

**PERFIL MOLECULAR E RESISTÊNCIA A
ANTIMICROBIANOS DE *Salmonella* ISOLADA EM
LINFONODOS MESENTÉRICOS DE SUÍNOS**

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UNIVERSIDADE ESTADUAL PAULISTA
FACULDADE DE MEDICINA VETERINÁRIA E ZOOTECNIA

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Resumo

O presente trabalho avaliou 250 animais de 25 lotes distintos abatidos em 4 estabelecimentos do estado de São Paulo para a presença de *Salmonella* nos linfonodos mesentéricos, e caracterizou o perfil de resistência das cepas isoladas aos principais antibióticos. O patógeno estava presente em 36,4% das amostras e 72% dos lotes analisados. Dos 91 isolados, 67 foram sorotipados, e os principais sorovares encontrados foram *S. Typhimurium* (n=13), *S. 1.4,5,12:i:-* (n=12) *S. Infantis* (n=12) e *S. Havana* (n=11). Os compostos com menor eficácia frente aos isolados foram estreptomicina e tetraciclina (68,1% de resistência) ampicilina e sulfonamidas (62,6%), cloranfenicol (56,0%), trimetoprim-sulfametoxazol (41,8%) e ácido nalidíxico (40,7%). Os mais efetivos foram aztreonam e cefoxitina, (ambos com 3,3% de resistência) e cefepima e ceftriaxona, (ambos com 7,7%). Cepas multidrogas resistentes (MDR) corresponderam a 70,3% dos isolados. Oito cepas foram submetidas ao MLST: quatro *S. Typhimurium* e uma *S. 1.4,5,12:i:-* todas pertencentes ao ST 19, duas *S. Infantis* pertenceram ao ST 32 e uma *S. Derby*, pertencente ao ST 40. A grande prevalência do patógeno nos animais analisados, com altas taxas de resistência aos antibióticos e pertencentes a grupos genéticos frequentemente associados a surtos e doenças em humanos demonstram que a cadeia produtiva da carne suína é uma fonte de contaminação em potencial nos casos de salmonelose, sendo necessárias medidas preventivas eficazes para o controle do patógeno e diminuição do risco de veiculação de patógenos por alimentos.

Abstract

This study evaluated 250 animals of 25 different batches processed in four slaughterhouses in São Paulo state - Brazil for the presence of *Salmonella* in the mesenteric lymph nodes, and characterized the resistance profile for the main antibiotics. The pathogen was present in 36.4% of samples and 72% of the analyzed batches. Of the 91 isolates, 67 were serotyped, and the main serovars found were *S. Typhimurium* (n = 13), *S. 1.4,5,12:i-* (n = 12) *S. Infantis* (n = 12) and *S. Havana* (n = 11). The compounds with less efficacy were streptomycin and tetracycline (68.1% resistant) ampicillin and sulphonamides (62.6%), chloramphenicol (56.0%), trimethoprim-sulfamethoxazole (41.8%), and nalidixic acid (40.7%). The most effective were cephalothin and aztreonam, (both with 3.3% resistant) and ceftriaxone and cefepime (both with 7.7%). Multidrug-resistant strains (MDR) accounted for 70.3% of the isolates. Eight strains were submitted to MLST: Four *S. Typhimurium* and one *S.1.4,5,12:i-* all belonging to the ST 19, two *S. Infantis*, belonging to the ST 32 and one *S. Derby*, belonging to ST 40. The high prevalence of the pathogen in the analyzed animals, with high rates of resistance to antibiotics and belonging to genetic groups that are often associated with outbreaks and disease in humans, shows that the production chain of pork is a potential source of contamination in salmonellosis cases, with the necessity of effective preventive measures for pathogen control and lower the risk of foodborne diseases transmission.

Capítulo 1

Introdução

A carne suína representa uma importante fonte de nutrientes para a população, apresentando elevados níveis de proteínas de alto valor nutricional, aminoácidos essenciais, vitaminas do complexo B e minerais (KAUFFMAN, 2001). Atualmente é a mais consumida no mundo, sendo que sua produção ultrapassa 100 milhões de toneladas/ano. No cenário mundial, o Brasil é o quarto maior produtor e exportador do segmento, tendo abatido em 2014, se considerarmos os somente os estabelecimentos com inspeção oficial, mais de 32 milhões de animais e apresentando um consumo per capita de 14,60 Kg/habitante (ABPA, 2015).

Neste contexto, a preocupação com a segurança alimentar se faz necessária para assegurar o fornecimento de produtos livres de patógenos. Dentre os principais micro-organismos causadores dessas enfermidades, pode-se destacar *Salmonella*. Dados parciais de 2014 revelaram que nos Estados Unidos, este foi o patógeno de maior incidência e responsável pelo maior número de óbitos em humanos dentre os veiculados por alimentos contaminados (CRIM et al., 2015). Por apresentar sintomas relativamente comuns nos indivíduos afetados e por falta de empenho ou condição por parte dos órgãos médicos e de vigilância epidemiológica, sua ocorrência é subnotificada, mas calcula-se que nos EUA 1,4 milhões de pessoas são acometidas anualmente e os custos diretos com medicamentos e internações atingem em torno de 2,6 bilhões de dólares (MEAD et al., 2010).

