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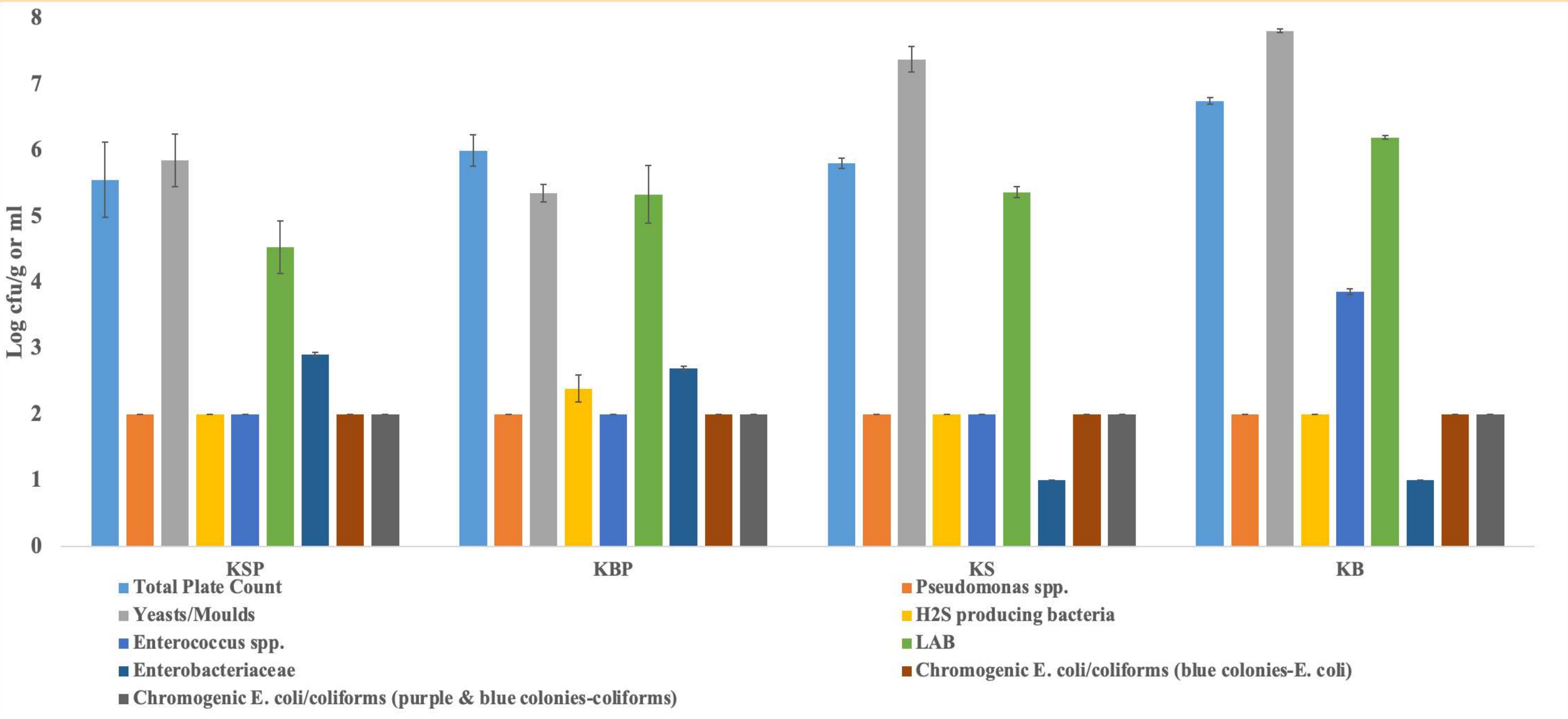
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Aim

The global food sector is being experienced a significant shift toward plant-based alternatives, driven by the nowadays consumer awareness of health and sustainability concerns. Among others, plant-based kefir has emerged as a promising case, harmonizing to broader trends of scientific interests, consumer demands and producers attempts to meet the needs of individuals with lactose intolerance, dairy allergies, vegan preferences, etc. This work aims to shed light on the microbiota profile of plant-based kefir produts by classical and molecular methods, constituting a first attempt in understanding the microbial ecology of such products.

