GROWTH OF *BROCHOTHRIX THERMOSPHACTA* AND *PSEUDOMONAS* SPP. ON MEAT UNDER VARIOUS TIME VERSUS TEMPERATURE CONDITIONS

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Background
The chilling and storage of meat is performed under various time versus temperature conditions. Using mathematical models, the growth of bacteria may be calculated for different scenarios. Several models have been published where the effect of temperature and other environmental factors such as pH and water activity may be predicted (Davey, 1989; Gill & Jones, 1992; McClure *et al.*, 1993; Baranyi *et al.*, 1995). *Pseudomonas* spp. and *Brochothrix thermosphacta* are able to reach high numbers on aerobically stored meat, and are, thus, important target bacteria when evaluating the importance of temperature history on the hygienic quality of meat.

Objective
The objective was to evaluate the growth of *Pseudomonas* spp. and *B. thermosphacta* on pork during varying time-temperature profiles, and to compare growth predicted from mathematical models with growth observed on meat.

Methods
Pieces of pork (25 cm^2/sample) excised from *Longissimus dorsi* were put into stomacher-bags, and subsequently incubated at ten time-temperature profiles (Figure 1) in a water-bath. The temperature was monitored using temperature loggers (OML, Danelco, Helsingborg, Sweden). On each sampling occasion (start and end of incubation) two samples were analysed for each temperature profile. Samples were homogenised with 25 ml peptone water and spread onto agar-plates for the enumeration of *Pseudomonas* spp (CFC-agar: cetrimide, fucidin, cephaloridine; incubated 25°C, 48 h) and *B. thermosphacta* (STA-agar: streptomycin, thallous acetate; incubated 30°C, 48 h). The pH-value (PHM82 Standard pH meter, Radiometer, Copenhagen, Denmark) was determined in the homogenate and the water activity (CX-2 wateractivity system, AQUA lab, Deacon Devices Inc., USA) was determined on pieces of pork.

Prediction of the growth of *Pseudomonas* spp. was carried out using the models (Table 2) of Davey (1989), and Gill & Jones (1992), as well as one unpublished model of Gustavsson & Borch. For *B. thermosphacta,* the models of Baranyi *et al.* (1995), and McClure *et al.* (1993), as well as one unpublished model of Gustavsson & Borch were used. The measured temperature histories were divided into finite intervals for which the number of generations was calculated and finally integrated for the whole temperature history.

Results and discussion
The initial count on the naturally contaminated pork was 0.9 ± 0.7 *B. thermosphacta* /cm^2 and 3.4 ± 0.5 *Pseudomonas* spp./cm^2. pH-values and water activities are given in Table 1. The increase in *B. thermosphacta* and *Pseudomonas* spp. was affected by the different time-temperature scenarios. Low increases of *B. thermosphacta* and *Pseudomonas* spp. (< 2 log cfu/cm^2) were found for scenarios 3, 5 and 9 comprising an initial rapid chilling (25°C to 5°C within 10 hours) and/or prolonged storage below 3°C (Figure 1; Table 1). High increases of *B. thermosphacta* and *Pseudomonas* spp. (> 3 log cfu/cm^2) were found for scenarios 1, 6 and 10 comprising an initial slow chilling or prolonged storage at 6°C. Besides the time and temperature, there were also some variations in pH and water activity that may have affected proliferation (Table 1).

Models for predicting the growth of *B. thermosphacta* developed by Baranyi *et al.* (1995) and Gustavsson & Borch, showed high correlations ($r > 0.8$) to the observed growth (Figure 2). The proliferation was over-predicted by the model of Baranyi *et al.* (1995), but under-predicted by the models of McClure *et al.* (1993) and Gustavsson & Borch. The mathematical model for predicting the proliferation of *Pseudomonas* spp. (Figure 3) developed by Gill & Jones (1992) showed a high correlation ($r > 0.8$) to the observed proliferation, while models developed by Davey (1989) and Gustavsson & Borch did not show that high correlation ($0.6 > r < 0.7$). The three models studied for the proliferation of *Pseudomonas* predicted a higher proliferation than observed. Thus, the predicted proliferation from some of the studied models shows a high correlation to the observed proliferation, there was little numerical similarity. However, the models can be used to study the level of proliferation at different temperature histories.

Conclusion
The integrated temperature history must be taken into account for, when assessing the hygienic adequacy of cooling processes. However, the predictive models for *B. thermosphacta* and *Pseudomonas* spp. studied can only be used for rating processes.

