International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
IJCS 2018; 6(2): 2615-2619

Received: 04-01-2018
Accepted: 07-02-2018

Amita Tiwari
Department of Veterinary Medicine, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P.), India

PC Shukla
Department of Veterinary Medicine, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P.), India

Devendra Gupta
Department of Veterinary Medicine, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P.), India

Brejesh Singh
Department of Veterinary Medicine, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P.), India

Arpana Raikwar
Department of Veterinary Medicine, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P.), India

Amir Amin Sheikh
Department of Veterinary Physiology and Biochemistry, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P), India

Rakshanda Bhagat
Division of Veterinary Medicine, F.V.Sc and A.H., Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, R.S.Pura, Jammu, Jammu & Kashmir, India

Correspondence
Amir Amin Sheikh
Department of Veterinary Physiology and Biochemistry, College of Veterinary Science and Animal Husbandry, N.D.V.S.U., Jabalpur (M.P), India

Schmallenberg virus infection: An emerging vector borne disease

Amita Tiwari, PC Shukla, Devendra Gupta, Brejesh Singh, Arpana Raikwar, Amir Amin Sheikh and Rakshanda Bhagat

Abstract
Term emerging infectious diseases describes new or unrecognized diseases that are spreading to new geographic areas and hosts. Schmallenberg virus (SBV) is an enveloped, negative-sense, segmented, single-stranded RNA virus. Analysis of viral sequences has led to the classification of SBV in the *Bunyaviridae* family and the *Orthobunyavirus* genus. A very little is known about the life cycle of SBV. The replication cycle of bunyaviruses is exclusively cytoplasmic. SBV appears to cause disease in domestic and possibly wild ruminants. Cattle, sheep, and goats are susceptible. According to experimental challenge trials, calves inoculated intravenously or subcutaneously were seropositive 2 to 5 days post-inoculation. Symptoms are more apparent in adult cows and include loss of appetite, hyperthermia and diarrhoea, which can lead to a 50% reduction in milk production. The viraemia induced by SBV is short-lived, lasting for 2 to 6 days in cattle. Infected females are able to transmit the virus to foetuses (ovine, caprine and bovine), which developed atypical malformations leading most frequently to intra-uterine death or death immediately after birth. Diagnosis of SBV infection relies on the detection of the viral genome by RT-qPCR. At present no therapeutic drugs or vaccines are available for SBV induced disease. One possible option is to control the Culicoides vectors.

Keywords: Bunyaviridae, emerging, orthobunyavirus genus and schmallenberg virus

Introduction
The term emerging infectious diseases describes new or unrecognized diseases that are spreading to new geographic areas and hosts (Marsh, 2008) [1]. Noticeably, the rate of emerging infectious diseases is increasing (one new emerging or re-emerging disease every eight months) (Lefrançois and Pineau, 2014) [2]. The rapid pace of infection emergence is not only connected to more suitable conditions for pathogen appearance and spreading, it is also linked to improved methods and technologies for surveillance, pathogen detection, and identification. One such emerging infection was introduced to the world at the end of the summer and in the autumn 2011 when hyperthermia and drop in milk production were reported in adult dairy cows in north-west Germany and The Netherlands. In some cases, transient diarrhoea was also recorded in the Netherlands. Some of the symptoms observed were similar to the disease caused by Bluetongue virus (BTV) and a re-emergence of this virus that led to a major epizooty in 2006–2008 in Europe was feared but no known bovine pathogen was identified in samples from symptomatic cases. In November 2011, the Friedrich-Loëffler Institute (FLI) in Germany detected viral RNA belonging to a new virus in a pool of blood samples from clinically affected dairy cows using a metagenomic approach (Hoffmann *et al*., 2012) [3]. This new virus was called Schmallenberg virus (SBV) after the place of origin of the collected samples. Analysis of viral genomic sequences revealed similarities with Akabane, Aino and Shamonda viruses, all belonging to the *Orthobunyavirus* genus from the *Bunyaviridae* family.

Timeline of SBV infection
SBV was first detected in Germany and The Netherlands in 2011. In December 2011, The Netherlands reported a teratogenic effect of SBV in sheep with the birth of malformed lambs with crooked neck, hyrocephalus and stiff joints (Hoffmann *et al*., 2012) [3]. The presence of SBV was then reported in Belgium at the end of December 2011 and in the United Kingdom on the 22nd of January 2012.