Method

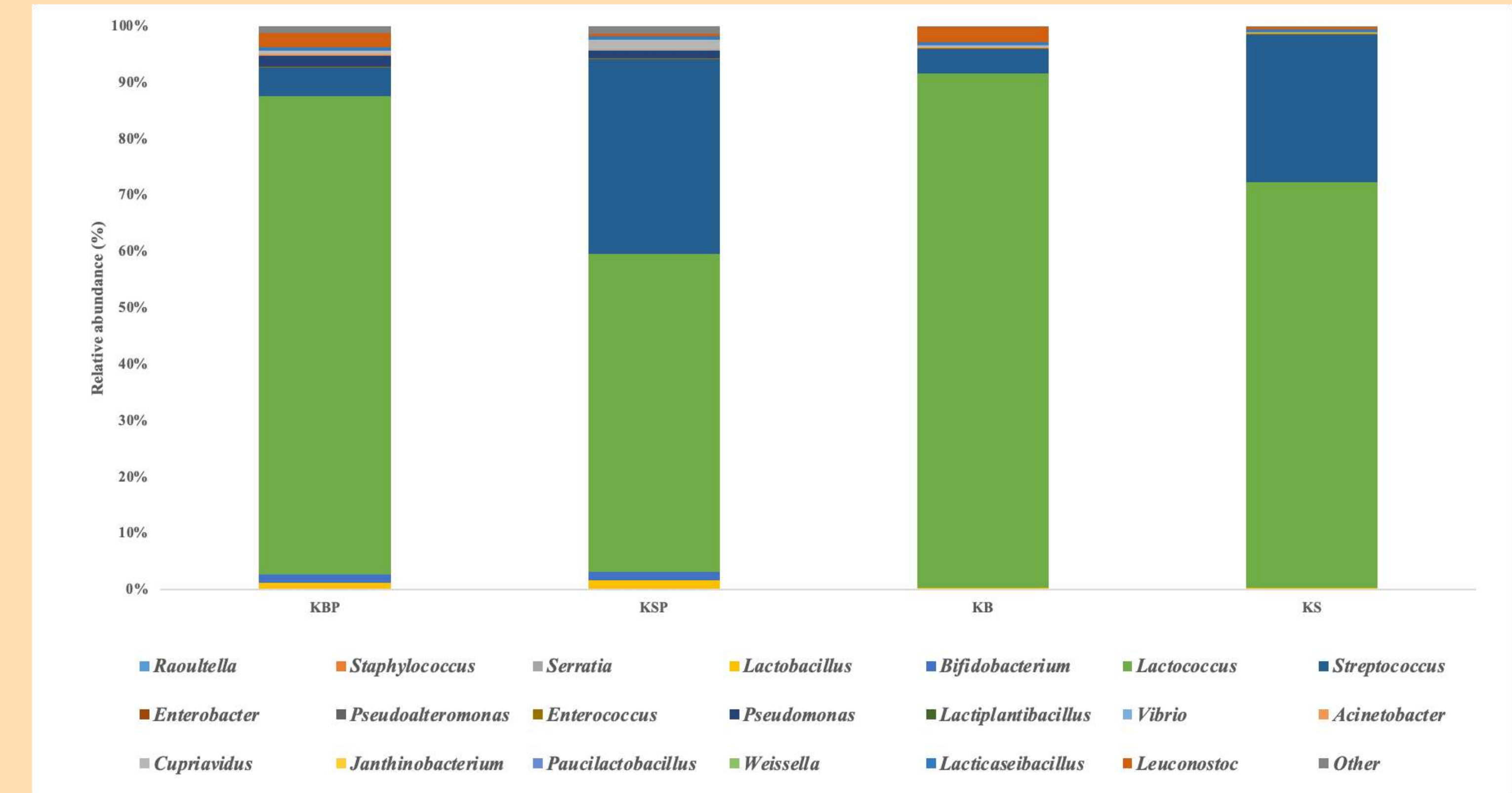
Kefir of both animal (milk/milk with fruits) and plant origin (soy/soy with fruits) were purchased from the market and analyzed via culture-based (Total viable counts, Lactic acid bacteria, yeasts/moulds, Enterobacteriaceae, *Enterococcus*) and culture-independent techniques. DNA was extracted directly from the samples, followed by the amplification of V3-V4 region of 16S rRNA and ITS 1-2 loci for bacterial and fungal diversity, respectively.



