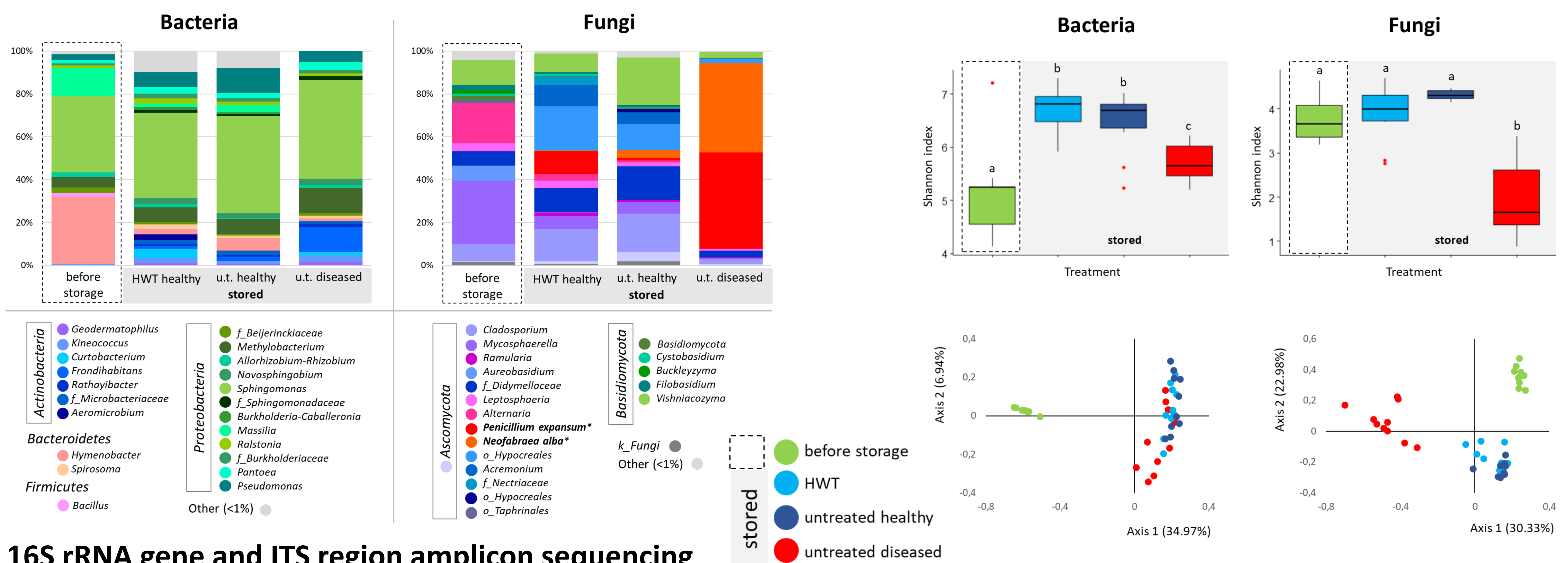


Apple microbiome response to HOT WATER TREATMENT and the potential of BIOLOGICAL CONTROL