France reported its first case of SBV on the 25th of January 2012 after the virus genome was detected by RT-qPCR in brain samples from malformed lambs born on farms located in the territorial divisions of "Moselle" and "Meurthe et Moselle" in north-eastern France. The presence of SBV was then reported in Luxembourg on the 16th of February. On the 17th of February, SBV was confirmed in a malformed goat in north-east Italy and on the 12th of March, in Spain (Andalusia), in a newborn lamb.

By the end of April 2012, SBV had been detected in 3628 herds in Europe. In May 2012, acute SBV infections were detected in cattle in south west France in the Pyrénées-Atlantiques territorial division, indicating that SBV was able to re-circulate after the winter period. Similar conclusions were also made after the detection of the virus in the United Kingdom in newborn lambs born in May and June 2012 and in Germany in cattle, sheep and goat holdings sampled in 2012. On the 5th of June 2012, Denmark reported the presence of antibodies against SBV in two cattle from southern Jutland and on the 20th of July, Switzerland confirmed its first cases of acute SBV infection in cows from two farms in the canton of Berne.

By August 2012, more than 5500 cases of SBV infection in ruminants had been recorded across northern Europe. In mid-September; anti-SBV antibodies were detected in Austria in cattle and sheep. At the beginning of October 2012, the presence of antibodies to SBV was reported in western Poland in goats and in Sweden in cows. In mid-October, anti-SBV antibodies were detected in northern Scotland and in two cows from Finland. Further studies suggested that the virus had spread to South Finland during the summer and early autumn of 2012. At the end of October 2012, the presence of SBV was detected in Ireland in a bovine foetus and a few days later, in Northern Ireland in a malformed calf.

In November 2012, antibodies against the virus were detected in milk from cattle herds in Norway and an outbreak of SBV was reported in Italy (Sardinia) in a sheep flock with cases of abortion and foetal malformations. At the end of December 2012, SBV was detected for the first time in the Czech Republic following the birth of malformed lambs. In mid-January 2013, the first cases of SBV were confirmed in Estonia in sheep foetuses and at the end of January the presence of SBV was confirmed in sheep in Slovenia (Doceul *et al*., 2013) [4].

Molecular Virology

Schmallenberg virus (SBV) is an enveloped, negative-sense, segmented, single-stranded RNA virus. As mentioned above it was first detected at the FLI, Germany using metagenomic analysis and named after the German town 'Schmallenberg' from which the first positive samples came. Scientists from the FLI led by Dr. Harald Granzow of the Institute of Infectology visualised SBV using high-resolution electron microscopic analyses of infected cells. The virus was visible as a membrane-enveloped particle with a diameter of about 100 nm.

Analysis of viral sequences has led to the classification of SBV in the *Bunyaviridae* family and the *Orthobunyavirus* genus. Viruses from this family infect vertebrates with the exception of tospoviruses that are plant viruses. The *Orthobunyavirus* genus is composed of more than 170 viruses divided into 18 serogroups. SBV belongs to the Simbu serogroup that also includes Simbu virus, Oropouche virus, Akabane virus, Douglas virus, Sathuperi virus, Aino virus, Shamonda virus, Peaton virus and many others.

Genome and Structure

The bunyavirus genome consists of 3 segments of negative-sense single-stranded RNA: the L (large), M (medium) and S (small) segments (Bouloy *et al*., 1973) [5]. The L segment encodes the RNA-dependent RNA polymerase (RdRp) L (or L protein), the M segment encodes a precursor polyprotein that is co-translationally cleaved into the envelope glycoproteins Gn and Gc and the non-structural protein NSm and the S segment encodes the nucleoprotein N and the non-structural protein NSs in an overlapping open reading frame. The three segments of the SBV genome have been fully sequenced but its structure and the different encoded proteins are not yet well-characterised and can only be predicated from the data available on related viruses.

Virions from bunyaviruses are enveloped, spherical and have a diameter of approximately 80 to 120 nm. They acquire their membrane when budding at the Golgi apparatus lumen (Kuismanen *et al*., 1982) [6]. Electron microscopy performed at the FLI confirmed that, similarly to other bunyaviruses, the SBV virus particle has a diameter of approximately 100 nm and is membrane-enveloped. Virus particles of bunyaviruses are constituted of 4 structural proteins: the two surface glycoproteins Gn and Gc and the viral polymerase complex composed of the polymerase L protein and the nucleoprotein N. This complex is responsible for the transcription and replication of the viruses that occur exclusively in the cytoplasm. Inside the virus particle, the viral genome is present as a ribonucleoprotein (RNP) associated with many copies of the nucleoprotein N and a few copies of the polymerase L.

