

MICROBIOLOGICAL AND PHYSICOCHEMICAL CHARACTERIZATION OF DEFECTIVE TEXTURE DRY-CURED HAM

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Background

The quality of dry-cured ham is strongly affected by its texture (Guerrero et al., 1999). A defective texture significantly detracts the quality of ham as the end product is too soft and greasy to the touch (Parolari et al., 1994). These anomalies have been detected in different types of dry-cured hams such as Parma and Spanish dry-cured hams (Parolari et al., 1988; García-Garrido et al., 1999). Defective texture anomalies have been related to uncontrolled proteolytic activity resulting in high increases of non protein nitrogen (Virgili et al., 1995). The mechanism by which uncontrolled proteolysis takes place is still not fully known. It has been suggested that lysosomal enzymes (cathepsins N, B+L, H and D) might be wholly or partly responsible for proteolysis that takes place which leads to defective texture (Virgili et al., 1995; García-Garrido et al., 2000). In addition it is possible that microbial proteases from micro-organisms growing on the hams could contribute to uncontrolled proteolysis. Chemical characteristics such as high moisture and water activity and low salt concentration may also contribute to defective texture (Guerrero et al., 1999) due to their effect on tissue or microbial proteolytic activity.

Objectives

The aim of this work has been to characterise microbial population and those physicochemical parameters usually associated to defective texture in dry-cured ham.

Material and Methods

The study involved forty-four dry-cured hams ripened under same conditions, fifteen defective texture hams and twenty-nine unaltered considered as control hams. For sampling ripened hams were sterilised on the surface by searing to avoid external contamination. Approximately twenty g of the internal muscle (*biceps femoris*) of hams were homogenised in 90 ml sterile 1% peptone in a Stomacher for 5 min. Appropriate dilutions were made with 1% peptone and 1 ml were plated. For microbial examination the following criteria were assessed: a) Plate Count Agar (PCA) at 30°C, 48h for total aerobic counts; b) Rose Bengal Agar (RBC) at 25°C, 7 d to enumerate yeasts; c) Violet Red Bile Dextrose Agar (VRBG) at 30°C, 48h for Enterobacteriaceae; d) Mannitol Salt Agar (MSA) at 30°C, 48h to enumerate Micrococcaceae; e) De Man Rogosa, Sharp broth (MRS) at 30°C, 48h for lactic acid bacteria; f) Agar Brucella whit 7% sterile sheep blood-desfibrinated and 0.1 % vitamin K1 at 30°C, 48 h in anaerobic conditions for anaerobic microbial counts.

Moisture was determined following the ISO recommended methods (ISO/1442) and water activity (A_w) was determined with a GBS Scientific Instruments FA-st/1 system (Romans, France). The chlorides were quantified by the Carpentier Vohlard method by titration with $AgNO_3-NH_4CNS$ (AOAC, 1984). Non protein nitrogen (NPN) was analysed in the extracts of muscles made with $HClO_4$ 0.6 N (De Ketelaere et al., 1974) following the Nessler method.

Results and discussion

Defective texture hams showed higher levels of total aerobic counts (TAC) than unaltered control (Fig. 1). Micrococcaceae (M), lactic acid bacteria (LAB) were higher in defective hams. Microbial counts of defective texture hams were higher than those reported for different types of normal ripened hams (Baldini and Ranczynski, 1978; Huerta et al., 1988; Rodríguez et al., 1994). Furthermore, anaerobic micro-organisms, which most of them could have active proteases, were higher in defective hams. Although microbial levels were always lower than 10^5 cfu/g, it should be noted that these counts corresponding to final product and in deep tissues. There was not significant differences in moisture, water activity and salt content between defective and unaltered hams (Figures 2, 3 and 4). Thus, differences in microbial population are not related to physicochemical conditions of the hams, since these parameters showed similar values in the two batches analysed. Non protein nitrogen showed higher values in defective than unaltered control hams (Figure 5). Similar concentration of NPN have been referred for defective texture hams (Parolari et al., 1994; Virgili et al., 1995; García-Garrido et al., 2000). Thus, a higher proteolysis took place in defective than unaltered control. The difference in proteolysis between defective texture and unaltered control are not due to NaCl concentration, since no differences were found in the two batches analysed. Although microbial proteases could be contributing to proteolysis, it can not be concluded that the differences in proteolysis are caused by microbial activity. Even, it is possible that the major microbial counts of defective hams could be due to higher levels of non protein nitrogen caused by exaggerated proteolysis originated by cathepsins (García-Garrido et al., 2000). In conclusion, higher microbial counts and NPN concentration were found in defective texture than unaltered hams, while no differences were found in NaCl, moisture and water activity. It is necessary further investigation to know microbial activity, specially of the anaerobic micro-organisms, during processing in hams becoming in defective texture.

