ERADICATION OF PRRSV (PORCINE REPRODUCTIVE AN RESPIRATORY SYNDROME VIRUS) FROM A CLOSED PIG HERD

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Introduction

Eradication of the PRRSV war attempted in a closed nucleus herd of 200 sows (Large White). The herd has SPF status with exemplary hygiene and management. The replacement rate is 70%
The herd broke with PRRSV in May 2000. Because of the valuable genetic status, the eradication programme was initiated.

Meterial and Methods

Key control tool of eradication was a vaccination programme with the vaccine Ingelvac® PRRS MLV (Boehringer Ingelheim). The vaccination schedule is represented in table 1.

Table 1: Vaccination Schedule

Type of vaccination	Animal group	Time of vaccination
Whole herd	All animals of the herd	Twice with an Interval of 42 days
Revacci-nations	Sows	Day 40-60 of pregnancy
	Suckling pigs	Week 2-3 of live
	Growing pigs	Day 120-140 of live

Starting with the first vaccination of the total herd, the vaccination programme was continued for 150 days.
Blood samples, tonsil scrapes and organ samples were analysed for PRRSV specific antibodies or genome fragments with IDEXX-ELISA, IPMA and RT-PCR to monitor the progress of the eradication.

Results

Following the vaccination phase, the herd was PRRSV stable and without any clinical symptoms. All tested sows were positive for PRRSV specific antibodies. Piglets (unvaccinated) were serological negative at the age of about 10 weeks. Pigs in the growing unit seroconverted soon after introduction and PRRS vaccine virus but no field virus was demonstrated. Due to market situations, the final step of the eradication attempt was interrupted. When the eradication programme was restarted in autumn 2003, no virus could be found in the growing area any more and pigs at the end of the nursery were still seronegative.
In November 2003, all sows and gilts were tested serologically and by RT-PCR for PRRS-specific antibodies and genome fragments. 24 sows were serologically positive and all animals were negative in PCR (Table 2).

Due to these results, the original plan of depopulation of the growing area was dispensed. The serologically positive sows are continually removed from the herd after farrowing and weaning. Replacement gilts, suckling and growing pigs are tested for PRRSV specific antibodies on a regular basis. Up to now positive results have been observed only in suckling pigs from seropositive sows. All PCR results were negative.

Table 2: Diagnostic samples and results

Date	Animals tested	N	ELISA positive	PCR pos.	
				EU	US
10/ 2003	Sows	15	1	0	0
	Gilts	10	0	0	0
	Piglets	5	0	0	0
	growers	35	0	0	0
11/ 2003	Sows	204	23	0	0
	Gilts	36	1	0	0
	Growers	20	0	0	0
11/03 to 02/04	Piglets	107	5*	0	0
	Growers	40	0	0	0
	gilts	44	0	0	0

* suckling pig from seropositive sows

Discussion

Due to the immediate vaccination programme following the PRRSV outbreak (1st step of the eradication programme), an immediate and stable immunity within the whole herd was established by which the PRRS field virus was successfully eliminated from the herd. When vaccination was discontinued, PRRS vaccine virus was found only in the growing facility. There was no transmission of this vaccine virus to sows or nursery pigs, even though replacement gilts were recruited from this vaccine virus positive growing unit. From diagnostic results it can be concluded that the vaccine virus died out by itself.
Although the vaccination phase was very short, the PRRS field virus was successfully eliminated. From today`s knowledge, at least partial depopulation of the growing unit would have been necessary to avoid any persistence of the vaccine virus within the growing unit.
To minimize any risk of undetected virus carrier animals which could transmit PRRSV to negative herds, it seems to be necessary to control this obviously regained negative status very intensely for some more time. Beside regular serological control, over a period of three month, starting with the elimination of the last seropositive sow, tonsil scrapes from slaughter sows and suckling pigs as well as blood samples will be tested for PRRSV genome fragments.