Life Cycle

A very little is known about the life cycle of SBV. The replication cycle of bunyaviruses is exclusively cytoplasmic. It begins with the recognition of the cellular receptor, unknown for the majority of bunyaviruses, by the Gn/Gc heterodimers present at the surface of the virion membrane (Elliott, 1990) [7]. Virions enter the cell via endocytosis. Change of pH in vesicles induces conformational modifications of the viral glycoproteins and the exposure of the Gc fusion peptide (Plassmeyer *et al*., 2007) [8]. The viral envelope fuses with the membranes of the endosomes and the RNP are released inside the cytoplasm. The primary transcription can start and produce viral mRNA via a mechanism of catch-snatching (Bouloy *et al*., 1990) [9]. The L protein cleaves a sequence of 10 to 18 nucleotides from the 5' end of capped mature cellular mRNA to use it as a primer for the initiation of viral transcription. Viral mRNA are synthesised and translation by host cell ribosomes leads to the production of viral proteins. The L and N proteins are needed for replication of the viral genome and the glycoproteins Gn and Gc form heterodimer complexes in the endoplasmic reticulum. Both glycoproteins are then transported to the Golgi apparatus via a Golgi-retention signal, located on Gn for most bunyaviruses, where their glycosylation is completed (Walter and Barr, 2011) [9].

Assembly of bunyaviruses is thought to occur mostly in tubular virus factories containing both cellular and viral components situated around the Golgi complex. From free nucleotides, the viral L polymerase produces complementary copies of the whole viral genome called antigenomes that are also present as RNP and are needed for the production of high

quantities of viral genomes. Newly-formed genome RNP then accumulate in the Golgi complex where they directly interact with the C-terminal domains of the glycoproteins Gn and Gc. Maturation of viral particles occurs via budding through the modified membrane of the Golgi apparatus. Mature virus particles are then transported in vesicles to the plasma membrane where they are released in the extracellular compartment by exocytosis. Further morphological changes then occur resulting in the release of fully infectious extracellular virus particles (Doceul *et al*., 2013) [4].

Ecology

General Overview

Members of the Simbu serogroup are distributed throughout Asia, Africa, the Middle East, and Australia. Prior to November 2011, Simbu serogroup viruses had not been detected in Europe. Cases have now been reported in countries including Germany, the Netherlands, Belgium, the United Kingdom, Luxembourg, Italy, France, Spain, Switzerland, Austria, Ireland, Finland, Norway, Sweden, Poland, and Estonia.

Susceptible Species

SBV appears to cause disease in domestic and possibly wild ruminants. Cattle, sheep, and goats are susceptible. The large majority of affected animals are sheep. Bison are also susceptible and bison calves have been observed with teratogenic disease. Evidence of SBV infection has also been detected in wild British red deer (Cervus elaphus), fallow deer (Dama dama), roe deer (Capreolus capreolus), and Reeve's muntjac (Muntiacus reevesi); whether wild ruminants experience clinical disease is unknown (Barlow *et al*., 2013**)** [11]. Other potential susceptible wildlife include mouflon sheep (Ovis aries) and wild boar (Sus scofra).

Origin

The history and geographical origins of SBV emergence remain unknown. Although SBV was discovered only recently, there is no doubt that its origins are more ancient and that it might have co-evolved with other closely related viruses. Viruses belonging to the Simbu serogroup have not been well studied and epidemiological data are poor. Nevertheless, phylogenetic analyses based on samples taken in different regions of the world at different periods of time suggest that these viruses evolve slowly. For example, the nucleotide sequences of Japanese strains of the Shamonda virus isolated in 2005 differ by only 3% from those of strains isolated in Nigeria 30 years before (Yanase *et al*., 2005) [12].

Transmission

Studies have shown that viruses within the Simbu serogroup are mostly transmitted by culicoides, but also by mosquitoes from the *Aedes* and *Culex* genus and by several species of ticks. Recently, a study has reported the presence of the SBV genome in a pool of culicoides (*C. obsoletus complex*, *C. chiopterus* and *C. dewulfi*) trapped from July to October 2011 in Belgium (De Regge *et al*., 2012) [13]. Culicoides from the *C. obsoletus* group trapped in Denmark during the same period also contained SBV RNA (Rasmussen *et al*., 2012) [14]. Furthermore, SBV RNA was detected in *C. obsoletus complex* and *C. chiopterus* collected in August-September 2011 in the Netherlands where the prevalence of SBV among Culicoides at this period was estimated to be around 0.25% (Elbers *et al*., 2011) [15]. The virus has also been found in biting midges in Norway, Poland and Sweden (Larska *et al*., 2013) [16]. These studies suggest that species of culicoides identified as vectors for BTV also act as vectors for the transmission of SBV.

