

Review Article

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A new approach for maedi visna virus infections: a review

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Abstract

Maedi-Visna virus belonged to a lentiviruus genus which is one of two subfamilies of retroviridae family, the name retro refers to "reverse, backward" derives from the reverse transcriptase (RNA-dependent DNA polymerase). Morphologically, MV virus is enveloped derived from the host cell membrane, it is spherically shaped with a diameter from 80–100 mµ, consists of three-layered structures, the envelope has tiny spikes (about 8 nm) dispersed evenly over the structure. The core structure is cylindrical and composed of gag proteins: p24, p17, p9, and p7. The MVV genome is comprised of a single sense, two identical positive and stranded RNA subunits each strand contains three structural genes: env, gag, and pol, three regulatory genes include rev, vif and tat, and long terminal repetitive regions, non-coding (LTRs). Infection with MVV causes dyspnea, loss of weight, mastitis, and arthritis, depending on where the lesions are located. This virus causes antibodies to develop, which you may test for using agar gel immunodiffusion, ELISA, and serum neutralization assays Because there is no antiviral therapy or vaccine available, diagnostic testing constitutes the backbone of most prevention strategies. Due to the limitations of sensitivity and specificity of current serological tests, molecular biological techniques are being developed to identify viruses in peripheral blood and milk samples as well as tissue samples.

Keywords MVV, Virus, Sheep, Lentivirus

Introduction

Maedi-Visna is a lasting and long-lived viral winning catastrophe of store and now size up caused by the Maedi-Visna germ, credentials Retroviridae, subfamily Orthoretrovirinae, school Lentivirus, which is genetically related to caprine arthritis encephalitis virus (CAEV) (Fauquet et al., 2005). There are two forms of the disease. Maedi is the respiratory form and Visna is the nervous form (Radostits et al., 2017; Akkan et al., 2009). Maedi-Visna leads to multi-systemic fomenting torment. The join first tissues feigned are the lungs, mammary glands, joints, and CNS. Still, disordered lesions buttocks additionally to be freaky in second choice organs aside from the point of

departure , liver, feather , lymph swelling, bust vessels, and bone substance. Maedi-Visna make a mess of has a unequivocal distress incubation time eon and the clinical reminder carry through scream show up on hold the era of three period and unlike parentage submit to asymptomatic carriers for their exemplary rebound. (Sargan et al., 1991; Herrmann-Hoesing et al., 2010). The clinical minutes of Maedi are experimental forth routine than Visna. The clinical symbolism of Maedi are coughing, dyspnea, emaciation and mastitis. Abortions mewl counting factual but united surrounding immediacy of idiot ruin (Straub, 2004; Christodoulopoulos, 2006). Clinical symbolism of Visna are abate in swain paws, arthritis, steadiness run out of steam, mastitis and progress to faultless grief and seldom CNS disorders are barring pra (Straub, 2004). Translation of Maedi-

Visna ball up faddist groundwork be obligated by clinical wit and the confirmative sorting out be dressed be concluded by methods such as review labotatory breakdown. Histopathological chancre, jerk serology and clandestineness. Span methods are hand-me-down for serological working-out of Maedi-Visna fault moreover AGID, ELISA, RIA, RIPA and PCR (Herrmann-Hoesing et al., 2010; Asadpour et al., 2014). The pain is width by respiratory fustigate or by ingestion of sick extort and by utero illness. Lamb may about the electronic eavesdropper at origination, or as soon as resulting, non-native correspond round near reference to infirm ewes or ingestion of infirm colostrum and bleed. Mononuclear cells in colostrum and wrest of infirm ewes are diseased everywhere creepycrawly go off alien these cells may gill throught the natural bar to malign the lambs. The mania is exclusive of dramatis personae in the semen of the contaminated rams depart strive leukospermia. Macrophages are contrasting in the lungs of clich la-di-da orlah-di-dah with pulmonary adenomatosis and these cells sturdiness be ill with yielding way-out pneumonia child position just about is a overlapped shortcoming (Radostits et al., 2017). In the present, Maedi-Visna spreads sheep all in all world in most European countries and saw in a couple of central areas, for instance, USA, Africa and Asia where the affliction caused huge money related setbacks. Very few countries are freed from MVV like New Zealand and Australia. In various countries, MV was not depicted and investigated starting as of late like Algeria, Egypt, Lebanon, Libya and Tunisia (Gurcay and Parmaksiz, 2013).

History of MVV

Maedi-Visna disease was first uncovered in Netherland, in 1862, when Loman portrayed in rams imported from Spain, an infirmity with worked breathing he called Zwoegerziekte. At the beginning of the XXth century, Robertson, (1904) portrayed in south Africa, a determined catarrhal pneumonia called Jagziekte, further followed by Mitchell in 1915 and Cowdry in 1925 with point by point epidemiological, etiological, clinical and lesional studies (Mitchell, 1915; Cowdry, 1925). Swamp declared the essential data in 1923 on the MVV or Montana ailment in the USA, yet when 1915, his power reports were recorded (Marsh, 1923). After two years, Cowdry distributed his examinations concerning the beginning of epithelial expansions in Jagziekte of South Africa (Cowdry, 1925). Contrasting the portrayal of Montana sickness and the Jagziekte depiction they inferred that they were most likely indistinguishable (Cowdry and Marsh, 1927). Afterward, the neoplastic idea of the sores of Jagziekte in sheep was thought of (De Kock, 1929). In 1933, after the appearance of Karakul rams from Germany, the presence of Maedi in Iceland was suspected: the main clinical side effects seemed six years after the fact, when the sickness had spread to numerous sheep crowds in Iceland (Ingvarsson, 2013). A new demyelinating contagious infection happened in sheep in Iceland as well, this neurological problem was called Visna (Sigurdsson et al., 1957). In the next century, various investigations of the etiology of Maedi and Visna were performed by Icelandic specialists (Sigurdsson et al. (1962). figured out how to confine the etiological specialist of Visna infection, trailed by the seclusion by Sigurdardottir and Thormar, (1964) of the aetiological

specialist of Maedi illness. From that point onward, reasoning that Maedi and Visna infection have a similar aetiological specialist (Sigurdardottir and Thormar, 1964; Blacklaws, 2012).

Genome

Complete genomic sequences of Maedi-Visna virus strains isolated from bovine peripheral blood mononuclear cells (PBMCs) have been reported (Bartak et al., 2018). The viral genome is a 9.2 kb positive polarity RNA strand dimer that is R-Transcriptase into provirus DNA, Any of this is inserted into host in the region of chromosomal DNA. The genome consists of three main genes. This is essential for the encoding of structural proteins and enzymes important for the replication of viruses: env (envelope), gag (group-specific antigens), pol (polymerase) are the main genes. The Maedi-Visna virus has a typical genetic organization of the lentivirus. Three regulatory or accessory genes are available:-rev, tat and vif. In addition for the long terminal repeats (LTR). It consists of three U3, R, and U5 regions and has been identified as promoters of viral transcription, particularly the U3 region that potentializes transcription factor binding sites (Peters et al., 2013).

The structure genes

gag gene

The gag gene codes the Maedi-Visna virus' key structural proteins. There are three proteins in the gag precursor (pr55gag): the capsid (CA; p25), the matrix (MA; p16) and the (neucleocapsid NC; p14) (Murphy et al., 2010). The hydrophobic base of the Virion shapes the CA protein. The CA protein induces a potent antibody response during infection, which is essential for diagnosis. Within the CA protein, the RNA genome is bound to NC proteins. Between the CA protein and the viral membrane, the MA protein is localized (Pepiin et al., 1998).

Env genes

The env quality is converted into a solitary polyprotein antecedent isolated into two proteins, the surface glycoprotein (SU) and the transmembrane glycoprotein (TM), by a host protease. In the envelope lipid bilayer, the transmembrane glycoprotein is secured, while the surface glycoprotein is noncovalently bound to the transmembrane glycoprotein. (Pepin et al., 1998). A SU trimer joined to a TM trimer is made of each spike on the Virion's surface. Env proteins are the important determinant of contamination restricting receptors.

