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#### Summary

Zusammenfassung

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# Prevalence and risk factors for Maedi-Visna in sheep farms in Mecklenburg-Western-Pomerania

Prävalenz und Risikofaktoren von Maedi-Visna bei Schafen in Mecklenburg-Vorpommern

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Despite indications of a considerable spread of Maedi-Visna among sheep flocks in Germany, prevalence studies of this important infection are hardly available. Prior to any health schemes and guidelines, knowledge about regional disease distribution is essential. Depending upon herd size, 70 farms were randomly selected, of which 41 cooperated. A total of 2229 blood samples were taken at random and serologically examined. For assessment of selected farm characteristics a questionnaire exercise was conducted at all farms involved. The average herd prevalence is 51,2%, the within-herd prevalence is 28,8%. In the unvariate analysis of risk factors, small (10–100 sheep) and large (> 250 sheep) farms are more MVV-affected than medium sized farms. The average stable and pasture space per sheep is larger at non-infected- compared to infected farms. Owners judgement on general herd health turns out to be better at non-infected compared to infected farms. Taking infected farms only, the risk of within-herd prevalence above 20% is significant higher in crossbred than in purebred flocks.

**Keywords:** maed-visna, prevalence, sheep, risk factors, Mecklenburg-Western Pomerania

Systematische Untersuchungen auf Maedi-Visna in Schafbeständen wurden in Deutschland bislang kaum durchgeführt, obgleich die Infektion eine substantielle Gefahr für die Herdengesundheit darstellt und von einem hohen Infektionsrisiko auszugehen ist. Vor der Verabschiedung von Landes-Sanierungsrichtlinien wurde die Durchführung einer solchen Untersuchung für zwingend erforderlich gehalten.

Abgestuft nach Bestandsgröße, wurden siebzig zufällig selektierte Schafhalter im Land ausgewählt, wovon 41 kooperierten. Parallel zu Entnahme von insgesamt 2229 zufällig entnommenen Einzeltierproben und der serologischen Untersuchung auf Maedi-Visna, wurden Informationen zur Bestandscharakteristik mittels Fragebogen erfaßt, Die durchschnittliche Herdenprävalenz über alle Bestandskategorien hinweg beträgt 51,2 %, – die durchschnittliche Einzeltierprävalenz in infizierten Betrieben 28,8 %. Bei der univariaten Analyse von Risikofaktoren zeigt sich, daß kleine (bis 100 Tiere) und große (> 250 Tiere) Herden stärker durchseucht sind als mittelgroße Herden. Die verfügbaren Stall- und Weideflächen je Tier sind bei nicht infizierten Herden tendenziell größer als bei durchseuchten Beständen. Herdengesundheitsparameter inkl. das Verlammungsrisiko werden bei infizierten Beständen von den Besitzern schlechter eingeschätzt als bei Nicht-infizierten. Innerhalb der Gesamtheit infizierter Betriebe ist das Risiko von Einzeltierprävalenzen > 20 % in Gebrauchskreuzungen signifikant höher als in Herdbuchbeständen.

Schlüsselwörter: Maedi-Visna, Prävalenz, Schafe, Risikofaktoren, Mecklenburg-Vorpommern



### Introduction

Maedi-visna virus (MVV) is classified as a lentivirus of the retroviridae family. The name of the disease is formed by the two Icelandic words that describe the clinical signs it produces - maedi ("laboured breathing" affecting the lungs) and visna ("shrinking" or "wasting" affecting the central nervous system). The world organisation for animal health (OIE) also uses the terms ovine- or chronicor marsh's progressive pneumonia, respectively. The virus can infect sheep at any age, but signs of the disease are not usually seen until at least three years of age. These may include pneumonia, weight loss, joint problems, mastitis and in rare cases, nervous signs. In goats, the main clinical sign of Caprine-Arthritis-Encephalitis (CAE) is lameness. Weight loss and shrinkage of the udder may also be present. It has been demonstrated that MVV can infect goats, and CAEV can infect sheep (Castro et al., 1999, Zanoni, 1998). However, it is unclear how and to what extent infection crosses the species barrier. The most likely risk factors are ingestion of viruscontaminated ovine colostrum and milk by goats and vice versa, as well as a close contact between the species in overstocked barns (Peterhans et al., 2004).

