Combination of the Finite Elements Method (FEM) and kinetic models to simulate microbial inactivation during cooking of a solid food product

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Background

The application of predictive models to ensure the safety of cooking conditions has gained popularity during the last years. However, due to the thermal inertia of solid food products, the temperature is heterogeneous in the product during cooking. Most models overcome this issue using the conservative assumption that the temperature in the whole product is the one of its coldest point. This results in an overprocessing of the product, which may have a negative impact on sensorial quality. The aim of this research was to develop a kinetic model for microbial inactivation in chicken meat linked to a protocol that takes into account the temperature distribution in the meat during cooking.

Objectives

- Definition of an experimental protocol to analyze microbial inactivation during cooking of solid food matrixes (applied to meat).
- Development of a computational model for the temperature transfer in meat during cooking.
- Development of a predictive model for inactivation of *Listeria monocytogenes* during cooking combining microbial kinetics and a 3D heat transfer model.

Thermal model

The domain of the FEM model includes the meat and the surrounding water bath. Water temperature control and heat transference between the two media are considered in the model. The specific heat capacity of chicken meat was determined using a differential scanning calorimeter (Mettler Toledo). The density was calculated from the diameter of the sphere which was 3 cm, which was measured with a Vernier caliper. The thermal conductivity of the meat was obtained using data available in the literature.

The mathematical model was validated experimentally. Samples of chicken meat of 25g with an spherical shape were suspended in a water bath at different temperatures. The model predictions were compared against the temperature measured in the center of the sample using a thermocouple.

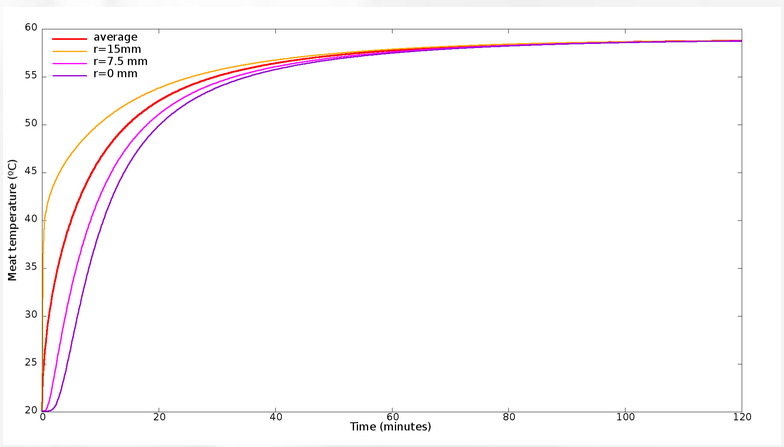

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Figure 1. CFD simulation of the temperature field within the meat during cooking. Scan the QR code for a link to the video.

Microbial kinetics

The inactivation kinetics of *L. monocytogenes* in chicken meat was described using an empirical model. Samples of spheres of minced meat of 25 g and 3 cm in diameters were made. Small spheres of calcium alginate were made (the size of a drop made with a Pasteur pipette), where a concentration of *Listeria monocytogenes* of 10^8 CFU / mL was inoculated. The calcium alginate sphere was introduced into the "cold point" of the meat sphere (1.5 cm). Lastly, the meat balls were placed inside a Stomacher bag. The bag was then introduced in a water bath at the desired temperature during pre-set times. Treatments were carried out at four different temperatures: 53.6ºC (125 min), 56ºC (60 min), 59.5ºC (10 min) and 62ºC (5 min). For all the treatments, at least 6 log-reductions in the count of *L. monocytogenes* were attained.

The microbial counts were described using the Geeraerd model. A secondary log-linear model was defined to describe the relationship between the D-value and temperature.

$$\frac{dN}{dt} = -\frac{1}{1+C_c}\frac{\ln 10}{D(T)}\left(1-\frac{N_{res}}{N}\right)N$$

$$\frac{dC_c}{dt} = -\frac{\ln 10}{D(T)}C_c$$

$$D(T) = D_{ref}10^{-\frac{T-T_{ref}}{z}}$$

Tail effects were observed for every pressure tested, indicating that a fraction of the cells are resistant to the treatment. Their value depended on the pressure level, being the highest at 300 MPa (2.48 log CFU/ml). For the remaining pressures, the treatment was able to cause 6 log-reductions of *L. monocytogenes*.

A strong positive correlation was observed between the inactivation rate and the intensity of the treatment. A linear model was fitted to the k_{max} vs pressure plot, with a good fit ($R^2 = 0.91$). Nevertheless, further data points should be required to confirm the secondary model.

3D prediction of microbial inactivation

The microbial inactivation model for the inactivation of *L. monocytogenes* was coupled with the thermal model. The resulting models enables to predict the reduction of the microbial count on each point of the meat product (Figure 2). Therefore, it calculates the microbial inactivation attained on each point of the meat product; i.e. the variability in the inactivation between different points of the product. It is, thus, more insightful than models providing an average microbial inactivation. This information can further improve quantitative risk assessment for solid products.

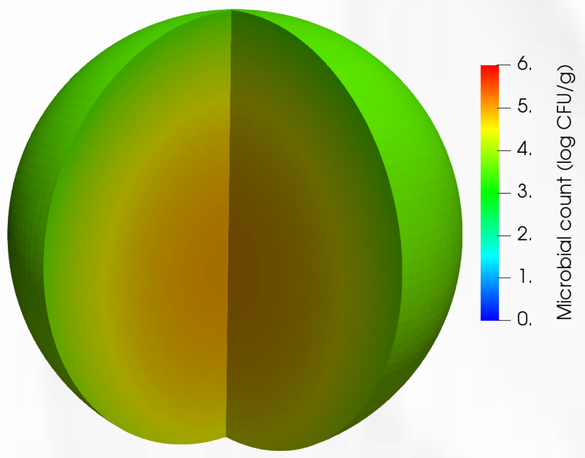

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Figure 2. Simulation of the inactivation in the meat during cooking. Scan the QR code for a link to the video.

Conclusions

- The protocol (experimental and computational) was successful at describing the relevant factors and microbial inactivation.
- The mathematical models provide a more accurate description of cooking than methods based on the "coldest point".
- The tools developed can be applied to optimized cooking conditions for minimally processed food products.

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