Pol gene

Pol gene is a viral enzyme that is encoded. The gag-pol precursor (pr150gag-pol) is split from the DUPase, integrase, protease and reverse transcriptase (Pepin et al., 1999).

Reverse transcriptase

There are three consecutive biochemical cycles in Retroviral RT: RNA-subordinate DNA polymerase action, ribonuclease H

movement (RNase H), and DNA-subordinate DNA polymerase action.

Together these exercises permit the chemical to transform single-abandoned RNA into twofold abandoned cDNA (Danchin et al., 2018). This cDNA can then be fused into the host genome in retroviruses from which new RNA duplicates can be created by means of host-cell record. A similar response grouping is generally utilized in the lab for sub-atomic cloning, RNA sequencing, polymerase chain response (PCR) or genome examination to change RNA over to DNA (Luciw and Leung, 1992; Pepin et al., 1999).

Intrgrase (IN)

Fundamental capacity is to tie the viral DNA to the host's chromosomal DNA, a stage essential for MVV replication. Mix, which turns into a super durable transporter of the viral genome (provirus), For the cell, this is a 'final turning point.' Integration is mindful to some extent for the determination of retroviral contaminations. Viral quality articulation and molecule creation can happen right away or at some stage after future coordination, the circumstance of which relies upon the movement (Turner and Summers, 1999).

Protease (PR)

The Gag-Pol polyprotein contains proteins that are rashly coded, including PR. [9] PR is situated between the (TFR) switch transcriptase (which is at the C-end of PR) and p6pol (which is at the N-end of PR) (Pettit et al., 2004).

The dUTPase

The quality between RNase H and integrase is situated in the pol quality. DUTPase has been shown in MVV, CAEV, FIV and EIAV, yet not in HIV and other primate lentiviruses (Petursson et al., 1998; Pepin et al., 1998). The dUTP/TTP ratio is reduced by DUTPase. Cellular dUTPase activity in dividing cells is greater than that of nondividing cells. In sheep macrophages, MVV can replicate in vitro and in vivo without a functioning dUTPase (Petursson et al., 1998).

The Regulatory genes

vif gene

Vif is a 29 KDa protein that is located in a position similar to HIV-1 in the MVV vif gene (Franzdottir et al., 2016). Of all the lentiviruses except EIAV, Vif is retained. In MVV and CAEV, for example, the amino acid sequence is identical, but the amino acid sequences are very different in distantly related lentiviruses. Among closely-related lentiviruses, the Vif amino acid sequence is preserved. The protein's carboxyl end has a preserved sequence of SLQXLA (Yu et al., 2003). This arrangement has been related with replication of all lentiviruses aside from EIAV and it has been displayed to build HIV-1 infectivity by up to 1000 overlay (Kristbjornsdottir et al., 2004). A practical vif quality is normally required for the improvement of the inflectional vif quality and its capacity to recreate in many cells (non-oermissive cells) is seriously limited (Borman

et al., 1995). The non-tolerant aggregate after the combination of non-lenient cell lines was predominant over the tolerant one (Simon et al., 1998). This suggested that in the non-permissive phenotype, an anti-viral factor influence was seen and that this effect was counteracted by vif. This anti-viral factor was then referred to as the enzyme APOBEC3GG cytosine deaminase (Sheehy et al., 2002).

Tat gene

Situated among pol and env qualities, there is an open understanding framework (ORF) called tat. In both MVV and CAEV that encodes a protein of 10 KDa, which play significant rolefor viral replication, the SIV, HIV-1, BIV, and EIAV tat protein is emphatically and expected for trans-initiating of the LTR by restricting to a trans-enacting responsive component (TAR) (Bose et al., 2015). TAR is a stem-circle structure found toward the finish of each of the 5-end started viral records. There is no TAR grouping for MV, CAEV and FIV, However, it has been shown that the MVV and CAEV Tat proteins have a feeble trans-actuating impact on the comparing LTR. There is no transactivating impact of this type of the protein FIV Tat (Villet et al., 2003). The MVV quality was named tat on the grounds that trans-enactment was known and the quality position was equivalent to the tat quality in HIV-1. In examination with HIV-1, the action of basal LTR advertisers in MVV and CAEV is exceptionally high or if nothing else multiple times higher. Dissimilar to HIV-1, which needs it for effective replication, this high advertiser movement might be the explanation that MVV and CAEV don't require transinitiation from the Tat protein (Saltarelli et al., 1993). Late proof shows that in design and capacity, Tat in MVV is like Vpr in HIV-1111 (Villet et al., 2003).

Rev gene

Fire up is a polypeptide of 19 KDa encoded by two exons which are situated at the env quality's 5 and 3 finishes. Fire up is communicated early and the fire up protein makes it conceivable to trade unspliced and to some extent grafted viral RNA from the core to the cytoplasm and enacts the connection with the polyribosomes of these viral RNAs. Cytoplasmic expression of incompletely spliced mRNA requires Rev expression to encode the viral envelope protein(Clements and Zink, 1996).In MVV, the rev binds to (RRE). The N terminus of the TM protein is encoded by a stem-loop framework in the RNA (Tiley and Cullen, 1992). The function of the Rev protein is maintained amongst lentiviruses and is essential for viral infectivity (Tiley and Cullen, 1992).

Long Terminal Repeat (LTR)

LTRs are situated on the fifth and third finishes of the viral DNA. Three parts are separated into the LTR: R, U3 and U5. Average for both the 3 and 5 finishes of the virion RNA, the R area contains the cap refer to end signal, polyadenylation sign, and RNA record signal. The U3 locale is situated on the third finish of the viral RNA and contains the RNA record commencement enhancer and advertiser parts. The U5 locale is situated at the fifth finish of the viral RNA, and the nucleotide

succession is corresponding to mammalian lysine tRNA promptly downstream of the U5 area and goes about as a focal restricting site for the converse record of RNA to DNA (Gonda, 1994).

Transmission

MVV is a transmissible disease could be vertically and horizontally Transmitted to susceptible animals from an infected animal, the transfer of MVV infected cells via several potential routs is essential for dissemination of the disease (Leginagoikoa et al., 2006). The key route of transmission of MVV is through the ingestion by lambs of infected colostrum and milk, and horizontal transmission by infected secretion inhalation has also been reported and is primarily regarded as a transmission route in intensive and indoor production systems (Villoria et al., 2013; Junkuszew et al., 2016). The two courses of transmission are not fundamentally unrelated, and the most probable situation is that after the tainted colostrum is ingested, sheep and contaminated grown-up creatures are raised together (level transmission) and more presented to the infection (Junkuszew et al., 2016). Programs involving the exchange and export of sheep and goats have commonly recognized the horizontal transmission route as responsible for the spread of MVV between various geographical regions (Peterhans et al., 2004).

(i) direct contact: long-term and closed contacts between animals are one of the essential ways in which for instance, broken skin and mucous membranes occur via blood and exudates. Likewise contact transmission happens by means of a combination of regular sources: blood and exudates as nasal emission and salivation (Blacklaws et al, 2004). In the transmission of MVV within herds, another possible method may play a major role.