MVV spreads easily between sheep and can cause high economic losses. A Scottish report on MVV estimates 10–20% adult mortality once clinical signs are present (www.sac.ac.uk/main). Peterhans et al. (2004) describe the infection and its economic consequences as an interaction of MVV with the host as well as herd management, genetic factors, breed, husbandry practices and co-infections. Subclinical MVV-infection can be a gateway for a range of serious herd health problems (Behrens, 1987). MVV commonly coincides with diarrhea, lung affections, internal parasites, poor body condition and reproductive performance of different causal origin.

As neither antiviral treatment nor vaccination is available, diagnostic tests are the backbone of most of the schemes implemented to prevent the spread of MVV (Pépin et al., 1998).

Considering studies on the occurrence of the Infection in sheep around the globe, herd and within-herd prevalence rates vary between 1 and 90% and 3 and 70%, respectively (Schaller et al., 2000; Sihvonen et al., 1999; Kita et al., 1990; Cutlip et al., 1992; Simard and Morley, 1991; Baumgartner et al., 1990; Madewell et al., 1987; Caporale et al., 1983).

In Germany, no systematic MVV-screening was performed, neither at the national nor at the regional level. Graber and Ganter (2005) concluded from a retrospective study that merely 0.21% of German sheep and 0.93% of flocks are MVV-accredited. Apart from few random sampled breeding flocks in some federal states, little knowledge exists on the prevalence of MVV among sheep. Before adding to the already existing about two dozen different lentivirus-health schemes and guidelines for sheep and goats masters, offered by respective authorities, a representative MVV-screening in Mecklenburg-Western Pomerania (M-V) was targeted.

## Questionnaire for Maedi-Visna – Screening M-V 2009

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FIGURE 1: Maedi-Visna-Questionnaire M-V 2009.

# **Material and Methods**

#### Sampling and diagnostic tests procedure

The target population for this cross-sectional study consisted of 4900 Farms with about 126 000 sheep in M-V. Three categories of farms were selected by using the random generator function in MS-Office: 20 small (10-100 sheep), 25 medium (> 100-250 sheep) and 25 large farms (> 250 sheep). Of these 70 farms, 41 responded positively and were included anonymously into the serological screening. Of them, 20 were classified as small, 7 as medium and 14 as large farms. Random selection of individual animals across age group, sex and paddock was conducted in the course of blood sampling. Twenty, 60 and 80 sheep more than one year of age for small, medium and large farms, respectively, were sampled



**FIGURE 2:** Average within-herd prevalence of MVV-infected flocks according to herd size.

between February and October 2009. A total of 2229 individual samples were taken. For the detection of antibodies , the Idexx Chekit-ELISA CAEV/MVV test (Idexx GmbH, Ludwigsburg, Germany) was employed.

#### Questionnaire

A single page questionnaire (Fig. 1) was drawn. Main sections were comprised of farm location, herd characteristics and animal health parameters. Based on a farmer's judgement on the importance of parasites, diarrhea, pneumonia and abortion, ranking from one to three, general herd health was evaluated for all farms. Similarly, the level of lamb mortality was assessed, ranging one to four. The questionnaire was tested at three farms and amended before it was applied in this study. Interviews lasted about 20 minutes on average.

#### Data analysis

Data were stored using Microsoft ACCESS 2006 (Microsoft Corporation, Redmond, USA). The statistical analyses were performed using SPSS for Windows version 16 (SPSS Inc., Chicago, Illinois, USA). Univariate analyses were applied to describe the differences between farm groups. For analysis of categorical data Pearson's chisquare and Fishers exact test were used. One way analysis of variance was applied for comparison of means. For ordinal data Man-Whitney- and Kruskal-Wallis-test were used (Sokal and Rohlf, 1995, Thrusfield, 1997). P-levels ≤ 0.05 were considered significant.