Recently, SBV RNA has been detected in the semen of naturally infected bulls and SBV infection was reported in calves inoculated experimentally with SBV RT-qPCR-positive semen. These findings show that the semen of bulls naturally infected with SBV can be infectious (Doceul et al., 2013) [4].

Incubation Period

According to experimental challenge trials, calves inoculated intravenously or subcutaneously were seropositive 2 to 5 days post-inoculation. The World Organization for Animal Health (OIE) additionally reports that in experiments with both adult cattle and sheep incubation time was 1 to 4 days and viremia lasted for 1 to 5 days (OIE, 2013) [17]**.**

M**orbidity and Mortality**

Morbidity in adult animals may be in apparent or present with non-specific signs of illness. Recovery occurs within a few days for individual animals and within 2 to 3 weeks for the herd. Herd morbidity rates can be high (20 to 70 percent). Mortality appears to be mainly confined to aborted fetuses.

Pathogenesis

The outcome of infection is different for invertebrates and vertebrates. Although the virus replicates cyttoplasmically, infection of mammalian cells is cytolytic and results in cell death, whereas infection of insect cells lead to persistence as no cytopathic effects are visible postinfection. The initial replication of the virus inside the vector occurs in the midgut epithelium. Subsequently, the virus disseminates into the hemocoel, permitting carriage in the hemolymph. Finally the virus enters cells of salivery glands, replicates and reaches the salivery ducts. In ruminants, the viruses replicate in the periphery and cause a subsequent transient viremia in their hosts.

Clinical Signs

Sheep and goats seem to be very mildly affected by SBV infection. Symptoms are more apparent in adult cows and include loss of appetite, hyperthermia and diarrhoea, which can lead to a 50% reduction in milk production. Symptoms usually disappear within a few days. The viraemia induced by SBV is short-lived, lasting for 2 to 6 days in cattle. Infected females are able to transmit the virus to foetuses (ovine, caprine and bovine), which developed atypical malformations leading most frequently to intra-uterine death or death immediately after birth. Common congenital malformations and clinical signs in aborted and stillborn animals include a neuro-musculo-skeletal disorder called arthrogryposis, severe torticollis, ankylosis, kyphosis, lordosis scoliosis, brachygnathia inferior and neurological disorders such as amaurosis, ataxia and/or behavioral abnormalities.

In case of twin gestation, one twin can suffer from arthrogryposis and the other from neurological disorders. One twin can also be born malformed and the other one viable or only affected by a delayed growth.

Newborns suffer from severe neurological disorders that generally lead to death of the animal several hours to several days after birth. It was reported that a SBV-positive one-week old calf born at term showed severe central nervous system lesions, severe dysfunctions of the cerebral cortex, basal ganglia and mesencephalon, severe porencephaly or

hydranencephaly but no arthrogryposis (Garigliany *et al*., 2012) [18].

Histological studies have revealed lymphohistiocytic inflammation in the central nervous system and glial nodules in the mesencephalon and hippocampus in ovine species. Histological examination of the brain and spinal cord of a ten-day old SBV RT-qPCR-positive calf has also reported the presence of meningoencephalitis and poliomyelitis. Furthermore, immunohistochemistry and in situ hybridisation methods performed on brain sections have suggested that neurons are the major target for SBV replication in naturally infected newborn lambs and calves (Hahn *et al*., 2012) [19].

SBV can infect bison as reported in Germany. The virus is also able to infect wild cervids and llamas but no clinical signs or macroscopic abnormalities were recorded for these species (Linden *et al*., 2012) [20]. The virus might infect other wild species and domestic animals such as horses or dogs, as reported for viruses belonging to the *Orthobunyavirus* genus. However, SBV infection has not yet been reported in these species. Most of the viruses from the Simbu serogroup are not considered to be zoonotic, with the exception of Oropouche virus, which can infect humans and provoke severe flu-like symptoms. To date, no evidence of SBV infection in humans has been reported and no SBV-neutralising antibodies have been detected in sera from persons (farmers and veterinarians) exposed to the virus (Ducomble *et al*., 2012) [21].