(ii) For MVV, the primary objective organ in the respiratory lot is the lungs. The infection contaminates lung monocytes, macrophages and dendritic cells and can spread on a level plane through these cells containing respiratory discharges (Blacklaws et al., 2004; Blacklaws, 2012). The spread of MVV by pulmonary exudates can also lead to co-infections with other viruses or bacteria. Moreover, MVVV is responsible for characteristic interstitial pneumonia lesions. Generally, The lower respiratory tract is the main route of infection in intensive and permanently housed sheep in sheds with poor ventilation and elevated stocking density (Minguijón et al., 2015). The mechanisms and role of MVV intrauterine (vertical transmission) have not been fully clarified yet (Blacklaws, 2012). Distributed information shows that up to 6 percent of sheep brought into the world by cesarean area might have intrauterine transmission. In spite of the presence of infections in the regenerative lot, uninfected ova or early undeveloped organisms can be gotten from dams that are either tainted or defiled with semen and uninfected sheep or goat undeveloped organisms can be delivered by in vitro preparation from contaminated sires or dams assuming specific safeguards are taken (Al Ahmad et al, 2012; Feini et al., 2012). It is difficult to determine the function of this vertical transmission mechanism, and the findings, which differ according to the technique used

and the immune response to the virus, should be compared with the dam-infected virus if PCR is used to detect the virus in the fetus derived from caesarean. The long and variable time to seroconversion will make it difficult to confirm when serologic is used that transmission occurred through the intrauterine route (Blacklaws, 2012). The effectiveness of eradication programs dependent on birth elimination and bovine colostrum rearing, however, indicates that intrauterine viral transmission is mainly of minor importance (Houwers et al., 1989), A origin of infection can also be placenta contamination by maternal blood. Semen has been shown to contain viruses, but it has not been evaluated for its role in viral transmission (Preziuso et al., 2003). Virus-infected rams and bucks, however, may infect females by other paths. Recently, evidence was obtained for the presence of viral nucleic acids in seminal plasma and tissues of the genital tract of male small ruminants suggesting the possibility venereal transmission either through the natural route or via artificial insemination, but its contribution to the epidemiology of MVV is considered of minor importance (Herrmann-Hoesing et al., 2007; Ali Al Ahmad et al., 2008). The main route of transmission of the MVV is through colostrum or milk from the infected ewe to the lamb (Preziuso et al., 2003). The penetrability of the infant digestive system permits contaminated cells or irresistible particles in the tainted colostrum to go through (Alvarez et al., 2006). A high pace of viral replication during the neonatal period and mastitis because of different microbes work with this transmission, leaning toward the presence of tainted cells in the udder.



Fig. 1 Schematic design of maedi visna infection (MVV) genome and the viral molecule. The viral genome, alongside the chemicals vital for record, joining, and development, is encapsidated inside the center framed by capsid proteins. This is encircled by the grid and by the lipid bilayer in which the envelope glycoproteins are embedded (Gomez-Lucia et al., 2018).

Epidemiology of MVV

Maedi-Visna virus in World

Currently, in most European countries, MVV has spread to sheep around the world and is recognized in several continents, such as the USA, Africa and Asia, where the disease has caused significant economic losses. Very few countries, like New Zealand and Australia are free (Gurcay and Parmaksiz, 2013). The long brooding time of MVV causes a gradually creating, ongoing disease that influences the lungs, cerebrum, joints and mammary organs of sheep. The infection spreads while purchasing live creatures, as first announced in Iceland and afterward in numerous European nations (Thormar, 2013). The epidemiological situation of MVV prevalence in worlds is more uncertain, the MVV for a number of countries such as Syria, Egypt, Algeria Indonesia, China and Mongolia, studies on the occurrence of Maedi-Visna virus do not exist (OIE, 2015). Seroprevalence rates in Lebanon were found to be 71% and 100% at the individual and herd levels respectively (Tabet et al., 2017), demonstrated that the individual seroprevalence rates exceeded 50% whilst one study suggests a very high MVV herd prevalence in North-east Spain where97% of sheep herds were seropositive (Perez et al., 2010) was the first detection of the MVV in Spain by using a enzyme-linked immunosorbent assay, in other countries Italy, the herd prevalence of MVV is also relatively high, as it can reach 90% f the flocks in some districts (Tolari, 2000). Regarding the Middle East countries, all studies suggested that the incidence of MVV infection was much lower than in other countries around the world (Ameen and Karapinae, 2018) in the regions of Iran and Turkey The degree of spread and prevalence of MVV in these neighboring countries of Iraq have some importance. In Turkey referred to the restricted spread and low percentage of 0.02% in some sheep according to pathological changes of the lungs in slaughter houses. In order to determine its persistence in animal tissue, Tan and Alkan, (2002) recorded a 26.7 percent rate of isolation of the virus from seropositive sheep, while Karaoglu et al. (2003) observed antibodies in 2.6 percent of turkey tests from different areas. Then again, Muz et al. (2013) observed seropositivity paces of 68.3 percent in investigations of statepossessed enterprises.In Iran, Seroprevalence of MVV contamination was 2.175 percent in the main review evaluating seroprevalence of the infection in the Kerman Province (Sakhaee and Khalili, 2010). And Sayari and Lotfi, (2001), as previously mentioned. Who found that from the total inspected lungs and Maedi like lesions, 0.54 percent. In a recent study in Iran, a study of ELISA detected seropositive on the level of herd infectivity was (7 percent) out of one hundred female sheep infected (Doust et al., 2020).

Economic Impacts

The economic losses due to infection with MVV are important. Review of literature, however, found that data on such losses are incomplete and in some cases, contractor. Complexity and participation of MVV's interaction with its hosts result from management factors are the reasons for this (Snowder et al., 1990). Factors affecting economic losses are as follows:

(a) The MVV infection-induced clinical disease progresses slowly.

(b) only about 30 percent of animals infected develop clinical diseases.

(c) Seroprevalence is associated with symptoms of disease and economic loss in herds with a low prevalence of infection and no clear signs of infection.

(d) The seriousness of the infection is impacted by hereditary elements in sheep, powerlessness to sickness can be impacted by breeds, while in goats this is related with specific significant histocompatibility haplotypes present in every one of the varieties inspected

(e) certain administration exercises, for example, milk handling or creature lodging and swarmed lodging increment the pace of viral transmission (Keen et al., 1997).

(f) Accompanying contaminations that might change with conceded geological regions and techniques for the executives, for example, Maedi-Visna with co-disease, for example, jaagsiekte retrovirus brought about by ovine aspiratory adenocarcinoma, an infectious lung growth prompting bothered sickness, may influence indications of illness (Gonzalez et al., 1993; York and Querat, 2003).

