and mean P-N value among positive samples. When these hepatitis cases were analyzed by subgroup, the highest prevalence (47%) of antibody to the SMSV pool was in the cases of Non-A-E hepatitis associated with transfusion or dialysis. Cases of Non-A-E hepatitis with an unknown exposure source had an estimated prevalence (19%) similar to that (21%) of the high ALT donors and cases of HBV or HCV hepatitis had an estimated prevalence (10%) similar to that of healthy donors. The increase of anti-SMSV pool prevalence along the axis "Normal donor–high ALT donor–Non-A-E hepatitis case associated with transfusion or dialysis" was highly significant ($P < 0.001$, χ^2 for the trend). The mean P-N value of the positive samples from the Non-A-E hepatitis group was lower than that of the other groups studied ($P > 0.05$ for these comparisons). The patterns of significant differences in estimated prevalence were similar and statistically significant for a range of antibody assay cut-points, up to 0.200, although estimated prevalence declined as the cut-point increased.

Detection of *Vesivirus* RNA in Human Sera

Total RNA was extracted from 30 donor sera and tested by RT-PCR 1. The laboratory performing this testing had no prior experience with *Vesivirus* genomes in the facility. RT-PCR 1 generated a *Vesivirus* amplicon in one of these samples that was confirmed by dot-blotting (Fig. 2) and sequencing.

To reduce the possibility that a positive result for serum *Vesivirus* genome detection was generated by laboratory contamination at the first facility, a further 82 donor samples were tested in a second laboratory routinely performing RT-PCR and that had prior experience with *Vesivirus* RNA, but using newly designed primers to amplify a genomic region not previously amplified (RT-PCR 2). Ten of these 82 samples yielded amplicons of the expected size (Fig. 3).

Ten (11%) amplicons came from 91 high ALT donor samples and 1 (4.8%) amplicon from 21 Normal donor samples ($P = 0.64$, Yates' corrected χ^2). Five (15%) of the amplicons were from 34 sera that scored EIA-positive and 6 (7.7%) from 78 sera that scored EIA-negative ($P = 0.42$, Yates' corrected χ^2).

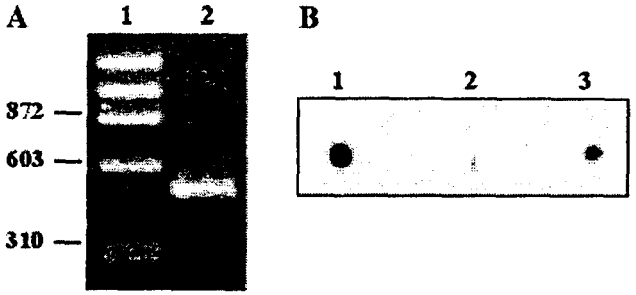

Fig. 2. RT-PCR 1 product and confirmatory dot blot. RT-PCR 1 testing of blood donor sera revealed an amplicon of the expected size for *Vesivirus* RNA (A) and dot blot probing of total RNA from the same serum provided evidence of *Vesivirus* viremia (B). In (A), **Lane 1**: molecular weight ladder; **lane 2**: RT-PCR 1 amplicon. In (B), dot 1 is 20 ng of RNA extracted from CsCl-banded SMSV-5, dot 2 is 50 ng of total RNA from mouse embryo, and dot 3 is 50 ng of total RNA extracted from the donor serum sample.

Sequence Comparisons of the RT-PCR Amplicons

Six amplicons from the RT-PCR 2 (polymerase region) sample set and the one from the RT-PCR 1 (capsid region) sample set were successfully sequenced. Amplicons not successfully sequenced yielded a band too faint for successful direct sequencing and were not successfully cloned. Five of the six polymerase region amplicons were distinct from each other but closely related (1–6% divergence). The sixth amplicon, study number N104, was distinct from the other five polymerase region amplicons (24–38% divergence from N104). When the five similar polymerase region amplicons were compared with GenBank entries spanning the amplification region of RT-PCR 2, the two best matches were with primate *Vesivirus Pan-1* (88–96% identity) and SMSV-6 (88–94%) and lower match was with SMSV-5 (84–86%).

