Introduction

Traditionally, meat fermentation was based on the use of natural flora, including the “back-slopping”, or addition of a previous successful fermented sausage. However, these practices gave a great variability in the developed flora and affected the safety and quality of the sausages (Toldrà, 2002; Toldrà & Flores, 2007). The natural flora of fermented meat has been studied for many years (Leistner, 1992; Toldrà, 2006a), and more recently, these micro-organisms have been isolated and biochemically identified through molecular methods applied to extracted DNA and RNA (Cocolin, Manzano, Aggio, Cantoni, & Comi, 2001; Cocolin, Manzano, Cantoni, & Comi, 2001; Comi, Urso, Lacumin, Rantsiou, Cattaneo & Cantoni, 2005). Today, most of the fermented sausages are produced by using microbial starters, usually from both *Lactobacilli* and *Micrococaceae* because this combination ensures rapid acidulation and optimal flavor development (Demeyer & Toldrà, 2004; Toldrà, Nip, & Hui, 2007). The main groups of micro-organisms used as starters are briefly described below.

Main Groups of Microbial Starters

**Lactic Acid Bacteria (LAB)**

Lactobacilli are the most competitive micro-organisms usually found in fermented meat products and are also essential components of starter cultures. These bacteria are able to metabolize glucose or any other available carbohydrate to generate lactic acid through either homo or heterofermentative pathways. The accumulation of lactic acid produces a pH drop towards acidic values. The homofermentative pathway only produces lactic acid but in the case of heterofermentative pathway, some undesirable secondary products (i.e., acetic acid, hydrogen peroxide, acetoin, ...
etc.) may also be produced (Demeyer, 1992). *Lactobacillus sakei* and *Lactobacillus curvatus* grow well at mild temperatures (20–25°C), and this is the main reason why they are mainly used in European sausages (mild fermentation temperatures). On the other hand, *L. plantarum* and *Pediococcus acidilactici* are used in the U.S because they grow better at higher temperatures (30–35°C) (Toldrá, 2007a). LAB have a proteolytic system, with a good number of peptidases, which may partly contribute to the degradation of muscle proteins. Most important proteases found in *L. sakei* are reported in Table 9.1. Further description on the genetics of LAB is given in Chap. 6.

**Micrococcaceae**

*Staphylococcus* and *Kocuria* (formerly *Micrococcus*) are the main representatives of this family. These micro-organisms have important enzymes like some proteases and lipases that contribute to flavor generation as will be later described. Other interesting enzymes are nitrate reductase, that reduces nitrate to nitrite and contributes to the formation of nitrosylmyoglobin giving rise to the typical color formation and safety of the sausage and catalase that helps to prevent lipid oxidation and improve flavor formation and color stability (Talon, Walter, Chartier, Barriere, & Montel, 1999).

**Yeasts**

*Debaryomyces hansenii* has been found as the predominant yeast in fermented sausages. This yeast grows preferentially in the outer area of the sausage due to its aerobic metabolism. *D. hansenii* has a good proteolytic activity (Bolumar, Sanz, Aristoy, & Toldrá, 2003a, 2003b, 2005) as shown in Table 9.1, and its lipolytic activity is able to generate flavored volatile compounds from branched-chain amino acids (Durá, Flores, & Toldrá, 2004a). Another important contribution to sausage flavor is through its deaminase/deamidase activity on certain free amino acids that generate ammonia as a by-product which rises the pH in the sausage (Durá, Flores, & Toldrá, 2002). Further description on the genetics of yeasts is given in Chap. 7.

**Molds**

A white coating on the surface of dry fermented sausages is typical in certain areas like the Mediterranean. The most usual molds identified are *Penicillium nalgiovense* and *P. chrysogenum* (Sunesen & Stahnke, 2003). They contribute to the flavor through their proteolytic and lipolytic activity as well as to the ammonia generated by deamination and deamidation. Further extensive description on molds is given in Chap. 8.