O gênero *Salmonella* compreende bacilos Gram-negativos, não formadores de esporos, pertencentes à família Enterobacteriaceae. São ainda micro-organismos anaeróbios facultativos, capazes de utilizar citrato como única fonte de carbono, quase sempre produzem gás a partir da glicose e raramente fermentam lactose ou sacarose. Em sua maioria, são móveis, pois possuem flagelos peritríquios (FRANCO; LANDGRAF, 1996).

Hald et al. (2004) destacaram o consumo de carne suína como um importante fator na ocorrência da veiculação de patógenos por alimentos. Dentre as carnes vermelhas, a suína é a mais frequentemente associada à *Salmonella*, estando o

patógeno intimamente ligado à cadeia produtiva do animal, da fazenda ao varejo, tendo sido detectado em diversas etapas e insumos envolvidos na produção (SANCHEZ et al., 2007; ZHENG; BONDE; SØRENSEN, 2007; LITTLE et al., 2008; YANG et al., 2010). Dados da literatura revelaram que na Alemanha, 20% dos casos de salmonelose foram associados ao consumo deste tipo de carne (STEINBACH; HARTUNG, 1999). Em um estudo de caso-controle para estimar os fatores de riscos associados à salmonelose, Mughini-Gras et al. (2014) afirmaram que 39,9% dos casos esporádicos da doença em ambiente doméstico estavam associados ao consumo de carne suína na Holanda.

Lo Fo Wong et al. (2002) relataram que a introdução de animais positivos no frigorífico e subsequente transmissão para animais negativos durante o processamento, estavam relacionados com a alta prevalência do micro-organismo no produto final, ressaltando fatores importantes como o estresse do animal na chegada ao abatedouro, influenciando na excreção de *Salmonella* por portadores e o manejo e fluxograma de abate, como pontos que possibilitavam a contaminação dos demais animais.

Revisão da literatura

- Prevalência e caracterização dos sorovares de *Salmonella* em suínos

Trabalhos em diversos países reportaram a prevalência de *Salmonella* nas diferentes etapas da cadeia produtiva da carne suína, utilizando-se de diferentes metodologias e reportando diferentes números. Sanchez et al. (2007) ao realizarem uma metanálise de artigos que relataram a prevalência da bactéria em diversas unidades de produção de suínos na Europa, durante o período de 1990 até 2005, encontraram valores médios de 59% de propriedades positivas e 17% de animais positivos. Foram também determinados no trabalho os principais pontos responsáveis pelos resultados de prevalências divergentes dentre as diversas pesquisas, sendo destacados: o método microbiológico utilizado, o número de amostras analisadas e o país onde o estudo foi realizado como os fatores mais significativamente envolvidos em tal variação.

Ao compararem a sensibilidade do uso de “pools” de *swabs* de carcaças com a pesquisa individualizada para *Salmonella*, utilizando um total de 18.984 amostras obtidas em abatedouros na Dinamarca, Sørensen et al. (2007) reportaram uma baixa prevalência de resultados positivos (1,4%) quando utilizaram 5 animais aleatoriamente selecionados por dia, amostrados individualmente. Quando 5 animais foram amostrados em *pool*, tal prevalência aumentou para 4,1%.

Na Itália, Piras et al. (2011) relataram uma prevalência de animais positivos na ordem de 30,5% quando eram analisados os linfonodos mesentéricos, 16,4% quando a pesquisa era realizada em fezes e conteúdo intestinal, e 14,1% quando foram utilizados *swabs* de carcaças e fígado. Foi realizada ainda a pesquisa do patógeno nas superfícies do abatedouro, sendo positivas 38,0% das que não estavam em contato direto com a carne, e 35% das que tinham contato direto com a mesma. Os pesquisadores reportaram ainda que de 31 animais identificados como portadores do patógeno (presença nos linfonodos e/ou conteúdo intestinal) somente em oito foi isolada *Salmonella* na carcaça. Foram determinados oito diferentes sorovares no trabalho, sendo *S. Derby* e *S. Typhimurium* os mais prevalentes (42,7% e 23,3%, respectivamente).

Em ambas as situações, deve-se destacar o considerável aumento de resultados positivos quando a pesquisa utilizava linfonodos ou conteúdo intestinal como unidade analítica ao invés de *swabs* de carcaças

Pesquisas brasileiras também reportaram a presença do patógeno nos animais abatidos. Silva et al. (2009) relataram que no estado do Mato Grosso foram detectados 16,6% dos animais positivos para o patógeno quando pesquisados linfonodos mesentéricos e tonsilas. Os principais sorovares isolados foram novamente *S. Derby* (16%) e *S. Typhimurium* (14%), seguidos por *S. London* e *S. Give* (ambos 12%).

Em trabalho semelhante, realizado no Rio Grande do Sul, Bessa et al. (2004) encontraram uma maior prevalência do patógeno, da ordem de 55,6% de positivos. Tal trabalho também se utilizou da análise de linfonodos mesentéricos e conteúdo intestinal para a pesquisa de *Salmonella*. Destacaram ainda que a prevalência de animais positivos nos linfonodos foi de 17,6% e nas fezes 18,6%. Os sorovares que

se destacaram como mais isolados foram *S. Typhimurium* (24,3%), *S. Agona* (19,9%), *S. Derby* (13,2%) e *S. Bredeney* (12,0%).

