During COVID-19, industries made operational adjustments and put in place new procedures and sanitization processes. What was the impact of these new procedures, new staffing management, behavior (more work on-shift and remote, mandatory frequent hand-sanitization, face masks, gloves, no physical contact between people), and new supply chain/raw material sources on industrial microflora? What new lessons can be learned to move a step forward in the improvement of the quality of pharmaceutical manufacturing?

Microbial identification is a critical piece of Contamination Control Strategy since accurate and reproducible identifications are imperative for risk assessments and mitigations, confident operational decisions, and safe product release. Accurate data can be confidently trended, gathering valuable insight regarding microflora distribution and changes. Modern microbial identification methods, together with the power of data analytics, represent a powerful tool to recognize and respond quickly to changes and industry needs.

2 DATASET

To evaluate possible differences or shifts in microflora diversity from pre- to post-COVID pandemic, we selected data coming from 10 Pharma industries fully outsourcing their identifications to Accugenix® laboratories from 2018 to Jul 2022. A total of 276,046 identifications corresponding to the same number of samples were analysed. Pre-COVID was defined as identifications in 2018 and 2019, whereas post-COVID was defined as identifications in 2020, 2021, and through July 2022. Twenty-eight customers occasionally outsourcing their identifications (typically, in case of No ID obtained with their in-house identification system) were also considered, with a total of 17,848 samples. An initial general comparison between the two datasets was performed to evaluate a possible trend in the number of IDs performed (Fig.1) and possible differences in terms of microflora outsourced for identification from 2018 to Jul 2022 (Fig.2).
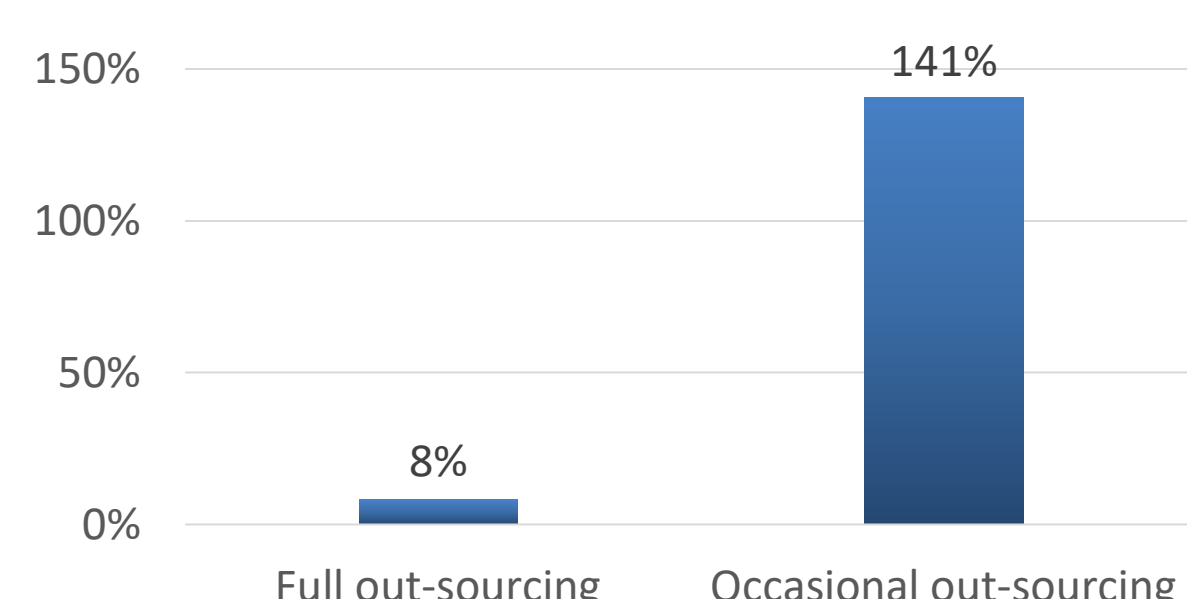

