

Seroconversion against SU5 derived synthetic peptides in sheep experimentally infected with different SRLV genotypes

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15 Abstract

Synthetic peptides were generated, corresponding to SU5 domain of envelope glycoprotein of 16 Italian SRLV isolates It-561 and It-Pi1, belonging respectively to MVV- and CAEV-like 17 genotypes. The peptides, encompassing an N-terminal variable and a C-terminal conserved 18 19 antibody-binding site, were used in an ELISA assay to analyse the sera of two groups of sheep experimentally infected with these isolates. The kinetics and specificity of the humoral response 20 21 to the homologous and heterologous antigen and the affinity maturation of the sera were evaluated. Seroconversion occurred between week 3 and 8. The response to SU5 antigen was 22 mostly type-specific. The few broadly reacting sera may reflect the production of antibodies 23

directed to the SU5 constant antibody-binding site. All sera underwent with time avidity maturation, resulting in the appearance of high affinity antibodies. This study suggests constant monitoring of the circulating viral variants to develop a panel of diagnostic peptides representative of local genotypes.

28

29 Keywords

30 Small Ruminant Lentiviruses, envelope glycoprotein, SU5 peptides, type-specific
 31 seroconversion.

32 Introduction

Maedi Visna Virus (MVV) and Caprine Arthritis Encephalitis Virus (CAEV) are non oncogenic 33 34 lentiviruses of the Retroviridae family, presently referred to as Small Ruminant Lentiviruses 35 (SRLVs) (Zanoni, 1998). A recent phylogenetic classification of these viruses defines two main 36 groups, A and B, including respectively MVV-like and CAEV-like genotypes (Shah et al., 2004). 37 SRLV infections occur almost worldwide and cause relevant economic losses. Therapy and effective vaccine are not yet available (Gonzalez et al., 2005; Petursson et al., 2005; 38 39 Torsteindottir et al., 2007; Niesalla et al., 2008; Reina et al., 2008), therefore eradication and prevention of the infection largely depend on early, efficient and correct identification of infected 40 animals (de Andrés et al., 2005). This is routinely done by serological analysis, the ELISA 41 42 assay being the most sensitive and suitable technique both for large scale screening and 43 individual examination. Several ELISA protocols have been developed so far, mostly based on 44 antigens from a single viral strain. The specificity of these assays is generally high, but the sensitivity shows extensive variability (de Andrés et al., 2005) due to antigenic heterogeneity of 45

SRLVs. Recent analysis of two Italian SRLV isolates, MVV-like It-561 and CAEV-like It-Pi1, 46 47 demonstrated that gag-encoded capsid (CA) and matrix (MA) proteins carry type-specific epitopes and most sheep and goat sera reacted to these antigens in a type-specific manner, 48 49 irrespective of the species of origin (Grego et al., 2002; Grego et al., 2005). Furthermore, 50 homologous CA-MA fusion protein was able to detect seroconversion at an earlier stage 51 compared to the heterologous protein (Lacerenza et al., 2006). The present study extends the 52 analysis of the humoral response induced by It-561 and It-Pi1 to SU5, one of the major epitopes 53 of the envelope (Env) protein (Bertoni et al., 2000; Valas et al., 2000). Two SU5 synthetic 54 peptides were generated, corresponding to It-561 and It-Pi1 sequences. The peptides were used as antigens to assay sera from two groups of sheep experimentally infected with these 55 viruses, in order to investigate the kinetics and specificity of the humoral response to the 56 57 homologous and heterologous antigen.

58 Materials and Methods

59 Viral strains and experimental infection

SRLV strains It-561 (genotype A) and It-Pi1 (genotype B) (Grego et al., 2002) were used in the
present study. Infection of sheep with these strains has been described by Lacerenza et al.
(2006). Detection of viral sequences in blood of experimental sheep was done by *LTR* PCR
(Extramiana et al., 2002) and *Pol* PCR (Grego et al., 2002).

64 Cloning, sequencing and sequence analysis of env region coding for SU5

An env gene fragment encompassing the 75bp "SU5 total" domain (Mordasini et al., 2006) 65 coding sequence (nt 7800-7874) was amplified from DNA of foetal ovine lung fibroblasts 66 infected respectively with It-561 and It-Pi1 viral stocks. Primer sequences (Bertoni et al., 2000) 67 follows: 563F: GAYATGRYRGARCAYATGAC 68 were as (nt.7272-7291); 567F: GGIACIAAIACWAATTGGAC (nt. 7482-7501); 564R:GCYAYATGCTGIACCATGGCATA (nt. 69

8089- 8067). The nucleotide positions refer to the CAEV sequence published by Saltarelli et al.
(1990; Genbank accession number M33677). Amplified fragments were cloned and sequenced.
Genetic distances were calculated with MEGA 3 (Kumar et al., 2001) and used to construct a
neighbor-joining tree with the Tamura-Nei two-parameter distance option (Tamura et al., 1993). *Peptide ELISA*

Peptides corresponding to the 25aa "SU5 total" domain of both viruses, were resuspended in 0.1M carbonate buffer pH 9.6 at 5 μ g/mL. ELISA plates were coated overnight at 37°C (50 μ L/well), incubated for 1 hour at 37°C with sera diluted 1/20 and for 1 hour at room temperature with a 1:8000 dilution of peroxidase-labelled anti-sheep/goat IgG monoclonal antibody (Sigma). Optical density was measured at 405 nm wavelength after 40 min incubation with ABTS (Sigma).

