

= Playa de Oro virus =

Playa de Oro virus (OROV) is a probable species of hantavirus found in the rodents *Oryzomys couesi* and *Sigmodon mascotensis* in the Mexican state of Colima . The former is thought to be the main host . The sequences of parts of the virus 's RNA @-@ based genome have been determined ; they differ by 7 ? 10 % in amino acid composition and 22 ? 24 % in nucleotide composition from closely related viruses .

Playa de Oro virus was identified as a new species in 2008 and is most closely related to Bayou virus , Catacamas virus , Muleshoe virus , and Black Creek Canal virus , found in other species of *Oryzomys* and *Sigmodon* . Catacamas virus is found in a different population of *Oryzomys couesi* , and the presence of different viruses in these two species has been used as an argument for classifying the two populations of the host as separate species .

= = History and occurrence = =

Playa de Oro virus was first identified in rodents collected in 2004 as part of a survey of wild mammals at Playa de Oro in Manzanillo , Colima , western Mexico . The discovery was published in 2008 by Yong @-@ Kyu Chu and colleagues . Among 600 small mammals , antibodies against the hantavirus Sin Nombre virus were found in 23 individuals (out of 358 studied) of *Oryzomys couesi* , a rice rat that was the most common species found , six (out of 87) of the cotton rat *Sigmodon mascotensis* , and one (out of 77) of the pygmy mouse *Baiomys musculus* . In addition , twelve *O. couesi* and one *S. mascotensis* yielded hantavirus RNA . Viruses were found in males more often than in females . Because the amino acid sequences in sequenced parts of the virus 's genome differed by as much as 7 to 10 % from closely related hantaviruses , Chu and colleagues identified the virus found at Playa de Oro as a new species , called Playa de Oro virus or OROV . Although the authors could not prove that the virus fulfilled all the criteria for identifying a new virus species , they argued that it was likely that it did fulfill those criteria . It is currently treated as a probable species in the Hantavirus genus .

= = Virology = =

Hantaviruses have a genome that consists of three segments of single @-@ stranded , negative @-@ sense RNA (see RNA virus : Replication) , called the large (L) , medium (M) , and small (S) segments . The entire S segment and a fragment of the M segment have been sequenced .

The S segment consists of 1953 bases , of which 1287 (starting at position 43) code for the nucleocapsid protein . In addition , a second 192 @-@ base open reading frame occurs in the middle of this sequence (starting at position 122) , as in several other hantaviruses . Among three specimens of *O. couesi* , the sequence in this segment differed by only 1 % , and all changes were silent mutations . The amino acids of the S segment differ by 7 to 10 % from those of the related hantaviruses Bayou virus (BAYV ; from the marsh rice rat , *Oryzomys palustris*) , Catacamas virus (CATV ; from a Honduras population of *Oryzomys couesi*) , and Black Creek Canal virus (BCCV ; from the hispid cotton rat , *Sigmodon hispidus*) . The nucleotide sequence differs by 24 % from those viruses .

Among 1537 @-@ base fragments of the sequence of the M segment , several variable sites were observed , including some non @-@ silent mutations . The sequence differs by 8 to 10 % from BAYV , CATV , and BCCV in terms of amino acids and by 22 % in terms of nucleotides .

= = Epidemiology and effects = = =

Because OROV occurs frequently in *Oryzomys couesi* , Chu and colleagues suggested that it is the primary host of the virus and that infections in *Sigmodon mascotensis* are the result of spillover between these two rodent species , which occur closely together . Hantavirus pulmonary syndrome , the disease caused by hantaviruses such as Sin Nombre virus , has never been reported in Mexico ,

but antibodies against hantaviruses have been found in human blood samples in Yucatán and various wild rodents are known to be reservoirs of hantavirus species . Thus , there is a potential risk of OROV infection in humans . Before the discovery of OROV , one hantavirus species had been identified in Mexico ? El Moro Canyon virus from the small rodent *Reithrodontomys megalotis* .

= = = Relationships = = =

According to phylogenetic analyses based on the sequences of both the S and M segments , OROV is most closely related to the clade formed by BAYV , CATV , BCCV , and Muleshoe virus (MUL ; from the hispid cotton rat) . In 2009 , Piet Maes and colleagues proposed that the closely related BAYV , BCCV , and MUL be united into a single species . Chu and colleagues were surprised to find that the same species , *Oryzomys couesi* , harbored different viruses (OROV and CATV) , though noted that the subspecies infected by the two viruses were different . In 2010 , Delton Hanson and colleagues suggested on the basis of various lines of evidence , including the presence of different hantaviruses , that western Mexican populations of *Oryzomys couesi* represent a different species , *Oryzomys mexicanus* .