Fig. 1 **Change in the Number of Outsourced Identification Samples PRE- VS. POST-COVID.** Numbers show a general increase in the number of outsourced identifications in post-COVID, especially for occasional out-sourcing companies.
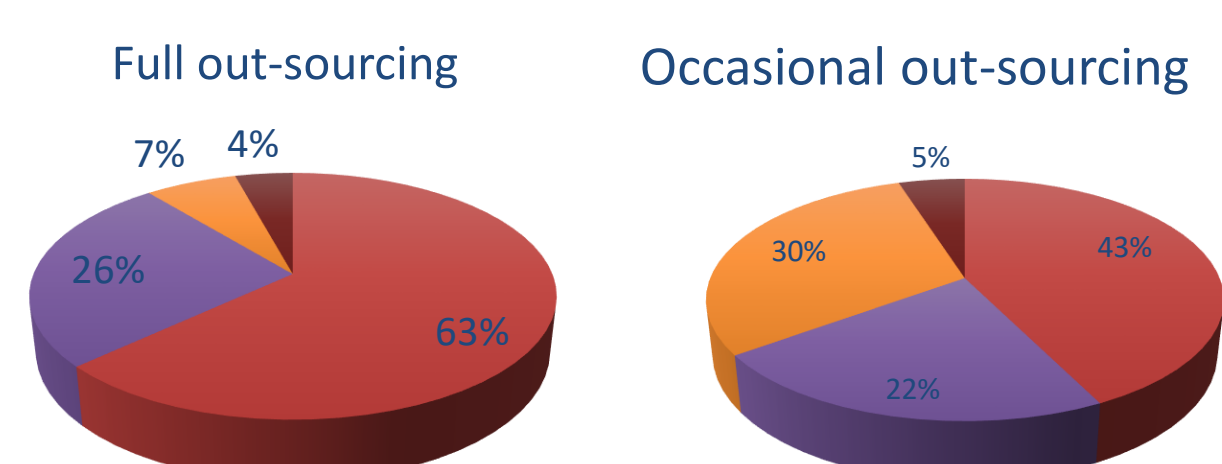
Fig. 2 **Differences in microflora distribution between full and occasional outsourced identifications.** Occasional outsourced samples have a higher proportion of Yeasts and Fungi (Y/FF) compared to Gram positive (Gram +), Gram negative (Gram -) or Gram Variable (Variable) bacteria.

4 CONCLUSIONS

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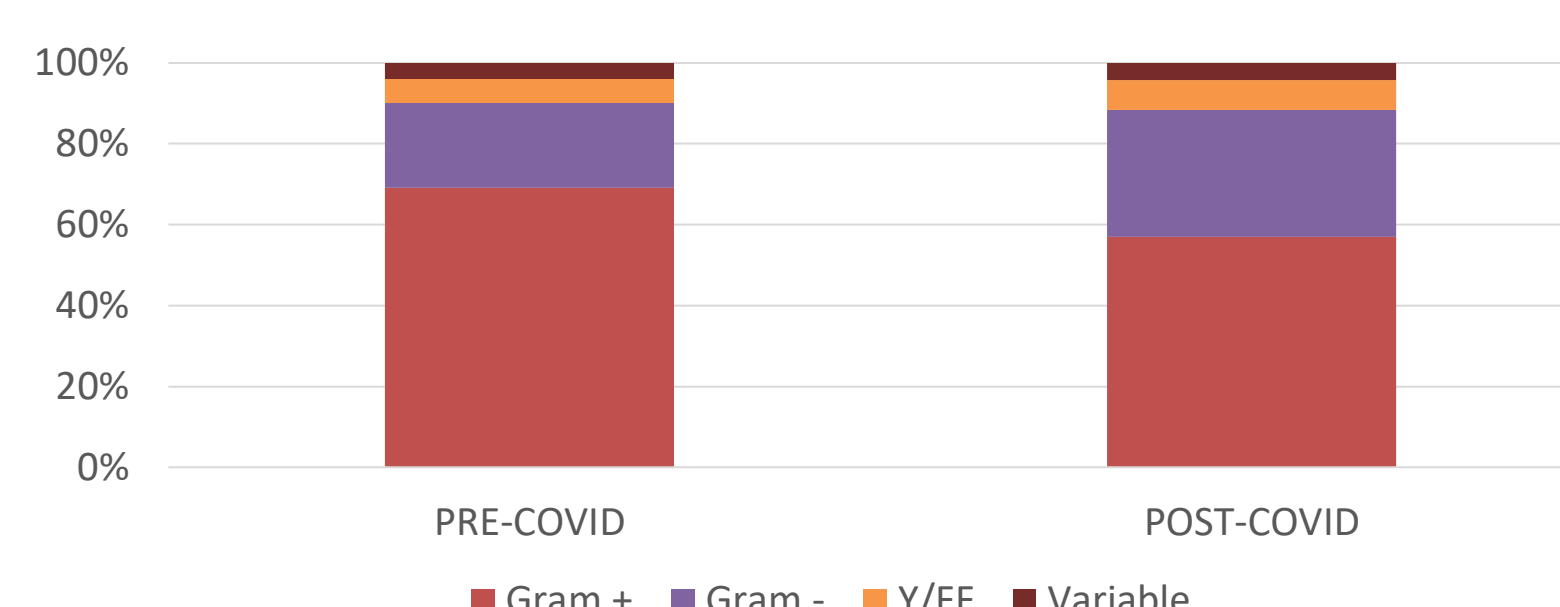## 3 MICROFLORA DIVERSITY PRE- VS. POST-COVID