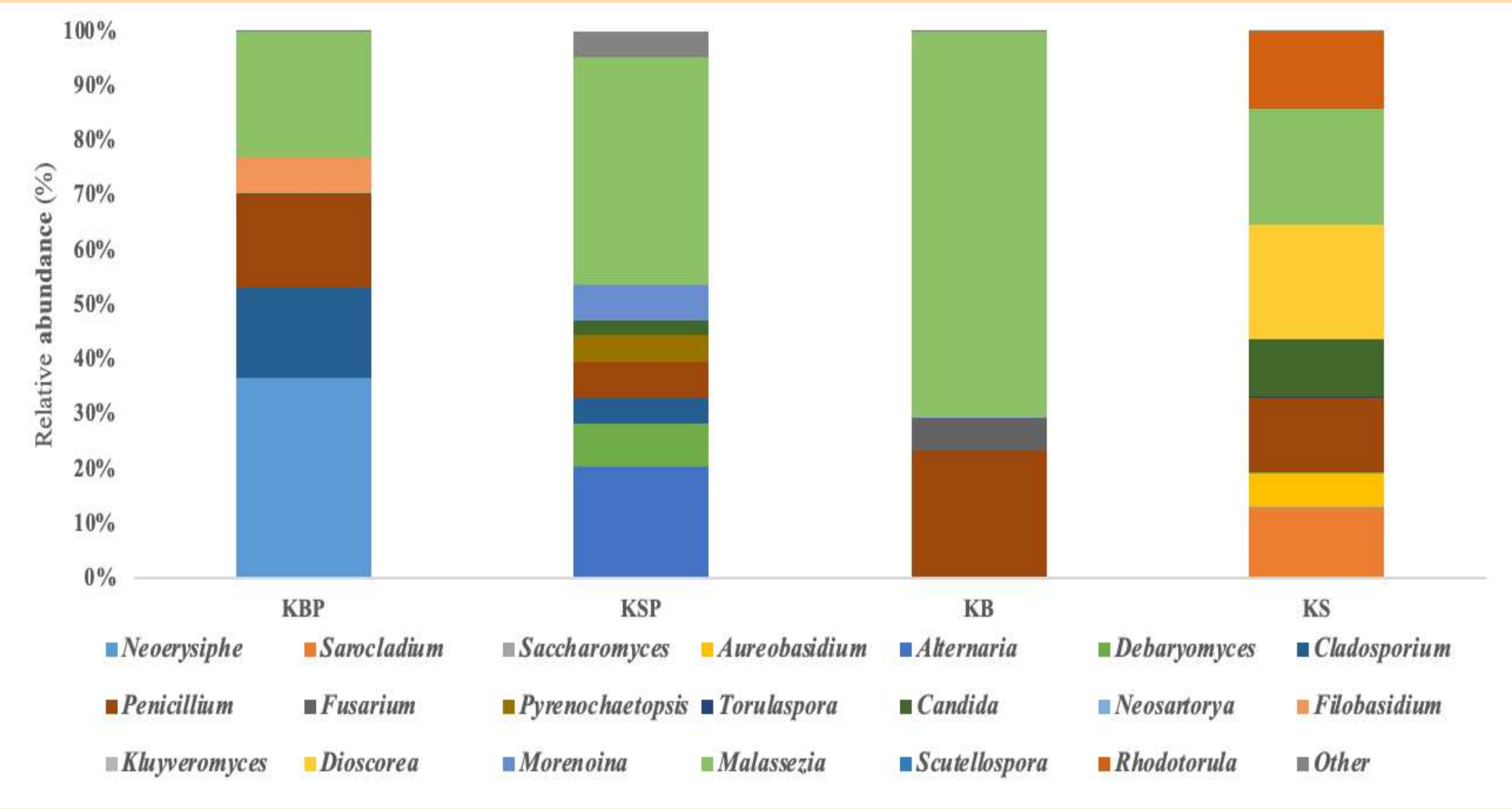
**Fig. 1:**Microbial population changes of dairy and plant-based dairy products (KSP: Plant-based Kefir, KBP: Plant-based Kefir with blueberry and cherry, KS: Dairy Kefir, KB: Dairy Kefir with blueberry). Total Viable Counts (TVC), *Pseudomonas* spp., H2S producing bacteria, LAB, yeasts, Enterobacteriaceae, *E. coli*/Coliforms. Each point is the mean of three replicates. Error bars represent the standard error.

Results

Classical microbiological analysis revealed the undisputed dominance of yeasts, followed by LAB. Metabarcoding analysis showed a very similar bacterial profile among the studied samples, since *Lactococcus* was by far the most abundant genus in all cases, while the presence of *Streptococcus* was more limited. Notwithstanding, fungal analysis indicated a noteworthy different profile among the samples, since *Malassezia* followed by *Penicillium*, and *Malassezia* followed by *Dioscorea* were the dominant fungi in dairy kefir and dairy kefir with fruits, respectively. Oppositely, genera such as *Neoerysiphe*, followed by *Malassezia*, *Penicillium* and *Cladosporium* were detected at high abundances in plant-based kefir with fruits, while *Malassezia*, followed by *Alternaria* and *Debaryomyces* were found in plant-based products without fruits.



**Fig. 2:** Relative abundance (%) of fungal genera of dairy and plant-based dairy products as revealed by ITS metabarcoding analysis (KSP: Plant-based Kefir, KBP: Plant-based Kefir with blueberry and cherry, KS: Dairy Kefir, KB: Dairy Kefir with blueberry.)



**Fig. 3:** Relative abundance (%) of bacterial genera of dairy and plant-based dairy products as revealed by 16S rRNA metabarcoding analysis. (KSP: Plant-based Kefir, KBP: Plant-based Kefir with blueberry and cherry, KS: Dairy Kefir, KB: Dairy Kefir with blueberry.)

Conclusion

The present work shed light on the microbial composition of plant-based kefir, revealing some noteworthy differences compare to dairy products. These findings could be used as benchmark for better understanding the microbial ecology of this emerging product and contributing to its consistent quality and safety ensurance.

Acknowledgements

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