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Canada

Distribution of *Streptococcus suis* (from 2012 to 2014) and *Actinobacillus pleuropneumoniae* (from 2011 to 2014) serotypes isolated from diseased pigs

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Streptococcus suis is an important pathogen of swine and serotype determination remains a valuable tool for veterinary practitioners and/or diagnosticians to understand the epidemiology of the infection and to evaluate the need for serotype-specific vaccines in a herd (1). Due to the fact that we have a reference laboratory for *S. suis* serotyping, more than 60% of worldwide data on serotype distribution is from Canada (2). From January 2012 to December 2014 a total of 472 isolates were received in our laboratory for serotyping. Except for a few isolates that came from Ontario, most isolates originated from the Diagnostic Service of the Faculty of Veterinary Medicine of the Université de Montréal and from provincial laboratories. All isolates originated from tissues of diseased pigs with a variety of clinical signs such as respiratory and nervous signs, septicemia with sudden death, arthritis, and endocarditis. Serotyping was carried out by using a coagglutination test. Untypable isolates were tested by polymerase chain reaction (PCR) for the identification of *S. suis* species and for further serotyping (2,3).

The distribution of serotypes is presented in Table 1. These data are not intended to suggest that *S. suis* was the sole causative agent of the pathological conditions. There are some differences from previously reported data (3), although serotypes 2, 1/2, 3, 4, 5, 7, and 8 are still among those more frequently detected. For example, the frequency of detection of serotype 3 clearly decreased, while that of serotype 9 increased, a tendency already observed in 2011 (3). As previously reported, although serotype 2 is the most frequently described serotype worldwide, it is isolated at a relatively low frequency in Canada, indicating a lower virulence than that of Eurasian serotype 2 isolates (1). Although serotypes 20, 22, 26, 32, 33, and 34 have been suggested to be a species different from *S. suis* (2), isolates belonging to these serotypes (with the exception of serotype 20) were still identified in this study. Strains belonging to serotypes 17, 24, or 29 were also absent during the studied period. The percentage of untypable strains was < 20%, as previously reported (3). It seems that there is no clear justification for the characterization of new serotypes.

Table 1. Distribution of serotypes of 472 strains of *Streptococcus suis* recovered from diseased pigs during the 3-year period 2012–2014

Serotype	%	Serotype	%
1	4	18	1
1/2	10.5	19	1
2	13.5	20	0
3	7	21	1
4	7	22	4.5
5	2	23	3
6	< 1	24	0
7	6	25	< 1
8	5	26	0
9	4	27	< 1
10	< 1	28	< 1
11	< 1	29	0
12	< 1	30	1
13	< 1	31	< 1
14	2.5	32	< 1
15	< 1	33	< 1
16	1.5	34	< 1
17	0	UT	18.5

UT — untypable.

Porcine pleuropneumonia caused by *Actinobacillus pleuropneumoniae* (App) is a contagious disease reported to cause economic losses worldwide (4). Serotyping is still of major interest for App since different serotypes have different virulence potential, depending on the geographical origin (5). In addition, serological surveillance to detect sub-clinically infected animals in conventional herds must be directed towards the most important serotypes causing disease in pigs in a given country or continent. Importantly, during the last 20 y, almost no data are available from most countries (including Canada) concerning

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Table 2. Distribution of serotypes of 134 strains of *Actinobacillus pleuropneumoniae* recovered from diseased pigs during the 4-year period 2011–2014

Serotype	Number of isolates	%
1	6	4.5
2	6	4.5
5	52	39
7	50	37
8	11	8
12	9	7

the distribution of prevalent serotypes of App recovered from diseased animals (5). Hence, it is unknown if past data are still pertinent (6). From January 2011 to December 2014 a total of 147 strains biochemically identified as App and isolated from lungs of diseased pigs with respiratory signs, that were sent to the App serotyping laboratory at the Diagnostic Service of the Faculty of Veterinary Medicine of the Université de Montréal, were analyzed. Twelve strains belonged to a species different from App by molecular typing (5). One strain was characterized as an atypical biotype II App, and is still under characterization. The remaining 134 strains were further serotyped by serological and molecular techniques (5). The distribution of serotypes is presented in Table 2. Almost 80% of isolates belong to either serotype 5 or serotype 7, in similar proportions, followed by serotypes 8 and 12 and then by serotypes 1 and 2. This distribution is highly different from that in the last published report, dating more than 20 y ago (6), in which serotype 1 (68%) was followed by serotype 5 (23%), and all other serotypes together represented 9%. The dramatic reduction of serotype 1 isolates may be due, at least in part, to the serological control of breeders in Quebec and Ontario through different programs applied during the intervening years. Interestingly, cases due to serotypes 8 and 12 mainly occurred in high health status herds. Serotype 2 isolates, although responsible for clinical diseases and mortality, still lack one of the toxins typically absent in North American isolates, but produced by highly virulent European serotype 2 strains (5). Although not present during the studied period, isolates of serotypes 4 (once), 6 and 15 have previously been recovered in Canada (4). Detection of herds subclinically infected with App is highly important to prevent the introduction of the infection into naïve herds. In this regard, serology should be used to perform routine surveillance of possibly infected herds. Data presented in this report suggest that herds should be priority tested for serotype 1 (to prevent it from reappearing) as well as serotypes 5 and 7. High health status herds should be, if possible, free of all serotypes.

References

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