Fig. 3 **Microorganism Variation (PRE- vs. POST-COVID).** Considering full outsourcing, an increase of Gram-negative microorganisms (+10%) and a relative decrease of Gram positive (-12.5%) was detected. Along with that, a slight increase in fungal samples (+1,5%) and no significant change in Gram variable species.
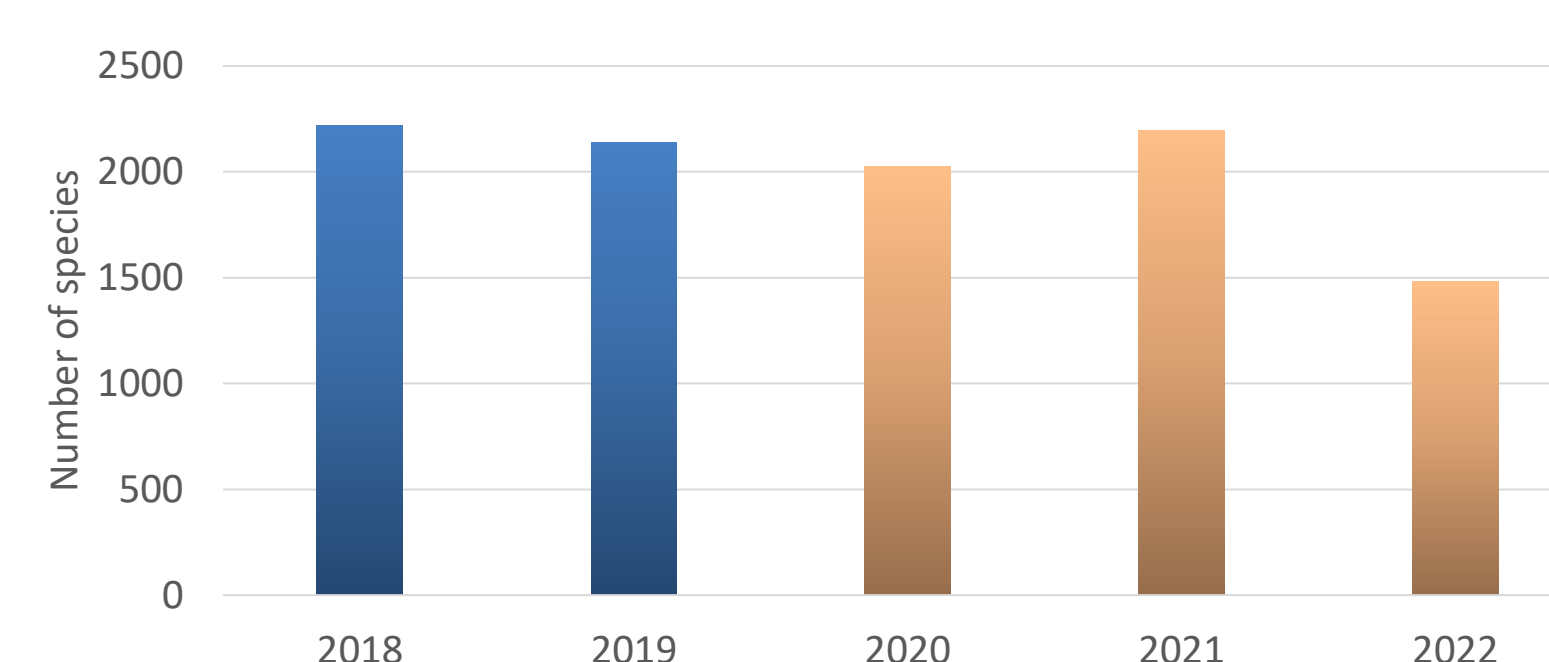