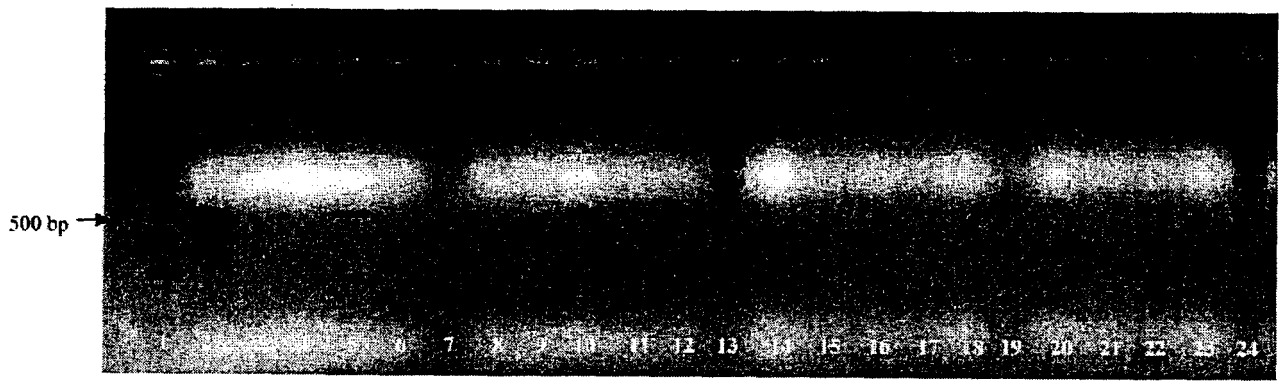

Fig. 3. RT-PCR 2 products from blood donor sera. Several amplicons generated by RT-PCR 2 were of the expected size (**lanes 5, 10, 19, and 22**). **Lanes 1, 13, and 24**: molecular weight ladder. **Lane 2**: positive-control RT-PCR 2. **Lanes 3, 11, and 20** are negative controls containing all RT-PCR reagents without test specimen.

The sixth polymerase region amplicon (N104), was closest (68% identity) to SMSV-13 and 44% identical to F9. The capsid gene sequence from RT-PCR 1 best (97% identity) matched SMSV-5.

A smaller nucleotide (113 nt) region of the six polymerase region amplicons was shared with 22 SMSV-like *Vesivirus* entries in GenBank (Fig. 4). The five similar polymerase region amplicons were distinct from each of the GenBank entries and diverged from published *Vesivirus* sequences for the most part at sites where other *Vesivirus* strains also differed from each other (Part A). The amplicon from donor N104 also had a *Vesivirus* sequence, but was distinct from other *Vesivirus* strains, including F9, differing from published *Vesivirus* most at the 5′ end of the sequence, in a manner akin to how FCV differed from SMSV-like *Vesivirus* strains. Strain *Hom-1* derived from a skin vesicle of a previously reported case of human *Vesivirus* infection [Smith et al., 1998a] had a short (47–64 nt) region of overlap with the serum-derived polymerase region amplicons. In this region of overlap, nucleotide sequence identity with the polymerase region amplicons ranged from 66% to 83%.

DISCUSSION

In this report, the detection of antibodies to *Vesivirus* and of SMSV-like *Vesivirus* viremia in blood donors is described at a U.S. regional blood bank serving eight Northwestern states. A higher prevalence of anti-*Vesivirus* antibody was observed, in comparison with normal blood donors, in donors with elevated serum ALT values, and the highest prevalence, among the groups tested, in cases of clinical hepatitis of unknown etiology associated with transfusion or dialysis. In addition, *Vesivirus* RNA was detected in healthy and high ALT blood donors, occurring numerically but not statistically significantly more frequently in the high ALT blood donors than among the healthy donors tested. The findings of this study and the attributes of *Vesivirus* calicivirus strains in mammals extend the potential for *Vesivirus* disease in humans from a few well-described cases to a broader population.

The complementary evidence for viremia included positive results from separate laboratories testing separate sample sets, utilization of RT-PCR assays that amplified non-overlapping genomic regions, direct detection of genomic RNA by hybridization, and amplicon sequencing that revealed non-identity of sequence compared with known *Vesivirus*, including strains characterized in one of the laboratories previously [Rinehart-Kim et al., 1999] and among the set of characterized amplicons themselves. These results together indicate that the positive laboratory results were not because of contamination in sample collection and handling.

The antigens utilized for detection of anti-*Vesivirus* antibody were purified by cesium chloride banding, which yields a homogenous population of viable particles. A pool of three SMSV strains was utilized, with each strain representing a different potential mechanism for exposure of humans to *Vesivirus*: SMSV-5 detected previously in a human case, SMSV-13 known to cause disease in two livestock species, and SMSV-17 recovered from edible shellfish. The separate phylogenetic cluster within the *Vesivirus* genus defined by FCV was represented by a live vaccine strain widely administered to cats. The noted differences among serum groups in patterns of estimated prevalence remained across a broad range of potential assay cut-points. It would be unexpected for humans to have *Vesivirus* viremia, but not exhibit serologic evidence of infection.

Viremia was expected to be part of the natural history of *Vesivirus* infections in humans because one of two cases described had a disseminated vesicular exanthem of the hands and feet from which *Vesivirus* was cultivated [Smith et al., 1998a]. The *Vesivirus* strains causing *Vesivirus* viremia in this study were closest by genome sequence comparison to SMSV, marine *Vesivirus*. SMSV *Vesivirus* are widely distributed in marine and some terrestrial animals and may routinely "traffic" among these hosts, cycling from their large marine reservoirs onto land and perhaps back again. An ocean presence has been established by the isolation of virus, the presence of specific neutralizing antibodies, or by genome amplification and sequencing for 43 of the 46 known serotypes of the genus *Vesivirus*, including serotypes isolated initially from terrestrial hosts and named feline (FCV), primate (PCV *Pan-1*), bovine (BCV *Bos-1*), reptilian (RCV *Cro-1*), swine (VESV-A_{48}-K_{56}), mink (MCV), and human (SMSV-5 *Hom-1* and HuCV *Hom-1*) caliciviruses [Evermann et al., 1983; Smith et al., 1983, 1998a,b, 2002b; Seal et al., 1995; Reid et al., 1999]. Another marine *Vesivirus* isolated from walrus (WCV) causes hepatitis in domestic animals [Smith, 2000; Ganova-Raeva et al., 2004]. *Vesivirus* caliciviruses are resistant to environmental degradation; stable in aquatic substrates; multiply to high titer, with an estimated 10^{13} virions released into the ocean daily by a single California gray whale (*Eschricitus gibbosus*) [Smith et al., 1998b, 2004] and, in the case of FCV, have a cosmopolitan distribution [Studdert, 1978; Smith et al., 1998b]. Such attributes indicate the potential for frequent contact between a diversity of *Vesivirus* biotypes and hosts.