Clinical signs

Maedi-Visna (MV) It is a chronic viral disease, that is widespread in sheep, characterized by respiratory form determined by chronic interstitial pneumonia called Maedi, and nervous form determined by meningoencephalitis in adult sheep called Visna, Sheep of any age may be infected with the MV virus, Medical symptoms, lack of available occur in sheep under the age of two years. In addition to respiratory conditions, the onset of illnesses is incremental, resulting in relentless weight loss. There are also additional signs of cough, abortion, respiratory problems, depression, chronic mastitis and arthritis (Blacklaws, 2012). These side effects likewise happen in creatures beyond three years old and can frequently spread to different groups before a clinical finding can be gotten. Creatures with the above side effects will kick the bucket following a half year of disease (Larruskain and Jugo, 2013). Because of MVV contamination, mortility in the enzootic locale is low, yet is exceptionally impacted by accompanying sickness, cultivation, diet and ecological elements. Perceptions made during the epizootic MV in Iceland show that mortality can surpass 30% in recently tainted creatures (Sigurdardottir and Thormar, 1964). In sheep, the respiratory form is the most common clinical form. It affects adult animals older than two years, and the life expectancy of the animals does not exceed 1 year until the signs are noticeable (Watt, 1992). The first clinical signs to be found are exercise intolerance, followed by dyspnea at rest, accompanied by abdominal breathing, extension of the nostril, widening of the neck and open mouth with respiration (Barquero et al., 2015). The animal suffers from anorexia, weight loss and eventually cachexia as the disease progresses. Nasal exudate only occurs in the presence of bacterial secondary diseases. Mammary disease, due to frequency of incidence and economic losses is the second major type. The mammary syndrome is hard to diagnose and consists primarily of induration of the mammary gland, loss of milk production and slow lamb development (Minguijón et al., 2015). It may be more frequent in some breeds (as in the Spanish Rasa Aragonesa) than in the respiratory form (Lujan et al., 1991) It commonly affects adult animals between the ages of 3 and 5 years, but it has also been found in animals aged 1 year and is more common in intensively reared animals and mechanical milking (Barquero et al., 2015). Mastitis with swollen mammary lymph nodes is typically sub-clinical, indurative, recurrent, diffuse, bilateral, and non-painful. It is possible to reduce milk production and its macroscopic properties: color and consistency, do not differ (De la Concha-Bermejillo, 1997; Barquero et al., 2013a). Subsequent to lambing or joking, injuries are just noticeable. The pathology uncovers persistent interstitial mastitis, described by mononuclear cell invasion around the mammary acini and milk pipes. This enacts ductal epithelium hyperplasia, vacuolization, and desquamation. The sore gradually becomes fibrotic, causing milk duc stenosis and mammary induration (Gayo et al., 2019). Milk yield in seropositive animals can be reduced by 6.7 percent compared with the control pair for indurative mastitis, which is also a sign of MVV infection (Juste and Minguijon, 2020). Accurate data is not available because standardized milk production evaluation procedures are more common in dairy cattle than in small ruminants. It should be noted that husbandry activities impact decreased milk production (Ploumi et al., 2001). MVV infection reduces lamb weight gain, probably duo to indurative mastitis with depressed milk yield. Losses may rise at weaning from 0.3 to 3.0 kg per lamb (Arsenault et al., 2003). The reduced weight gain in offspring born from lamb dams and shown in most indicates that losses affect next-generation studies productivity (Greenwood, 1995). In MV, arthritis is the least common, but is prevalent in CAE. It is caused by animals which are between two and three years of age. Typically it affects the tarsal and carpal joints, so lameness marks the process. It may also affected to a lesser extent by Atlanta bursa and nuchal ligament. The treatment starts with the joint synovial membrane and capsule edema and congestion, which allows the joints to thicken and expand all structures. Along with frequent articular surface erosions, synovial membrane proliferation and periarticular tissue are hardened, which may extend to bone destruction (Pérez et al., 2015). The nervous form In sheep, often seen in stable animals, very rare. Animals aged > 2 years are affected. It can occur in younger animals in some breeds such as Assaf (Benavides et al., 2007). Ataxia and Hind-limb fatigue, hypermetria, and paralysis are nervous symptoms that typically contribute to recumbency, although the animal remains reacts to external stimuli and alert (Benavides et al., 2006).

Diagnosis

The determination of MVV disease depends on clinical signs, pathologic sores and research center testing. Clinical signs related with MVV contamination can anyway be connected with different illnesses, and the illness is for the most part asymptomatic. The disease is distinguished either by roundabout procedures of counter acting agent recognition or direct strategies of infection discovery, and the two methods are suggested for early determination and consolidated use (Barquero et al., 2011). In 2004, in order to detect seropositive animals, the OIE suggested. the use of either the enzymelinked immunosorbent assay (ELISA) or Agar gel immunodiffusion (AGID). The antibody present is typically persistent and because it is a life-long infection, seropositive animals are considered MVV carriers. Isolation from tissue explants or co-culture of contaminated fluids or cells may be used to detect viruses (Reina et al., 2009). For provirus or virus identification used molecular biology techniques such as RT-PCR and PCR, respectively for diagnosis MVV in sheep.

Hematological assay

There is a dynamic moderate hypochromic pallor with a drop in hemoglobin levels from 12-14g/dl to 7-8g/dl and some red propensity towards cell gloom, а leukocytosis., hypergammaglobulinemia additionally is present. lymphocytes and nutrophils are expanding in number in bronchoalveolar lavage liquid with an ascent in CD+8 cells and a lessening in CD+4 cells and a reversal of CD+4/CD+ (Radostits et al., 2017).

Serological assays

Sheep, the normal host, remain infection transporters for life once tainted with MVV and start to show an immunizer reaction inside quite a while after disease and consistently produce MVV antibodies that can be identified in an assortment of examines for the finding of MVV contaminated creatures incorporates, agar gel immunodiffusion (AGID), supplement obsession test, ELISA, Western smear (WB), and radioimmunoassay, various serological strategies have been utilized. AGID, ELISA and Western smudge (WB) are the three most normal serological tests utilized in the finding of MVV (Alves et al., 2018).

Enzyme linked immunosorbent assay (ELISA)

ELISA is satisfactory and more touchy than AGIDD for examining enormous quantities of tests. Countless various antigens are utilized for the discovery of antiviral antibodies by ELISA, including total infections, recombinant proteins and peptides containing immunodominant epitopes (Herrmann et al., 2003). Biphasic tests are best on the grounds that vague responses have a lower recurrence. On account of recombinant proteins, This response can be made by glutathione-S-transferase antibodies the cell parts of the whole ELISA infection or by bacterial constituents. As of late. Explicit peptides and an original consolidated peptide have been utilized in ELISA to identify antiviral antibodies against MVV primer outcomes look encouraging (Sanjosé et al., 2015). The review discoveries show that the consolidated peptide ELISA can be utilized for the serological analysis of SRLV disease and that solitary peptide ELISA can be utilized for ensuing serotyping purposes.

Agar gel immunodiffusion test (AGID)

This test was used to detect antibodies in animals against small ruminant lentiviruses (Potarniche et al., 2020). The enzymelinked immunosorbent assay (ELISA) and agar gel immunodiffusion test (AGIDT) are the most often used in laboratory methods for MV diagnosis in the United Kingdom. AGIDT is high but less responsive than ELISA compared to ELISA (Synge and Ritchie, 2010), and has been found to be 98% specific and 76% sensitive (De Andrés et al., 2005). Therefore, AGIDT is mainly used to confirm that ELISA is more sensitive because of its high specificity and low sensitivity.

Western blots (WB) analysis

Western blots is a laboratory confirmatory procedure used to detect serum antibodies that identify viral proteins. WB is typically more susceptible than ELISAs, but has a lower performance and is more importent. Nnon-unique cellular proteins with Cross-reactivity is also an issue. There is no systematic protocol for Western blotting success or interpretation in MVV diagnostics at present (Herrmann-Hoesing et al., 2010).

Other serological methods

Radioimmuno precipitation and radioimmunoassay are largely minimal experimental work and are not known to be standard diagnostic procedures (Gogolewski et al., 1985).

Molecular Assays

Polymerase chain reaction (PCR)

Polymerase chain reaction Techniques, which are most widely used for the direct evaluation of the presence of viral nucleic acid. Real-time PCR has been less investigated of Conventional PCR for diagnostic purposes than. (Zhang et al., 2000; Gudmundsson et al., 2003). In early 1990, the first traditional PCR protocols for Maedi-Visna virus detection were released (Zanoni et al., 1990). Polymerase chain reaction was initially considered effective in the diagnosis of the Maedi-Visna virus due to its ability to specifically detect viral particles either as a provirus (DNA) in the infected cell or in blood containing free virus particles (RNA: reverse transcription-PCR) (Leroux et al., 1997). In various animal samples, namely PBMCs, various studies have shown the usefulness of traditional PCR to detect Maedi-Visna virus infections (Leginagoikoa et al., 2009), peripheral blood leukocytes (PBL) (Chassalevris et al., 2020), mammary secretions (Gayo et al., 2018; Jarczak et al., 2019), synovial fluid (Reddy et al., 1993), Semen (Ali Al Ahmad et al., 2008; Lima et al., 2017), Lung (Dousti et al., 2020) and other tissue (Brellou et al., 2007). The low viral load present in infected animals, the low percentage of permissive cells in some tissues (104-105 PBMC has one infected monocyte) (Zhang et al., 2000), and the high genetic heterogeneity may hamper PCR diagnosis of Maedi-Visna virus (Peterhans et al., 2004). Similar PCR sensitivities have also been observed using

qPCRR in PBMCs and milk cells (Adjadj et al., 2019). However, studies also report a decreased sensitivity by using 23% milk samples compared to 33.3% blood samples using a gag or LTR-PCR technique (Extramiana et al., 2002). In the Maedi-Visna virus genome, including env, gag, pol and LTR regions, target sequences for the design of PCR primers are widespread (Extramiana et al., 2002; Carrozza et al., 2003; Marinho et al., 2018).PCR-positive reactions are also among seronegative animals (false negatives) that subsequently seroconvert to Maedi-Visna virus infections by demonstrating a lack of serological method sensitivity compared to PCR in specific conditions (Cardinaux et al., 2013).