Fig. 4 **Species diversity in Full Outsourcing (2018-Jul 2022).** The number of identified species per year is comparable between the past 4 years. The year 2022 apparently shows less species, but it considers only 7 months for the current study.

Species diversity (total 3929 species)

| 904 | 1978 | 1047 |

PRE-COVID   POST-COVID

Genera diversity (total 864 genera)

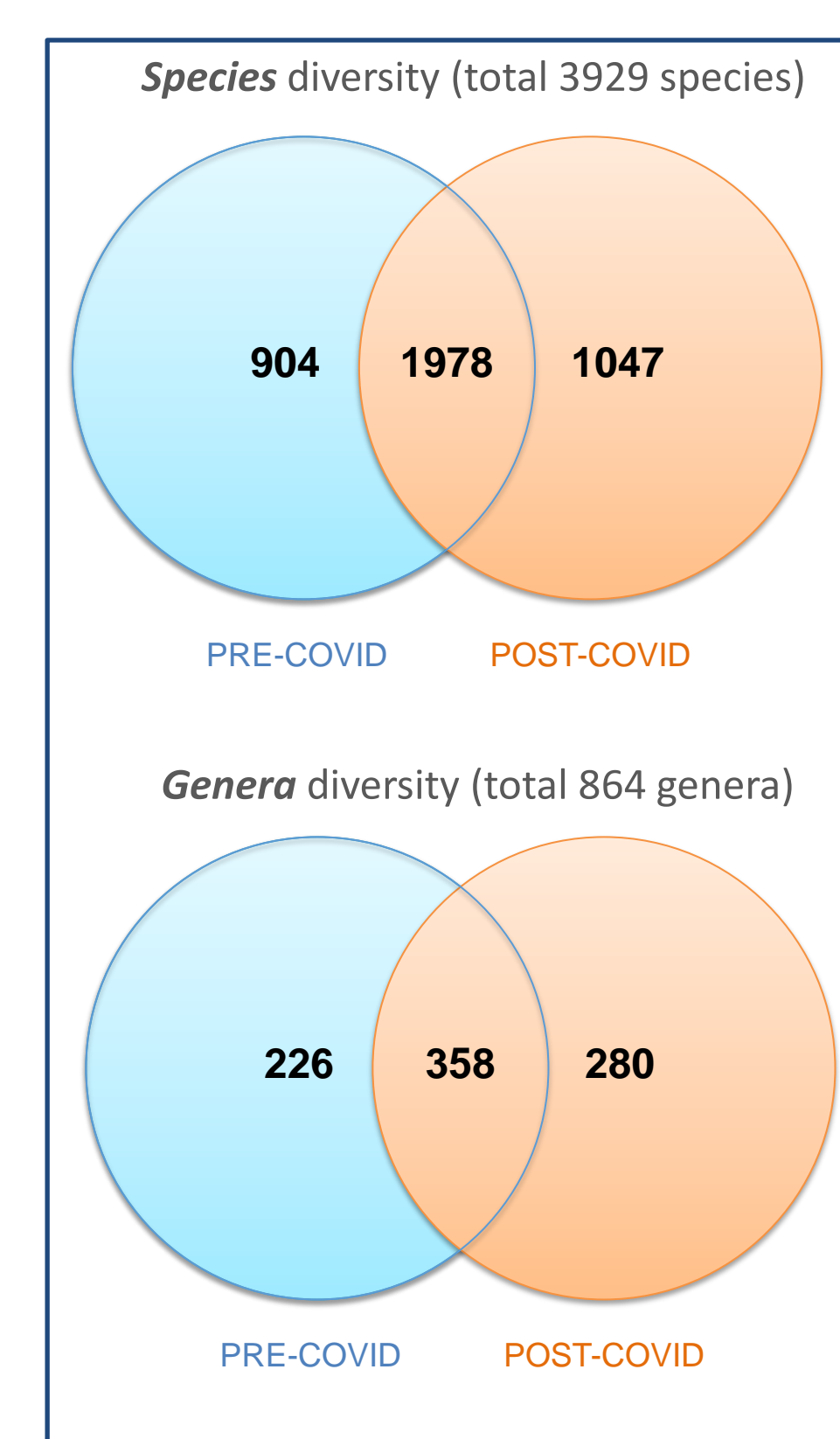| 226 | 358 | 280 |

PRE-COVID   POST-COVID

Fig. 5 **Species and Genera diversity in Full Outsourcing.** Only 1978 Species out of 3929 (left panel) and 358 Genera out of a total of 864 (right panel) were shared PRE- and POST-COVID.

TOP 50 FOO PRE-COVID	TOP 50 FOO POST-COVID
Bacillus	Bacillus
Staphylococcus	Staphylococcus
Micrococcus	Micrococcus
Pseudomonas	Pseudomonas
Corynebacterium	Corynebacterium
Paenibacillus	Paenibacillus
Kocuria	Kocuria
Dermacoccus	Ralstonia
Microbacterium	Serratia
Lysinibacillus	Herbaspirillum
Ralstonia	Microbacterium
Serratia	Sphingomonas
Sphingomonas	Stenotrophomonas
Penicillium	Lysinibacillus
Stenotrophomonas	Klebsiella
Klebsiella	Penicillium
Brevibacterium	Aspergillus
Streptococcus	Burkholderia
Methylobacterium	Cladosporium