Known examples of such interaction include mussels and oysters, aquatic filter feeders that concentrate particulates, including viruses, from the water column, preserve viral viability for 60 days or more and thereby can deliver large doses of viable *Vesivirus* to species ingesting contaminated shellfish [Smith, 2000; Burkhardt et al., 2002]. Another example is from the mid-Pacific (French Frigate Shoals), where *Vesivirus*-infected fingerlings of two fish genera (*Aterinomorous spp.* and *Encrasicolina spp.*) were eaten by white tern (*Gygis alba*) hatchlings that developed a *Vesivirus*-associated blistering disease of the feet [Poet et al., 1996]. As mentioned above, whales (California gray) that can shed large numbers of *Vesivirus* particles per

A

Vesivirus Strain	Nucleotide Sequence
chimpanzee Pan-1	ACCACTCATA TCATCTGTCA TGCCCAAAGT CTTCACCAAC CTGAAACAGT TTGGTCTGAA ACCGACCCGG ACCGACAAAA CGGATGCTGA GATAACGCCT ATCCCTGCTG ATG
Study N330	---------- ---------- ---------- ---------- ---------- ----C----- ---------- ---------- ---------- ---------- ---------- ---
Study N102	---------- ---------- ---------- ---------- ---------- ----G----- ---------- ---------- ---------- ---------- ---------- ---
Study 310	--G---T--- ---------- ---------- ---------- ---------- ----C----- ---------- ---------- ---------- ---------- ---------- ---
Study 214	-G-------- ---------- ---------- ------G--- ---------- ----C----- ---------- ---------- ---------- ---------- ---------- ---
Study 298	---------- --G------- ------T--- ------G--- ---------- ----C----- ---------C --------G- ---------- ---------- ---------- --
SMSV-6	G--------C ---------- ---------- ----T----- ---------- ----C----- ---------- ---------- ---------- ---------- ---------- ---
VESV E54	---------C ---------- --A------- ----G-T--- --A------- ----C----- ---------- ---------- ---------- ---------- ------CAC- ---
VESV A48	G--G-----C ---------- ---------- ----G-G--- ----G----- ----C----- ---------- --------GT ---------- ---------- ---------- ---
SMSV-4A	---G-----C ---------- -------T-- ----G-A--- ---------- ----C----- ---------- ---------T ---------- ---------C ---------- ---
skunk 4-2S	---G-----C ---------- -------G-- ----G-A--- ---------- ----C----- ---------- ---------T ---------- ---------C ---------- ---
SMSV-4B	---G-----C ---------- -------G-- ----G-A--- ---------- ----C----- ---------- ---------T --------C-- ---------C ---------- ---
VESV 1934b	---C------ --C------- ---------- ------A--- --ACG----- ----C----- ---------- ---------- ---------- ---T------ ---------- ---
skunk 4-1L	---G-----C ---------- ---------- ----T-A--- --ACG----- ----A----- ------T--- ---------- ---------- A--------C ---------- ---
skunk 7-2	---G-----C ---------- ---------- ----T-A--- --ACG----- ----A----- ------T--- ---------- ---------- A--------- ---------- ---
SMSV-1A	---G-----C ---------- ---------- ----T-A--- --ACG----- ----A----- ------T--- ---------- ---------- A--------- ---------- ---
SMSV-2	G--------C --C------- ---------- ----T-A--- T-ACG----- ----C----- G--------- ---------- ---------- ---------- ---------- ---
SMSV-1B	---G-----C ---------- ---------- ----G-G--- --ACG----- ----C----- ---------- ---------G ---------- ---------- ---------- ---
SMSV-5	---T-----C --T------- ---------- ---TG-G--- --ACG----- -C--C----- ---------- -----T---- ---------- ---------- --------A- ---
walrus	---------T -----C---- ----A----- ----G-G--- ---------- ----C----- ---------- ---------- ----C----- ---------A -----CAAA- ---
SMSV-7	---------T -----C---- ----G----- ---TG-G--- ---------- ----G----- ---------- ---------- ----C----- ---------- -----CAAA- ---
rabbit	---G-----C ---------- ----G----- ---TG-A--- --A------- ----C----- ---------- ---------- ----C----- ---------- -----CA-A- ---
VESV C52	---G-----C ---------- ----G----- ---TG-A--- --A------- ----C----- ---------- ---------- ----C----- ---------- -----CA-A- ---
bovine	---G-----C ---------- ----G----- ---TG-A--- --A------- ----C----- ---------- ---------- ----C----- ---------- -----CA-A- ---
VESV I55	---------C -----A---- --A------- ----G-T--- -----GAC-- ----C----- ---------- ---------- ---------- ---------C -----CCAC- ---
SMSV-14	---------C -----A---- ----G----- -C--G----- ---------- ----C--A-- G--------- ---------- ----C----- ---------A -----C----- ---
SMSV-13	---T-----C --T------- ------G--- ---------- ---------- ----C----- ---------- ---------- ---------- --------T- ---------- ---
Study N104	G--CGAGGCT CAT-G-CGGT C-G-G--G-- G-----G--G ---GG----- ----A---G- ---------- ---------- --A------- ---------- ---------- ---
feline F9	TATTA-GTAT G--AG-A-T- GTGA-C--A- T--TGGA--T --TTCTTCC- A---C----- ---A--T--- GTT-----GT ---T--GA-C A--TGA----- --TGA-C--- -CT