Treatment

Palliative treatment which used for treatment of infected sheep can reduce the spread of the disease, as there is no effective treatment to prevent Ovine progressive pneumonia virus infection and no available vaccine. In order to identify and eliminate infected animals, attempts to treat OPP in flocks must be oriented. Serological testing can be used to effectively eliminate Ovine progressive pneumonia virus from flocks as the virus is harbored by all people with positive AGIDT (Cutlip et al., 1985) as a monitoring and removal tool. All seropositive sheep and goats under 1 year of age are removed. The flock is kept closed and only isolated seronegative animals are introduced and annual serological flock tests are recommended. Another control strategy for making a clean flock is isolation and artificial rear progeny on pasteurized milk or milk replacer (Cutlip et al., 1985).

Control

The management of MVV is related to the understanding of its epidemiology. Airborne, through respiratory secretions, are the most significant routes of MVV transmission (Berriatua et al., 2003) and colostrum and milk called lactogenic (Pritchard and Dawson, 2000; Villoria et al., 2013). Vaccination programs have been implemented in many countries and the disease has been eradicated in several of them by widespread culling and elimination of non-infected animals or seronegative sheep (Sihvonen et al., 2000; Peterhans et al., 2004). Or the gradual culling of vulnerable plants, as in the Netherlands and Finland, (Houwers et al., 1989; Sihvonen et al., 2000).A variation of the following activities can include MVV seroprevalence control methods

(a) Removal and substitution of herds with uninfected sheep.(b) selective culling only through the ELISA check of positive animals.

(c) the replacement of the offspring of seronegative ewes by sheep only.

(d) early slaughter of seropositive animals, with initial clinical symptoms.

(e) the artificial rearing of lambs immediately after birth, except the mother who is HIV-positive.

(f) Division of the flock into two flocks on the basis of serological status, followed by separate control of the resulting flocks in order to prevent horizontal transmission (Reina et al., 2009; Pérez et al., 2010). The majority of these steps are only available in herds with moderate seroprevalence of MVV. The

segregation approach could be the most effective in the case of highly infected flocks, be that as it may, it is just possible assuming the responsibility is reasonable and there are ranch offices accessible. It is for the most part acknowledged that creature isolation as indicated by serological status is a decent way to deal with MVV control, yet there are no experimental investigations accessible supposedly that give information on the pace of decrease of seroprevalence and the time taken to accomplish leftover seroprevalence. In most countries, the standard method used for diagnosis MVV-infected animals and checking the infected with MVV in a flock is periodic serological testing by using AGID or ELISA. In the event that new stocks are added to run liberated from MVV contamination. Acquiring domesticated animals from a licensed without my rush is the main reasonable approach to staying away from the presentation of the illness. For the destruction of the disease in the contaminated herds, different conventions were given. Since colostrum and milk are of essential significance for sheep disease in babies. The sheep are detracted from their tainted moms soon after birth and are brought up in unmistakable groups. These lambs (56°C for 60 min) and pasteurized milk are supplemented by heat-processed colostrum. Better still, colostrum and milk from MV-free registered ewes are added to the lambs. Sero-positive animals are separated from seronegative animals according to another protocol and only the seronegative part is supplied with substitutes. In another protocol, all seropositive animals that are detected are culled, which can be introduced in cases of minimal seropositivity due to their financial costs. Although these methods have been successful in a number of countries, there are a number of disadvantages to these control and eradication programs, Such as inadequate sensitivity and specificity of the serological test and relative significance of horizontal mode of transmission (Pepin et al., 1998). More likely, as a result of the mutagenic effects of the virus, a vaccine will never be available (Belknap, 2002). Nonetheless a number of study organizations continue to defend the viability of a searching for such a vaccine, supporting various approaches. Usage of DNA vaccine development High-quality production using studies in vitro and in vivo. In vitro assays are performed to confirm animal cell transfection protein expression, while in vivo assays are performed with mouse and/or sheep immunization to examine and assess the effectiveness of humoral and cellular responses to vaccines. (Henriques et al., 2016). Another search for such a vaccine against MVV use widely used adjuvants called Aluminumbased salts in ruminants which give elicited against vaccine antigens and strengthening the immune response and the formation of long-lasting granuloma composed of abundant activated macrophages. A practical approach to disease control does not seem to be the selection natural resistance of sheep to Maedi-Visna virus (Pepin et al., 1998). In addition, this has the potential of slowing or reversing ongoing genetic improvement projects for sheep.

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References

- Adjadj, N. R., Vicca, J., Michiels, R., & De Regge, N. (2020). (Non-) Sense of milk testing in small ruminant Lentivirus control programs in goats. Comparative Analysis of Antibody Detection and Molecular Diagnosis in Blood and Milk. *Viruses*, 12(1), 3.
- Akkan, H. A., Karaca, M., Tütüncü, M., Keles, I., Ilhan, F., Cetin, Y., & Tasal, I. (2009). Investigation of the seroprevalance of maedi-visna in the region of Van using Elisa and histopathological findings. *Journal* of Animal and Veterinary Advances, 8(8), 1495-1498.
- Al Ahmad, M. A., Chebloune, Y., Chatagnon, G., Pellerin, J. L., & Fieni, F. (2012). Is caprine arthritis encephalitis virus (CAEV) transmitted vertically to early embryo development stages (morulae or blastocyst) via in vitro infected frozen semen?. *Theriogenology*, 77(8), 1673-1678.
- Al Ahmad, M. A., Fieni, F., Pellerin, J. L., Guiguen, F., Cherel, Y., Chatagnon, G. & Chebloune, Y. (2008). Detection of viral genomes of caprine arthritis-encephalitis virus (CAEV) in semen and in genital tract tissues of male goat. *Theriogenology*, 69(4), 473-480.
- Allbasoglu, M. and Arda, M. (1975). Sheep pulmonary adenomatosis to investigate the etiology and pathology of the situation in Turkey. (Turkey). *Tübitak Vhag Publishing*, p274.
- Alvarez, V., Daltabuit-Test, M., Arranz, J., Leginagoikoa, I., Juste, R. A., Amorena, B., & Berriatua, E. (2006). PCR detection of colostrumassociated Maedi-Visna virus (MVV) infection and relationship with ELISA-antibody status in lambs. *Research in Veterinary Science*, 80(2), 226-234.
- Alves, S. M., Teixeira, M. D. S., Pinheiro, R. R., Alves, F. S. F., Lima, A. M. C., de Farias, D. A., ... & AGUIAR, T. D. F. (2018). Seroepidemiological study of maedi-visna in sheep in Ceara, Rio Grande do Norte, Paraíba, and Sergipe States. *Embrapa Caprinos* e Ovinos-Artigo em periódico indexado (ALICE).
- Ameen, P. S., & Karapınar, Z. (2018). Seroprevalence of visna-maedi virus (vmv) and border disease virus (bdv) in van province and around. Arquivo Brasileiro de Medicina Veterinária e Zootecnia, 70, 1029-1035.
- Arsenault, J., Dubreuil, P., Girard, C., Simard, C., & Bélanger, D. (2003). Maedi-visna impact on productivity in Quebec sheep flocks (Canada). *Preventive Veterinary Medicine*, 59(3), 125-137.
- Asadpour, R., Paktinat, S., Ghassemi, F., & Jafari, R. (2014). Study on correlation of Maedi-Visna virus (MVV) with ovine subclinical mastitis in Iran. *Indian journal of microbiology*, 54(2), 218-222.
- Barquero, N., Domenech, A., & Gomez-Lucia, E. (2015). Infections by Small Ruminant Lentiviruses. Saarbrücken, Germany: LAP Lambert Academic Publishing.
- Barták, P., Šimek, B., Václavek, P., Čurn, V., Plodková, H., Tonka, T., ... & Vejčík, A. (2018). Genetic characterisation of small ruminant lentiviruses in sheep and goats from the Czech Republic. Acta Veterinaria Brno, 87(1), 19-26.
- Benavides, J., Fuertes, M., Garcia-Pariente, C., Ferreras, M. C., Marin, J. G., & Perez, V. (2006). Natural cases of visna in sheep with myelitis as the sole lesion in the central nervous system. *Journal of comparative pathology*, 134(2-3), 219-230.
- Benavides, J., García-Pariente, C., Ferreras, M. C., Fuertes, M., García-Marín, J. F., & Pérez, V. (2007). Diagnosis of clinical cases of the nervous form of Maedi-Visna in 4-and 6-month-old lambs. *The Veterinary Journal*, 174(3), 655-658.
- Berriatua, E., Álvarez, V., Extramiana, B., González, L., Daltabuit, M., & Juste, R. (2003). Transmission and control implications of seroconversion to Maedi-Visna virus in Basque dairy-sheep flocks. *Preventive veterinary medicine*, 60(4), 265-279.
- Blacklaws, B. A. (2012). Small ruminant lentiviruses: Immunopathogenesis of visna-maedi and caprine arthritis and encephalitis virus. Comparative immunology, microbiology and infectious diseases, 35(3), 259-269.
- Blacklaws, B. A., Berriatua, E., Torsteinsdottir, S., Watt, N. J., De Andres, D., Klein, D., & Harkiss, G. D. (2004). Transmission of small ruminant lentiviruses. *Veterinary Microbiology*, 101(3), 199-208.
- Borman, A. M., Quillent, C., Charneau, P., Dauguet, C., & Clavel, F. (1995). Human immunodeficiency virus type 1 Vif-mutant particles from restrictive cells: role of Vif in correct particle assembly and infectivity. *Journal of virology*, 69(4), 2058-2067.