A pesquisa de *Salmonella* nos linfonodos mesentéricos é comumente utilizada para indicar o *status* do animal como portador deste patógeno (BAHNSON et al., 2006) e quando a amostragem é realizada a partir do conteúdo intestinal, pode demonstrar seu caráter excretor (DAVIES et al., 1998). Autores relatam que a infecção dos animais pela bactéria ocorre predominantemente por via oral e os linfonodos mesentéricos atuam primariamente como uma barreira, porém posteriormente se tornam reservatórios do patógeno, que pode sobreviver intracelularmente nos macrófagos e neutrófilos até que alterações fisiológicas desencadeadas pelo stress, como a liberação de catecolaminas e alterações da motilidade intestinal, propiciem sua liberação nas fezes em poucas horas (STRAW et al., 2012).

- Resistência a antimicrobianos de cepas de *Salmonella* isoladas de suínos

Sendo a salmonelose uma enfermidade transmitida primariamente por alimentos, com destaque para os de origem animal, a ocorrência de micro-organismos resistentes a antimicrobianos nos produtos alimentícios originários de tais fontes pode ser considerada um grave problema de saúde pública, agravado se forem consideradas as drogas que são concomitantemente utilizadas no tratamento dos animais e dos seres humanos (THAI et al., 2012).

Apesar de promover uma infecção auto limitante na maior parte dos casos, sem necessidade de antibioticoterapia, por vezes, *Salmonella* não tifoidal pode causar enfermidades mais severas, principalmente quando ocorre o acometimento de outros sistemas além do trato gastrointestinal. Em tais situações, o uso de fármacos se faz necessário para salvaguardar a vida do indivíduo acometido (ANGULO et al., 2000; PARRY; THRELFALL, 2008). Estudos relataram o isolamento de diversas cepas de *Salmonella* resistentes aos principais grupos de antimicrobianos utilizados tanto na produção animal, quanto no tratamento de seres humanos.

Gomez-Laguna et al. (2011) determinaram o perfil de resistência a antimicrobianos em cepas de *Salmonella* isoladas em suínos que foram criados em sistema *free-range* na Espanha, e destacaram como os compostos com maior incidência de resistência: estreptomicina (46%), tetraciclina (30%), sulfonamidas (25%) e ampicilina (23%). Revelaram ainda que 36% das cepas que apresentaram algum tipo de resistência, foram concomitantemente resistentes a 4 ou mais compostos antimicrobianos, sendo consideradas pelos autores como multidrogas resistentes (MDR).

Durante estudo similar realizado no Vietnã, porém contemplando carne de origem avícola e suína, Thai et al. (2012) determinaram que 78,4% dos isolados eram resistentes a pelo menos um antimicrobiano. Os compostos menos efetivos foram tetraciclina (58,5%), sulfonamidas (58,1%), estreptomicina (47,3%) ampicilina (39,8%), cloranfenicol (37,3%), trimetoprim (34,0%), e ácido nalidíxico (27,8%). Um total de 23,2% dos isolados foi classificado como MDRs, sendo que 8,3% foram resistentes a mais de 9 antibióticos.

Dados brasileiros revelaram perfis semelhantes de resistência. Castagna et al. (2001) ao analisarem amostras de suínos provenientes do Rio Grande do Sul, destacaram como principais compostos aos quais as cepas do patógeno apresentaram resistência: sulfonamidas (83,9%), tetraciclina (37,4%), cotrimoxazol (25,2%), ampicilina (20,2%), cloranfenicol (16,1%), estreptomicina (14,1%), ácido nalidíxico (10,1%). As amostras MDR representaram 24,2% do total de isolados.

Weiss et al. (2002), também em estudos no Rio Grande do Sul, utilizando-se de fezes, *swabs* retais, e linfonodos mesentéricos, isolaram cepas de *Salmonella* resistentes a sulfonamidas (97,8%) estreptomicina (82,6%), tetraciclina (36,9%) e sulfazotrim (15,2%).

O isolamento de *Salmonella* resistente aos antimicrobianos em suínos é relativamente comum, e o uso inadequado de antibióticos na cadeia produtiva dos animais, seja com finalidade terapêutica, como medidas profiláticas, ou como promotores de crescimento, está relacionado com tal ocorrência (ANGULO et al., 2000; STRAHILEVITZ et al., 2009). Destaca-se ainda o grande número de cepas

resistentes aos compostos convencionalmente utilizados no tratamento da salmonelose em humanos, como a ampicilina e cotrimoxazol.

-Determinação do perfil molecular pela técnica de MLST (*MultiLocus sequence typing*)

A determinação das fontes de contaminação dos animais por *Salmonella*, bem como a distribuição do patógeno através dos rebanhos é de fundamental importância para compreender sua epidemiologia e traçar medidas efetivas de controle, porém a grande variabilidade de sorovares isolados na produção de suínos, associados com a grande quantidade de vetores e portadores assintomáticos dificultam substancialmente a determinação da origem da bactéria (KICH et al., 2007). Por mais de sete décadas a sorotipagem das cepas de *Salmonella*, baseada na determinação dos epítomos dos antígenos capsulares (O) e flagelares (H), tem sido a principal ferramenta para estudar a epidemiologia do patógeno. Tal classificação é amplamente utilizada pela comunidade científica e órgãos de saúde pública, e sua nomenclatura normalmente é associada aos quadros clínicos e espécies acometidas, ou a região onde foi isolado primariamente (por exemplo: *S. Choleraesuis*, *S. Abortusequi*, *S. London*, *S. Dublin*). Recentemente, a nomenclatura de novos sorovares de *Salmonella* foi padronizada de modo a contemplar sua fórmula antigênica (como *S. 1,4,5,12:i:-*) (GRIMONT; WEILL, 2008). Todavia tal classificação não leva em conta a perspectiva evolutiva dos isolados, agrupando por vezes cepas com pouca similaridade genética e em outras não conseguindo agrupar micro-organismos provenientes de linhagens semelhantes (ACHTMAN et al., 2012).

