# Virus Research News

Volume 1 No. 1 December 2012

A Half Yearly News Letter of Indian Virological Society on Research and Development in the Field of Virology


## Editorial

Indian Virological Society (IVS) was established in December 1984. The IVS provides platform for promotion of research and development in Virology. IVS publishes original research work on virology through its official journal Indian Journal of Virology. The highly technical research publication has a limitation to reach the wider sections of the society. In an effort to outreach the benefit of virus research to the society, it was thought that a newsletter would be useful for dissemination of current research outcome in Agriculture, Medical, Veterinary, Fishery and Insect Virology. The IVS newsletter will be launched in the XXI IVS National Conference organized at Indian Veternary Research Institute, Mukteshwar. The newsletter will be available at www.ivsnet.in.

## In this Issue



## Editorial Board



## Guidelines

Submit news article, which has some application prospect to any one of the editors. The article to be written in a popular format not exceeding 1000 words with a few simple table and or high quality figures. Article structure: Title, author(s), full address, email, telephone, self photo of corresponding author, running text and references not required.

## From IVS President Desk

### Human Influenza

Among zoonotic diseases, human influenza today has not only emerged as an important infection but most of time, as a pandemic threat. We all, without an exception, have suffered from influenza not once but several times in our life. But most of us have ignored the infection as common cold. Influenza is not just cold. In risk group and where infection gets complicated with super imposed infection and with the existing chronic conditions, influenza is not only serious, but may be fatal.

Influenza virus under goes antigenic drift and shift in the surface antigen. The drift as per the change causes outbreak and shift causes pandemic. Seasonal Influenza vaccine is good and is the best way to protect from the circulating influenza vaccine but not against the pandemic strain. In the absence of pandemic strain there is no vaccine and the communities do not have any protective immunity.

The influenza virus has three subtypes: type A, B and C. Influenza type A causes infection, out breaks, epidemics & pandemics in human and animals including birds. Influenza type B & C causes infection in human only. Influenza type A has 16 sub types of haemagglutins; (HA) 1-16; and 9 sub types of neuraminidase; NA 1-9. Human influenza strains have few HA (1-3) and NA (1-2) only, but birds influenza virus have all the sub types of HA & NA. This makes the situation adverse for human influenza strains and possibilities are there of host barrier jump from other species to become human pathogen.

In dual infection in other hosts with the human strain and strain from other species, human strain acquires gene segment get re- assorted. The human affinity in the re-assorted strain can result into a pandemic strain. This is what happened in 2009 for the pandemic pH1N1 (swine strain) from Mexico, which had three gene re-assortments (Human, pig & Avian). This virus was very invasive and spread in human fast and just in three months time spread to most of the countries in the world, that the WHO had to declare the outbreak as 'Influenza Pandemic', first of this century. The virus fortunately had low pathogenicity. Although over 170 countries got infected by this virus, but with very little deaths. The three pandemic of the last century has a death toll, estimated to be 50-100 millions all over the world.

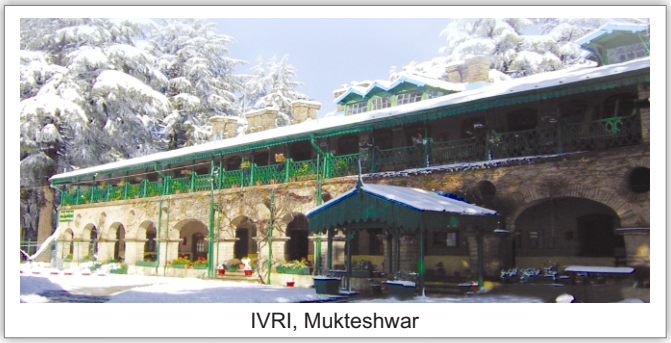
Ever since 1997, the bird flu virus (H5N1) has been a hanging fire for a pandemic. This virus can infect human but has no ability to pass from human to-human. The virus causes a fatal infection in birds and is highly pathogenic to human. The fear of Bird flu is not yet dead and most of the countries are keeping watch on H5N1 in birds as well incidence in human. There is no vaccine available to protect from this virus in human. The virus is present in India in poultry with possible stray incidence in human (?).

