

Application and Experimental Validation of the TTI Based Chill Chain Management System SMAS for MAP Lamb Products

Petros S. Taoukis, George Katsaros, Eleni Gogou, Thofania Tsironi, Maria Tsevdou

Laboratory of Food Chemistry and Technology, School of Chemical Engineering,
National Technical University of Athens, Greece, taoukis@chemeng.ntua.gr

Ability to monitor storage conditions, from production to consumption, is prerequisite for the optimisation of the chilled distribution of fresh meat products. Time Temperature Integrators (TTI) allow control down to product unit level. A novel chill chain management system, coded SMAS, based on the real quality and risk profile of products, was developed. Structural elements of SMAS are validated predictive models of growth of spoilage and risk microbial indices and kinetic models of TTI response. SMAS uses the information from the TTI at designated points of the chill chain, ensuring that temperature-burdened products reach consumption at acceptable quality level. The objective was to demonstrate the effectiveness of SMAS.

Growth of lactic acid bacteria and *Listeria monocytogenes* in MA packed fresh ground lamb was modelled as a function of temperature and CO₂. Growth was measured on naturally contaminated products inoculated with the pathogen, at isothermal and dynamic conditions from 0 to 15° C. Enzymatic TTI with suitable response were also modelled. 120 products of MA packed ground lamb (20%CO₂), were then used in a chill chain simulation. On half, TTI were attached at packing. All products were stored, in programmed cabinets simulating the conditions of the real chill chain to the consumption point. At the decision point, at 64h from packing, the products were split in half and were stored for 3 different short times and 3 longer times (local and distant market scenaria). The products without TTI were split randomly. Split and further handling of products with TTI was based on their integrated temperature history and the SMAS scheme. According to the final microbiological measurements of all products at “consumption time” the spoilage profile of the products with TTI was significantly improved. 22% of randomly handled samples were spoiled at consumption time (LAB>log8) compared to less than 6% handled with the SMAS approach. Respectively 28% exceeded a set limit for *Listeria* compared to less than 3% handled with SMAS.

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