FIL/IDF – Brasil

Comitê Brasileiro – Sub Comitê de Higiene e Segurança (HS)

MINAS LACTEA
EXPOLAC/EXPOMAQ

Juiz de Fora- Minas Gerais
17-19 de julho de 2019

Célia Lucia de Luces Fortes Ferreira
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FIL/IDF – Brasil

Comitê Brasileiro – Sub Comitê de Higiene e Segurança (HS)

List of IDF Topics - Selected

36-Surveillance of relevant information and reporting of emerging hazards associated with milk and milk products

96-Guidelines for the validation of screening methods for residues of veterinary medicines

141-Fermented milk products -- Bacterial starter cultures -- Standard of identity

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Comitê Brasileiro – Sub Comitê de Higiene e Segurança (HS)

36-Surveillance of relevant information and reporting of emerging hazards associated with milk and milk products

1-**Screening** de *Staphylococcus aureus* resistente a meticilina em leite e produtos lácteos no território nacional

96-Guidelines for the validation of screening methods for residues of veterinary medicines

2- **Screening antibióticos, pesticidas e agrotóxicos** em leite e produtos lácteos no território nacional

141-Fermented milk products -- Bacterial starter cultures -- Standard of identity

3- Efeito da alteração do ambiiente de maturação de queijos feitos com leite cru na biodiversidade e virulência de fungos

Comitê Brasileiro da FIL-IDF - Sub-Comitê de Segurança e Higiene (SH) Encaminhamento dos temas para pesquisa e revisão [03-03-2019] - [08-04-2019]

1-**Screening** de *Staphylococcus aureus r*esistente a meticilina em leite e produtos lácteos no território nacional

2-Efeito da **alteração do ambiente de maturação de queijos feitos com leite cru** na **biodiversidade** e **virulência de fungos**

3-**Screening** de **antibióticos, pesticidas e agrotóxicos** em leite e produtos lácteos no território nacional

Comitê Brasileiro da FIL-IDF - Sub-Comitê de Segurança e Higiene (SH) Encaminhamento dos temas para pesquisa e revisão [03-03-2019] - [08-04-2019] - [02-12-2019]

1-**Screening** de *Staphylococcus aureus r*esistente a meticilina em leite e produtos lácteos no território nacional

2-Efeito da **alteração do ambiente de maturação de queijos feitos com leite cru** na **biodiversidade** e **virulência de fungos**

3-**Screening** da presença de **antibióticos, pesticidas e agrotóxicos** em leite e produtos lácteos no território nacional

FIL/IDF – Brasil

Comitê Brasileiro – Sub Comitê de Higiene e Segurança (HS)

QUALIDADE DO LEITE EM NATUREZA, DO TANQUE DE EXPANSÃO AO SILO INDUSTRIAL

Aspectos Microbiológicos

FIL/IDF – Brasil

Comitê Brasileiro – Sub Comitê de Higiene e Segurança (HS)

QUALIDADE DO LEITE EM NATUREZA, DO TANQUE DE EXPANSÃO AO SILO INDUSTRIAL [1]

Prezados senhores: No âmbito da FIL/IDF, o sub-comitê de Higiene e Segurança esta procedendo a um levantamento sobre a qualidade do leite no Brasil, em suas diferentes regiões e solicita sua colaboração prestando as informações solicitadas. Informamos que os dados recebidos serão mantidos em sigilo e utilizados para informações gerais, não sendo necessário identificar-se como empresa, mas em termos de região do país (e Estado) e quantidade de leite trabalhada diariamente, em média. Desde já agradecemos.

Os dados a serem inseridos nesta planilha podem ser aqueles referentes ao ano de 2018. Caso não se refiram a 2018, fineza indicar o período correto. Mesmo que não possuam todas as informações solicitadas, por fineza, incluam as que possuírem.

Os resultados serão divulgados oportunamente, no site do Comitê Brasileiro da FIL/IDF.

Desde já agradecemos sua colaboração.

