

Comparison between swabbing devices in order to analyze the microbial flora found on surfaces of community kitchens by classical microbiology and 16S rRNA amplicon sequencing

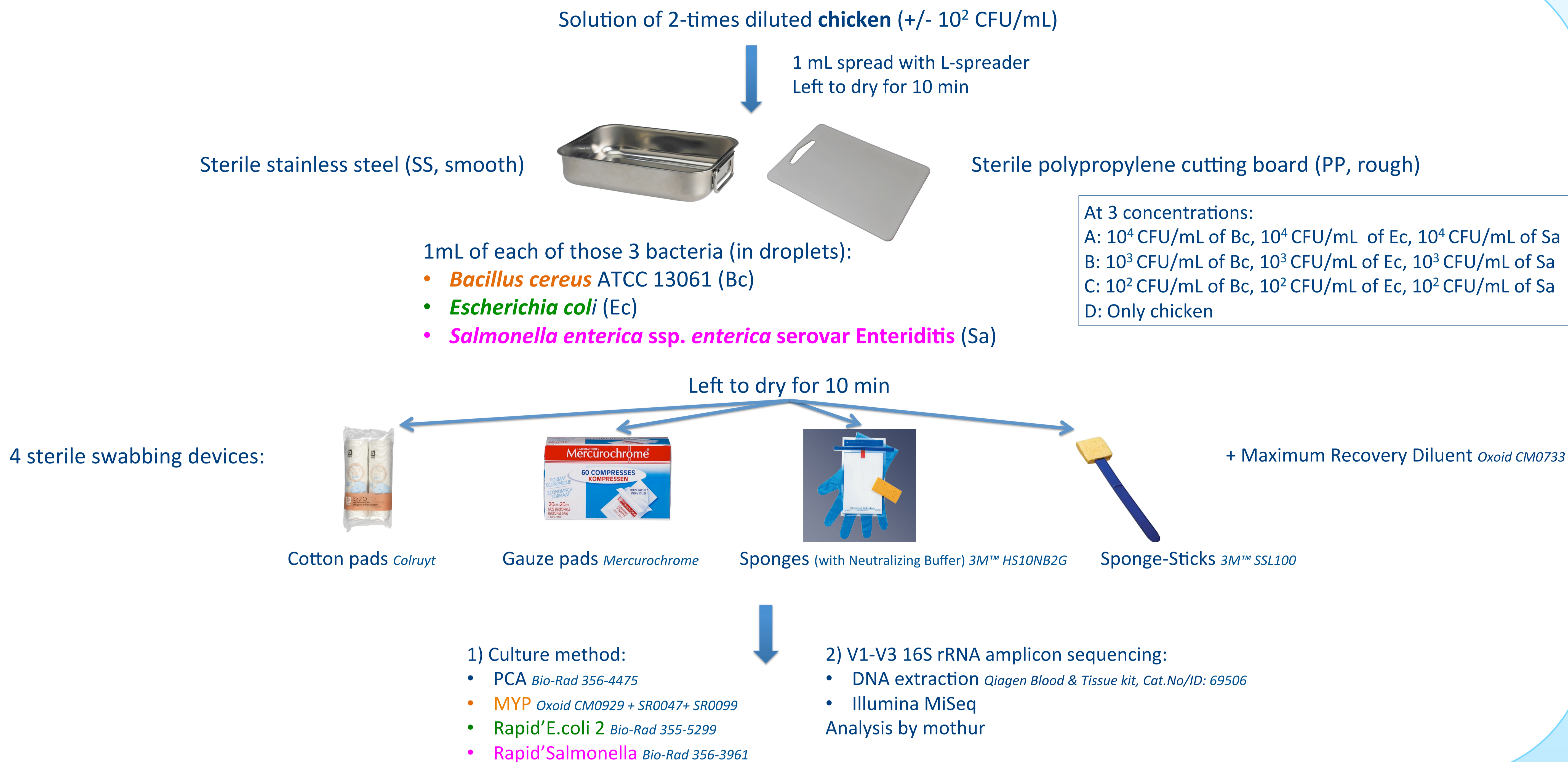
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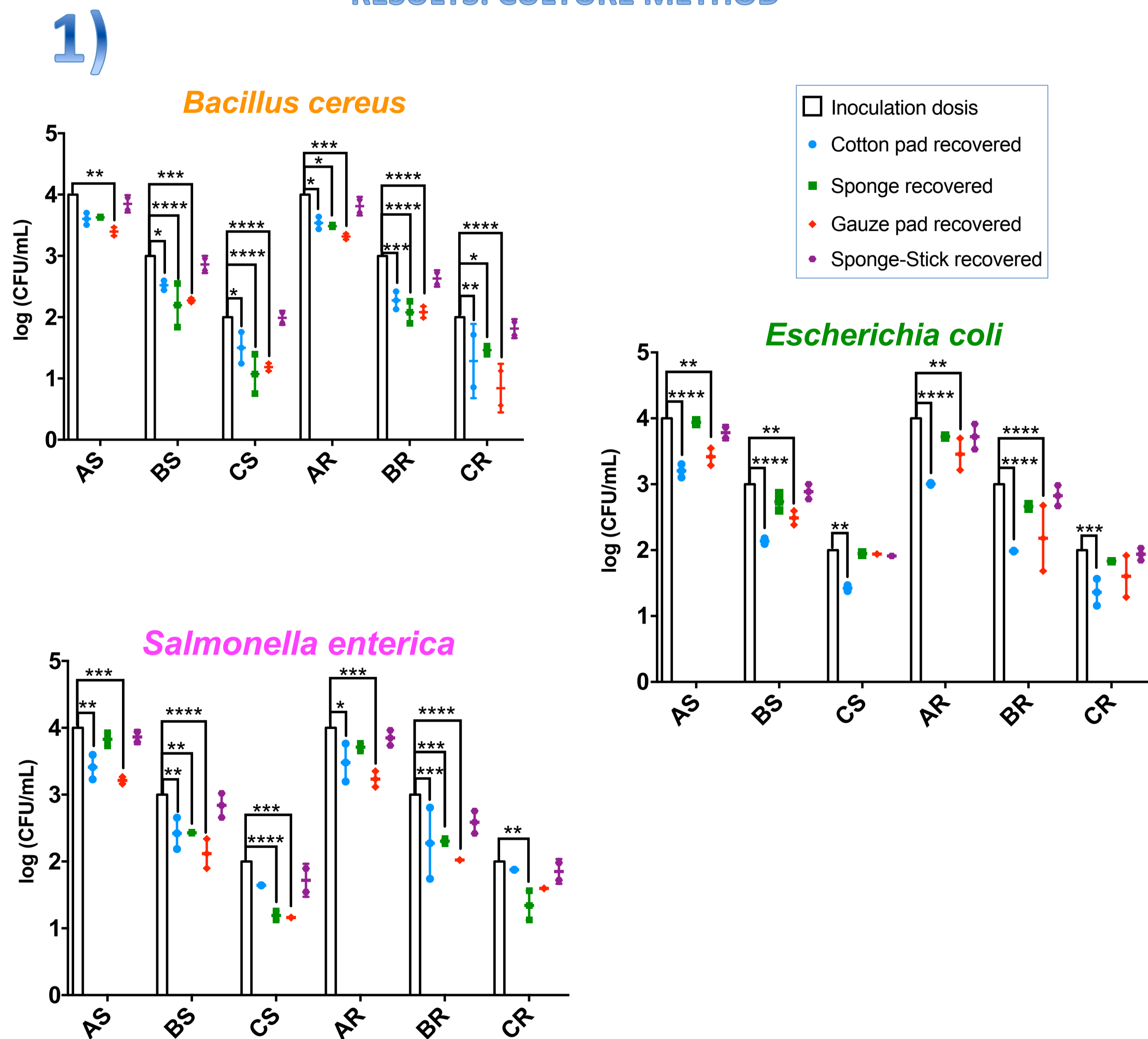
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INTRODUCTION: The work in community kitchens involves several **manual steps** bearing the **risk of transmitting pathogenic microorganisms**. This fact justifies accurate control of surfaces to prevent foodborne illnesses. In this study, the efficiency of different swabbing devices was tested in terms of recovery of microorganisms by **culture methods** and **culture-independent 16S rRNA amplicon sequencing**.