## Results

Twenty-one (51,2%) of all participating farms showed at least one individual that tested serologically positive. At these infected farms almost a third (28,8%) of all individu-

als tested serologically positive on average. Figure 2 summarizes the findings according to herd size for infected flocks while Table 1 shows the results in more detail.

The average herd size for all participating farms is smaller compared to infected flocks. Considering infected flocks only, small flocks have the highest MVV prevalence, followed by large flocks and medium size herds. For analysing risk factors associated with farm status for all participating and infected farms, respectively, comparison of means and ranks were evaluated (Tab. 2 and 3).

Infected herds tend to be larger, have on average less stable space and pasture per capita available and have to deal with poor herd health indicators more often. None of the differences are statistically significant. Distinguishing low and high within-herd prevalence rates at infected farms at a 20% cut-off (Tab. 3) shows, that flocks with lower within-herd prevalence tend to have on average more stable space and pasture per capita available and have to deal less with poor herd health situations. Differences are not statistically significant.

For analysis of low/high infected flocks towards their crossbred or purebred management, data were cross-tabulated as shown in Table 4.

The difference of infection levels in purebred compared to crossbred flocks is statistically significant (p = 0.04, CI 95%)

## Discussion

Our findings confirm international data on the occurrence of MVV among sheep. Arsenault et al. (2003) conducted a MVV-impact study in Quebec in 29 commercial flocks involving 1954 sheep of which on average 29% (3–70%) of sheep tested positive. In Switzerland, random testing of 5084 sheep in 241 flocks resulted in herd prevalence rates

**TABLE 1:** Average MVV-detection according to farm size and MVV-status

participating fams					infected farms	
farm size	farms (n)	Ø no. of sheep (SD)	farms (n)	%	Ø no. of sheep (SD)	% infected sheep
small (10–100)	20	<b>36</b> (27,3)	7	35,0	<b>50,3</b> (30,0)	29,2
medium (101–250)	7	<b>155,7</b> (68,8)	_4	57,1	<b>195,8</b> (57,1)	15,4
large (> 250)	14	<b>923,4</b> (599,7)	10	71,4	<b>937,4</b> (85,7)	41,8
	41	<b>378,2</b> (551,7)	21	51,2	<b>500,4</b> (624,4)	<b>28</b> ,8

between 0.4 and 36% that varied according to six different breeds in purebred- and crossbred flocks (Schaller et al., 2000). Kita et al. (1990) found within-herd prevalence rates between 1.4 and 46.9% by investigating 4284 sheep in 18 herds in Poland, using an agar gel diffusion test. Cutlip et al. (1992) reported up to 90% of sheep infected in flocks in the US. In their own study, they tested 16 827 sheep of 164 flocks from 29 states serologically and found an average of 26% of sheep and 48% of flocks MVV-positive. Madewell et al. (1987) who tested 3369 sheep and 1394 goats in Peru by using agar gel diffusion test, stated on average 19,0% (1.7–40.6%) of sheep per flock MVV-positive. In Austria Hönger et al. (1990), also using the agar gel diffusion test, reported breed-dependent within-herd prevalence rates between 1.7 and 47.7%.

The authors emphasize the remarkable range of flockspecific within-herd prevalence rates as confirmed in our study. While breed, among other risk factors such as age (Cutlip et al., 1992), separation of lambs born to primiparous ewes (Madewell et al., 1987), contact exposure (Leginagoikoa et al., 2010; Berriatua et al., 2003), sheepgoat-transmission (Gjerset et al., 2009) and husbandry (Schaller et al., 2000), reportedly is associated with MVVinfection level, little valid statistical data are obtainable to quantify this. In this view, a distinct susceptibility of texel or milk sheep remains to be confirmed. The scope of our own data, however,

did not permit inclusion of breed into the analysis.