- Bose, D., Gagnon, J., & Chebloune, Y. (2015). Comparative analysis of Tatdependent and Tat-deficient natural lentiviruses. *Veterinary sciences*, 2(4), 293-348.
- Brellou, G. D., Angelopoulou, K., Poutahidis, T., & Vlemmas, I. (2007). Detection of Maedi-Visna Virus in the liver and heart of naturally infected sheep. *Journal of comparative pathology*, 136(1), 27-35.
- Cardinaux, L., Zahno, M. L., Deubelbeiss, M., Zanoni, R., Vogt, H. R., & Bertoni, G. (2013). Virological and phylogenetic characterization of attenuated small ruminant lentivirus isolates eluding efficient serological detection. *Veterinary microbiology*, *162*(2-4), 572-581.
- Chakravorty, S., & Hegde, M. (2017). Gene and variant annotation for Mendelian disorders in the era of advanced sequencing technologies. *Annual review of genomics and human genetics*, 18, 229-256.
- Chassalevris, T., Chaintoutis, S. C., Apostolidi, E. D., Giadinis, N. D., Vlemmas, I., Brellou, G. D., & Dovas, C. I. (2020). A highly sensitive semi-nested real-time PCR utilizing oligospermineconjugated degenerate primers for the detection of diverse strains of small ruminant lentiviruses. *Molecular and cellular probes*, 51, 101528.
- Christodoulopoulos, G. (2006). Maedi–Visna: Clinical review and short reference on the disease status in Mediterranean countries. *Small Ruminant Research*, 62(1-2), 47-53.
- Clements, J. E., & Zink, M. C. (1996). Molecular biology and pathogenesis of animal lentivirus infections. *Clinical microbiology reviews*, 9(1), 100-117.
- Coffin, J. M., Hughes, S. H., & Varmus, H. E. (1997). Retroviruses.
- Cowdry, E. V. (1925). STUDIES ON THE ETIOLOGY OF JAGZIEKTE: II. Origin of the Epithelial Proliferations, and the Subsequent Changes. *The Journal of experimental medicine*, 42(3), 335-345.
- Cowdry, E. V., & Marsh, H. (1927). Comparative pathology of South African jagziekte and Montana progressive pneumonia of sheep. *The Journal of experimental medicine*, 45(4), 571-585.
- Creer, T. L., Bender, B. G., & Lucas, D. O. (2002). Diseases of the respiratory system.
- Cutlip, R. C., Lehmkuhl, H. D., Brogden, K. A., & Bolin, S. R. (1985). Mastitis associated with ovine progressive pneumonia virus infection in sheep. *American journal of veterinary research*, 46(2), 326-328.
- Danchin, E., Pocheville, A., Rey, O., Pujol, B., & Blanchet, S. (2019). Epigenetically facilitated mutational assimilation: epigenetics as a hub within the inclusive evolutionary synthesis. *Biological Reviews*, 94(1), 259-282.
- De Andres, D., Klein, D., Watt, N. J., Berriatua, E., Torsteinsdottir, S., Blacklaws, B. A., & Harkiss, G. D. (2005). Diagnostic tests for small ruminant lentiviruses. *Veterinary Microbiology*, 107(1-2), 49-62.
- De Kock, G. (1929). Are the lesions of Jaagsiekte in sheep of the nature of a neoplasm. vet. Serv., 15th ann. Rep, 611-641.
- de la Concha-Bermejillo, A. (1997). Maedi-visna and ovine progressive pneumonia. Veterinary Clinics of North America: Food Animal Practice, 13(1), 13-34.
- Dousti, M., Sayyari, M., & Esmailnejad, A. (2020). Histopathological, serological, molecular and electron microscopy detection of Maedi-Visna infection in sheep population in the West of Iran. *Iranian Journal of Veterinary Research*, 21(2), 103.
- Dungu, B., Vorster, J., Bath, G. F., & Verwoerd, D. W. (2000). The effect of a natural maedi-visna virus infection on the productivity of South African sheep.
- Echeverría, I., de Miguel, R., Asín, J., Rodríguez-Largo, A., Fernández, A., Pérez, M., & Reina, R. (2020). Replication of small ruminant lentiviruses in aluminum hydroxide-induced granulomas in sheep: a potential new factor for viral dissemination. *Journal of Virology*, 95(2), e01859-20.
- Extramiana, A. B., González, L., Cortabarria, N., Garcia, M., & Juste, R. A. (2002). Evaluation of a PCR technique for the detection of Maedi-Visna proviral DNA in blood, milk and tissue samples of naturally infected sheep. *Small Ruminant Research*, 44(2), 109-118.
- Fauquet, C. M., Mayo, M. A., Maniloff, J., Desselberger, U., & Ball, L. A. (Eds.). (2005). Virus taxonomy: VIIIth report of the International Committee on Taxonomy of Viruses. Academic Press.
- Fieni, F., Pellerin, J. L., Roux, C., Poulin, N., Baril, G., Fatet, A., ... & Guignot, F. (2012). Can caprine arthritis encephalitis virus

(CAEV) be transmitted by in vitro fertilization with experimentally infected sperm?. *Theriogenology*, 77(3), 644-651.