81 Cut-off

A panel of sera collected before experimental infection as well as sequential sera from two mock-infected sheep, were repeatedly assayed: no significant interplate variation of the absorbance was observed. The cut-off was calculated as mean absorbance of negative sera + 3x Standard Deviation. Samples with absorbance higher than 0.3 were considered positive with a 99% confidence level. A serum collected from a sheep belonging to a long term seronegative flock was loaded on each plate.

88 Antibody avidity measurements

The avidity index values of SU5-specific antibodies were measured by testing the stability of the antigen-antibody complexes following a wash in 8 M urea (Mordasini et al., 2006). Antibodies with avidity indexes <30% were considered to be of low affinity; those with values between 30% and 50% of intermediate avidity and those with values >50% of high avidity.

93 **Results**

94 Cloning and sequencing of SU5-encoding env region

The env sequences encompassing respectively the SU5 domain of It-561 and It-Pi1 strains 95 96 (Genbank accession numbers: It-561: EU702487: It-Pi1: EU709743) were aligned with MVV 97 and CAEV prototypic env sequences of worldwide origin. It-561 clusters with representatives of 98 group A genotypes and It-Pi1 with B genotypes (fig.1 a), in agreement with the results of a 99 phylogenetic analysis of gag and pol sequences (Grego et al., 2002; 2005). The SU5 aminoacid sequences of It-561 and It-Pi1 share homology in the N-terminal region, which is well 100 101 conserved among MVV and CAEV strains, and diverge in the C-terminal, more variable portion 102 (fig.1 b).

103 Peptide ELISA

104 Peptide ELISA assays were performed on a panel of sera obtained over a period of up to 92 105 weeks p.i. from three groups of experimentally infected sheep: group A, sheep 1 to 5, infected with It-561; group B, sheep 6 to 9, infected with It-Pi1 (fig.2 a, b) and group C, four mock-106 107 infected sheep. Group C sheep remained seronegative throughout the study (data not shown). 108 Group A sheep 1 to 4 seroconverted to the homologous antigen between week 4 and 8 and 109 remained positive throughout the study. Sheep 1 to 3 were completely negative to the 110 heterologous It-Pi1 peptide, while sheep 4 raised a weak humoral response to It-Pi1, from week 111 77 onwards. Sheep 5 did not seroconvert and was the only one negative to both LTR and Pol 112 PCR assays performed throughout the study to confirm the presence of virus in the infected 113 animals (data not shown). Group B sheep seroconverted to the homologous antigen between 114 week 3 and 8; all sheep remained positive until the end of the experiment, with high absorbance 115 values. Only sheep 9 responded to the heterologous antigen from week 8 onwards. The

absorbance, which was about two- to threefold lower than for the homologous antigen, reached

117 a peak at week 22 and gradually decreased thereafter, to values just above the cut-off.

118

119 Kinetics of antibody avidity maturation

The avidity maturation of sera was assayed at week 8 p.i., corresponding to the first antibody peak, at week 35 and at week 78. The results obtained for group A sheep are depicted in fig.3 a. Sheep 2, 3 and 4 underwent a marked increase of antibody avidity over the period analyzed. All avidity indexes of sheep 1 were low; therefore additional time points were analyzed. Maturation to high avidity was detected at week 56, followed by a gradual decrease to low avidity by the end of the experiment (data not shown. Group B sheep underwent a marked avidity maturation, reaching the highest values at week 35 p.i (fig.3b).

127 Discussion

Most ovine isolates collected in Italy belong to the CAEV-like group (Grego E. et al., 2002) and 128 129 coinfection of goats with both MVV- and CAEV-like strains in an Italian flock has recently been 130 reported (Pisoni et al., 2007). In the last years serological assays based on Gag antigens 131 derived from Italian isolates belonging to both phylogenetic groups were developed and applied 132 in field conditions: the response obtained was largely type-specific, indicating the opportunity to 133 use antigens representative of both genotypes to improve the sensitivity of the diagnostic 134 assays (Grego et al., 2002; 2005). Furthermore, when sequential sera collected from sheep 135 experimentally infected with either It-561 or with It-Pi1, were analyzed by ELISA with both 136 homologous and heterologous CA-MA fusion proteins, the homologous antigen detected 137 infected animals up to months before the heterologous antigen (Lacerenza et al., 2006). In this