**Dr. A.K. Prasad**

## IVS NATIONAL CONFERENCE

### Virocon 2012 : National Conference

IVS organizes National Conference on virology every year, which is named as 'Virocon'. Indian Veterinary Research Institute (IVRI) is one of the premier research institute dedicated to livestock research in India will be organizing Virocon-2012 at Mukteswar from 8-10 November 2012. IVRI-



IVRI, Mukteshwar

Mukteswar, the centre of origin of veterinary research in India was established way back in 1893. The Institute has a glorious scientific heritage. The Nobel laureate, Robert Koch visited this place. Mukteswar is a place in Himalayan mountain, where God unleashed his creative and artistic genius for inner calm and peace. The Virocon-2012 is the XXI National conference of IVS on Immunology and management of viral diseases in 21st century". Scientists and students working on viruses affecting human, animal, plant, fish and insect are expected to attend the conference.

## IVS JOURNAL NEWS

### Special issues of Indian Journal of Virology

**Bikash Mandal**

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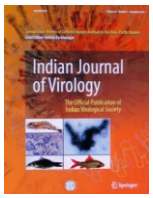


Indian Journal of Virology (INJV), the official journal of Indian Virological Society (IVS) publishes original research work on Medical Virology, Plant Virology, Veterinary Virology, Fish Virology, Insect Virology or any other viruses and virus like pathogens infecting living beings. INJV is published through Springer (www.Springer.com/13337).

A Special issue of INJV on "Viruses of cultured aquatic animals in the Asia-Pacific region" has been recently published. Prof. Indrani Karunasagar has played a key role of Guest Editor to bring out the special issue, which includes 16 review articles covering wide range of topics on viral diseases affecting both finfish and crustacean. Another special issue has been planned for 2013 on Veterinary Virology: "Emerging viral diseases of wild and domestic animals in the developing world". Dr. Jagadeesh Bayry (Jagadeesh.Bayry@crc.jussieu.fr) will be the guest editor of the special issue on animal viruses. Currently, articles are being invited at http://www.editorialmanager.com /injv.

## RESEARCH NEWS

### Diagnostic kits for some chronic and emerging plant viruses in India

**Bikash Mandal and Rakesh Kumar Jain**

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India's trade in agriculture is exponentially growing which is offering economic opportunities, but also inviting new risks of phytopathogens. Viruses are difficult to manage and therefore, introduction of new viruses in agri-ecosystem is a major concern. One of the important ways of reducing the virus-associated risks is to use high quality diagnostic tools and methods for the detection of viruses. Adequate virus testing facilities and expertise are lacking to support the growing horticulture industry in India. Ready to use broad spectrum diagnostic kits are not commercially available for plant viruse detection in India.

The plant virus genera *Cucumovirus*, *Potyvirus* and *Tospovirus* containing chronic and emerging plant viruses such as *Cucumber mosaic virus* (CMV), *Papaya ring spot virus* (PRSV) and *Groundnut bud necrosis virus* (GBNV), which are serious constraints in numerous crops in India.

The polyclonal antibodies (PAb) to plant viruses are conventionally produced by immunizing rabbits or mice with the native virus particles purified from plant tissues, which is a cumbersome process and is difficult to reproduce the same quality of antibodies as the long time maintenance of live

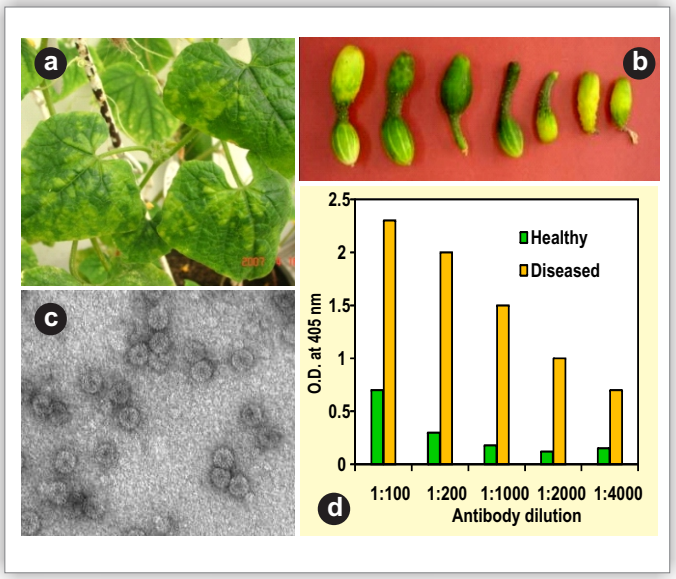


Fig.1. Detection of *Cucumber mosaic virus* (CMV) by ELISA kit. (a) Cucumber plant showing mosaic symptom following inoculation of CMV. (b) Distorted small fruit from the CMV infected plants. (c) CMV particle and (d) ELISA detection of CMV by using polyclonal antibodies to recombinant capsid protein of CMV

