

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

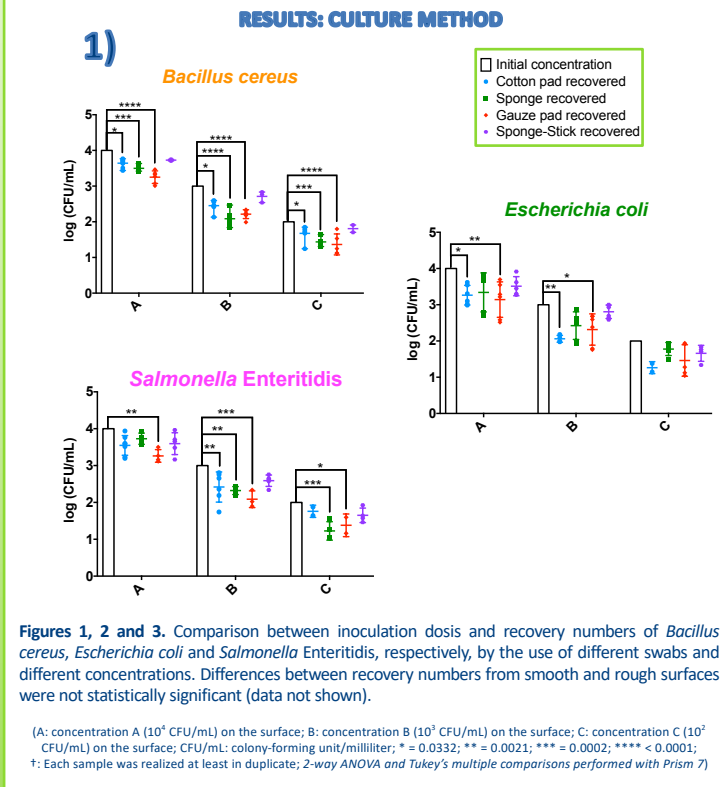
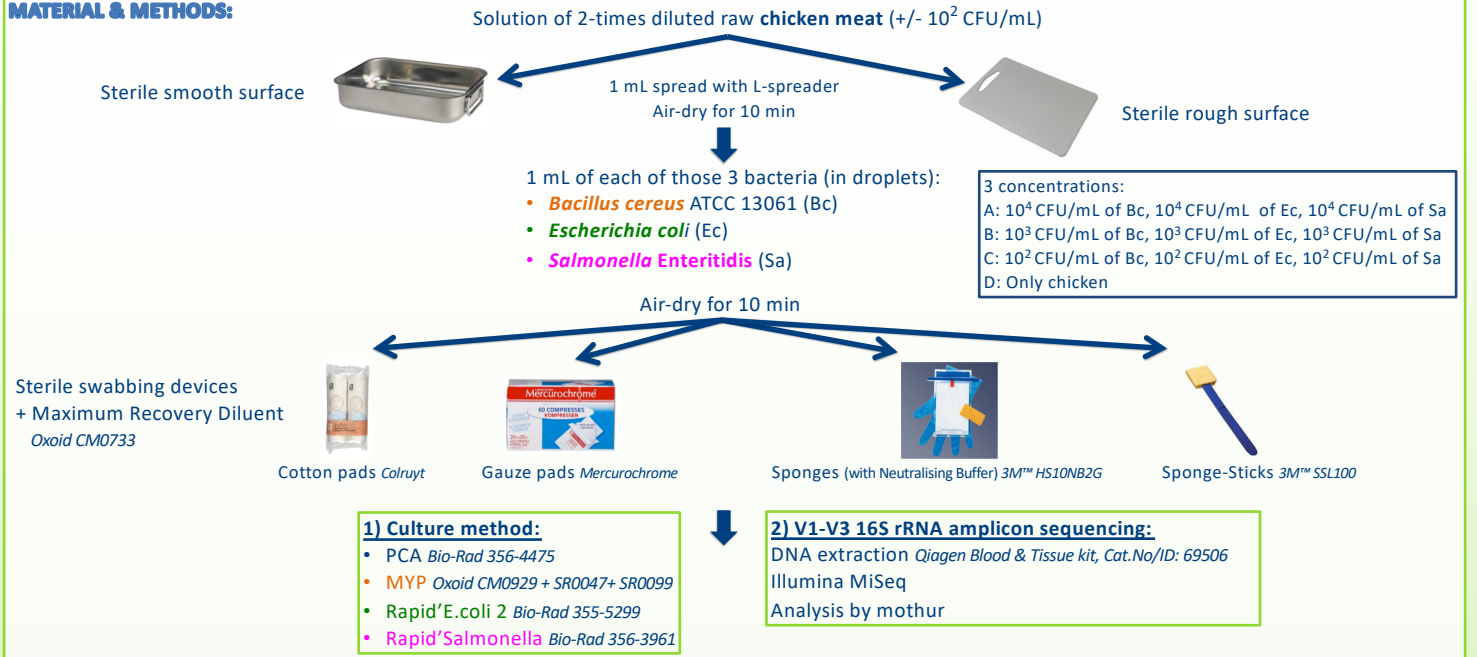
Krings S.^{*1}, Crèvecoeur S.¹, Rodriguez C.¹, Fall P. A.², Taminiou B.¹, Daube G.¹