Diversas alternativas têm sido desenvolvidas, visando estreitar as classificações para *Salmonella* e outros micro-organismos. Técnicas como o PFGE (*Pulse field gel electrophoresis*) e MLVA (*MultiLocus Variable number of tandem repeats Analysis*) se mostraram valiosas para estudar as similaridades ou diferenças de cepas isoladas em surtos ou regiões, porém não são capazes de determinar a relação evolutiva das cepas em relação a outros isolados (ACHTMAN et al., 2012). Métodos que utilizam a análise de partes conservadas do genoma

bacteriano, que sofreriam pouca ou nenhuma pressão de seleção genética, foram desenvolvidos para estimar tal relação e determinar clones semelhantes e as árvores evolutivas dos patógenos, possibilitando um estudo epidemiológico mais aprofundado. Ao final da década de 80, foi desenvolvido o MLEE (*MultiLocus Enzyme Electrophoresis*, onde se inferiu a presença de diferentes alelos de um mesmo gene através da verificação da migração de proteínas em um gel de eletroforese (SELANDER et al., 1986). Posteriormente, com o advento da análise genômica e métodos de sequenciamento de DNA, foi desenvolvida a técnica de MLST (*MultiLocus sequence typing*).

O MLST para *Salmonella* consiste no sequenciamento de sete genes conservados do genoma bacteriano, visando determinar qual alelo de cada gene específico está presente na amostra, atribuindo um número para cada alelo pesquisado. Desta forma, cada amostra recebe uma sequência de sete números, os quais irão determinar sua *sequence type* (ST). Os diferentes alelos para cada gene e os ST já catalogados são disponibilizados online no site <http://mlst.warwick.ac.uk/mlst/dbs/Senterica> e este banco de dados pode ser alimentado por diversas instituições de pesquisa, possibilitando-se a comparação dos diferentes isolados em diversas fontes e regiões geográficas (JOLLEY; MAIDEN, 2014).

Almeida et al. (2013) pesquisaram o perfil molecular de *S. Infantis* obtidas no estado de São Paulo ao longo de 25 anos, isoladas em pacientes humanos e alimentos, e descobriram que todas as cepas avaliadas através do MLST (n=16) pertenciam ao ST32. Os autores afirmaram que este seria o principal perfil clonal para o sorovar em questão, e juntamente com a PFGE, concluíram que o mesmo subtipo do patógeno estava presente na maior parte dos pacientes e alimentos estudados.

Cai et al. (2016) demonstraram que cepas de *Salmonella* com perfis semelhantes foram isoladas em abatedouros de suínos e mercados varejistas na China, utilizado também as técnicas de MLST e PFGE. Destacaram ainda que os mesmos perfis são isolados frequentemente em surtos de salmonelose por órgãos de saúde pública, demonstrando um possível elo epidemiológico para a doença.

Em um estudo similar na Alemanha, porém contemplando o sorovar *S. Derby*, Hauser et al. (2011) também conseguiram detectar um subtipo prevalente do patógeno circulante nos suínos, sua carne e em humanos, ressaltando a relevância deste ciclo de transmissão.

Assim, tendo em vista o papel dos suínos como fonte de proteína animal e, paradoxalmente, a sua participação como veículos de *Salmonella* ao homem, torna-se importante avaliar sob nossas condições, a prevalência do patógeno nos rebanhos aqui criados, bem como o perfil de resistência das cepas isoladas a alguns antimicrobianos empregados na criação animal e na terapêutica humana, além da circulação do patógeno dentre os diferentes núcleos de produção.

Objetivos

- Determinar a prevalência de *Salmonella* em linfonodos mesentéricos de suínos abatidos em frigoríficos com inspeção oficial no estado de São Paulo, além de caracterizar seus sorovares.
- Determinar a resistência das cepas isoladas aos principais compostos antimicrobianos.
- Determinar o perfil molecular de cepas isoladas através da técnica de *MultiLocus Sequence Typing* (MLST) e comparar os perfis encontrados com as diferentes origens dos lotes analisados e dados da literatura.

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Capítulo 2

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***Salmonella* in pig's mesenteric lymph nodes**

Multilocus sequence typing and antimicrobial resistance characterization of *Salmonella* isolates from mesenteric lymph nodes of swine.

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Introduction

Pork stands as an important protein source for the population, being the most consumed meat in the world, with its production surpassing 100 million tons/year. Brazil stands in the fourth position in the global production and exportation ranking, and slaughtered in 2014 more than 32 million swine under federal inspection (1).

In this context, concern about food safety is necessary to ensure the supply of pathogen-free products thereby preventing the occurrence of foodborne pathogens. Among the main microorganisms associated with these diseases, we can highlight *Salmonella*, being the most incident and responsible for the highest number of deaths in the United States (19).

