Interpreting culture reports from swine lungs

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From time to time, practicing veterinarians ask for help in interpreting results of bacteriologic examination of lung samples. Usually, the practitioner has necropsied an affected pig and sent a section of pneumonic lung or a swab to the diagnostic laboratory for bacterial culture. When the culture results are received, they may not point to a clear-cut diagnosis. At this point, the significance of isolating a certain organism from the lung is questioned. Many researchers have examined the relationship of infectious agents to the presence of pneumonia. Twenty-two publications report results of microbiologic surveys of swine lungs.[1–22] All but three studies included bacterial/mycyoplasmal evaluation; some also tested for viruses and parasites. The findings of these studies are presented in Table 1 (next page). The frequency of isolation of the 10 most common bacteria from normal and pneumonic lungs are summarized in Table 2. A Chi-square test was used to test for the bacterial isolation rates between grossly abnormal and normal lungs.

Actinobacillus pleuropneumoniae and *Salmonella cholerasuis* were only isolated from lungs with gross abnormalities. *Pasteurella multocida* was isolated 4.7 times more frequently in lungs with gross abnormalities than in normal lungs. Similarly, *Bordetella bronchiseptica* was 2.5 times more likely to be isolated from pneumonic lungs than from those with no abnormal regions. Streptococcal and staphylococcal organisms were isolated more frequently from normal lungs than abnormal lungs (Table 2).

It appears that little or no clinical significance can be attached to the isolation of *Actinomyces pyogenes*, *Mycoplasma hyopneumoniae*, *Mycoplasma hyorrhinis*, coliforms, streptococcal species, or staphylococcal species. If the streptococcal organism has been further characterized as *Streptococcus suis*, it may be a greater contributor to the pneumonia complex; however, *S. suis* is commonly recovered from tonsils of normal swine.[23] Conversely, when *A. pleuropneumoniae*, *S. cholerasuis*, or *P. multocida* are found, they are likely to be an important contributor to the disease process.

For practitioners, the problem with trying to interpret a single lung culture lies in the fact that most bacteria can be found in both healthy and diseased lungs. When several lungs are sampled, and culture results examined, a more definite pattern emerges. Another indication of etiologic contribution is whether an organism is found in relatively pure culture or whether it is one organism among many isolated. Heavy growth of *S. suis* with an occasional coliform supports a diagnosis of a streptococcal component much more strongly than a mixed culture with a few *S. suis*, a few coliforms, and an occasional *A. pyogenes*. The addition of histopathologic examination also assists with interpretating the results. The general rule is that compatible lesions plus organism identification indicate an active disease process.

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Diagnostic notes are not peer-reviewed.

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Table 2

Relative frequency of isolation of common infectious agents from grossly normal and grossly pneumonic swine lungs in 21 studies: 1922–1990 (3286 pneumonic lungs, 584 normal lungs)

Percent of normal lungs with organism	Organism	Percent of pneumonic lungs with organism	Relative risk ratio
6.8	*P. multocida*	30.9	4.5
16.3	*M. hyopneumoniae*	29.4	1.8
2.1	*B. bronchiseptica*	3.8	1.8
7.9	*M. hyorhinis*	13.6	1.7
0.2*	*A. pleuropneumoniae*	1.8	10.4
0.2*	*S. cholerasuis*	1.0	5.9
8.8	Coliforms	7.9	0.9
23.6	*Streptococcus*	13.8	0.6
9.4	*Staphylococcus*	5.0	0.5

* 1:584 assumed to avoid zero

Table 1

Infectious agents associated with pneumonia in swine

Reference	1		2		3	4	5	6	7		8		9	10		11	12		13	14		15	16		17	18	19	20	21	22
Year	1922		1940		1947	1953	1953	1954	1961		1975		1976	1975		1976	1980		1981	1981		1982	1982		1985	1986	1990	1990	1990	1990
Lung condition	P	N	P	N	P	P	P	P	P	N	P	N	P	P	N	P	P	N	P	P	N	P	P	N	P	P	P	P	N	P
Number of samples	314	100	166	38	100	30	49	108	86	15	65	44	44	68	11	685	237	172	50	231	116	143	97	17	334	205	208	297	51	440
Bacteria:																														
A. pleuropneumoniae									2				9			1				2					2	31	1	10		+
P. multocida	54	4	27		55	17		58	41		+	+	32	37	27	18	17	1	80	48	20	1	34	12	34	33	11	32		+
B. bronchiseptica	3	3			5			40	1	13	+	+		2		2	+	+								4	13	2	4	+
Salmonella spp.					5	3	+	25	1																					
Streptococcus spp.	35	12	40	1	5	17	+	40	41	33	+	+	20	44	27	4	+	+		18	12	1	3			15	15	+	86	+
Staphylococcus spp.			1		5	3	+		23	53	+		5	3							7		3	6		5	52		59	+
A. pyogenes					35		12		9	20			16	3		+			2	13						4	2		16	
H. parasuis											+	+		2									2	6	2			+	4	+
Haemophilus spp.						3	10	5								7	+					7			24					
Pseudomonas					3			3																			4		10	
Coliforms			7		10		+		9	20	+		6							11	13					18	75		50	+
Klebsiella												+		19	27													+	28	
Proteus									5	13	+			2													10			
Listeria								1	1																					
Fusobacterium																				1										
Bacillus													16	1	9								2							
Micrococcus														15	18				6											
Diplococcus			6					6						4			+													
Neisseria														4																
Mycoplasma:																														
M. hyopneumoniae											+		57	53	27		27	26	54	1		22	93	35	24			37		
M. hyorhinis									51	7	+	+	16	69	36		17	10	52	10	1	9	16	18						+
M. arginni														12						1			18	29						
M. hyosynoviae														4			8													
Viruses:																														
pseudorabies																														
influenza											+																			+
TGE																														
resp. corona virus																														
adenovirus											+	+																		
enterovirus											+																			
cytomegalovirus																														
reovirus											+	+																		
Helminths:																														
Ascaris suum											+	+																		
Metastrongylus											+																			

P Grossly pneumonic

N Grossly normal

\+ less-frequently isolated organisms in unstated percentages

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