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The occurrence of chlamydiae in German holdings of South American camelids

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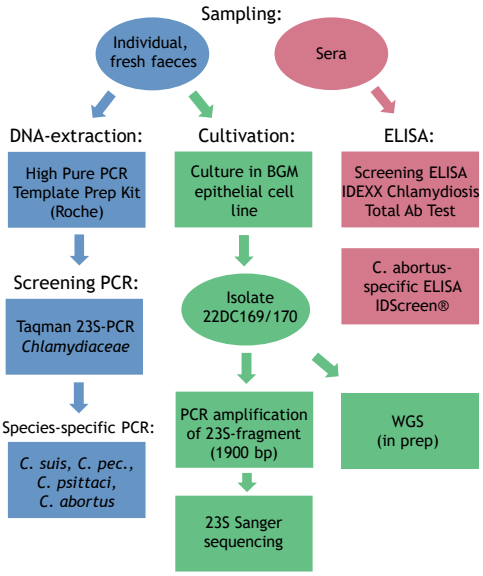
Background

South American camelids (SAC) are kept in Europe in increasing numbers for wool-production, leisure activities, therapy, landscape conservation or breeding. Although they often live in close contact to humans and livestock, little is known about zoonotic and epizootic agents that could affect their health or reservoir status. Since chlamydiae are important endemic pathogens residing in the reproductive or gastrointestinal systems of the closely related ruminants, they were targeted in a systematic investigation of llamas and alpacas in ten representative holdings crossover Germany.

Workflow



Tab 2. ELISA screening (IDEXX Chlamydiosis Total Ab Test) in ten German SAC holdings

Flock	Samples	IDEXX pos.	% Seroprevalence Chlamydiaceae
1	38	7	18,4
2	23	6	26,1
3	22	3	13,6
4	40	4	10,0
5	17	0	0,0
6	30	5	16,7
7	38	2	5,3
8	34	7	20,6
9	20	0	0,0
10	30	5	16,7
Total	292	39	13,4
95 % CI			9.5-17.3

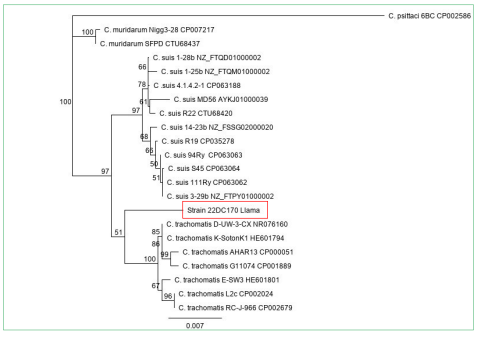


Fig. Phylogenetic reconstruction (Geneious Alignment, Jukes-Cantor, Neighbour-Joining) based on a 1900 bp 23S-fragment of the new isolate 22DC170, and GenBank-derived *C. suis*, *C. trachomatis* and *C. muridarum* strains. *C. psittaci 6BC* was used as an outgroup.

Tab 1. Chlamydia detection and typing in ten German SAC holdings by rtPCR (*C. pec.* - *C. pecorum*)

Flock	Flock size	Contact livestock	Diseases	Samples	*Chlamydiaceae*	% *Chlamydiaceae*	*C. pec.** pos.	% *C. pec.**	*C. suis* pos.	% *C. suis*
1	105	diverse	diarrhea, weak offspring	38	15	39,5	4	26,7	5	33,3
2	23	poultry, sheep	none	23	4	17,4	0	0,0	2	50,0
3	98	none	none	22	1	4,5	0	0,0	1	100,0
4	121	cattle	none	40	16	40,0	4	25,0	9	56,3
5	57	none	none	20	0	0,0	0	0,0	0	0,0
6	100	horses	none	30	5	16,7	2	40,0	2	40,0
7	301	none	abortions	38	8	21,1	1	12,5	4	50,0
8	36	none	none	34	17	50,0	0	0,0	16	94,1
9	70	none	none	20	0	0,0	0	0,0	0	0,0
10	62	none	none	30	13	43,3	3	23,1	7	53,8
Total	973			295	79	26,8	14	17,7	46	58,2
95 % CI						21.7-31.9		9.3-26.1		46.1-67.9

Results

Shedding of chlamydiae was detected in eight of ten SAC holdings and in 26.8% of animals (n=79, 95% CI 22.0-32.2%). The positivity rate was similar in llamas (28.0%) and alpacas (26.2%). Typing with species-specific PCR identified *Chlamydia (C.) suis* as the predominant species with 58.2% of *Chlamydiaceae*-positive samples, followed by *C. pecorum* with 17.7%. No *C. abortus*- or *C. psittaci*-specific DNA was detected. 26.6% of samples could not be typed, probably due to low DNA-content.

Two isolates were recovered from a flock with high chlamydial loads (Cq values 22) and further characterized by sequencing of a 1900 bp fragment of the 23S-rRNA gene. Phylogenetic analysis revealed that the isolates clustered in the *C. trachomatis*/*C. suis* clade, but apart from porcine *C. suis and* human *C. trachomatis* isolates. Ongoing WGS-based typing will allow to determine the exact phylogenetic position of the new agent.

Chlamydiaceae-specific antibodies were detected in the eight PCR-positive holdings. The overall seroprevalence was 13,4 %. The sera did not contain antibodies against *C. abortus* (IDScreen negative).

Conclusions

Our findings suggest that South American camelids are carriers of chlamydiae and that a *C. suis*-like agent predominates in faecal shedding. Its pathogenic and zoonotic impact remains to be elucidated. No evidence of the occurrence of the abortion pathogen *C. abortus* was found.

Acknowledgement

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