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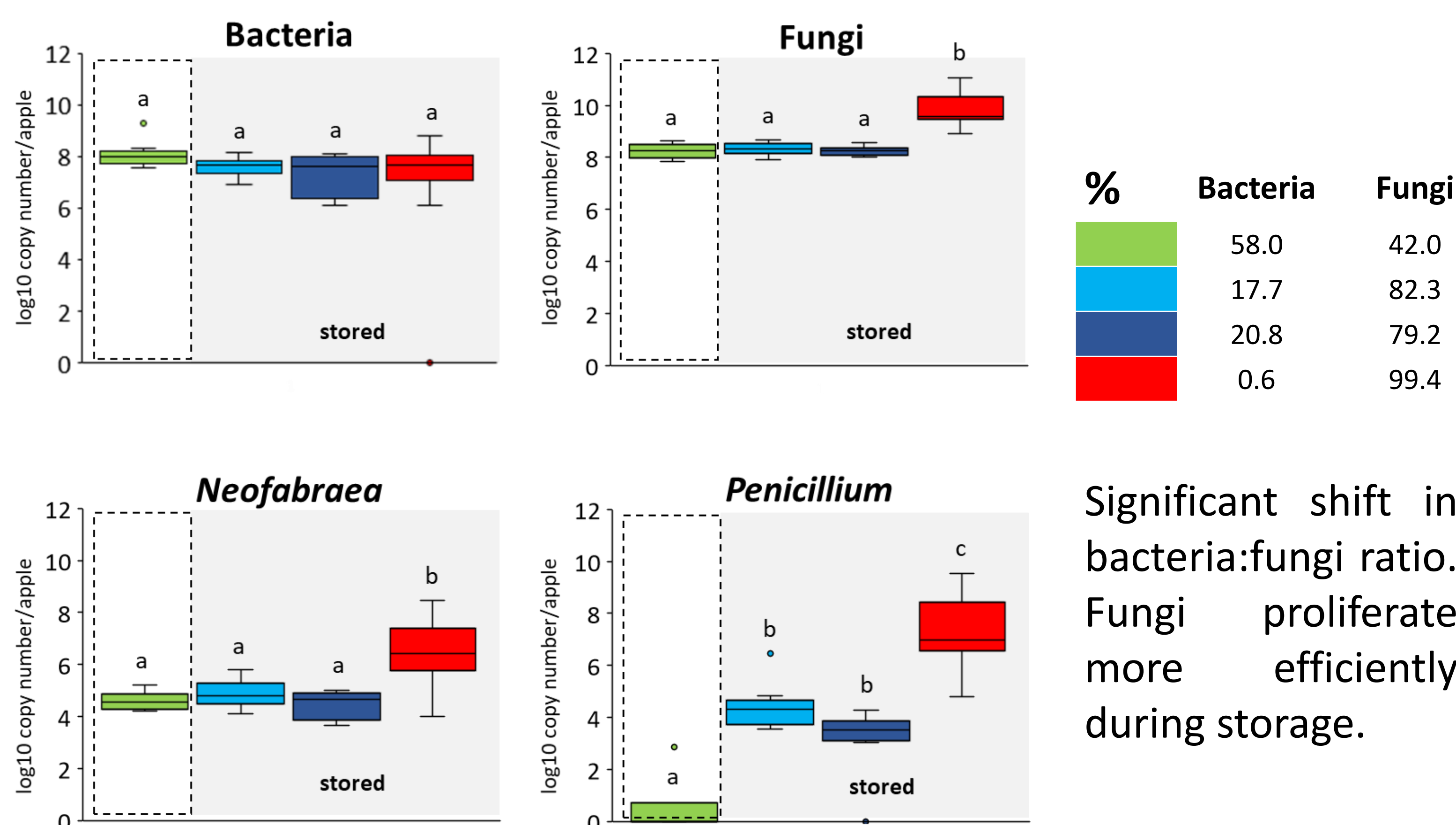
About one third of all produced food is either lost or wasted globally. Especially the postharvest period plays a crucial part and has a lot of potential for improvements. Hot water treatment (HWT), a sustainable method to reduce pathogen-induced postharvest fruit decay, has been proven to be effective on a variety of crops. However, the microbiome response to HWT is still unknown and the role of postharvest microbiota for fruit quality is

largely unexplored. The present study provides the first investigation of the apple microbiome changes induced by the currently in-use HWT on an industrial scale. Additionally, the indigenous apple microbiome was harnessed for biocontrol agents to combat postharvest pathogens *Penicillium expansum* and *Neofabraea sp.* Their additive protective effect as well as their applicability in the HWT process was evaluated.