ATT

Celia Lucia de Luces Fortes Ferreira

Coordenadora do Sub Comitê Higiene e Segurança, Comitê Brasileiro da FIL/IDF

Quaisquer informações adicionais, fineza entrar em contato com: clferrei@ufv.br

Encaminhar o questionário preenchido para: clferrei@ufv.br

Data limite para encaminhamento do questionário preenchido: 12 de julho /2019

Resultados médios parciais de Contagem Padrão em Placas(CPP- UFC/mL) e Contagem de Células Somáticas (CCS) em Amostras de Leite coletado na Fazenda, Transporte e Silo Industrial				
Ponto de coleta	CPP (>)	CPP (<)	CCS (>)	CCS(<)
	[na propriedade ou tanque comunitario]a partir de 1-07-2019 máximo $1,0 \times 10^5$		Ma propriedade ou tanque comujitario]a partir de 1-07-2019 máximo $4,0 \times 10^5$	
Fazenda	$4,83 \times 10^6$	$3,81 \times 10^3$	$3,4 \times 10^6$	$2,0 \times 10^6$
Transporte	$9,7 \times 2,4^7$	$2,4 \times 10^5$	--------	-------
Silo Industrial	$6,2 \times 10^6$	$9,45 \times 10^5$	--------	-------

Identidade e Qualidade de Leite Cru Refrigerado, o Regulamento Técnico de Identidade e Qualidade de Leite Pasteurizado e o Regulamento Técnico da Coleta de Leite Cru Refrigerado e seu Transporte a Granel, alterada pela Instrução Normativa nº 7, de 3 de maio de 2016, passa a vigorar com a seguinte redação:

Índice medido (por propriedade rural ou por tanque comunitário)	A partir de 01/07/2008 Até 31/12/2011 Regiões: S/SE/CO A partir de 01/07/2010 até 31/12/2012 Regiões: N/NE	A partir de 01/01/2012 até 30/06/2014 Regiões: S/SE/CO A partir de 01/01/2013 até 30/06/2015 Regiões: N/NE	A partir de 01/07/2014 até 30/06/2019 Regiões: S/SE/CO A partir de 01/07/2015 a 30/06/2019 Regiões: N/NE	A partir de 01/07/2019 Regiões: S/SE/CO A partir de 01/07/2019 Regiões: N / NE
Contagem Padrão em Placas (CPP), expressa em UFC/mL (mínimo de 01 análise mensal, com média geométrica sobre período de 03 meses)	Máximo de 7,5 x 105	Máximo de 6,0 x 105	Máximo de 3,0 x 105	Máximo de 1,0 x 105
Contagem de Células Somáticas (CCS), expressa em CS/mL (mínimo de 01 análise mensal, com média Geométrica sobre período de 03 meses)	Máximo de 7,5 x 105	Máximo de 6,0 x 105	Máximo de 5,0 x 105	Máximo de 4,0 x 105
Pesquisa de Resíduos de Antibióticos/outros Inibidores do crescimento microbiano: Limites Máximos previstos no Programa Nacional de Controle de Resíduos - MAPA				
Temperatura máxima de conservação do leite: 7ºC na propriedade rural / Tanque comunitário e 10ºC no estabelecimento processador.				
Composição Centesimal: Índices estabelecidos na Tabela 1 do presente RTIQ.				

https://alimentusconsultoria.com.br/instrucao-normativa-no-31-de-29-de-junho-de-2018-mapa/

FIL/IDF - Brasil
Comitê Brasileiro - Sub-Comitê de Higiene e seguança (HG)

QUALIDADE DO LEITE EM NATUREZA DO TANQUE DE EXPANSÃO AO SILO INDUSTRIAL

The evolutionary history of methicillin-resistant *Staphylococcus aureus* (MRSA)

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Edited by Christopher T. Walsh, Harvard Medical School, Boston, MA, and approved April 16, 2002 (received for review February 22, 2002)

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of hospital-acquired infections that are becoming increasingly difficult to combat because of emerging resistance to all current antibiotic classes. The evolutionary origins of MRSA are poorly understood, no rational nomenclature exists, and there is no consensus on the number of major MRSA clones or the relatedness of clones described from different countries. We resolve all of these issues and provide a more thorough and precise analysis of the evolution of MRSA clones than has previously been possible. Using multilocus sequence typing and an algorithm, eBURST, we analyzed an international collection of 912 MRSA and methicillin-susceptible *S. aureus* (MSSA) isolates. We identified 11 major MRSA clones within five groups of related genotypes. The putative ancestral genotype of each group and the most parsimonious patterns of descent of isolates from each ancestor were inferred by using eBURST, which, together with analysis of the methicillin resistance genes, established the likely evolutionary origins of each major MRSA clone, the genotype of the original MRSA clone and its MSSA progenitor, and the extent of acquisition and horizontal movement of the methicillin resistance genes. Major MRSA clones have arisen repeatedly from successful epidemic MSSA strains, and isolates with decreased susceptibility to vancomycin, the antibiotic of last resort, are arising from some of these major MRSA clones, highlighting a depressing progression of increasing drug resistance within a small number of ecologically successful *S. aureus* genotypes.