Hald et al. (25) highlights the consumption of pork as an important factor in food-associated pathogens. Among the red meats, pork is the most frequently associated with *Salmonella*, and is closely related to its production chain, from farm to fork, being detected in several steps of production and raw materials (35, 42, 54, 56).

The isolation of *Salmonella* in mesenteric lymph nodes of pigs is used to evaluate the carrier status of the animal (6). The infection by these bacteria occurs primarily orally, with mesenteric lymph nodes acting as barriers, but later becoming pathogen reservoirs, which can survive intracellularly in macrophages and neutrophils until physiological changes triggered by stress, such as the release of catecholamines and changes in intestinal motility, propitiate its fecal release in few hours (47). This can lead to the contamination of the industrial environment and retail

market products if slaughterhouse steps fails to prevent cross-contamination (37, 41).

Other important concern about salmonellosis transmitted by animal origin products is the occurrence of antibiotics resistant strains, exacerbated if the drugs that are concomitantly used in the treatment of animals and humans are considered (49)

Although promotes self-limiting infection in most cases, and do not require treatment with antibiotics, sometimes nontyphoidal *Salmonella* can cause more severe illnesses, especially when there is impairment of more systems than the gastrointestinal tract. In these situations, the use of drugs is necessary to safeguard the life of the affected individual (4, 40). Several studies have reported the isolation of *Salmonella* strains that are resistant to the main groups of antimicrobials, used both in animal production and the treatment of humans (14, 23, 49, 53). Ampicillin, sulfonamides, streptomycin and tetracycline are highlighted as ineffective drugs for many of these strains, and special attention is given to a high prevalence of multi drugs resistant (MDR), when four or more compounds are ineffective (40).

The determination of the contamination sources, as well as the distribution of the pathogen through livestock is of fundamental importance to understand its epidemiology and design effective control measures, however the great variability of serotypes isolated in swine production, associated with the large number of vectors and asymptomatic carriers, substantially hinder the determination of bacterial origin (33). For this reason, several alternatives have been developed, to help with a better discrimination of *Salmonella* serotypes and other microorganisms.

Among then, MLST is highlighted as an interesting tool to evaluate the genetic diversity and genealogy of the isolates, and provide substantial epidemiological and evolutionary data. This technique is based on sequencing seven housekeeping genes in the bacterial genome, to determine which allele of each particular gene is present in the sample, assigning a number to each one studied. Thus, each sample receives a sequence of seven numbers, which will determine its sequence type (ST). The alleles for each gene, and the cataloged STs are available online at <http://mlst.warwick.ac.uk/mlst/dbs/Senterica> and this database can be supplied by many research institutions, allowing the comparison of different isolates from different sources and geographical regions (31). *Salmonella* MLST data in Brazil is currently scarce, even more when related to swine isolates, and can provide relevant information about the epidemiology of the pathogen.

The aim of this study was evaluate the prevalence of *Salmonella* in pigs slaughtered under official inspection in São Paulo state – Brazil, and determinate the resistance of the isolates to the main antibiotics compounds of animal production and human therapeutics, besides the MLST characterization of the main serovars found.

Materials and Methods

- Samples collection

Mesenteric lymph nodes of 250 pigs were collected from 25 different batches of animals slaughtered in four plants with official inspection from São Paulo state, which were individually packaged in sterile plastic bags, and sent in cool boxes with ice to the laboratory. The animals were randomly selected and distributed throughout

the industrial batch processing, respecting an interval of at least three animals among the chosen. Each batch was raised in a different farm, and they were originated from 22 cities of 4 states in south and southeast of Brazil (figure 1). The sample size was estimated with the help of OpenEpi software (48), assuming a confidence interval of 95% and a 5% confidence limit. The population parameter was estimated based on the data from the Brazilian Institute of Geography and Statistics (IBGE) for livestock production, considering the number of animals slaughtered in the state of São Paulo in 2013 (1.7 million animals) (30) and an estimated prevalence for *Salmonella* of 20% in mesenteric lymph nodes (8, 44).

- Samples processing

The surface of the lymph nodes was cleaned with alcohol 70° GL and individual samples were sliced in petri dishes with a scalpel, both sterile, in laminar flow hood. Material portions of 10g were obtained from each animal.

- *Salmonella* research

The isolation of *Salmonella* occurred in accordance with the methodology recommended by Andrews et al. (3). For each 10g samples of lymph node was added 90 mL of buffered peptone water 1% (BPW 1% - Oxoid). After homogenization in stomacher (400 circulator - Seaward - UK) the mix was incubated at 36°C for 18 – 24 hours, for the pre-enrichment step. Posteriorly, 0.1 mL and 1.0 mL of the mix was transferred to 10 mL of the selective enrichment broths Rappaport-Vassiliadis (RV - Difco) and Tetrathionate (TT - Oxoid) respectively, being incubated at 42°C for 18 – 24h. Both culture media were then striated at the surface of petri dishes with

Bismute Sulphite agar (BS - Oxoid) and Xylose Lysine Deoxycholate agar (XLD - Oxoid), which were incubated at 36°C for 18-24h. Typical colonies were peaked in Triple Sugar Iron (TSI - Oxoid) and Lysine Iron Agar (LIA - Oxoid), being both incubated at 36°C for 18-24h. At least, the polyvalent antiserum O and H (Probac) was used to confirm the characteristic samples in biochemical tests.