Fig. 4. Nucleotide (A) and amino acid (B) alignment of shared sequence among *Vesivirus* polymerase region amplicons from blood of study subjects and from *Vesivirus* strains represented in GenBank. Study strain sequences shared with these GenBank entries are aligned and placed next to the strains with which they had the highest sequence identity. GenBank sequences are grouped according to similarity to each other. Five of the study strains were similar to each other and closest to chimpanzee *Pan-1* and San Miguel sea lion serotype 6 strains. The other polymerase study strain also was closest to known *Vesivirus*, but in the pattern of sequence homology similar to feline calicivirus.

B

Vesivirus Strain	Amino Acid Sequence
chimpanzee *Pan-1*	PLISSVMPKV FTNLKQFGLK PTRTDKTDAE ITPIPAD
Study N330	---------- ---------- ---------- -------
Study N102	---------- ---------- ---------- -------
Study 310	R--------- ---------- ---------- -------
Study 214	A--------- ---------- ---------- -------
Study 298	--------I- ---------- ---------- -------
SMSV-6	---------- -S-------- ---------- -------
VESV E54	-------T-- -A-------- ---------- -----H-
VESV A48	---------- -A--R----- ------S--- -------
SMSV-4A	--------N- -A-------- ---------- -------
skunk 4-2S	---------- -A-------- ------S--- -------
SMSV-4B	---------- -A-------- ------S--- -------
VESV 1934b	---------- ----R----- ---------- -------
skunk 4-1L	---------- -S--R----- ---------- -------
skunk 7-2 & 3L	---------- -S--R----- ---------- -------
SMSV-1A	---------- -S--R----- ---------- -------
SMSV-2	---------- -S--R----- ---------- -------
SMSV-1B	---------- -A--R----- ------A--- -------
SMSV-5	---------- -A--R----- ---------- -------
walrus	---------- -A-------- ---------- -----K-
SMSV-7	---------- -A-------- ---------- -----K-
rabbit	---------- -A-------- ---------- -----T-
VESV C52	---------- -A-------- ---------- -----T-
bovine	---------- -A-------- ---------- -----T-
VESV 155	-------T-- -A---T---- ---------- -----H-
SMSV-14	---------- LA-------- ---------- -------
SMSV-13	--------R- ---------- ---------- --L----
Study N104	**-EAHCRSA-- --K-G----E** -------N-- -------
feline F9	IMYA-ISDQI -G--SSY--- ---V--SVGA -E--DP-

Fig. 4. (*Continued*)

gram of feces per day also migrate thousands of miles annually between the Sea of Cortez and the Arctic Ocean [Akers et al., 1974; Smith et al., 2004]. *Vesivirus* has been recovered at titers of 10^7 infectious virions per gram of spleen in naturally and experimentally infected opal-eye fish (*Girella nigricans*). These fish are resident along the Southern California coast [Smith et al., 1980a,b, 1981] and are a sports and commercial fish and a common food source for seals, some of which also have extensive migration cycle. Seals reproduce on land or ice, where *Vesivirus*-induced reproductive failure and death occur, where foraging scavengers can further redistribute the viruses into terrestrial ecosystems, and where exposure to *Vesivirus* likely occurred for one human case [Smith et al., 1998a].

The present findings indicate a broader potential for *Vesivirus* infection and, perhaps, illness in humans than previously recognized. The strains causing viremia and to which antibody was detected in this study are similar to the *Vesivirus* with an ocean reservoir. A finding of subclinical viremia and the detected highest seroprevalence in cases of clinical hepatitis associated with transfusion or dialysis suggest that blood exposure that may have led to hepatitis also could lead to higher exposure to *Vesivirus*. If *Vesivirus* causes hepatitis in humans, then an estimated rate for such causation can be derived from the study findings, as follows: the rate of 10 of 91 donors amplicon-positive in the serum who also had elevated serum liver transaminases (ALT) values, together with the rate of high ALT values occurring in about 1 in 1,000 blood donors, would correspond to a rate of ~1 in 10,000 blood donors who might have active, subclinical *Vesivirus* hepatitis. The association of higher anti-*Vesivirus* antibody prevalence with clinical hepatitis of unknown etiology would require further study. The finding of *Vesivirus* viremia in otherwise normal blood donors indicates that blood exposure to caliciviruses of the genus *Vesivirus* could occur by multiple routes of exposure. The diversity of host species, mechanisms of exposure and tissue tropisms for *Vesivirus* with the findings of this study suggest additional *Vesivirus* disease manifestations might be found in humans with further investigation.