Methicillin was introduced in 1959 to treat infections caused by penicillin-resistant *Staphylococcus aureus*. In 1961 there were reports from the United Kingdom of *S. aureus* isolates that had acquired resistance to methicillin (methicillin-resistant *S. aureus*, MRSA) (1), and MRSA isolates were soon recovered from other European countries, and later from Japan, Australia, and the United States. MRSA is now a problem in hospitals worldwide and is increasingly recovered from nursing homes and the community (2, 3). The methicillin resistance gene (*mecA*) encodes a methicillin-resistant penicillin-binding protein that is not present in susceptible strains and is believed to have been acquired from a distantly related species (4). *mecA* is carried on a mobile genetic element, the staphylococcal cassette chromosome *mec* (SCC*mec*), of which four forms have been described that differ in size and genetic composition (5). Many MRSA isolates are multiply resistant and are susceptible only to glycopeptide antibiotics such as vancomycin and investigational drugs. MRSA isolates that have decreased susceptibility to glycopeptides (glycopeptide intermediately susceptible *S. aureus*, GISA) (6, 7), reported in recent years, are a cause of great public health concern.

Many studies have characterized MRSA isolates from individual hospitals or countries and have identified strains that appear to be well adapted to the hospital environment, are established in several hospitals within a country, or have spread internationally (epidemic MRSA, EMRSA). MRSA isolates are generally characterized by pulsed-field gel electrophoresis, a powerful technique for identifying the relatedness of isolates from recent outbreaks within a hospital, but are not well suited to long-term global epidemiology, which requires a procedure that is highly discriminatory but that indexes variation that accumulates slowly. Multilocus sequence typing (MLST) provides such a procedure and characterizes isolates of bacteria unambiguously by using the sequences of internal fragments of seven housekeeping genes (8, 9). MLST has been developed and validated for *S. aureus* (10) and provides a discriminatory method that allows related strains recovered in different countries to be readily identified.

The origins of the major MRSA clones are still poorly understood. Kreiswirth *et al.* (11) proposed that all MRSAs were descended from a single ancestral *S. aureus* strain that acquired *mecA*, but more recent studies (12, 13) show that some MRSAs are very divergent, implying that *mecA* has been transferred between *S. aureus* lineages. The data from MLST can be used to probe the evolutionary and population biology of bacterial pathogens and to predict ancestral genotypes and patterns of evolutionary descent within groups of related genotypes. We have applied MLST to an international collection of 359 MRSA isolates, which includes examples of the previously described EMRSA and GISA clones, and compare these to a collection of 553 methicillin-susceptible *S. aureus* (MSSAs). We demonstrate the limited number of major EMRSA genotypes and provide an unambiguous method for characterizing MRSA and GISA clones and a rational nomenclature. We also identify the ancestral MRSA clone and its MSSA ancestor and suggest the evolutionary pathways by which MRSA clones have repeatedly emerged from successful MSSA clones.

Materials and Methods

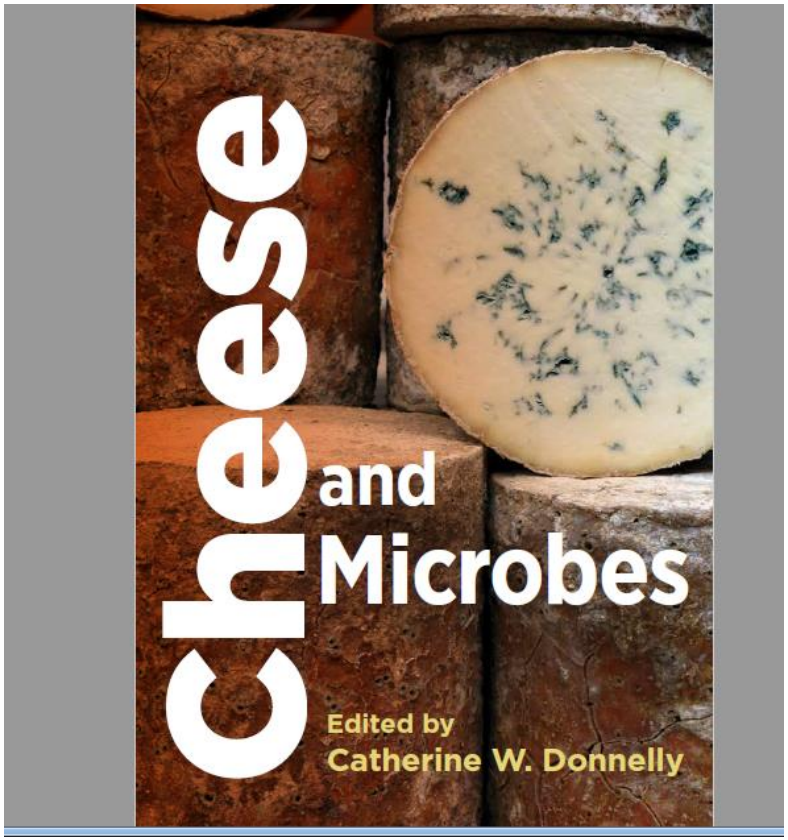
Bacterial Isolates. A total of 359 MRSA isolates were collected between 1961 and 1999 from 20 countries. Isolates were confirmed as MRSAs in our laboratory by detecting the presence of the *mecA* gene with PCR (14). The collection contains members of previously described EMRSA clones, including the Iberian (15), Portuguese/Brazilian (16), Vienna (17), New York/Japan (18, 19), pediatric (20), Berlin (17), Hannover (17), South German (17), EMRSA-3, -15, and -16 (21), and six of the first GISA isolates (minimum inhibitory concentration ≥8 μg vancomycin ml^{-1}) from Japan, the United States, and Scotland (6, 7). The allelic profiles of the MRSA isolates were compared with those of 553 MSSA isolates from disease and carriage; details of all isolates are available at the MLST database (http://www.mlst.net).