cultures of virus/strain and their purification are difficult. To overcome these limitations in preparing plant virus antigen and for renewable use of the same viral antigen for the production of PAb, the conserved capsid protein gene sequence of CMV, PRSV and GBNV representing *Cucumovirus, Potyvirus* and *Tospovirus* were expressed in bacterial system. The PAbs to the recombinant capsid protein of these viruses were produced in rabbits and was used to standardize enzyme linked immunosorbent assay (ELISA) for the detection of cucumo-, poty- and tospoviruses in India.

The constructs of conserved core capsid protein gene sequence of both CMV and PRSV and full length nucleoprotein sequence of GBNV were highly expressive in *E. coli,* which are highly suitable for the commercial utilization to produce unlimited quantity of highly immunogenic recombinant antigens. The PAb to the core CP of CMV efficiently detected both the subtypes of CMV occurring in India (Fig. 1). The PAb to PRSV (Fig 2) detected PRSV and several other potyviruses, *Bean common mosaic virus, Chilli venal mottle virus, Potato virus Y* and *Zucchini yellow mosaic virus*. The PAb to GBNV (Fig. 3) detected the homologous virus and in addition it also detected Watermelon bud necrosis virus and Capsicum chlorosis virus.

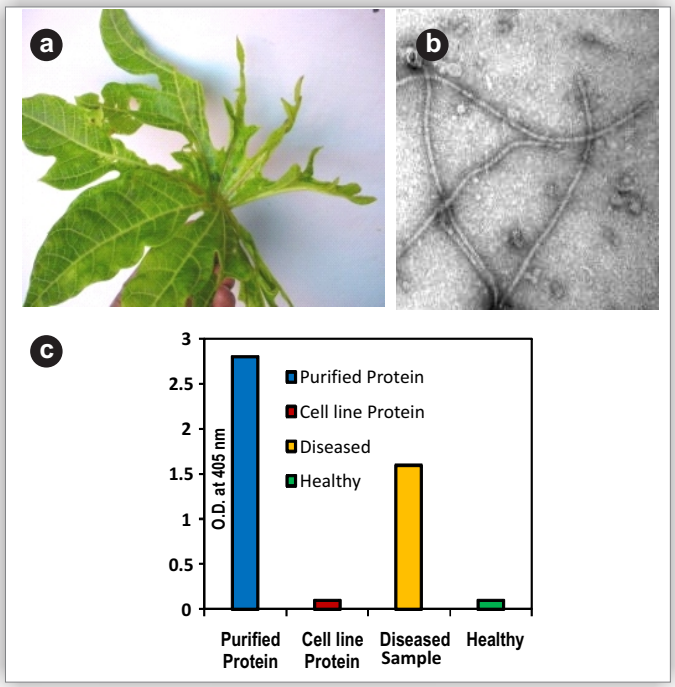


Fig.2. Detection of *Papaya ring spot virus* (PRSV) by ELISA. (a) Papaya plant showing leaf distortion symptoms, (b) PRSV particles and (c) Detection of PRSV by ELISA

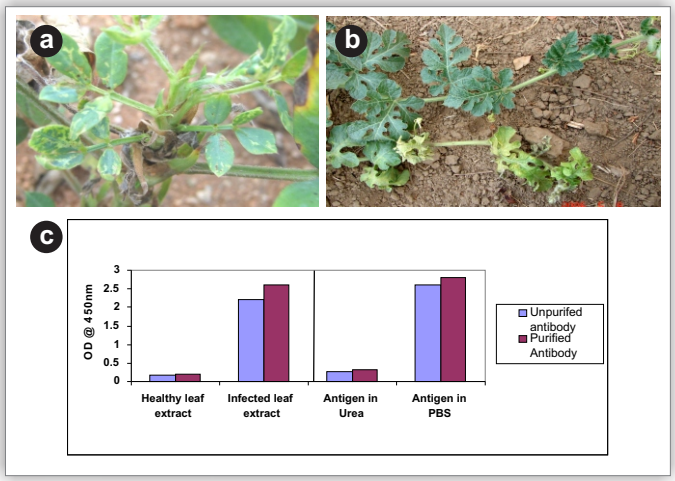


Fig.3. *Groundnut bud necrosis virus* (GBNV) and Watermelon bud necrosis virus infection in groundnut (a) and watermelon (b). Detection by ELISA using PAb to recombinant nucleocapsid protein of GBNV

The broad spectrum ELISA kit has a sensitivity of detecting up to 10-20 ng of viral antigen/100 µl of sap. The typical ELISA kit for the detection of these viruses comprises of the major components containing PAb to the specific virus, positive control and negative control. The prototype of the ELISA kits developed at the Advanced Centre for Plant Virology, IARI, New Delhi are suitable for upscaling commercial usages.