The isolates were sent on nutrient agar (Difco) to the Enteropathogens Laboratory of the Instituto Adolfo Lutz for confirmation and determination of serotype with agglutination of specific *Salmonella* antisera produced by the institution according to the standardized methodology. The serotype was defined by the characterization of its somatic and flagellar antigens according to the Kauffmann-White-LeMinor scheme (24).

- Antibiotics resistance determination

The antimicrobials were chosen based on the Clinical Laboratory Standards Institute (CLSI) guidelines (17), using the agar diffusion method as recommended by Kirby & Bauer (7). The strains were suspended in sterile saline (0.85% NaCl) to obtain turbidity compatible with the 0.5 McFarland scale level (approximately 1.5×10^8 CFU / mL). The bacterial suspension was seeded on the surface of Mueller-Hinton agar plates (Oxoid), with the aid of a sterile swab, and to these were added antibiogram discs of the compounds to be tested. The plates were incubated at 35 °C for 18h. After this period, the inhibition zones were read and the results were interpreted as resistant (R), intermediate resistant (R) or susceptible (S) according to the CLSI Manual, thus allowing to infer the effectiveness of antimicrobials. The

chosen compounds were ampicillin (10 µg), cefepime (30 µg), cefotaxime (30 µg), cefoxitin (30 µg), ceftazidime (30 µg), ceftriaxone (30 µg), meropenem (10 µg), aztreonam (30 µg), amikacin (30 µg), gentamicin (10 µg), streptomycin (10 µg), nalidixic acid (30 µg), sulfonamides (300 µg), trimethoprim-sulfamethoxazole (01.25 / 23.75 µg), chloramphenicol (30 µg), and tetracycline (30 µg) (17). All resistant or intermediate resistant strains were considered non-susceptible to the referred antibiotic (36).

- MLST

MLST was performed using seven conserved housekeeping genes (*aroC*, *dnaN*, *hemD*, *hisD*, *purE*, *sucA* and *thrA*). The detailed protocol of the MLST procedure, including the housekeeping gene's amplification primers and the annealing temperatures, is available in the MLST database (<http://mlst.warwick.ac.uk/mlst/dbs/Senterica>). All amplifications were performed in a total volume of 50 µL as described by Souza et al. (46). A sample of the complete mix, without the DNA, was used as a negative control in all runs.

- Statistical analysis

The prevalence and 95% confidence limits (CL95%) of *Salmonella* were calculated considering the 250 animals and posteriorly the 25 batches of the study, being considered positive the batches with one or more positive results. The calculations were made with the PROC FREQ procedure of the Statistical Analysis Software – SAS 9.4 (43).

Results and Discussion

Salmonella was isolated in 91 samples, resulting in a prevalence of 36.4% (CL95% 30.4 – 43.4). Bessa et al. found 37.3% (CL95% 32.4 – 43.4%) of positives (8), and Silva et al. (44) reported a lower prevalence, of 19.4% in similar studies. This differences can be associated to several factors, but some can be highlighted, such as the kind of production cycle (when animals can be subjected to different handling stress due to the mixture of different batches and ages), the number of animals transported at the same time in the trucks and the waiting time in the slaughterhouse stalls (9, 44). If we take into consideration batches when the pathogen was isolated in at least one sample, 72% (18/25, CL95% 50.6 – 87.9%) of then were positive.

For the 91 isolates, 67 were serotyped, revealing 9 different serovars (table 1). The main serovars were *S. Typhimurium* (n=13) and its monophasic variant *Salmonella enterica subsp. enterica* 1.4,5,12:i:- (n=12), followed by *S. Infantis* (n=12) and *S. Havana* (n=11).

S. Typhimurium was isolated in two batches from slaughterhouse 1, one batch from slaughterhouse 3, and 2 batches from slaughterhouse 4 (total of 5 batches from 3 slaughterhouses). Its isolation is constantly related to animal origin food, specially pork meat, being a main serovars involved in human outbreaks and standing as one of the most prevalent worldwide (5, 9, 27, 38, 51). Monophasic strains of this serovar, such as *S. 1.4,5,12:i:-* had gained notoriety in the last years,

being considered an important emergent pathogen (21). Its isolation had raised substantially and several outbreaks had been reported (5, 12, 28, 38). In our research, *S. 1.4,5,12:i:-* was recovered from two batches in slaughterhouse 1 and three batches in slaughterhouse 3 (total of five batches in 2 slaughterhouses).

S. Infantis is also closely related to pork production (16, 20). It was isolated in two batches from slaughterhouse 1 and two batches from slaughterhouse 4 (total of 4 batches in 2 slaughterhouses). Although this serovar is considered to have less virulence factors than Typhimurium (52), its association to human salmonellosis is frequent (2, 16, 20).

S. Havana is less associated with pork production chain, with few relates of its isolation in swine (14, 55). In this research, all isolates were from only two batches, raised in the same city and processed in slaughterhouse 1. The possibility that these isolates represents a local circulating strain must be considered.