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別紙様式第2-1

No. 19

医薬品 研究報告 調査報告書

識別番号・報告回数			報告日	第一報入手日	新医薬品等の区分	機構処理欄
				2006. 2. 15	該当なし	

一般的名称	新鮮凍結人血漿	研究報告の公表状況	ProMED 20060205-0040, 2006 Feb 3. 情報源:[1]BBC News, UK, 2006 Feb 3. [2]Reuters alert. [3]Le Mauricien, 2006 Feb 3.	公表国	
販売名(企業名)	新鮮凍結血漿「日赤」(日本赤十字社)			[1][2]レユニオン [3]モーリシャス	

研究報告の概要

○チクングンヤ－レユニオンとモーリシャス

[1]レユニオン島でチクングンヤウイルスが猛烈な勢いで広まり、患者数は2006年1月下旬の1週間だけで1万5千人増え計5万人に達した。この疾患は致死的ではないが高熱と激痛をもたらす。治療法はなく、ワクチンもない。軍隊が派遣され、近日中に蚊の大量駆除が全島で行われる予定である。セイシェル、マダガスカルでも患者や疑い例が発生している。

[2]レユニオン入院管理局は、チクングンヤウイルスが1月に死亡した9歳の患者の死因と考えられると発表した。

[3]モーリシャス当局はMahebourgにおいてチクングンヤウイルスによる新規患者2例を確認し、ウイルスを媒介するヒトスジシマカ(Aedes albopictus)の駆除を決定した。1月から2月2日までに15例が報告されている。

仏政府はヒトに感染を起こしうる蚊を全て駆除するために機器を購入している。たとえ保健検査局が港湾や空港で目を光らせても、レユニオンからの旅客を検疫する協定は存在しない。保健省報道官は、検疫の対象は鳥インフルエンザとヒト－ヒト感染を起こしうる致死的疾患に限られる、と語った。保健省は全てのホテルと医師に疑わしい症例を報告するよう求めた。

モーリシャスでは2005年5月にチクングンヤの流行があり、週に数百名の患者が発生した。患者は6月には減り始め、9月までには散見される程度にまで減少した。2006年1月の患者の多くは最近レユニオンに行った人であった。ところが最近10日ほどは渡航歴のない患者が増えている。幾人かの血液検体からウイルスが検出された。Mahebourgでの集団発生を別にすると患者は様々な地域で発生している。

報告企業の意見	今後の対応
インド洋西部でチクングンヤウイルスによる感染症が流行しているとの報告である。	日本赤十字社では、輸血感染症対策として問診時に海外渡航歴の有無を確認し、帰国後4週間は献血不適としている。今後も引き続き、新たなウイルス等による感染症の発生状況等に関する情報の収集に努める。

使用上の注意記載状況・その他参考事項等

新鮮凍結血漿「日赤」

血液を介するウイルス、細菌、原虫等の感染
vCJD等の伝播のリスク

9

ProMED情報(詳細)

記事番号	20060205-0040
重要度	C
タイトル	PROChikungunya - Mauritius and Reunion Island (07): Reunion
感染症名	チクングンヤ
主症状	
日付	2006/02/03
流行国	
和訳概要	チクングンヤーモーリシャスとレユニオン(07):レユニオン# [1]レユニオン 情報源:BBC News レユニオン島でチクングンヤが猛烈な勢いで広まり、患者数は先週だけで1万5千人で計5万人に達した。この疾患は致死的ではないが高熱と激痛をもたらす。治療法はなく、ワクチンもない。軍隊が派遣され、近日中に蚊の大量駆除が全島で行われる予定である。 [モデレータ注:1週間に15000例とは驚異的である。読者には地理と気候について興味があるだろう。レユニオンはマダガスカルの東に位置し、マダガスカル諸島の一部である。赤道と南回帰線との間にあるので海洋熱帯性気候である。季節は涼しい乾季(5ー10月)と暖かい雨季(11ー4月)の二つに分かれる。今は雨季の真中であり、蚊族が最も活動的で多いときである。1946年までフランス領であり、現在はフランスの海外県] [2]レユニオン 情報源:Reuters alert 入院管理局は9歳の患者がチクングンヤで死亡した、と発表した。 [3]モーリシャス 情報源:Le Mauricien モーリシャス当局はMahebourgにおいてチクングンヤの新規患者2例を確認し、ウイルスを媒介するヒトスジシマカ(Aedes albopictus)を駆除することを決定した。1月から2月2日までに15例が報告されている。 政府はヒトに感染を起こしうる蚊族を全て駆除するために機器を購入している。たとえ保健検査局が港湾や空港で目を光らせても、レユニオンからの旅客を検疫する協定は存在しない。保健省報道官は人を検疫する方法はあるが、対象は鳥インフルエンザとヒトーヒト感染を起こしうる致死的疾患に限られる、と語った。保健省は全ホテルと全医師に疑わしい症例を報告するよう求めた。 Dr. MI Issack 病理学者(細菌学)の個人的コメント モーリシャスでは2005年5月にチクングンヤのアウトブレイクがあり、週に数百名の患者が発生した。患者は6月には減り始め、9月までには時折みられる程度にまでなった。2006年1月の患者の多くは最近レユニオンに行った人たちであった。ところが最近10日ほどは渡航歴のない患者が増えている。幾人かの血液検体からウイルスが検出された。 Mahebourgでの集団発生を別にすると他の患者は様々な地域で発生している。 これまでのところ、チクングンヤの状況はレユニオンに比べればはるかに良い。2005年12月は大変乾燥しており、夏の豪雨は1月23日まで始まらなかった。