**Acknowledgement:** The research work was supported by NAIP (ICAR-World Bank), project code-416501-02.

## Long-hairpin RNA expressing plasmid vaccine to control *White spot syndrome virus* in tiger shrimp

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Infectious diseases, especially viral diseases are an important limiting factor in aquaculture production. *White spot syndrome virus* (WSSV) is the most devastating virus with wide geographical distribution. WSSV causes catastrophic mortality in cultured shrimp within a short span of time. Considerable scientific effort has been directed at exploring the use of RNAi molecules for controlling this virus. This strategy is particularly attractive because the rudimentary specific immune system of shrimp limits the success of conventional strategies like protein based vaccination.

We have recently designed and constructed a DNA vaccine (pCMV-vp28-LH) to protect tiger shrimp, *Penaeus monodon* against WSSV (Fig. 1). When administered by dip treatment or injection, the plasmid construct is capable of expressing a long hairpin RNA (lhRNA) molecule that can triggering an RNA interference response against the target transcript vp28 that encodes an antigenic envelop protein. This vaccine that provides 75% survival in lab challenge studies compared to complete mortality of unvaccinated control group holds the promise of being a cost effective, stable and efficient approach to combat WSSV.

A single injection administered intramuscularly ensured the distribution of the construct to all parts of the shrimp body, as the construct could be PCR amplified from several tissues when tested 2 days after administration. In fact, it persisted for at least a month, and could possibly persist for at least two

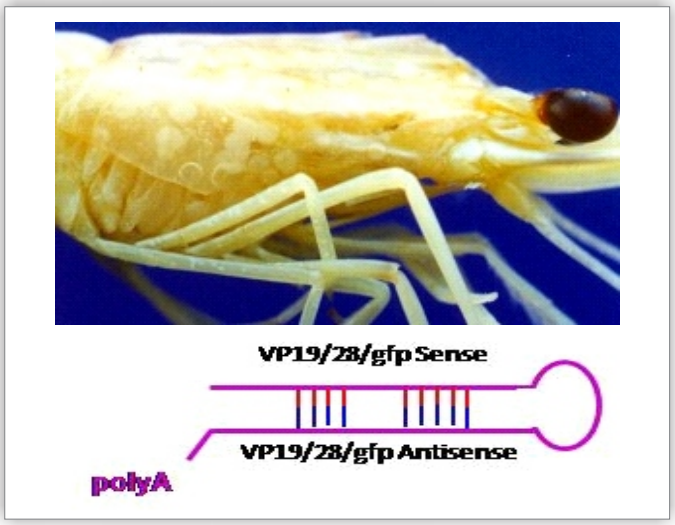


Fig. 1. Head portion of shrimp, Penaeus monodon infected with WSSV showing white spots on the carapace. Long Hairpin RNA constructs (below)

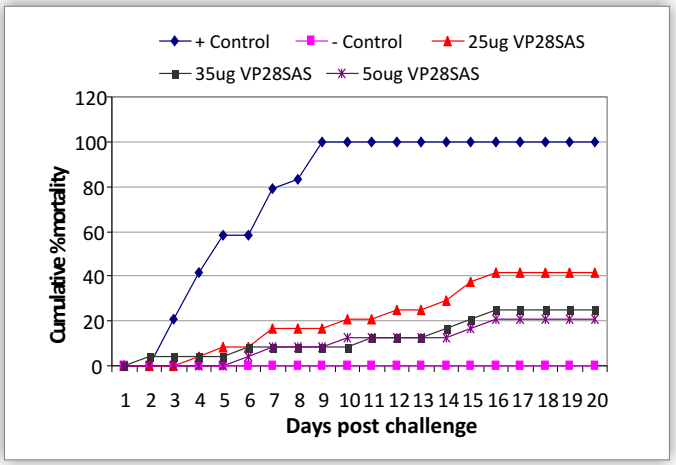


Fig. 2. Mortality pattern in shrimp vaccinated with different doses of RNAi constructs.