138 study the same panel of sequential sera was analyzed with an Env ELISA based on It-561 and It-Pi1 SU5 peptides. Five epitopes have been identified in the SU subunit of Env (Bertoni et al., 139 140 2000; Valas et al., 2000). SU5 in particular, a 25 aminoacid sequence located at the C terminus 141 of SU, is immunodominant and partly type-specific: it carries at least three antibody-binding sites, one in the N-terminal conserved region, one within the C-terminal most variable domain, 142 143 and the third encompassing the junction between the variable and conserved regions 144 (Mordasini et al., 2006). In this study, two env gene fragments encoding respectively It-561 and 145 It-Pi1 SU5, were sequenced. Alignment of these fragments with sequences of MVV and CAEV 146 prototypic strains of worldwide origin showed that It-561 clusters with the MVV strains and It-Pi1 147 is phylogenetically related to classical CAEV-like prototypes. The SU5 N-terminal aminoacid 148 sequences of the two strains share extensive homology; the C-terminal region is more 149 divergent, confirming the results of Mordasini et al. (2006). Seroconversion kinetics of group A 150 and B sheep were similar, with antibodies being mostly type-specific. The few broadly reacting 151 sera may reflect the production of antibodies directed to the constant antibody-binding site. The 152 antibody levels varied between animals and for the same animal during the time course of the 153 experiment. In group A, the first antibody peak was followed by a slight decrease of reactivity 154 and then by a rise to three to fourfold higher values. One sheep of this group did not 155 seroconvert. This result was most likely caused by a technical failure during the experimental 156 infection, since the sheep was repeatedly negative to both LTR and pol PCR assays which 157 were performed on blood samples of the experimental animals to confirm the presence of viral 158 genomes. Group B sheep developed immediately an antibody response well over the cut-off. All 159 sera underwent with time avidity maturation, resulting in the appearance of high affinity 160 antibodies, although with different kinetics. It-Pi1 sera, which developed higher antibody levels 161 from the beginning, underwent high avidity maturation at an earlier time point than It-561 sera.

162 Sheep 1 showed a peculiar pattern of avidity maturation, with indexes decreasing from week 56 onwards, to return to low values by the end of the experiment, in spite of a persisting high 163 164 antibody level. The reason for sheep 1 behaviour is unclear; the genetic variability of SU5 could 165 possibly explain the disappearance of the high affinity antibody-producing clone(s). Alternatively, this sheep may present some failure in the mechanisms that underly the ability to 166 167 maintain the production of high affinity antibodies. A failure of T helper function may be 168 responsible for the loss of high affinity antibodies as well as the associated decay of the 169 antibody titer, that have been reported in individuals who later developed AIDS (Chargelegue et 170 al., 1993; 1995; Thomas et al., 1996). SRLV infection, however, does not involve the 171 lymphocyte compartment, and sheep 1 antibody titer does not decrease, therefore a different 172 mechanism may be responsible. A comparison of the results obtained in this study and in 173 Lacerenza et al. (2006) shows that both CA-MA fusion antigens and SU5 peptides detect 174 infection at early stages, from week three onwards. Furthermore, while It-561 drives type-175 specific antibody response towards both Gag and Env antigens, It-Pi1 seems to drive 176 production of type-specific antibody only against SU5. In fact, all group B sheep reacted against the heterologous Gag subunits as well (Lacerenza et al., 2006). Since the humoral response to 177 178 SU5 is mainly directed towards the variable antibody-binding site, a constant monitoring of the 179 circulating viral variants will be necessary to develop a panel of SU5 peptides representative of 180 most local genotypes.

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183 Conflict of interest statement

All authors deny any financial and personal relationships with other people or organizations that could inappropriately influence this work.

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265 Fig.1:

a: Phylogenetic analysis of It-561 and It-Pi1 env fragments encompassing SU5 coding region. 266 267 The neighbor-joining tree was constructed using MEGA. Bootstrap values are based on 5000 268 repetitions. The accession numbers refer to the following strains: AF338227 (MVV K1514, Iceland); S51392 (MVV EV1, Great Britain); M31646 (SA-OMVV, South Africa); EF154467 269 (SRLV 12-5, Italy); U64439 (OLV 85/34, USA); EF154474 (SRLV 12-20, Italy); AY900630 270 271 (CAEV Gansu, China); M33677 (CAEV-Co, USA), AF322109 (CAEV 1GA, Norway); NC001482 272 (FIV). b: Alignment of SU5 aminoacid sequences of It-561 and It-Pi1 with MVV and CAEV 273 strains.

- 274
- 275 Fig. 2:

Kinetics of humoral responses of experimentally infected sheep to homologous (white bars) and heterologous (black bars) antigen. The cut-off was set at 0.3 OD. *: not available. a: It-561 infected sheep. b: It-Pi1 infected sheep.

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280 Fig. 3:

Avidity maturation of anti SU5 antibody taken at 8, 35, 78 weeks p.i. a: sheep infected with It-561; b: sheep infected with It-Pi1. Serum antibodies with avidity index values lower than 30% are designated low avidity antibody, those with avidity index values between 30 and 50% are intermediate-avidity antibodies, and those with values higher than 50% are considered high avidity antibodies.

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It-561 EF154467 U64439 S51392 M31646 AF338227 It-Pil EF154474 M33677 AY900630

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