情報詳細【和文】

チクングンヤーモーリシャスとレユニオン(07):レユニオン#
[1]レユニオン
情報源:BBC News
レユニオン島でチクングンヤが猛烈な勢いで広まり、患者数は先週だけで1万5千人で計5万人に達した。この疾患は致死的ではないが高熱と激痛をもたらす。治療法はなく、ワクチンもない。軍隊が派遣され、近日

中に蚊の大量駆除が全島で行われる予定である。
[モデレータ注:1週間に15000例とは驚異的である。読者には地理と気候について興味があるだろう。レユニオンはマダガスカルの東に位置し、マダガスカル諸島の一部である。赤道と南回帰線との間にあるので海洋熱帯性気候である。季節は涼しい乾季(5ー10月)と暖かい雨季(11ー4月)の二つに分かれる。今は雨季の真中であり、蚊族が最も活動的で多いときである。1946年までフランス領であり、現在はフランスの海外県]
[2]レユニオン
情報源:Reuters alert
入院管理局は9歳の患者がチクングンヤで死亡した、と発表した。
[3]モーリシャス
情報源:Le Mauricien
モーリシャス当局はMahebourgにおいてチクングンヤの新規患者2例を確認し、ウイルスを媒介するヒトスジシマカ(Aedes albopictus)を駆除することを決定した。1月から2月2日までに15例が報告されている。
政府はヒトに感染を起こしうる蚊族を全て駆除するために機器を購入している。たとえ保健検査局が港湾や空港で目を光らせても、レユニオンからの旅客を検疫する協定は存在しない。保健省報道官は人を検疫する方法はあるが、対象は鳥インフルエンザとヒトーヒト感染を起こしうる致死的疾患に限られる、と語った。保健省は全ホテルと全医師に疑わしい症例を報告するよう求めた。
Dr. MI Issack 病理学者(細菌学)の個人的コメント
モーリシャスでは2005年5月にチクングンヤのアウトブレイクがあり、週に数百名の患者が発生した。患者は6月には減り始め、9月までには時折みられる程度にまでなった。2006年1月の患者の多くは最近レユニオンに行った人たちであった。ところが最近10日ほどは渡航歴のない患者が増えている。幾人かの血液検体からウイルスが検出された。Mahebourgでの集団発生を別にすると他の患者は様々な地域で発生している。
これまでのところ、チクングンヤの状況はレユニオンに比べればはるかに良い。2005年12月は大変乾燥しており、夏の豪雨は1月23日まで始まらなかった。

情報詳細【英文】

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Archive Number 20060204.0358
Published Date 04-FEB-2006
Subject PRO/EDR> Chikungunya - Mauritius and Reunion Island (07): Reunion

CHIKUNGUNYA - MAURITIUS AND REUNION ISLAND (07): REUNION
****
A ProMED-mail post
<http://www.promedmail.org>
ProMED-mail is a program of the
International Society for Infectious Diseases
<http://www.isid.org>

In this issue:
[1] Reunion update
[2] Reunion - fatal case
[3] Mauritius

******
[1] Reunion
Date: Fri, 3 Feb 2006 05:56:22 -0500 (EST)
From: A-Lan Banks <A-Lan.Banks@thomson.com>
Source: BBC News, UK, 3 Feb 2006 [edited]
<http://news.bbc.co.uk/1/hi/world/europe/4674376.stm>

A crippling mosquito-borne disease is spreading at an accelerating rate on the French Indian Ocean island of Reunion, health officials say.

They say the number of cases of the viral illness, known as chikungunya, had risen to 50 000, an increase of 15 000 in the past week alone

The disease is not fatal, but those affected suffer high fever and severe pain. There is no cure or vaccine.

Hundreds of troops have been deployed on the island to eradicate mosquitoes.

Officials said the troops would be spraying the whole island against mosquitoes in the coming days.

The latest outbreak was first noticed there in February 2005 - but has spread at an accelerating rate since December.

Meanwhile, neighboring territories are mobilizing to contain the disease.

On the Seychelles - where 2,000 cases have been reported in the past 4 weeks - the army has been mobilized to exterminate mosquitoes, Reuters news agency reports.

The authorities in Madagascar also fear the disease may have reached their island, AFP news agency says.

Chikungunya fever is named after a Swahili word meaning "that which bends up" - referring to the stooped posture of those afflicted.

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ProMED-mail
<promed@promedmail.org>

[The spreading speed at 15 000 cases per week, or 2143 per day, is incredible. A bit of geography and climate may be of interest to our readers. Reunion is located east of Madagascar and is a part of the Madagascar archipelago. Situated between the equator and the tropic of Capricorn, Reunion's climate is of tropical type (southern

hemisphere) with oceanic influence. The island is home to one of the world's most active volcanoes. There are 2 seasons: cool or dry season (May till October) and warm or wet season (November till April). Currently it is in the middle of the warm season when mosquitoes are most active and proliferative. The island was ruled as a colony until 1946, when it was made a "departement" (=department), or administrative unit, of France. - Mod.RY]

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[2] Reunion - fatal case
Date: 4 Feb 2006
From: ProMED-mail <promed@promedmail.org>
Source: Reuters alert [edited]
<http://www.alertnet.org/thenews/newsdesk/L04459988.htm>

A crippling mosquito-borne disease has claimed its first life and infected more than 50 000 people on the volcanic French island of Reunion, spooking tourists in the region, local authorities said.