months as shown earlier for DNA vaccines. Protection efficiency was tested at various doses and found to be the best at 35 µg for shrimp weighing 10-12 g (Fig. 2). Apart from the survival study, vaccine efficacy was also estimated in terms of viral load. It was noted that the vaccine could restrict the viral copy number at 10-100, whereas in control animals the infection progressed to severe condition with 105 copies. It seems likely that it would also work as a therapeutic molecule as has been reported for RNAi molecules earlier. The ability of the lh-RNA to knockdown the expression of the target transcript was confirmed in human fibroblast cell lines by co-transfecting the vaccine construct with a full length expression construct of vp28 gene. It was concluded that this knockdown was the major mechanism of protection.

Furthermore, the recent dip treatment experiments have shown efficient uptake of the chitosan-DNA nanoparticles by post larvae. This method is most simple and easily applicable just before stocking grow-out ponds. Using freshwater prawn, Macrobrachium rosenbergii as a model organism it has also been shown that when immature and mature females (eggs-on-head) and mature males are injected with the vaccine, it passes on to the offspring. Although, this has not been tested in P. monodon yet, it is very likely that this can be an ideal and simple way of protecting brooders and young larvae.

## Diagnosis of baculoviral isolates in India and synthetic miRNA for larvicidal activity

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Insect viruses are excellent candidates for species-specific and narrow spectrum insecticidal applications and have been used successfully for controlling insect pests on pulses, oilseeds and sugarcane crops.

The largest and most studied group of DNA insect viruses is the baculovirus. The family Baculoviridae includes the nuclear polyhedrosis viruses (NPV) and Granulosis Viruses (GV) - both being dsDNA with rod-shaped nucleocapsids but occluded in protein bodies called polyhedra. The RNA insect viruses comprise of Cytoplasmic polyhedrosis viruses (CPV) belonging to the family Reoviridae and are occluded, nonenveloped dsRNA viruses. Unlike the NPVs, which replicate and form polyhedra in the host cell nuclei, CPV forms the polyhedra only in the cell cytoplasm.

Fig. 1. *Helicoverpa armigera* larvae infected by NPV on cotton. PCR detection of NPV based on lef-8, polyhedrin, *iap* and *pe- os* infectivity factor gene

The baculovirus genome size ranging from 80 - 180 kbp comprises of conserved genes which are involved in successful infection. Some of which are the polyhedrin (*polh*) gene encoding for the matrix protein of the virus occlusion body which provides the embedded virions protection against environmental decomposition; the late expression factor-8 gene (*lef*-8) that encodes the largest subunit of the virally encoded DNA-directed RNA polymerase specific for the transcriptional process; *per-os* infectivity factor gene, the product of which is an occlusion body-derived virion structural protein essential for first steps of oral infection; anti-apoptotic genes that prevent apoptosis exhibited by insect cells in response to baculoviral infection and DNA binding protein gene responsible for condensing the large dsDNA genome to facilitate packaging into the baculoviral nucleocapsids.

At NBAII, Bangalore, we have successfully characterized late expression factor- 8, polyhedrin, inhibitor of apoptosis, per-os infectivity factor and DNA binding protein gene with an intention to describe these genes as easy, reliable and quick identification of baculoviral isolates. The characterization was achieved using species specific primers and a hot-start PCR approach. The studies conducted with nine populations collected from the different parts of India indicated that virulence of Ludhiana NPV was 375-folds higher over other populations. Synthetic miRNA were designed from the pool of small RNAs involved in the up-regulation of the luciferase reporter gene and examined for larvicidal activity. Ultimately, it was found to be most effective in arresting the molting process of larva and has subsequently been used for developing transgenic plant..

**Acknowledgement:** The authors thank National Fund, Indian Council of Agricultural Research, New Delhi, India, for providing financial support.

## Hepatitis B virus subgenotypes in India: A window into human genetic diversity and population movements

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Genome diversity is a hallmark of hepatitis B virus (HBV) that resulted mostly from the copy errors introduced by the viral polymerase during replication of its DNA genome through reverse transcription of a pregenomic RNA. However, the long-term fate of these abundant genetic changes depends on the interactions of HBV with its host, the dramatic intrahost diversification and on different genetic processes such as selection, recombination, neutral genetic drift, population dynamics and biogeography. Comparisons of HBV nucleotide sequences derived from individuals in different geographical regions revealed the presence of ten genotypes (A-J), defined by genome dissimilarity from each other by more than 7.5%. Furthermore, within each HBV genotype (except for E, G and H), multiple subgenotypes that differ from each other by 4–7.5% have been identified.