Pertinent literature

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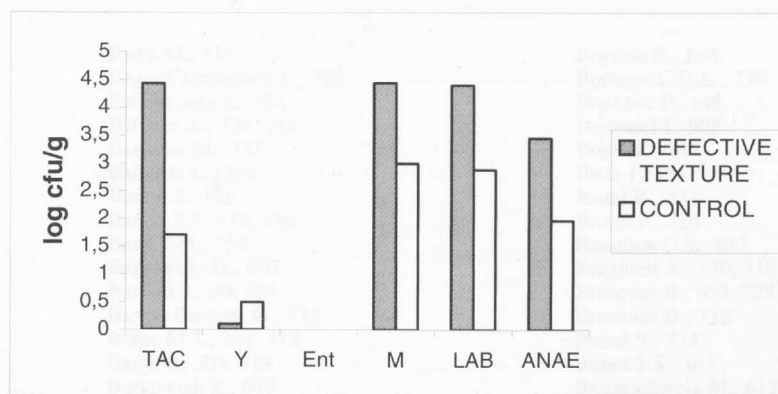


Fig. 1.-Microbial population (shown as mean of log cfu g⁻¹) of defective texture and control hams: total aerobic counts (TAC), yeasts (Y) Enterobacteriaceae (Ent), Micrococcaceae (M), lactic acid bacteria (LAB), anaerobic counts (ANAE).

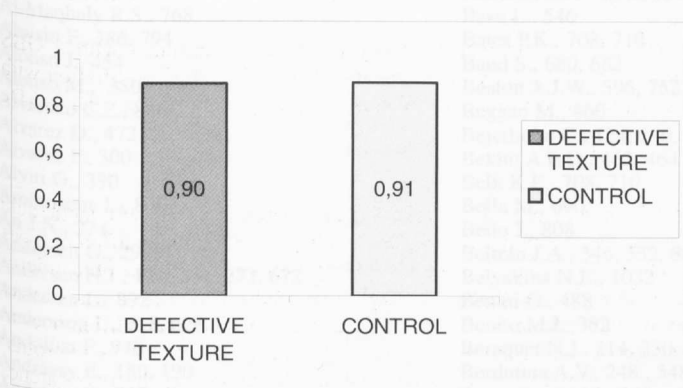


Fig. 2.- Water activity of defective texture and unaltered control hams.

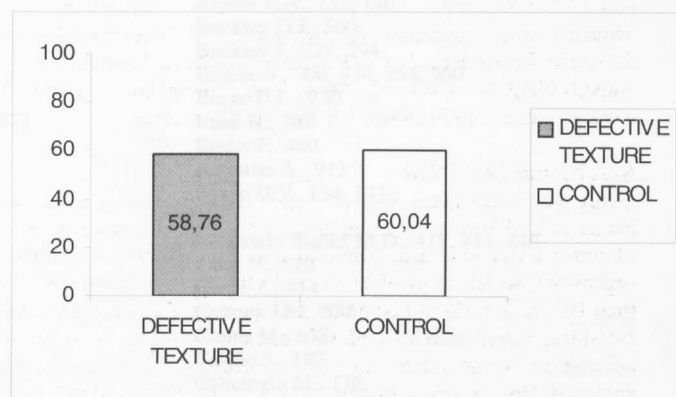


Fig. 3.- Moisture of defective texture and unaltered control hams.

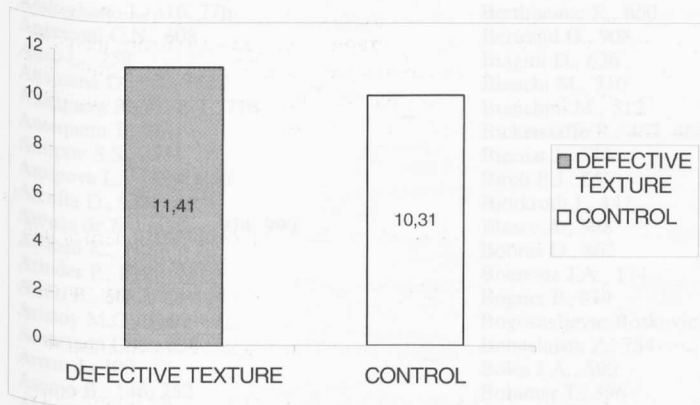


Fig. 4.- Concentration of chlorides (g/100g dry-matter) in defective texture and unaltered control hams.

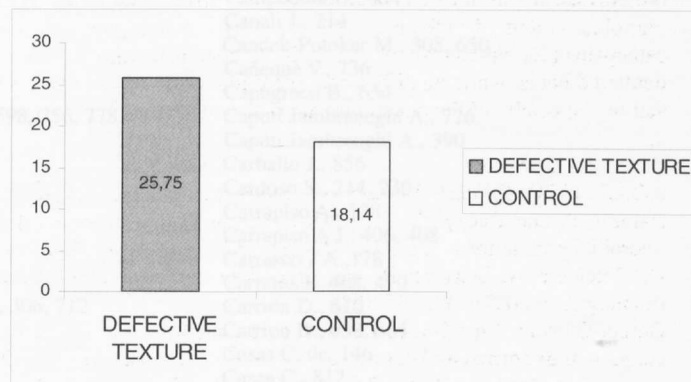


Fig. 5. Concentration of NPN (g/100g dry-matter) in defective texture and unaltered control hams.