Among the analyzed antibiotics, streptomycin and tetracycline were the less effective, followed by ampicillin and sulfonamides and chloramphenicol (table 1). The isolation of resistant strains to this antibiotic classes are of concern for the scientific community and public health organs, as this drugs are widely used both in human and animal therapeutics (29). Several studies have reported the isolation of similar resistance patterns (23, 32, 38, 49, 55). The most effective drugs were aztreonam and cefoxitin (table 1). The selective pressure made by the intense use of antibiotics through the years can be associated with the resistance to the earlier developed drugs, in comparison to the most recent compounds (55).

Most of the isolates were MDR (64/91 – 70.3%). Two isolates were resistant to ten antimicrobials simultaneously, six strains were resistant to nine antimicrobials

and eleven were resistant to eight strains. This could be associated with the presence of plasmids and integrons, which can transmit clusters of several resistance genes simultaneously from strain to strain, and have been studied and reported in swine isolates with elevated MDR rates (10, 22, 45).

Eight strains were selected for the molecular typing with MLST (Table 2). The five chosen *S. Typhimurium* strains were classified as ST 19. This is the main ST for this serovar, corresponding up to 74% of the isolates, and its ST complex (isolates with similar STs) represented 93% of *S. Typhimurium* strains in MLST database (34). This ST was isolated in different countries from many sources, including diseased humans (15, 18, 39, 50). The *S. 1.4,5,12:i:-* sample was also characterized as ST 19. The sharing of the same ST by both serovars is related to their genetic similarity (11), and reinforces the importance of the epidemiological surveillance for both classical and monophasic variants of *S. Typhimurium*.

The two *S. Infantis* samples analyzed belonged to ST 32. Its isolation is also reported in humans and animal sources (2, 15, 16). The same occurred for the *S. Derby* isolate evaluated (ST 40) (13, 26). Both STs of these strains stands among the most frequently reported in literature, suggesting that they are the main MLST profiles for these serovars.

The high prevalence of *Salmonella* in swine mesenteric lymph nodes, with the presence of STs which are clearly related to human gastroenteritis, isolated from bathes of distinct origins and slaughtered in different plants, associated with the high levels of antibiotics resistance, is an alarming fact as regards public health, indicating that swine production chain fails to control this pathogen dissemination, being a potential source for the occurrence of salmonellosis. Efforts must be spent to mince

the chance of *Salmonella* transmission by pork products and prevent new infections and outbreaks.

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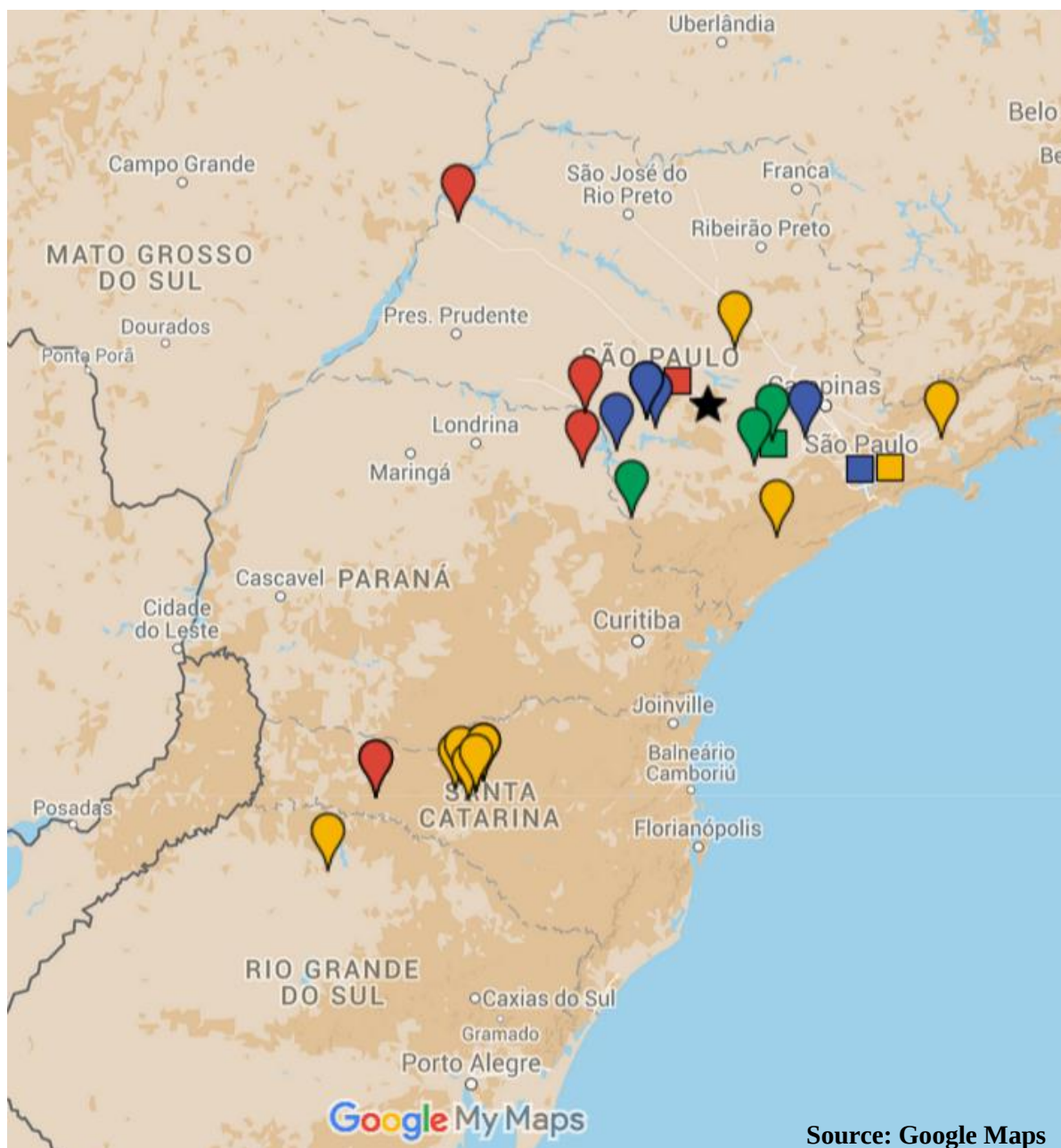