HBV infection is extremely common in India that is remarkable for her rich population genomic diversity. Taking into consideration the parallelism between host-pathogen co-evolution, it seems plausible that the HBV genome carries its own signature, preserved in defined population groups, that may reflect selection based on differences among human hosts in traits important to pathophysiology/transmission of the virus in that population. An important facet of HBV epidemiology in India is the predominance of HBV of genotype D and it had been suggested that the Indian sub-continent was the place in which HBV-D originated. India hosts five of the nine established HBV/D subgenotypes (D1, D2, D3, D5 and D9) and D5 and D9 had been first reported from this country. Our studies indicated significant differences in the distribution of HBV-D subgenotypes in India depending on the ethnicity and geographical location. Among the HBeAg-negative patients of eastern India, HBV/D5 was found to be the most abundant followed by D3, D9, D2 and D1. However in north-eastern India, HBV/D3 predominated in patients with chronic HBeAg-negative infection while D2, D4, D1 and D5 were also detected. Strikingly, HBV/D4, found in 18% of the patients of North-Eastern region, was not reported from any other parts of India till date and we observed unique molecular signatures in these North-Eastern isolates that distinguished them from all previously reported D4 strains from other parts of the world. The tribal people of India are considered to be the original inhabitants of the land and an exclusive presence of HBV subgenotype D5 was noted among the primitive hilly tribal community of eastern India. Intriguingly, HBV/D5 was the first to diverge from the other subgenotypes of D and hence could be considered as the most ancient of the D-subgenotypes seen in the country. It is thus tempting to speculate that D5 may be endogenous to these hilly tribes, reflecting an old association and intimate evolution of this viral subgenotype within this isolated primitive community and the consequent spread of D5 to the mainstream population of eastern India. However, there is also a possibility that the presence of D5 among the hilly may correspond to a recent introduction of the virus from the mainstream population and its transmission within this close-knit community. Another fascinating evidence of a link between human migration and HBV/D subgenotypes came from studies on recent immigrants from Bangladesh who were settled in the state of Tripura. About 80% of HBV isolates derived from the HBsAg-positive individuals of these immigrants carried HBV of subgenotype D2. Thus sequence variation within human HBV/D strains uncovers relationships between viral subgenotypes and ethnic groups and highlights the importance of studies of HBV genetics in well-separated human populations to understand viral transmission between communities and genome evolution. This might represent a promising alternative to classical

human genetic markers for analyzing human ancestry, migratory episodes, genetic fluxes and disease dissemination.

**Acknowledgment :** We thank Indian Council of Medical Research for funding the study.

## Accuracy of commercially available serological tests commonly used for laboratory diagnosis of dengue virus infection

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Dengue virus (DV) infection is a global public health concern, with an estimated incidence of 50-100 million cases of dengue fever (DF), resulting in 500,000 clinical cases of life threatening dengue hemorrhagic fever syndrome (DHF) and 24,000 deaths per year. Since the key to proper management of DF remains early diagnosis, use of commercially available diagnostic kits based on detection of either anti DV antibodies or non-structural protein 1 antigen (NS-1) remains the most readily available tool utilized in all public sector hospitals and the private labs. There are neither any recommendations nor systematic studies carried out in India to evaluate the diagnostic efficacy of these kits. Detection of anti-DV IgM and IgG antibodies and/ or NS-1 antigen using commercially available rapid diagnostic devices and commercial ELISA kits are usual diagnostic methods for diagnosis of dengue disease.

Here we are share our experience with various methods used for diagnosis of dengue disease. This experience is part of the work by Indian Council of Medical Research (ICMR) established diagnostic virology lab at King George's Medical University, one of the first lab developed with financial support from ICMR/DHR New Delhi. Serum samples from randomly selected 86 patients with clinical diagnosis of dengue illness were tested by all the following methods and kits.

