A FERMENTED MEAT MODEL SYSTEM FOR STUDIES OF MICROBIAL AROMA FORMATION

Karsten Tjener & Lone Andersen, Chr. Hansen A/S, DK-2970 Hørsholm, Denmark
Louise H. Stahnke & Jan Martinussen, Technical University of Denmark, DK-2800 Lyngby, Denmark

Background

During sausage processing, staphylococci produce volatiles that contribute to the characteristic dry sausage flavour (Montel et al., 1998; Stahnke et al. 2001). The aroma formation of staphylococci has been studied in some details (Masson et al., 1999; Stahnke, 1999a & b), but still very little is known about the actual capacity under various processing conditions. Since sausage production is a rather time and labour consuming process, one of the hurdles for obtaining more information on aroma formation is the establishment of a realistic model system.

Objectives

The objective of the study was to evaluate the applicability of a model system as a substitute for dry sausage fermentation when considering microbial aroma formation. An experiment was conducted in which pH and production of volatiles were followed over time in fermented, dry sausages and in a minced meat model system.

Methods

Fast and traditionally fermented sausages and model minces were produced following a standard recipe with starter cultures (*Pediococcus pentosaceus* 355 and *Staphylococcus xylosus* 363) but without spices (pepper, garlic, etc.). 0.1 of ppm manganese substituted the manganese that would have been added with the spices, and half of the minces and sausages were further added 1 of ppm of manganese in order to ensure a fast acidification. Minces were incubated in a water bath at 24°C for 7 days. Sausages were incubated in a climate chamber under controlled temperature and humidity for 21 days (day 0: 24°C, 95 %RH; Day 21: 17°C, 75 %RH). Thus, contrary to the model minces, the sausages experienced a decreasing temperature and water activity course. Samples for aroma analysis were taken on day 0, 1, 3, 7, 14 & 21 (day 14 & 21, sausages only). Volatiles were collected by dynamic headspace extraction onto adsorbent traps (purged with N_2, 50 mL/min. at 42°C for 30 minutes), subsequently identified and quantified (standard addition) by GC-MS. Two separate principal component regression (PCR) analyses were conducted with the quantified volatiles as X-variables and a set of binary Y-variables containing relevant sample information.

Results and discussion

In Figure 1 pH-measurements from fast and traditionally acidified sausages and model minces are presented. The pH profiles of fast fermented sausages and minces are similar, whereas the traditionally acidified sausages have a slightly higher pH towards the end of fermentation than the corresponding model minces.

Figure 2 is a PCR correlation loading plot of the volatiles in the sausage samples. Principal component 1 (PC1) describes variation caused by the time of ripening. It is seen that the levels of most of the components are positively correlated with time, i.e., they are produced during sausage processing. PC2 describes variation caused by two different acidification profiles. Fast acidification is positively correlated with the formation of ketones, sulphides, methyl-branched acids, hexanal and 1-hexanol, whereas traditional acidification is positively correlated with methyl-branched alcohols and aldehydes, their ethyl esters, phenylacetaldehyde and methional.

Figure 3 is a correlation loading plot similar to Figure 2 but with data collected from the model system. PC1 represents variation caused by time, and PC3 represents variation caused by differences in acidification profiles. PC2 (not shown) mainly represents variation caused by a high level of 1-hexanol and hexanal in samples from day 3. As in Figure 2, the traditional acidification is correlated with methyl-branched alcohols and aldehydes, their ethyl esters, phenylacetaldehyde and methional. The fast acidification is correlated with sulphides, methyl-branched acids, 2-pentanone, 1-hexanol and hexanal. Contrary to the sausage data, diacetyl and 2-butanone are not correlated with fast acidification in the model minces. Overall though, the correlation between X and Y data is very similar in Figure 2 and 3 and hence the interpretation of sausage and model data becomes very similar. The model therefore seems to be able to simulate microbial formation of aroma components during sausage production.

Conclusion

A fermented meat model able to simulate aroma formation during dry sausage ripening has been developed.

