ConFerm - A tool to predict the reduction of pathogens during the production of fermented and matured sausages - DTU Orbit (09/11/2017)

ConFerm - A tool to predict the reduction of pathogens during the production of fermented and matured sausages Existing growth models and non-thermal survival models for Salmonella, Shiga-toxin producing Eschericia coli (STEC) and Listeria monocytogenes primarily focus on the static effect of a(w), sodium nitrite (NaNO2), pH and temperature. However, during the production of fermented sausages, the intrinsic factors and temperature change, and there is a need to develop models that can predict pathogen survival under dynamic conditions. The objective of this study was to develop a novel mathematical model for predicting survival of Salmonella, STEC and L. monocytogenes, taking into account the dynamics of the sausage environment during fermentation and maturation of fermented sausages. A total of 73 experiments were carried out in sausages containing different levels of NaCl in the water phase (WPS) (3.9-6.8%), NaNO2 (0-200 ppm) and pH(48h) (4.3-5.6). The minced meat was inoculated with approx. 10(6) cfu/g of a multi-strain cocktail of 3 strains of Salmonella (S. Dublin, S. Typhimurium, S. Derby), 3 strains of STEC (O26:H-, O111:H- and O157) and five L. monocytogenes strains isolated from different meat products and environment. The sausages were fermented at 24 degrees C for 48 h using three different commercially available starter cultures followed by maturation at 16 degrees C until a weight loss of between 15% and 35% was achieved. Enumeration of Salmonella, STEC and L. monocytogenes was performed up to six times during fermentation and maturation, allowing for calculation of the logio reductions at each time point. The microbiological data, together with data for NaNO2 and changes in pH and WPS, were used to develop the "ConFerm" tool, which consists of three separate partial least squares regression (PLS) models for predicting the reduction of Salmonella, STEC and L. monocytogenes, respectively, as a function of weight loss, pH decrease, NaNO2 and WPS.The "ConFerm" tool was validated on a separate data set (n = 19). The Salmonella model had bias and accuracy factors of 1.02 and 1.15, the STEC model 1.04 and 1.24 and the L. monocytogenes model 0.99 and 1.27, respectively, indicating highly acceptable models. In conclusion, the models are applicable for predicting reduction of Salmonella, STEC and L. monocytogenes during the production of fermented sausages fermented at 24 degrees C and matured at 16 degrees C. The model has been made available to producers and other interested parties at http://dmripredict.dk (in English). (C) 2016 Elsevier Ltd. All rights reserved.

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