MLST. MLST was performed as described (10). Alleles at the seven loci were assigned by comparing the sequences at each

This paper was submitted directly (Track II) to the PNAS office.

Abbreviations: MRSA, methicillin-resistant *Staphylococcus aureus*; EMRSA, epidemic MRSA; MSSA, methicillin-susceptible *S. aureus*; SCC*mec*, staphylococcal cassette chromosome *mec*; GISA, glycopeptide intermediately susceptible *S. aureus*; MLST, multilocus sequence typing; ST, sequence type; SLV, single locus variant; CC, clonal complex.

†To whom reprint requests should be addressed. E-mail: m.c.enright@bath.ac.uk.



[2014]

FROM PASTEUR TO PROBIOTICS: A HISTORICAL OVERVIEW OF CHEESE AND MICROBES

Catherine W. Donnelly[1]

INTRODUCTION

Nowhere in the microbial world are microorganisms on more magnificent display than on the surfaces or in the interiors of the great cheeses of the world. Cheesemaking is inextricably linked to microbiology, which makes the study of cheeses, their history, and the vast science of cheese and microbes particularly fascinating. Over the past two decades, there has been explosive growth in the U.S. artisan cheese industry. The availability of artisan cheeses, made using traditional practices, has ignited renewed consumer interest in cheesemaking and cheese consumption. This affords a tremendous opportunity to educate a new population of students, scientists, cheesemakers, technologists, and cheese connoisseurs about the essential role which microorganisms play in the process of cheesemaking.

Many of the chapters in the book *Cheese and Microbes* (48) provide a scientific overview of the beneficial associations of microbes with cheese, through the lens of the numerous unique cheeses which result due to growth of bacteria, yeasts, and molds which play a crucial role in cheesemaking. Whether due to surface or internal mold, yeast, or bacterial ripening, growth, or metabolism, a vast array of products are able to be produced through transformation of a single starting material: milk. Cheeses in general are microbiologically safe foods, but there are occasional outbreaks of illness linked to cheese consumption. The chapters in *Cheese and Microbes* have been authored by scientists who are the leading researchers and experts on the various aspects of the association of microbes with traditional cheeses. Many of the authors reside in Europe, where the traditional cheeses which they study have been continuously produced for centuries. In addition to the informative overview of the science of cheesemaking and the microorganisms involved, selected photographs capture the culture, tradition, and vast array of unique cheese varieties, all of which are dependent on the action of a diverse population of bacteria, yeasts, and molds. New tools of molecular biology are informing the study of cheese microbiology in ways not previously possible, and this emerging science is providing new insights into the complexity of the microbial biodiversity of traditional cheeses. This inquiry will further advance our knowledge of some of the oldest traditional foods known to humankind.

[1]Department of Nutrition and Food Sciences and Vermont Institute for Artisan Cheese, The University of Vermont, Burlington, VT 05405.

Cheese and Microbes, Edited by Catherine W. Donnelly,
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Identidade e Qualidade de Leite Cru Refrigerado, o Regulamento Técnico de Identidade e Qualidade de Leite Pasteurizado e o Regulamento Técnico da Coleta de Leite Cru Refrigerado e seu Transporte a Granel, alterada pela Instrução Normativa nº 7, de 3 de maio de 2016, passa a vigorar com a seguinte redação:

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