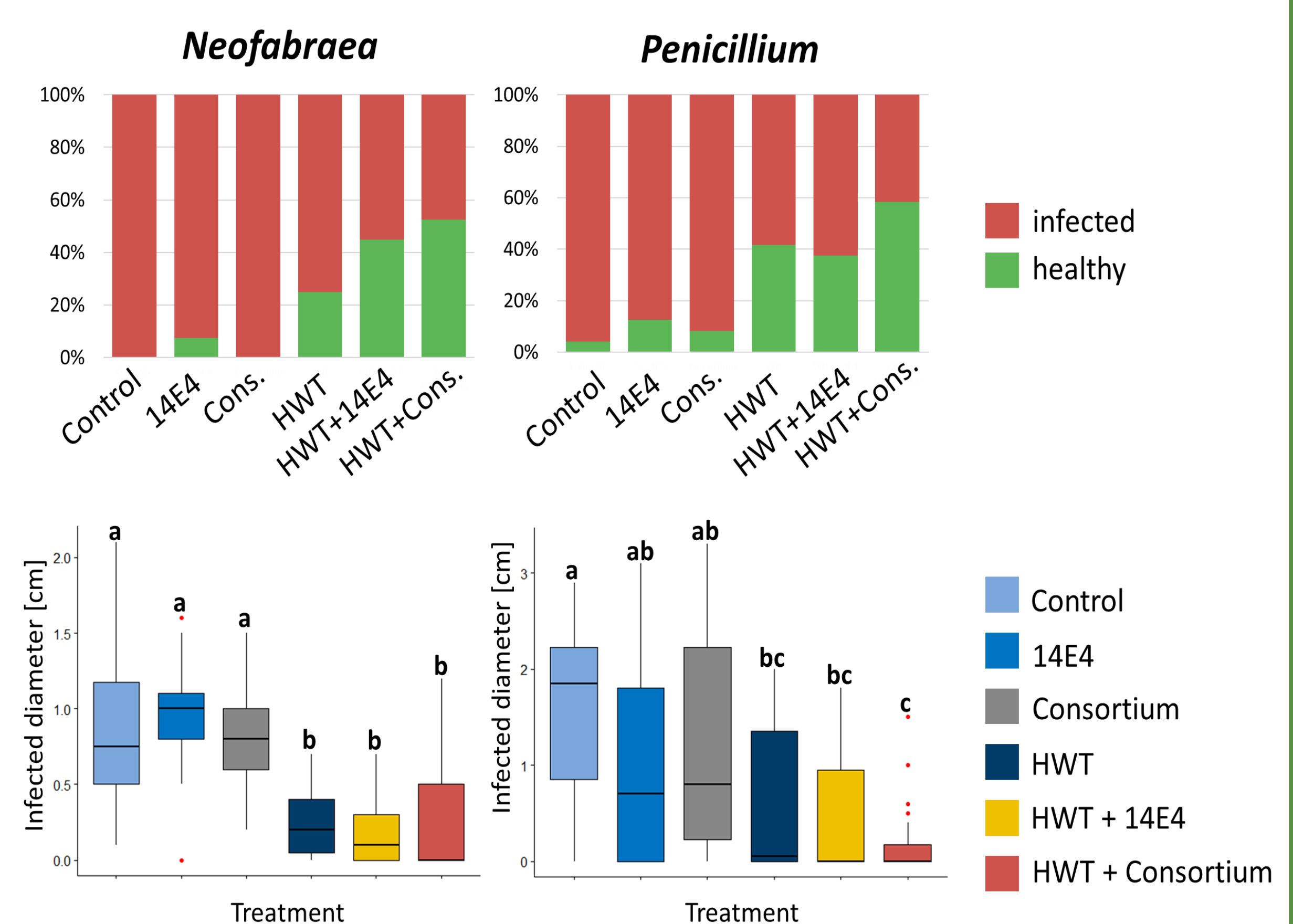
16S rRNA gene and ITS region amplicon sequencing

HWT was effective in reducing rot symptoms on the industrial scale. Efficiency was rather due to induced plant response than due to alterations of the microbiome. Fungal microbiota was only slightly, and the bacterial microbiota insignificantly affected by HWT. Pathogen infection significantly decreased bacterial and fungal diversity: 90% of the fungal community was covered by co-occurring storage pathogens *N. alba* and *P. expansum*. Bacterial diversity significantly increased during storage.



Quantitative real-time PCR

Bacterial abundance was not affected by storage, HWT and pathogen infestation. Diseased apples showed significantly increased fungal abundance. *Neofabraea* was already present in 'before storage' apples while *P. expansum* was almost absent.



Small-scale storage experiments

Combined approach of HWT and biocontrol consortium (*P. vagans* 14E4, *B. amyloliquefaciens* 14C9 and *P. paractis* 6F3) reduced total infection rates and infection diameter of both pathogens significantly.