FIGURE 1 – Geographical localization of the slaughterhouses and city of origin for the swine batches evaluated for Salmonella presence in the mesenteric lymph nodes.

- Squares indicate the slaughterhouses localizations, balloons indicate the origin cities of the batches and the star indicates the laboratory location (Botucatu City, SP)
- Markers (squares and balloons) with similar colors indicates that the batch was processed in the respective slaughterhouse

Table 1 – Number of samples and antibiotic resistant strains for the serovars isolated in mesenteric lymph nodes of swine in São Paulo state - Brazil

Serovar	n of isolates	amp	cpm	ctx	cfo	caz	cro	mer	atm	ami	gen	est	nal	sul	sut	clo	tet	MDR*
S. Typhimurium	13	8	1	2	0	1	0	2	1	1	3	7	8	8	7	8	9	9
S.l.4,5,12:i:-	12	7	2	2	0	3	1	2	0	2	4	7	2	8	11	5	12	10
S. Infantis	12	7	0	1	0	1	3	4	0	4	2	6	2	4	3	6	6	5
S. Havana	11	3	1	1	1	2	1	2	0	1	2	7	0	3	0	3	0	4
S. Panamá	7	7	0	0	0	0	0	2	0	3	0	5	7	7	7	7	7	7
S. Derby	6	1	1	1	0	1	0	4	1	4	0	6	0	2	1	0	6	5
S. Bovismorbificans	4	4	0	1	0	0	1	2	0	0	0	4	0	4	2	3	4	4
S. Coeln	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S. Newport	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Not serotyped	24	20	2	2	2	1	1	1	1	3	8	19	18	21	7	19	18	20
Total	91	57	7	10	3	9	7	19	3	18	19	62	37	57	38	51	62	64

amp = ampicillin (10 µg), cpm = cefepime (30 µg), ctx = cefotaxime (30 µg), cfo = ceftiofur (30 µg), caz = ceftazidime (30 µg), cro = ceftriaxone (30 µg), mer = meropenem (10 µg), atm = aztreonam (30 µg), ami = amikacin (30 µg), gen = gentamicin (10 µg), est = streptomycin (10 µg), nal = nalidixic acid (30 µg), sul = sulfonamides (300 µg), sut = trimethoprim-sulfamethoxazole (01.25 / 23.75 µg), clo = chloramphenicol (30 µg), tet = tetracycline (30 µg)

*Multi Drug Resistant

Table 2 – City of origin, ST characterization and antibiotic resistance pattern of *Salmonella* strains isolated from swine mesenteric lymph nodes submitted to MLST analysis.

Serovar	Slaughterhouse	City/State	ST	Number of resistant antibiotic	Resistance Pattern
Typhimurium	1	Quatiguá/PR	19	8	amp clo ctx mer nal sul sut tet
Typhimurium	1	Ourinhos/SP	19	5	clo nal sul sut tet
Typhimurium	3	Boituva/SP	19	1	ctx
Typhimurium	4	Jambeiro/SP	19	6	amp clo est nal sul tet
S.1.4,5,12:i:-	1	Quatiguá/PR	19	10	amp caz clo cpm cro ctx est sul sut tet
Infantis	1	Xavantina/SC	32	4	amp clo sut tet
Infantis	4	Jambeiro/SP	32	5	ami caz est gen mer
Derby	2	Arantu/SP	40	4	atm est mer tet

amp = ampicillin (10 µg), cpm = cefepime (30 µg), ctx = cefotaxime (30 µg), caz = ceftazidime (30 µg), mer = meropenem (10 µg), atm = aztreonam (30 µg), ami = amikacin (30 µg), gen = gentamicin (10 µg), est = streptomycin (10 µg), nal = nalidixic acid (30 µg), sul = sulfonamides (300 µg), sut = trimethoprim-sulfamethoxazole (01.25 / 23.75 µg), clo = chloramphenicol (30 µg), tet = tetracycline (30 µg).

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micrometer, μm micromole, μmol milliequivalent, meq milligram, mg milliliter, ml millimeter, mm millimolar, mM minute(s), min molar, M mole, mol most probable number, MPN nanometer, nm normal, N number, no. parts per billion, ppb parts per million, ppm percent, % PCR (never spelled out: polymerase chain reaction) pound, lb pounds per square inch, lb in² revolutions per minute, rpm second, s species (singular), sp. species (plural), spp. specific activity, sp. act UV (never spelled out: ultraviolet) volume, vol weight, wt

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