Literature

Masson, F., Hinrichsen, L., Talon, R. & Montel, M. C. (1999). *International Journal of Food Microbiology* **49**, 173-178.
Montel, M. C., Masson, F. & Talon, R. (1998). *Meat Science* **49**, S111-S123.
Stahnke, L. H. (1999a). *Lebensmittel Wissenshaft und Technologie* **32**, 357-364.
Stahnke, L. H. (1999b). *Lebensmittel Wissenshaft und Technologie* **32**, 365-371.
Stahnke, L. H., Holck, A., Jensen, A., Nilsen, A. & Zanardi, E. (2001). *Journal of Food Science, in press.*

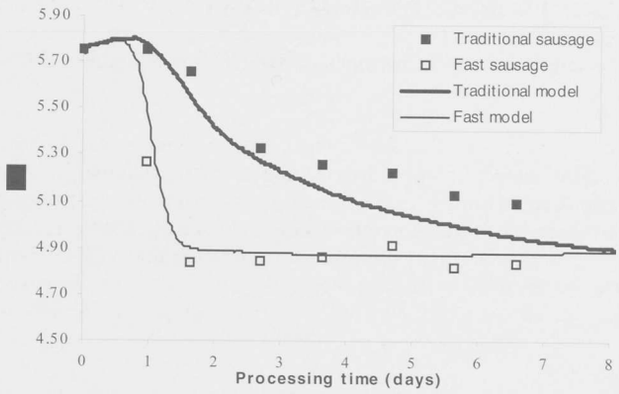

Figure 1: Acidification profiles of fast and slow-fermented sausages and model minces.

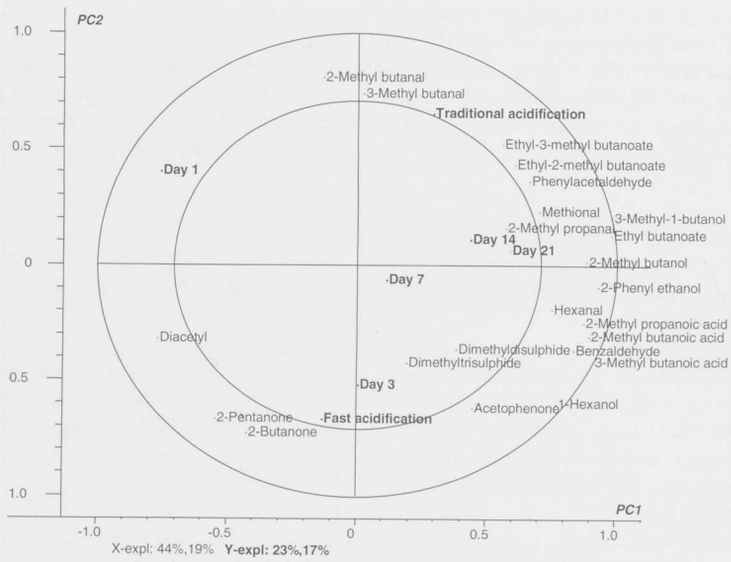

Figure 2: PCR correlation loadings for aroma analysis of **sausages**, day 1-21. Inner and outer circle represents 50 and 100 % explained variance, respectively.

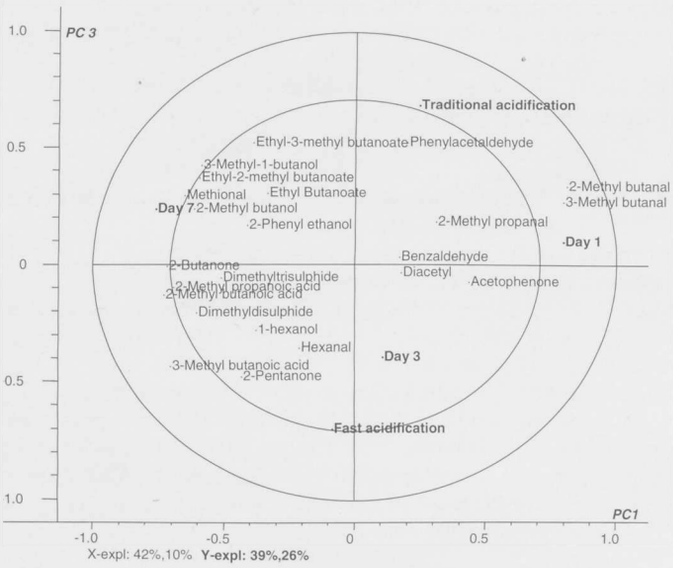

Figure 3: PCR correlation loadings for aroma analysis of **model minces**, day 1-7. Inner and outer circle represents 50 and 100 % explained variance, respectively.