Diagnosis

Diagnosis of SBV infection relies on the detection of the viral genome by RT-qPCR. It is a duplex assay that was initially developed by the FLI. The technique is based on the simultaneous amplification of a SBV gene and an endogenous gene, β-actin or GAPDH, which is used as an internal positive control (IPC) to ascertain RNA integrity and the absence of PCR inhibitors. Primers amplifying a part of the L gene segment were first used as a template for the detection of the SBV genome. Brain samples from aborted or stillborn lambs, kids and calves have mainly been used for diagnosis of SBV. Studies have shown that samples from the cerebrum, external placental fluid and the umbilical and spinal cord are suitable for the detection of SBV and that the highest concentration of SBV RNA is found in the brainstem. Viral isolation requires the inoculation of Vero (African green monkey kidney epithelial), BHK-21 (baby hamster kidney fibroblast) or KC (*Culicoides variipennis* larvae) cells with brain, serum or blood samples.

Virus neutralisation tests (VNT) and a plaque reduction neutralisation test were developed to detect antibodies present in the serum of infected animals. However, these methods are time-consuming (4 to 6 days) and cannot be automated. An indirect ELISA test based on a recombinant SBV nucleoprotein antigen produced by ID-VET (Montpellier, F-34070) was designed. This test was validated by the Animal Health laboratory at the French agency for food, environmental and occupational health and safety (ANSES) in Maisons-Alfort (Alfort ANSES laboratory) in April 2012 and currently provides a rapid and less expensive tool for serological diagnosis. A Dutch group has developed an ELISA based on SBV that has been cultured on partially purified and completely inactivated Vero cells. This assay was shown to be a sensitive test to detect antibodies in foetal or procolostral sera and diagnose SBV in newborn calves and lambs. ELISA tests have also been developed to detect anti-SBV antibodies in milk (Doceul *et al*., 2013) [4].

Prevention

At present no therapeutic drugs or vaccines are available for SBV induced disease. As it is a new disease further work is needed to determine what control measures may be appropriate. One possible option is to control the Culicoides vectors by employing methods such as the application of insecticides and pathogens to habitats where larvae develop; environmental interventions to remove larval breeding sites; controlling adult midges by treating either resting sites such as animal housing or host animals with insecticides; housing livestock in screened buildings; and using repellents or host kairomones to lure and kill adult midges. The treatment of livestock and animal housing with pyrethroid insecticide combined with the use of midge-proofed housing for viraemic or high-value animals and reduction of local breeding sites are the best options currently available. However, application of pour-on insecticides has been unsuccessful with no noticeable reduction in the density of biting midges in highly-challenged areas. Control of midges is unlikely to be effective given that they are extremely widespread, and appear to be very effective at spreading SBV. Furthermore, the timings of breeding or insemination of female animals can be selected such that the vulnerable stage of pregnancy does not lie within the vector-active season. However, the prospects for developing a SBV vaccine in the near future appear to be very good. Different research groups have developed prototypes for inactivated vaccines but none of them has been granted marketing authorisation yet. Merck Animal Health Company has produced a vaccine based on inactivated wild-type Schmallenberg virus, which should soon be available for use (Pawaiya and Gupta, 2013) [22].

Conclusions

The emergence of SBV at the end of 2011 is a reminder that the introduction of new diseases remains a threat for the livestock population. A certain level of protection exists within the ruminant populations but it is likely that a significant percentage of animals remains susceptible to SBV in areas where no or few cases of SBV have been reported. Maintaining an efficient surveillance would be essential to further describe the progression of the epidemic and its impact on the breeding industry. More studies are needed to determine the regions in which SBV is present, to understand its geographical and genetic origin and to identify its putative reservoirs. A better understanding of the pathogenesis associated with SBV infection and the ability of SBV antibodies to protect animals against the disease will also be useful to control the disease.