Anti DV IgM detection: Commercial antibody capture anti DV IgM ELISA kits available from (1) Pan Bio Diagnostics, Brisbane, Australia, (2) IVD Research Inc. U.S.A. and (3) J Mitra Pvt. Ltd., India were used. Dengue NS1

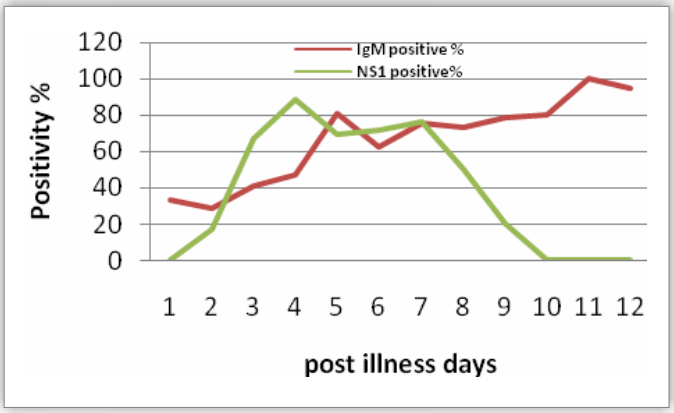


Fig.1 Positivity of dengue test at different days post illness.

Ag detection: Commercial microwell anti DV NS-1 Ag sandwich ELISA kit manufactured by J. Mitra & Co. Pvt. Ltd., India was used. Anti DV IgG detection: Commercial antibody capture anti DV IgG ELISA kit manufactured by J Mitra & Co. Pvt. Ltd, India was used. Rapid solid phase immuno-chromatographic test: Dengue NS-1 antigen and anti DV IgM and IgG antibodies was also done by Advantage dengue NS-1 Ag & Ab combi card, manufactured by J Mitra & Co. Pvt. Ltd., India was used. Sensitivity was calculated as the ratio of samples correctly identified as positive to the total number of samples in the panel.

Of 86 serum samples 44 were from patients who had fever for <5 days (group 1) and 42 were from patients who had fever for > 5 days (group 2) (Table 1). NS-1 antigen reacted positivity with 41.8%, being slightly higher (47.7%) in patients with <5 days illness. No positivity was seen after 9th day of illness (Fig. 1). Sensitivity of ICT (19.8%) was much lower as compared to microwell ELISA (41.8%). Anti DV IgM positivity was found effective for ELISA in patients with longer duration of illness more (76.2% for Panbio, 83.3% for IVD and 11.9% by J Mitra microwell ELISA & ICT) than that of shorter duration of illness (31.8% for Panbio, 40.9 % for IVD, 13.9% by J Mitra microwell ELISA & 11.3 % by ICT). Anti DV IgG positivity was higher (13.6% for ELISA and 11.3% for ICT) in patients with longer duration of illness than that of shorter duration of illness (9.5% for ELISA and 2.3% for ICT). Serum samples received from 25 healthy controls were negative for all the tests.

A great difference was observed in sensitivity of various commercial kits, because of post illness time and format applied for testing. Quality control and quality assurance of each kit is a key concern as increasing incidence of severe dengue infection had been seen all over the world. Quality control program and proficiency test must be done by each

**Table 1 Percent positivity of commercial kits used for diagnosis of dengue fever**

| No. of patients | NS-1 +ve | | IgM ELISA +ve | | | | IgG +ve | | Total |
|---|---|---|---|---|---|---|---|---|---|
| | Microwell ELISA | ICT | PanBio | IVD | J Mitra | ICT | ELISA | ICT | |
| Fever ≤ 5 days (44) (%) | 21(47.7) | 10 (22.7) | 14 (31.8) | 18 (40.9) | 06 (13.6) | 05 (11.3) | 06 (13.6) | 05 (11.3) | 36 (81.8) |
| Fever > 5 days (42) (%) | 15 (35.7) | 07 (16.7) | 32 (76.2) | 35 (83.3) | 05 (11.9) | 05 (11.9) | 04 (9.5) | 01 (2.3) | 38 (90.4) |
| Total positivity (%) | 41.8 | 19.8 | 53.4 | 61.6 | 12.8 | 11.6 | 11.6 | 7.0 | 86.0 |

level of laboratory to standardise and assure the quality of various commercially available kits. Further studies must be done in developing countries for quality assurance of kits and diagnostic methods.

**Acknowledgements:** Financial supports from ICMR, CSIR, New Delhi and is thankfully acknowledged.

## Government of India mulling control programme on classical swine fever

**Divakar Hemadri**

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Classical swine fever (CSF) is an economically important, highly contagious viral disease of pigs. The causative agent, classical swine fever virus (CSFV) is a member of the genus Pestivirus within the family Flaviviridae and is closely related to the viruses of bovine viral diarrhoea and border disease of sheep. CSF is endemic in many parts of the world including India.