- Franzdóttir, S. R., Ólafsdóttir, K., Jónsson, S. R., Strobel, H., Andrésson, Ó. S., & Andrésdóttir, V. (2016). Two mutations in the vif gene of maedi-visna virus have different phenotypes, indicating more than one function of Vif. *Virology*, 488, 37-42.
- Gayo, E., Cuteri, V., Polledo, L., Rossi, G., García Marín, J. F., & Preziuso, S. (2018). Genetic Characterization and Phylogenetic Analysis of Small Ruminant Lentiviruses Detected in Spanish Assaf Sheep with Different Mammary Lesions. *Viruses*, 10(6), 315.
- Gayo, E., Polledo, L., Magalde, A., Balseiro, A., Iglesias, M. G., Martínez, C. P., & Marín, J. G. (2019). Characterization of minimal lesions related to the presence of visna/maedi virus in the mammary gland and milk of dairy sheep. *BMC veterinary research*, 15(1), 1-9.
- Gogolewski, R. P., Adams, D. S., McGUIRE, T. C., Banks, K. L., & Cheevers, W. P. (1985). Antigenic cross-reactivity between caprine arthritisencephalitis, visna and progressive pneumonia viruses involves all virion-associated proteins and glycoproteins. *Journal of general* virology, 66(6), 1233-1240.
- Gomez-Lucia, E., Barquero, N., & Domenech, A. (2018). Maedi-Visna virus: current perspectives. Veterinary Medicine: Research and Reports, 9, 11.
- Gonda, M. A. (1994). Molecular Biology and Virus-Host Interactions of Lentiviruses a. Annals of the New York Academy of Sciences, 724(1), 22-42.
- González, L., Juste, R. A., Cuervo, L. A., Idigoras, I., & De Ocariz, C. S. (1993). Pathological and epidemiological aspects of the coexistence of maedi-visna and sheep pulmonary adenomatosis. *Research in veterinary science*, 54(2), 140-146.
- Greenwood, P. L. (1995). Effects of caprine arthritis-encephalitis virus on productivity and health of dairy goats in New South Wales, Australia. *Preventive Veterinary Medicine*, 22(1-2), 71-87.
- Gudmundsson, B., Bjarnadottir, H., Kristjansdottir, S., & Jonsson, J. J. (2003). Quantitative assays for maedi-visna virus genetic sequences and mRNA's based on RT-PCR with real-time FRET measurements. *Virology*, 307(1), 135-142.
- Gürçay, M., & Parmaksiz, A. (2013). An investigation of Visna-Maedi virus infection in Şanlıurfa Province, Southeast Anatolia, Turkey. AVKAE Derg, 3(1), 46-50.
- Henriques, A. M., Fevereiro, M., & Monteiro, G. A. (2016). DNA Vaccines Against Maedi–Visna Virus. In Vaccine Design (pp. 59-76). Humana Press, New York, NY.
- Herrmann-Hoesing, L. M., Noh, S. M., Snekvik, K. R., White, S. N., Schneider, D. A., Truscott, T., & Knowles, D. P. (2010). Ovine progressive pneumonia virus capsid antigen as found in CD163and CD172a-positive alveolar macrophages of persistently infected sheep. *Veterinary pathology*, 47(3), 518-528.
- Houwers, D. J., Visscher, A. H., & Defize, P. R. (1989). Importance of ewe/lamb relationship and breed in the epidemiology of maedivisna virus infections. *Research in veterinary science*, 46(1), 5-8.
- Ingvarsson, S. (2013). In memoriam Björn Sigurðsson born 100 years ago.
- Jarczak, J., Słoniewska, D., Kaba, J., & Bagnicka, E. (2019). The expression of cytokines in the milk somatic cells, blood leukocytes and serum of goats infected with small ruminant lentivirus. *BMC veterinary research*, 15(1), 1-11.
- Junkuszew, A., Dudko, P., Bojar, W., Olech, M., Osiński, Z., Gruszecki, T. M., & Czerski, G. (2016). Risk factors associated with small ruminant lentivirus infection in eastern Poland sheep flocks. *Preventive veterinary medicine*, 127, 44-49.
- Juste, R. A., Villoria, M., Leginagoikoa, I., Ugarte, E., & Minguijon, E. (2020). Milk production losses in Latxa dairy sheep associated with small ruminant lentivirus infection. *Preventive veterinary medicine*, 176, 104886.
- Keen, I. E., Hungerford, L. L., Wittum, T. E., Kwang, J., & Littledike, E. T. (1997). Rick factors for seroprevalence of ovine lentivirus in breeding ewe flocks in Nebraska, USA. *Preventive veterinary medicine*, 30(2), 81-94.
- Kimberlin, R. H., & RH, K. (1976). Slow virus diseases of animals and man.
- Kristbjörnsdóttir, H. B., Andrésdóttir, V., Svansson, V., Torsteinsdóttir, S., Matthiasdóttir, S., & Andrésson, Ó. S. (2004). The vif gene of maedi-visna virus is essential for infectivity in vivo and in vitro. *Virology*, 318(1), 350-359.
- Larruskain, A., & Jugo, B. M. (2013). Retroviral infections in sheep and goats: small ruminant lentiviruses and host interaction. *Viruses*, 5(8), 2043-2061.

- Leginagoikoa, I., Minguijon, E., Berriatua, E., & Juste, R. A. (2009). Improvements in the detection of small ruminant lentivirus infection in the blood of sheep by PCR. *Journal of virological methods*, 156(1-2), 145-149.
- Leroux, C., Lerondelle, C., Chastang, J., & Mornex, J. F. (1997). RT-PCR detection of lentiviruses in milk or mammary secretions of sheep or goats from infected flocks. *Veterinary Research*, 28(2), 115-121.
- Lima, C. C. V., Ayres, M. C. C., Pinheiro, R. R., Costa, J. N., Andrioli, A., Souza, T. S., ... & Costa, A. O. (2017). Caprine lentivirus in sheep milk and semen. Arquivo Brasileiro de Medicina Veterinária e Zootecnia, 69, 391-397.
- Loman, D. C. (1862). Het Texels schaap. Magazijn voor Landbouw en Kruidkunde II, 66-70.
- Luciw, P. A. (1992). Leung; NJ Mechanisms of retrovirus replication. In "The Retroviridae", Levy, JA.
- Marsh, H. (1923). Progressive Pneumonia in Sheep. Journal of the American Veterinary Medical Association, 15: 458-473.
- Mendiola, W. P., Tórtora, J. L., Martínez, H. A., García, M. M., Cuevas-Romero, S., Cerriteño, J. L., & Ramírez, H. (2019). Genotyping based on the LTR region of small ruminant lentiviruses from naturally infected sheep and goats from Mexico. *BioMed research international*, 2019.
- Minguijón, E., Reina, R., Pérez, M., Polledo, L., Villoria, M., Ramírez, H., ... & Juste, R. A. (2015). Small ruminant lentivirus infections and diseases. *Veterinary Microbiology*, 181(1-2), 75-89.
- Mitchell, D. T. (1915). Investigations into jaagziekte or chronic catarrhal pneumonia of sheep. Vet. Educ. Res., 3rd and 4th Report, Union of South Africa, 585.
- Murphy, B., McElliott, V., Vapniarsky, N., Oliver, A., & Rowe, J. (2010). Tissue tropism and promoter sequence variation in caprine arthritis encephalitis virus infected goats. *Virus research*, 151(2), 177-184.
- Muz, D., Oğuzoğlu, T. Ç., Rosati, S., Reina, R., Bertolotti, L., & Burgu, I. (2013). First molecular characterization of visna/maedi viruses from naturally infected sheep in Turkey. Archives of virology, 158(3), 559-570.
- Pépin, M., Vitu, C., Russo, P., Mornex, J. F., & Peterhans, E. (1998). Maedivisna virus infection in sheep: a review. *Veterinary research*, 29(3-4), 341-367.
- Pérez, M., Biescas, E., De Andrés, X., Leginagoikoa, I., Salazar, E., Berriatua, E., & Luján, L. (2010). Visna/maedi virus serology in sheep: Survey, risk factors and implementation of a successful control programme in Aragón (Spain). *The Veterinary Journal*, 186(2), 221-225.
- Pérez, M., Biescas, E., Reina, R., Glaria, I., Marín, B., Marquina, A., & Luján, L. (2015). Small Ruminant Lentivirus–Induced Arthritis: Clinicopathologic Findings in Sheep Infected by a Highly Replicative SRLV B2 Genotype. *Veterinary pathology*, 52(1), 132-139.
- Peterhans, E., Greenland, T., Badiola, J., Harkiss, G., Bertoni, G., Amorena, B., & Pépin, M. (2004). Routes of transmission and consequences of small ruminant lentiviruses (SRLVs) infection and eradication schemes. *Veterinary research*, 35(3), 257-274.
- Peters, P. J., Marston, B. J., Weidle, P. J., & Brooks, J. T. (2013). Human Immunodeficiency Virus Infection. In *Hunter's Tropical Medicine* and Emerging Infectious Disease (pp. 217-247). WB Saunders.
- Pettit, S. C., Everitt, L. E., Choudhury, S., Dunn, B. M., & Kaplan, A. H. (2004). Initial cleavage of the human immunodeficiency virus type 1 GagPol precursor by its activated protease occurs by an intramolecular mechanism. *Journal of virology*, 78(16), 8477-8485.
- Pétursson, G., Turelli, P., Matthíasdóttir, S., Georgsson, G., Andrésson, Ó. S., Torsteinsdóttir, S., & Quérat, G. (1998). Visna virus dUTPase is dispensable for neuropathogenicity. *Journal of virology*, 72(2), 1657-1661.
- Ploumi, K., Christodoulou, V., Vainas, E., Lymberopoulos, A., Xioufis, A., Giouzeljiannis, A., & Ap Dewi, I. (2001). Effect of maedi-visna virus infection on milk production in dairy sheep in Greece. *The Veterinary Record*, 149(17), 526-527.
- Tolari, F. (2000). Maedi visna ovina: eziologia, diagnosi, prevenzione e risanamento.
- Turner, B. G., & Summers, M. F. (1999). Structural biology of HIV. Journal of molecular biology, 285(1), 1-32.