The "chikungunya" disease, which is extremely painful and causes high fever, was not previously thought to be lethal and there is no known cure or vaccine.

The Reunion Regional Agency for Hospitalisation said late on Friday the virus was the only explanation for the death of a 9-year-old in January [2006].

The "chikungunya" fever is named after a Swahili word meaning "that which bends up," referring to the stooped posture of those afflicted.

First recognised in epidemic form in East Africa in 1952, it also leaves immune systems weak, providing opportunities for other diseases to set in.

The disease, which has already travelled to the nearby Indian Ocean islands of Seychelles, Mauritius and Mayotte, has prompted tourists to cancel bookings.

Since 23 Jan [2006], the Reunion Committee on Tourism said at least 1500 tours had been cancelled and the costs incurred from cancellations over the past 2 weeks were equal to its annual advertising budget. It did not provide any figures.

On Thursday [2 Feb 2006], Seychelles said it had mobilised its army to control the virus which has infected 2000 of the idyllic archipelago's 80 000 people.

Reunion last week earmarked $720 000 to fight the outbreak, drafting 400 extra troops to help fight the mosquitoes that have spread the disease for nearly a year.

In neighbouring Mauritius, authorities are screening people at the airport and port, spraying places near hotels and guest houses and warning the public to take precautions.

The Reunion authorities said they planned to set up a scientific committee to better understand the disease. They said they had registered some 25 deaths citing the virus as a possible cause.

Authorities say people should remove stagnant water, use mosquito repellents and bed nets and spray bedrooms at night.

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ProMED-mail
<promed@promedmail.org>

[Fatalities are not commonly seen with chikungunya. More information on these above mentioned cases would be appreciated. - Mod.MPP]

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[3] Mauritius
Date: Fri, 3 Feb 2006 14:43:53 -0500 (EST)
From: Mohammad Issack <missack@intnet.mu>
Source: Le Mauricien, 3 Feb 2006 [trans. and edited]

... //www.promedmail.org/pls/promed/f?p=2400:1001:3540070018127925427::NO::F2400_P1001_BACK_PAGE,

<http://lemauricien.com/mauricien/index.html>

Mauritian authorities are on high alert after the identification of 2 confirmed cases of Chikungunya in Mahebourg. A ministerial committee is chaired by the Prime Minister, Navin Ramgoolam, to decide on measures to take to prevent infection by the _Aedes albopictus_ mosquito, which transmits this viral illness that is characterized mainly by fever, muscular pain and joint swellings. 15 cases have been registered from January up to 2 Feb 2006; the ministry of Health in 2005 detected 3500 cases that it prefers to call suspected cases of Chikungunya.

The government is buying equipment for disinfection in order to destroy all mosquitoes liable to infect people. [Even if] the port and the airport are watched closely by the Health Inspectorate Division, there is no protocol to quarantine travellers arriving from Reunion Island. A spokesman for the Ministry of Health said this morning [3 Feb] that provisions for keeping people in quarantine exist [only] in protocols on avian influenza and in cases of a potentially fatal illness that is transmissible from person to person. The Ministry of Health is requesting all hotels and all medical practitioners in private practice to notify any suspect case.

Personal comment:

In Mauritius, the peak of the Chikungunya outbreak occurred in May [2005] when several hundred cases were reported per week. The number of cases started to fall in June and by September, only occasional cases were reported. Most cases reported in January [2006] occurred in people who had a history of recent travel to Reunion Island. However, in the [last] 10 days, some cases in people without history of travel have been reported. Some have been confirmed by virus isolation in tissue culture from blood samples. With the exception of the cluster in Mahebourg, the other cases live in different regions of Mauritius.

Up to now, the situation with Chikungunya virus has been much less dramatic than in Reunion Island. However, this may change. December [2005] was very dry in Mauritius, and heavy summer rainfall did not occur until 23 Jan 2006.

--
Dr. M. I. Issack
Pathologist (Microbiology)
Central Health Laboratory
Mauritius
<missack@intnet.mu>

[ProMED is grateful for the timely information and comment given by Dr. M. I. Issack from Mauritius. In the wake of the extraordinary epidemic of chikungunya on Reunion Island, spread of the epidemic to other islands seems inevitable. - Mod.RY]

[see also:
Chikungunya - Madagascar: susp., RFI 20060202.0340
Chikungunya - Mauritius and Reunion Island (06): Reunion 20060203.0343
Chikungunya - Mauritius and Reunion Island (05): Reunion 20060131.0306
Chikungunya - Mauritius and Reunion Island (04): Reunion 20060127.0254
Chikungunya - Mauritius and Reunion Island (03): Reunion 20060124.0230
Chikungunya - Mauritius and Reunion Island (02): Reunion 20060121.0202
Chikungunya - Mauritius and Reunion Island: Reunion 20060102.0007
2005

Chikungunya - Mauritius and Reunion Island (04): Reunion 20051231.3716
Chikungunya - Mayotte, Reunion, Comoros 20050913.2707
Chikungunya - Indonesia (Tangerang) 20050717.2059
Chikungunya - Mauritius and Reunion Island (03) 20050624.1770
Deaths at sea - France (Reunion Island): RFI 20050622.1759
Chikungunya - Mauritius and Reunion Island (2) 20050520.1384
Chikungunya - Mauritius and Reunion Island 20050519.1372
Chikungunya - Indonesia (West Lombok) 20050422.1121
Chikungunya - Comoros (Ngazidja) 20050405.0986
Chikungunya - Sri Lanka (02) 20050223.0581
2004

http://www.promedmail.org/pls/promed/f?p=2400:1001:3540070018127925427::NO::F2400_P1001_BACK_PAGE,...