Though being listed as one of the top five viral diseases of livestock in India, CSF has not received due attention, may be mainly because, pig rearing is mostly done in the north-eastern states and information flow from this part of India to mainland is slow. Besides, other factors such as religious sentiments and that pigs are reared by people belonging to economically and socially weaker section of the society too might have added to lack of attention. The disease is not new to India and earliest suspected CSF outbreaks in our country dates back to 1944 (Aligarh, Uttar Pradesh), followed by outbreaks in 1951 (West Bengal) and 1961 (Andhra Pradesh). Since then, outbreaks of CSF have been reported from almost all other states. The disease occurs throughout the year and there were 2126 CSF reported outbreaks during 1996-2011, which could be an underestimate considering the fact that the disease goes unreported in many states.

As per the 2007 livestock census, pig population of India stands at 11.134 millions, which is slightly lesser than 2003 census figure. Although overall figures for India show a negative growth in pig population, the north eastern states (Barring Manipur and Sikkim) have shown positive growth. With increased demand for pork in north eastern states, the traditional scavenging systems have given way to tethering and penning, and indigenous pigs are being replaced by cross breeds. Despite this encouraging trend, inadequate knowledge about feeding, health care and breeding management are perceived as major constraints to pig production. Given that there has been an increase in CSF outbreaks in recent years and that CSF has been one of the factors driving negative growth, Department of Animal Husbandry Dairying and Fisheries (DADF), Govt of India is planning to launch a nationwide control programme on this important disease. To this end DADF has recently conducted a meeting of the experts in the field and is working out strategies for vaccine production, quality control and implementation of vaccination programme.

## IVS AWARDS - 2012

### Prof. K.S. Bhargava Oration Award-2012

**Bhudev C. Das,** Dr. B.R. Ambedkar Centre for Biomedical Research (ACBR), University of Delhi (North Campus), Delhi.

### IVS Fellow-2012

**Medical Virology**

A.C. Mishra, National Institute of Virology, Pune

S. Broor, Dept of Microbiology, AIIMS, New Delhi

**Plant Virology**

V.K. Baranwal, Div of Plant Pathology, IARI, New Delhi

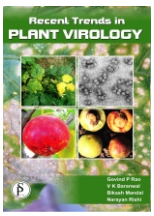
P. Sharma, Div of Biotechnology, DWR, Karnal, Haryana

**Veterinary Virology**

B.K. Singh, National Research Centre on Equines, Hisar

A.B. Pandey, Virology Division, IVRI, Mukteshwar

## BOOKS / BULLETIN




A reference book on plant viruses, 'Recent Trend in Plant Virology', edited by G.P. Rao, V.K. Baranwal, Bikash Mandal and Narayan Rishi (Studium Press, 502 pages, $ 94.95, http://studiumpress.in/ index.asp) has been published in 2012. The book provides the comprehensive information on the viral disease problems in the tropics and subtropics.

## PGIMER-IVS JOINT WORKSHOP

Indian Virological Society decided to carry out round the year academic activities in the fields of medical/ plant/ veterinary/ fish/ insect virology. A national workshop on "Advanced molecular techniques for arboviral diagnosis" under the aegis of Indian Virological Society was conducted at the Department of Virology, PGIMER, Chandigarh on September 4-5, 2012. Sixty young scientists / researchers from 13 states of India, in addition to Nepal were trained on hands-on training to carry out the most accurate and early diagnostic techniques: PCR, multiplex PCR, and real time PCR for

dengue, Japanese encephalitis virus and Chikungunya followed by molecular subtyping by sequencing and phylogenetic analysis.


## INTERNATIONAL MEETINGS

### Evolution, Ecology and Control of Plant Viruses

January 28 to February 1, 2013, Tanzania (http://www.isppweb.org/ICPVE/), Organized & Hosted by International Plant Virus Epidemiology Committee (IPVE) and the International Institute of Tropical Agriculture (IITA)

The 12th symposium focuses on emergence, epidemiology and control of native and new virus diseases to reflect on prevailing situation of virus diseases in the Africa and around the world that are not only ravaging the crop production, but also affecting the international exchange of germplasm and commerce. The symposium will provide a forum for exchange of latest knowledge and technologies to control virus diseases and pave way for an African and global strategy to combat emerging and reemerging plant virus diseases.

## EXECUTIVE COUNCIL OF INDIAN VIROLOGICAL SOCIETY



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