References

1. Marsh. The economic and social impact of emerging infectious disease: mitigation through detection, research, and response. Marsh Inc. Compliance # MA8-10342.Available online at:http://www.health-care.philips.com/main/shared/assets. 2008.
2. Lefrançois T, Pineau T. Public health and livestock: Emerging diseases in food animals. Ani Frontiers, 2014; 4(1): 4-6
3. Hoffmann B, Scheuch M, Hoper D, Jungblut R, Holsteg M, Schirrmeier H, *et al*. Novel orthobunya virus in Cattle, Europe, Emerg Infect Dis, 2012; 18:469-472.
4. Doceul V, Estelle L, Corinne S, Guillaume B, Jennifer R, Emmanuel B, Cyril V, Morgane D, Pascal H, Didier C, Alexandra D, Jerome L, *et al*. Epidemiology, molecular virology and diagnostics of Schmallenberg

virus, an emerging orthobunyavirus in Europe. Vet Res, 2013; 44:31
5. Bouloy M, Krams-Ozden S, Horodniceanu F, Hannoun C. Three-segment RNA genome of Lumbo virus (Bunyavirus). Intervirol, 1973; 2:173-180.
6. Kuismanen E, Hedman K, Saraste J, Pettersson R F. Uukuniemi virus maturation: accumulation of virus particles and viral antigens in the Golgi complex, 1982.
7. Elliott R M. Molecular biology of the Bunyaviridae. J Gen Virol, 1990; 71:501-522.
8. Plassmeyer M L, Soldan S S, Stachelek K M, Roth S M, Martin-Garcia J, Gonzalez-Scarano F. Mutagenesis of the La Crosse Virus glycoprotein supports a role for Gc (1066–1087) as the fusion peptide. Virology, 2007; 358:273-282.
9. Bouloy M, Pardigon N, Vialat P, Gerbaud S, Girard M. Characterization of the 5' and 3' ends of viral messenger RNAs isolated from BHK21 cells infected with Germiston virus (Bunyavirus). Virol, 1990; 175:50-58
10. Walter C T, Barr J N. Recent advances in the molecular and cellular biology of bunya viruses. J Gen Virol, 2011; 92:2467-2484.
11. Barlow A, Green P, Banham T, Healy N. Serological confirmation of SBV infection in wild British deer. Vet Record, 2013; 172(16): 429.
12. Yanase T, Maeda K, Kato T, Nyuta S, Kamata H, Yamakawa M, Tsuda T. The resurgence of Shamonda virus, an African Simbu group virus of the genus Orthobunyavirus, in Japan. Arch Virol, 2005; 150:361-369.
13. De Regge N, Deblauwe I, De Deken R, Vantieghem P, Madder M, Geysen D, Smeets, F, *et al*. Detection of Schmallenberg virus in different Culicoides spp. by real-time RT-PCR. Transbound Emerg Dis, 2012; 59:471-475.
14. Rasmussen L D, Kristensen B, Kirkeby C, Rasmussen T B, Belsham G J, Bodker R, Botner A. Culicoids as vectors of Schmallenberg virus. Emerg Infect Dis, 2012; 18:1204-1206.
15. Elbers A R, Meiswinkel R, Van Weezep E, Sloet van, Oldruitenborgh-Oosterbaan M M, Kooi E A. Schmallenberg virus in Culicoides spp. biting midges, the Netherlands, 2011. Emerg Infect Dis, 2013; 19:106-109.
16. Larska M, Polak M P, Grochowska M, Lechowski L, Zwiazek J S, Zmudzinski, J F. First report of Schmallenberg virus infection in cattle and midges in Poland, 2013.
17. OIE, 'Schmallenberg Virus." Technical Factsheet. www.oie.int. 2013.
18. Garigliany M M, Hoffmann B, Dive M, Sartelet A, Bayrou C, Cassart D, Beer M, Desmecht D. Schmallenberg virus in calf born at term with porencephaly, Belgium. Emerg Infect Dis, 2012; 18:1005-1006
19. Hahn K, Habierski A, Herder V, Wohlsein P, Peters M, Hansmann F, Baumgartner W. Schmallenberg virus in central nervous system of ruminants. Emerg Infect Dis, 2012; 19:154-155.
20. Linden A, Desmecht D, Volpe R, Wirtgen M, Gregoire F, Pirson J, Paternostre J, Kleijnen D, Schirrmeier H, *et al*. Epizootic spread of Schmallenberg virus among wild cervids, Belgium, Fall 2011. Emerg Infect Dis, 2012; 18:2006-2008.
21. Ducomble T, Wilking H, Stark K, Takla A, Askar M, Schaade L, Nitsche A, Kurth, A. Lack of evidence for Schmallenberg virus infection in highly exposed persons, Germany, 2012. Emerg Infect Dis, 2012; 18:1333-1335.
22. Pawaiya R V S, Gupta V K. A review on Schmallenberg virus infection: a newly emerging disease of cattle, sheep and goats. Veterinarni Medicina, 2013; 58 (10): 516–526.