Transmission of MVV through happens main routes like ingestion of infected colostrum and/or milk, or through inhalation of respiratory secretions (Blacklaws et al., 2004). Given this, available space per capita in barns and pasture area is of interest. A Spanish study conducted by Leginagoikoa et al. (2010) suggested that close contact between sheep support the efficiency of horizontal MVV transmission. In contrast, indirect aerogenous contact with sero-positive sheep was not associated with seroconversion as evidenced in replacement sheep, housed in separate pens in the same building as adult infected sheep for one year. Consequently, MVV may not be efficiently airborne over short distances, which is important for control of infection. The same authors concluded in an earlier study that extensive rearing of sheep as common in New Zealand or Australia indicates that MVV-control in extensive and semi-intensive flocks can be more simple and inexpensive (Leginagoikoa et al., 2006). This is in agreement with our data, whereby infected herds on average have less stable space and pasture per capita available, thus having closer contact to other sheep, compared to non-infected farms.

For all participating farms, farmers judgment of herd health parameters including the extent of lamb mortality in their flocks is broadly similar, thus not significantly different: herd health in non-infected compared to infected flocks, and low- compared to high-infected flocks, respectively, is more favourable.

Overall, our findings suggest a widely underestimated extent of MVV in sheep flocks in M–V which is most likely applicable to other German states too. We are in agreement with Peterhans et al. (2004) who recommended a systematic determination of MVV prevalence prior to eradication schemes within Europe.

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The authors declare that there are no protected, financial, occupational or other personal interests in a prod-

	infected? Ø (SD)		CI 95%, One-Way-Anova, Bonferd		onferoni
all farms	no yes		df	F	p-value
Ø herd size (n)	226,1 (442,2) 509,5 (610,8)		1	2,81	0,10
stable space (qm/sheep)	3,5 (5,1) 1,5 (1,3)		1	3,20	0,10
pasture (ha/sheep)	0,6 (1,1) 0,3 (0,3)		1	1,84	0,20
herd-health-factors (1–3)	Ø (	SD)	CI 95%, Kruskal-Wallis-test		est
			df	$\chi^2$	p-value
parasites	2,10 (0,77)		1	0,69	0,40
diarrhea	1,45 (0,51)		1	0,02	0,89
rsespiratory symptoms	1,52 (0,68)		1	0,49	0,19
abortion	1,48 (0,81)		1	1,16	0,25
	)				
lamb mortality factor (1–4)	Ø (SD)		Cl 95%, Man-Whtney-test		
			Z	Man-Whitney-U	p-value
lamb mortality	2,1 (0,96)		-0,137	204,00	0,89

**TABLE 2:** Comparison of means and ranks of different risk factors for all participating farms

<b>ABLE 3:</b> Comparison of means	and ranks of different	risk factors f	for infected farms
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_	infected? Ø (SD)		CI 95%, One-Way-Anova, Bonfe		nferoni	
infected farms	≤ 19%	≥ 20%	df	F	p-value	
Ø herd size (n)	315,0 (484,2)	574,6 (672,7)	1	0,73	0,40	
stable space (qm/sheep)	1,70 (1,0)	1,59 (1,4)	1	0,03	0,86	
pasture (ha/sheep)	0,35 (0,4)	0,18 (1,5)	1	2,10	0,16	
	7					
herd-health-factors (1-3)	Ø (SD)		CI	CI 95%, Kruskal-Wallis-test		
			df	$\chi^2$	p-value	
parasites	0,32 (0,47)		1	3,10	0,09	
diarrhea	0,32 (0,47)		1	0,44	0,53	
rsespiratory symptoms	0,27 (0,68)		1	0,57	0,48	
abortion	1,4 (0,67)		1	0,69	0,45	
			_			
lamb mortality factor (1–4)	Ø (SD)		CI	CI 95%, Man-Whtney-test		
			Z	Man-Whitney-U	p-value	
lamb mortality	2,1 (0,94)		-0,82	44,00	0,99	

infection level of in	fected farms			
management	infection level			
	≤ 19%	≥ 20%		
purebred	1	11		
crossbred	5	4		
	Fischer's exa	ct p: 0,04, 5,88		

**TABLE 4:** Cross-tabulation of farm management and

uct, service and/or a company which cold influence the content or opinions presented in the manuscript

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