医薬品
医薬部外品　　研究報告　調査報告書
化粧品

識別番号・報告回数			報告日	第一報入手日 2006年2月28日	新医薬品等の区分 該当なし	厚生労働省処理欄
一般的名称	①乾燥抗HBs人免疫グロブリン ②ポリエチレングリコール処理抗HBs人免疫グロブリン		研究報告の公表状況	ProMED20060225.0619	公表国 フランス	
販売名（企業名）	①ヘブスブリン（ベネシス） ②静注用ヘブスブリン－IH（ベネシス）					

研究報告の概要

インド洋地域からフランスへの帰国者の中に、蚊により感染するチクングンヤ感染者が発見されたと、保健局シニアスタッフが土曜に発表した。
フランス保健省によると、チクングンヤ熱は、治療法も予防法もなく、直接あるいは間接的に77人がアフリカ南東部のフランス領レユニオン島で死亡し、現在も人口の20%にあたる157000人が感染している。
モーリシャス政府によると、先週に患者数は341人から962人に増加した。

使用上の注意記載状況・その他参考事項等

代表として静注用ヘブスブリン－IHの記載を示す。
2. 重要な基本的注意
(1)本剤の原材料となる血液については、HBs抗原、抗HCV抗体、抗HIV-1抗体、抗HIV-2抗体陰性で、かつALT（GPT）値でスクリーニングを実施している。更に、プールした試験血漿については、HIV-1、HBV及びHCVについて核酸増幅検査(NAT)を実施し、適合した血漿を本剤の製造に使用しているが、当該NATの検出限界以下のウイルスが混入している可能性が常に存在する。本剤は、以上の検査に適合した高力価の抗HBs抗体を含有する血漿を原料として、Cohnの低温エタノール分画で得た画分からポリエチレングリコール4000処理、DEAEセファデックス処理等により抗HBs人免疫グロブリンを濃縮・精製した製剤であり、ウイルス不活化・除去を目的として、製造工程において60℃、10時間の液状加熱処理及び濾過膜処理（ナノフィルトレーション）を施しているが、投与に際しては、次の点に十分注意すること。

報告企業の意見

アフリカ南東部のフランス領レユニオン島において、チクングンヤ感染が大量に発生し、死亡例も発生しているとの報告である。
血漿分画製剤からのチクングンヤウイルス伝播の事例は報告されていない。また、万一原料血漿にチクングンヤウイルスが混入したとしても、BVDをモデルウイルスとしたウイルスバリデーション試験成績から、本剤の製造工程において十分に不活化・除去されると考えている。

今後の対応

本報告は本剤の安全性に影響を与えないと考えるので、特段の措置はとらない。

(12)

Archive Number 20060225.0619
Published Date 25-FEB-2006
Subject PRO/EDR> Chikungunya - Indian Ocean update (03): spread to France

CHIKUNGUNYA - INDIA OCEAN UPDATE (03): SPREAD TO FRANCE
****
A ProMED-mail post
<http://www.promedmail.org>
ProMED-mail is a program of the
International Society for Infectious Diseases
<http://www.isid.org>

Date: Sat, 25 Feb 2006 07:14:58 -0500 (EST)
From: Mary Marshall <tropical.forestry@btinternet.com>
Source: Reuters Alertnet, 25 Feb 2006 [edited]
<http://www.alertnet.org/thenews/newsdesk/L25768324.htm>

Doctors in mainland France have detected a mosquitoborne disease among people returning from the Indian Ocean region, where the virus is spreading rapidly, a senior health official said on Saturday.

France's health minister has blamed "Chikungunya" fever, for which there is no known cure or vaccine, for directly or indirectly killing 77 people on the French island of [the] Reunion off the south east coast of Africa. French health officials say 157 000 people have now been infected by the disease on Reunion, about one in 5 of the population.

"We have people returning from Reunion who have symptoms of chikungunya and their diagnoses have been confirmed," Francois Bricaire, head of the infectious diseases service at Pitie-Salpetriere hospital in Paris, told Europe 1 radio. "It's not surprising, quite simply because of the contacts between the island of Reunion and mainland France." He said about 30 cases had been found by his service and it was likely that other medical services had detected cases. The disease can only spread via mosquitoes and Bricaire did not say whether the people with symptoms were confined or allowed home.

Health minister Xavier Bertrand told Europe 1 that the mosquito which carries the virus could be present in south eastern France but gave no details. The illness, which has also been found in the nearby Indian Ocean islands of the Seychelles and Mauritius [and Mayotte. - Mod.RY], is marked by high fever and severe rashes. Most people recover but it is extremely painful.

The number of people infected in Mauritius has risen to 962 from 341 the previous week, the Mauritius government said.

French prime minister Dominique de Villepin is due to travel to Reunion on Sunday. He faces growing criticism over the failure to prevent the disease spreading and said this week that the entire island should be cleared of mosquitoes.