Literature
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Table 1. Proliferation of *Pseudomonas* spp. and *B. thermosphacta* on pork at different temperature histories. The pH-values and water activity of the pork are given. (n=4/scenario)

Scenario	Increase of *Pseudomonas* spp. generations	log cfu/cm^2	Increase of *B. thermosphacta* generations	log cfu/cm^2	pH initial ; final	water activity
1	15.2 ± 2.5	4.6 ± 0.8	15.2 ± 3.4	4.6 ± 1.0	5.74 ; 5.74	0.993
2	7.9 ± 2.0	2.4 ± 0.6	10.5 ± 2.1	3.1 ± 0.6	5.50 ; 5.45	0.994
3	1.6 ± 1.2	0.5 ± 0.3	2.2 ± 1.9	0.7 ± 0.6	6.04 . 5.86	0.996
4	5.9 ± 2.5	1.8 ± 0.7	9.5 ± 0.7	2.7 ± 0.2	5.50 ; 5.46	0.994
5	3.9 ± 1.5	1.2 ± 0.4	5.1 ± 1.2	1.5 ± 0.4	5.47 ; 5.46	0.990
6	14.5 ± 2.7	4.4 ± 0.8	12.3 ± 2.7	3.7 ± 0.8	5.74 ; 5.75	0.993
7	1.0 ± 1.5	0.3 ± 0.4	3.7 ± 1.1	1.1 ± 0.3	5.46 ; 5.48	0.991
8	3.5 ± 4.1	1.1 ± 1.2	7.0 ± 1.1	2.1 ± 0.3	5.36 ; 5.33	0.993
9	2.2 ± 2.5	0.6 ± 0.8	4.8 ± 2.4	1.5 ± 0.7	5.86 ; 5.80	0.994
10	10.4 ± 2.9	3.1 ± 0.8	13.6 ± 1.5	4.1 ± 0.4	6.04 ; 5.86	0.996

Table 2. Mathematical models for calculating the proliferation of *Pseudomonas* spp. and *B. thermosphacta*.

Reference	Organism	Model	
Baranyi *et al*. 1995	*B. thermosphacta*	μ_{max}= (0.0339*Temp+0.287)^2	
McClure et al.. 1993	*B. thermosphacta*	ln μ_{max}=-21.76+0.08936*Temp+5.984*pH+0.1739*NaCl+0.02077*Temp*pH-0.00319*Temp*NaCl-0.03155*pH*NaCl-0.004809*Temp^2-0.4716*pH^2-0.007618*NaCl^2	
Gustavsson and Borch	*B. thermosphacta*	μ_{max}= -2.054-0.027*Temp+0.292*pH+11.278*(1-a$_w$)$^{0.5}$+0.012*Temp*pH-0.176*Temp*(1-a$_w$)$^{0.5}$-1.633*pH*(1-a$_w$)$^{0.5}$	
Gill and Jones. 1992	*Pseudomonas* spp.	Generations*h^{-1} = (0.033*Temp+0.27)^2	when -2<Temp>25°C
		Generations*h^{-1} = 1	when 25<Temp>35°C
		Generations*h^{-1} = 0	when Temp<-20 or >35°C
Davey. 1989	*Pseudomonas* spp.	ln μ_{max}=-919.54+1.6033*10^5/Temp-2.3784*10^7/Temp^2+1317.7*a$_w$-669*a$_w$^{2}	
Gustavsson and Borch	*Pseudomonas lundensis*	μ_{max}= -0.759+0.091*Temp-0.013*pH+10.741*(1-a$_w$)$^{0.5}$-0.001*Temp^2-31.654*(1-a$_w$) -0.258*Temp*(1-a$_w$)$^{0.5}$	

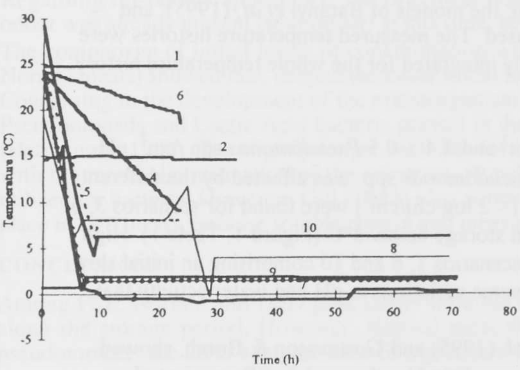

Figure 1. Temperature histories under different scenarios

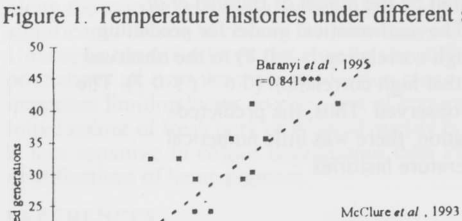

Figure 2. Validation of mathematical models for predicting the proliferation of *B. Thermosphacta*. r= correlation coefficient
* 0.01< P-value ≤0.05. ** 0.01≤ P-value >0.001
*** P-value ≤0.001 ■ Baranyi et al. 1995. □ McClure et al.. 1993.
● Gustavsson and Borch. 1994

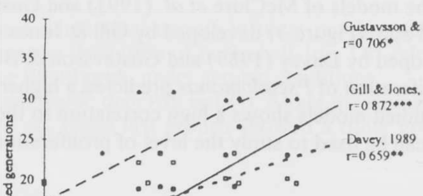

Figure 3. Validation of mathematical models for predicting the proliferation of *Pseudomonas* spp. r= correlation coefficient. * 0.01< P-value ≤0.05. ** 0.01≤ P-value >0.001
*** P-value ≤0.001 □ Davey. 1989. ■ Gill and Jones. 1993.
● Gustavsson et al.. 1995