¹University of Liège, Faculty of Veterinary Medicine, Department of Food Science & FARA, Liège, Belgium
²Genalyse Partner SA, Herstal, Belgium

*skrings@ulg.ac.be

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 sampling devices was tested in terms of recovery of microorganisms by culture methods and culture-independent 16S rRNA amplicon sequencing.

MATERIAL & METHODS:



Figures 1, 2 and 3. Comparison between inoculation dosis and recovery numbers of *Bacillus cereus*, *Escherichia coli* and *Salmonella Enteritidis*, respectively, by the use of different swabs and different concentrations. Differences between recovery numbers from smooth and rough surfaces were not statistically significant (data not shown).
 (A: concentration A (10² CFU/mL) on the surface; B: concentration B (10³ CFU/mL) on the surface; C: concentration C (10⁴ CFU/mL) on the surface; CFU/mL: colony-forming unit/milliliter; * = 0.0332; ** = 0.0021; *** = 0.0002; **** < 0.0001; †: Each sample was realized at least in duplicate; 2-way ANOVA and Tukey's multiple comparisons performed with Prism 7)

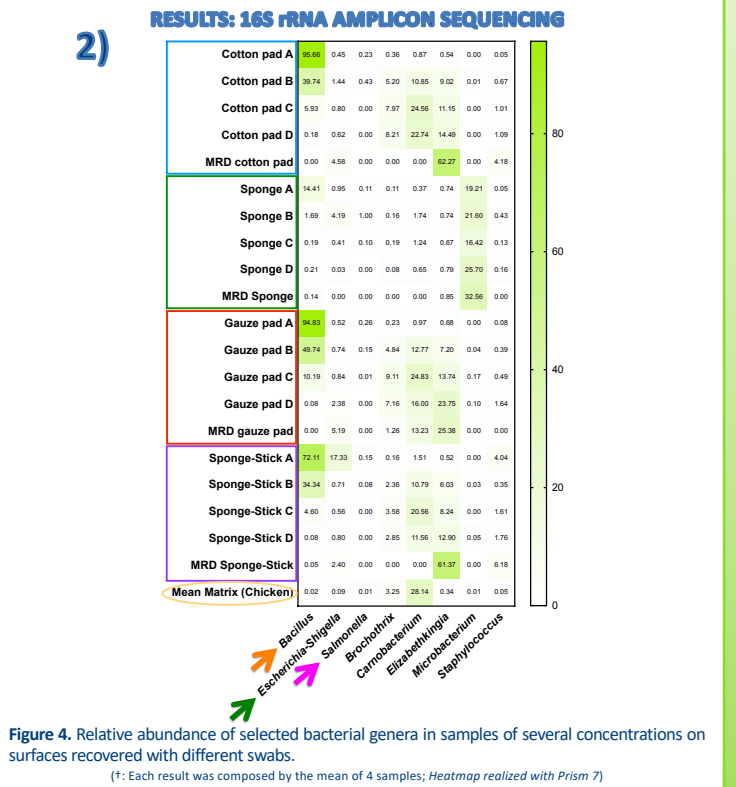


Figure 4. Relative abundance of selected bacterial genera in samples of several concentrations on surfaces recovered with different swabs.
 (†: Each result was composed by the mean of 4 samples; Heatmap realized with Prism 7)

CONCLUSIONS:

The perfect swab for kitchen analyses should recover the highest number of viable bacteria with a high population diversity from the surfaces. First of all, the difference of recovery from smooth or rough surfaces was not statistically significant (data not shown). 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 allowed to conclude that sponge samples were loaded with *Microbacterium* genus (from Neutralising 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 coli* 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 amounts of DNA in controls lead to the emergence of free DNA contaminants like *Elizabethkingia* population, which can be considered as a bias. In the end, these results attest the similarity of population diversity and good recovery numbers in cotton pad and Sponge-Stick samples, leaving the final choice to the operator.