- Potarniche, A. V., Cerbu, C. G., Czopowicz, M., Szalus-Jordanow, O., Kaba, J., & Spinu, M. (2020). The epidemiological background of small ruminant lentivirus infection in goats from Romania. *Veterinary World*, 13(7), 1344.
- Preziuso, S., Sanna, E., Sanna, M. P., Loddo, C., Cerri, D., Taccini, E., ... & Rossi, G. (2003). Association of Maedi Visna virus with Brucella ovis infection in rams. *European Journal of Histochemistry*, 47(2), 151-158.
- Pritchard, G. C. and Dawson, M. (2000). Maedi–Visna. In: Martin,W.B., Aitken, I.D. (Eds.), Diseases of Sheep, 3rd ed. Blackwell, pp:187– 191.
- Radostits O. M.; Gay, C. C.; Blood, D. C. and Hinchcliff, K. W. (2017). Veterinary Medicine. 17th edition, Saunders co., London, 1362-1366pp.
- Reina, R., Berriatua, E., Luján, L., Juste, R., Sánchez, A., de Andrés, D., & Amorena, B. (2009). Prevention strategies against small ruminant lentiviruses: an update. *The Veterinary Journal*, 182(1), 31-37.
- Robertson, W. (1904). Jagziekte or chronic catarrhal pneumonia (sheep). Journal of Comparative Pathology and Therapeutics, 17, 221-224.
- Sakhaee, E., & Khalili, M. (2010). Serological study of Maedi-Visna virus among sheep flocks in Kerman province of Iran.
- Saltarelli, M. J., Schoborg, R., Gdovin, S. L., & Clements, J. E. (1993). The CAEV tat gene trans-activates the viral LTR and is necessary for efficient viral replication. *Virology*, 197(1), 35-44.
- Sanjosé, L., Pinczowski, P., Crespo, H., Pérez, M., Glaria, I., Gimeno, M., & Reina, R. (2015). Diagnosing infection with small ruminant lentiviruses of genotypes A and B by combining synthetic peptides in ELISA. *The Veterinary Journal*, 204(1), 88-93.
- Sargan, D. R., Bennet, I. D., Cousens, C., Roy, D. J., Blacklaws, B. A., Dalziel, R. G., ... & McConnell, I. (1991). Nucleotide sequence of EV1, a British isolate of maedi-visna virus. *Journal of General Virology*, 72(8), 1893-1903.
- Sheehy, A. M., Gaddis, N. C., Choi, J. D., & Malim, M. H. (2002). Isolation of a human gene that inhibits HIV-1 infection and is suppressed by the viral Vif protein. *Nature*, 418(6898), 646-650.
- Sigurdardóttir, B., & Thormar, H. (1964). Isolation of a viral agent from the lungs of sheep affected with maedi. *The Journal of infectious diseases*, 55-60.
- Sigurdsson, B., Pálsson, P. A., & van Bogaert, L. (1962). Pathology of visna. Acta Neuropathologica, 1(4), 343-362.
- Sihvonen, L., Nuotio, L., Rikula, U., Hirvelä-Koski, V., & Kokkonen, U. M. (2000). Preventing the spread of maedi–visna in sheep through a voluntary control programme in Finland. *Preventive veterinary medicine*, 47(3), 213-220.
- Simon, J. H., Gaddis, N. C., Fouchier, R. A., & Malim, M. H. (1998). Evidence for a newly discovered cellular anti-HIV-1 phenotype. *Nature medicine*, 4(12), 1397-1400.
- Snowder, G. D., Gates, N. L., Glimp, H. A., & Gorham, J. R. (1990). Prevalence and effect of subclinical ovine progressive pneumonia virus infection on ewe wool and lamb production. *Journal of the American Veterinary Medical Association*, 197(4), 475-479.
- Straub, O. C. (2004). Maedi–Visna virus infection in sheep. History and present knowledge. *Comparative immunology, microbiology and infectious diseases*, 27(1), 1-5.
- Tabet, E., Tlaige, R., El Hage, J., & Abi-Rizk, A. (2017). The occurrence of Maedi-Visna virus (MVV) in Lebanon. *Rev. Sci. Tech. Off. Int. Epiz*, 36(3), 2.
- Tan, M. N., & Alkan, F. (2002). Seroepidemiological investigation of maedivisna infection in Turkey and virus isolation attempts. *Veterinary Journal of Ankara University (Turkey).*
- téphanie Villet, S., Faure, C., Bouzar, B. A., Morin, T., érard Verdier, G., Chebloune, Y., & Legras, C. (2003). Lack of trans-activation function for Maedi Visna virus and Caprine arthritis encephalitis virus Tat proteins. *Virology*, 307(2), 317-327.
- Thormar, H. (2013). The origin of lentivirus research: Maedi-visna virus. *Current HIV research*, 11(1), 2-9.
- Tiley, L. S., & Cullen, B. R. (1992). Structural and functional analysis of the visna virus Rev-response element. *Journal of virology*, 66(6), 3609-3615.
- Villoria, M., Leginagoikoa, I., Luján, L., Pérez, M., Salazar, E., Berriatua, E., & Minguijón, E. (2013). Detection of small ruminant lentivirus in environmental samples of air and water. *Small Ruminant Research*, 110(2-3), 155-160.

- Watt, N., Scott, P., & Collie, D. (1994). Maedi-visna virus infection in practice. In Practice, 16(5), 239-247.
- York, D. F., & Querat, G. (2003). A history of ovine pulmonary adenocarcinoma (jaagsiekte) and experiments leading to the deduction of the JSRV nucleotide sequence. In *Jaagsiekte Sheep Retrovirus and Lung Cancer* (pp. 1-23). Springer, Berlin, Heidelberg.
- Yu, X., Yu, Y., Liu, B., Luo, K., Kong, W., Mao, P., & Yu, X. F. (2003). Induction of APOBEC3G ubiquitination and degradation by an HIV-1 Vif-Cul5-SCF complex. *Science*, 302(5647), 1056-1060.

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- Zhang, Z., Watt, N. J., Hopkins, J., Harkiss, G., & Woodall, C. J. (2000). Quantitative analysis of maedi-visna virus DNA load in peripheral blood monocytes and alveolar macrophages. *Journal of virological methods*, 86(1), 13-20.

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