MATERIAL & METHODS:



RESULTS: CULTURE METHOD



Figures 1, 2 and 3. Comparison between inoculation dosis and recovery numbers of *Bacillus cereus*, *Escherichia coli* and *Salmonella enterica*, respectively, by the use of different swabs and different concentrations.

(AS/AR: concentration A (10⁴ CFU/mL) on the smooth/rough surface;
BS/BR: concentration B (10³ CFU/mL) on the smooth/rough surface;
CS/CR: concentration C (10² CFU/mL) on the smooth/rough surface;
CFU/mL: colony-forming unit/milliliter;
* = 0.0332; ** = 0.0021; *** = 0.0002; **** < 0.0001;
†: Each sample was realized in duplicate;
2-way ANOVA and Tukey's multiple comparisons performed with Prism 7)

RESULTS: 16S rRNA AMPLICON SEQUENCING

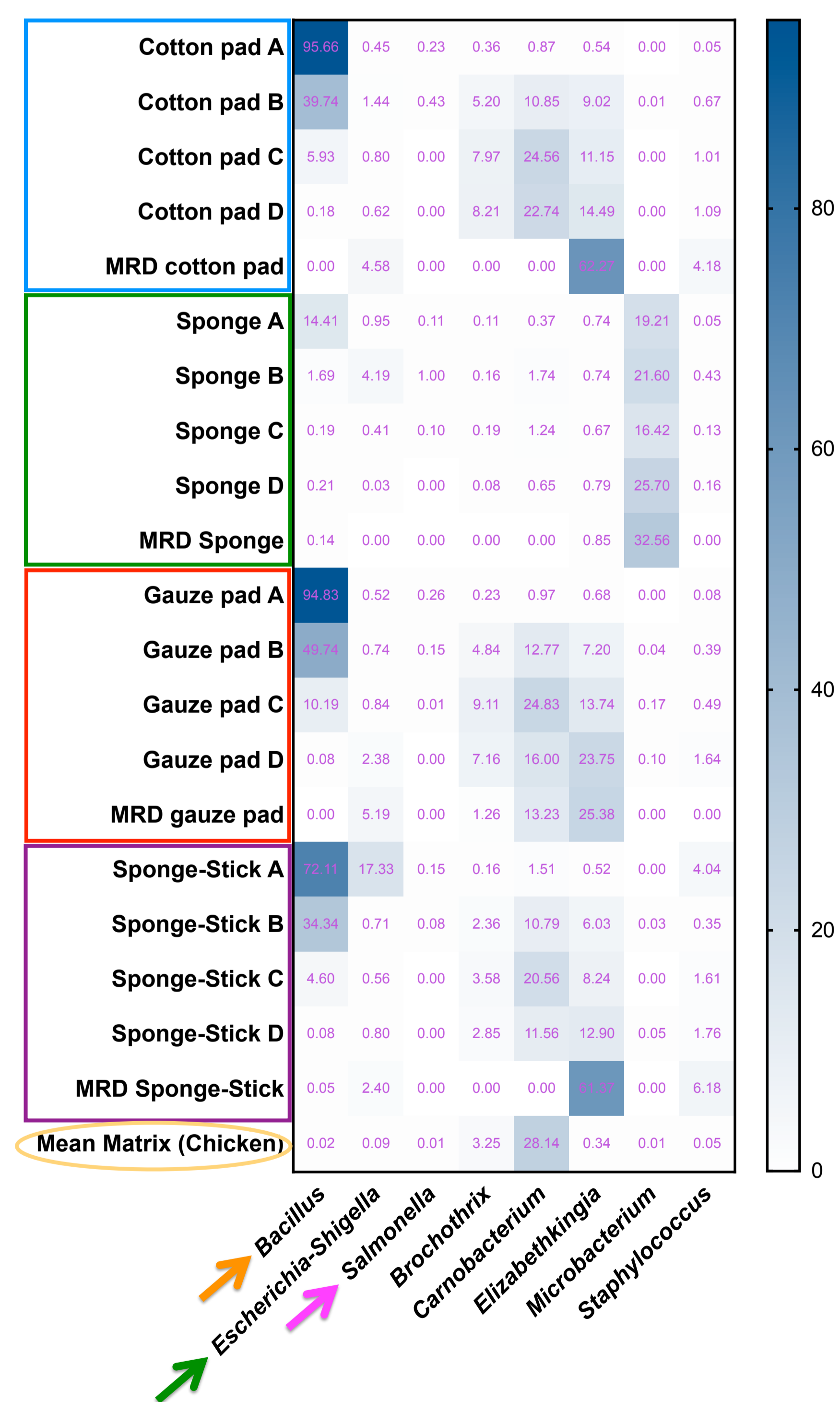


Figure 4. Relative abundance of selected bacterial genera in samples of several concentrations on surfaces recovered with different swabs.

(†: Each result was composed by the mean of 4 samples; Heatmap realized with Prism 7)

CONCLUSIONS:

The perfect swab for kitchen analyses should recover the **highest number of viable bacteria** with a **high population diversity** from the surfaces. Classical culture method showed best recovery numbers for the 3 inoculated bacteria with Sponge-Sticks (no significant difference between inoculation dosis and recovered number of bacteria, $p > 0.1234$). The 16S rRNA amplicon sequencing allows to conclude that sponge samples were loaded with *Microbacterium* genus (from Neutralizing buffer). Furthermore, a **high relative abundance** of *Bacillus* genus was found in cotton pad, gauze pad and Sponge-Stick samples. *Salmonella* genus was detected in only **low proportions**, whereas *Escherichia* genus are problematic as their DNA can be **contaminants of reagents** used during library creation. However, differences in recovery or enumeration with each method must be considered, as they can induce estimation bias on the initial concentration or recovered CFU/mL. Finally, low amount of DNA in controls lead to the emergence of free DNA contaminants like *Elizabethkingia* population, which can be considered as a bias. Further studies will be performed to **assess the recovery of bacteria after longer drying times** in order to approach real kitchen conditions and make the final swab decision.