Aspergillus	Enterobacter
Acinetobacter	Methylobacterium
Enterobacter	Pseudomonas(Stenotrophomonas)
Dietzia	Bradyrhizobium
Moraxella	Moraxella
Burkholderia	Acinetobacter
Cladosporium	**Paraburkholderia**
Ochrobactrum	**Delftia**
Pseudomonas(Stenotrophomonas)	Dietzia
Wickerhamomyces	**Psychrobacter**
Gordonia	Wickerhamomyces
Bradyrhizobium	Candida
Brevundimonas	Streptococcus
Janibacter	Dermacoccus
Brachybacterium	Enterococcus
Kytococcus	Mycobacterium
Mycobacterium	Brevibacterium
Achromobacter	Achromobacter
Candida	Pelomonas
Leifsonia	Kytococcus
Calidifontibacter	Ochrobactrum
Rothia	Cupriavidus
Enterococcus	**Acidovorax**
Pelomonas	Brevundimonas
Aureobasidium	Brachybacterium
Propionibacterium(Cutibacterium)	**Aerococcus**
Pantoea	Janibacter
Rhodotorula	**Halomonas**
Arthrobacter	**Oceanobacillus**
Cupriavidus	Alternaria
Herbaspirillum	**Macrococcus**

Fig. 6 **Analysis of the TOP 50 genera recovered PRE- and POST-COVID.** The first 7 species are in the same rank in both periods. However, 9 Genera recovered in PRE-COVID are no more in the TOP 50 POST-COVID Genera list. Similarly, 9 new Genera ranked up it the TOP 50 POST-COVID Genera list.