

# DETECTION OF MOSAIC VIRUS INFECTING YAMBEAN

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## INTRODUCTION

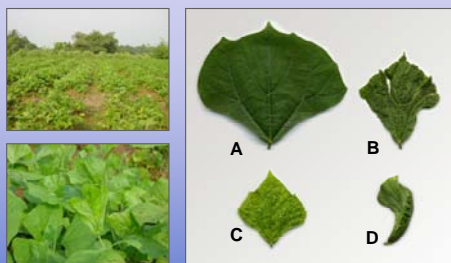
Yam bean (*Pachyrhizus erosus* L. Urban) (Fabaceae) is one of legumes which is well known as 'Bengkuang' in Indonesian. Yam bean is cultivated mainly in several areas of West and Central Java in Indonesia. Based on symptom expressions, in several of yam bean fields around Darmaga Bogor showed that yam bean leaves are infected severely by unknown virus. The first evidence of the disease was found on 1982 in Darmaga (Suseno *et al.*, 1982) and no further report related to the virus identity. The infected plant showed severe mosaic, vein-banding, leaf wrinkling and in severe infection causing plant growth retardation. These may lead yield tuber decreased obviously. The aims of the research are to (1) detecting the viral protein serologically by using viral antiserum from different group of plant viruses, (2) identifying the viral particles identity under electron microscope, and (3) testing the viral host range by mechanical inoculation of infected plant sap to several plants in different families (in progress). Here we reported the disease incidence and a partial of biological characters of the virus to determine the identity of the virus.

## MOSAIC DISEASE INCIDENCE IN THE FIELD

Location	n / N	DI (%)
Babakan Raya	301 / 2126	14
Cibeureum-1	56 / 60	93
Cibeureum-2	6627 / 8138	81
Situgede	4610 / 4610	100
Cifor	1344 / 5051	27

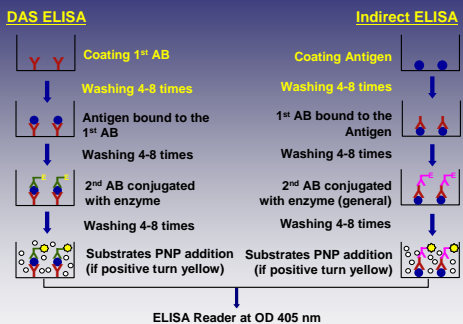
Incidence of Yam bean Mosaic Disease in Several Fields around Darmaga, Bogor  
 N ; total number of plants, n ; number of infected plants, DI ; disease incidence (n/Nx100%).

## SYMPTOM EXPRESSIONS OF INFECTED YAM BEAN



Symptom expressions of infected yam bean plants in the field (I) and its close up symptom (II).  
 [A] Healthy plant leaf. The main symptom is dark green vein-banding [B], severe mosaic [C] and leaf size reduction [D].

## DETECTION of VIRAL PROTEIN by ELISA TEST



## ELISA TEST RESULT

Viral Group	Antiserum	ELISA Result
Comovirus	Squash Mosaic Virus (SqMV)	-
Cucumovirus	Cucumber Mosaic Virus (CMV) *	-
Potyvirus	General Potyvirus	+
	Chilli Vein Mottle Virus (ChiVMV) *	-
	Turnip Mosaic Virus (TuMV)	-
	Potato Virus Y (PVY)	-
	Zucchini Yellow Mosaic Virus (ZYMV)	+
Watermelon Mosaic Virus-2 (WMV-2)	+	
Papaya Ring spot Virus (PRSV)	-	
Peanut Stripe Virus (PSTV)	+	
Tobamovirus	Tobacco Mosaic Virus (TMV) *	-

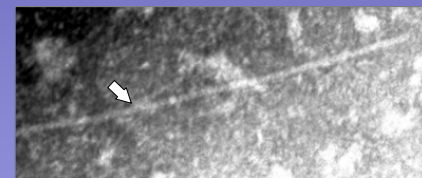
Serological test of infected plants detected with several viral antiserum. (+) indicates the accumulation of viral protein at least 2 times of negative control (healthy plant). (-) indicates the accumulation less than 2 times of negative control. \*, it means DAS-ELISA.

## VIRAL PARTICLES

### A. Leaf dip preparation

- (1) Collodion-coated Grid (diameter 3 mm)
- ↓
- Leaf sliced + PTA  
(Sodium Phosphotungstate)
- (2)
- ↓
- Grid dipped in (2) briefly, then put it on the paper
- (3)
- ↓
- Taken photograph of Virus particles in grid under electron microscope
- ↓
- Negative film scanned

### B. Virus Particle



- A. Leaf dip method to identify the viral particles under electron microscope
- B. Electron Micrograph of Viral Particle. Magnification is 40.000 times. Filamentous Particle is indicated by an arrow

## CONCLUSIONS

Based on field studies, we concluded that the yam bean fields around Darmaga Bogor are severely infected by a plant virus. The virus mechanically transmitted from infected plants to the healthy ones. In addition, it may seed-borne transmitted due to the high disease incidence in the field. It well known that most of cultivated yam bean seeds are obtained from previous planting season.

ELISA test suggested that the yam bean mosaic virus is caused by a **Potyvirus**. Further, the virus positively detected by ZYMV, WMV-2 and PSTV antiserum, suggested that the virus has serological relationship with those of viruses. PSTV well known mainly infects peanut and other legumes, while ZYMV and WMV-2 mainly infects cucurbits. However, as secondary host WMV-2 also infect Legumes, especially Fabaceae.

In the future, serological relationship study, detection of the genome by PCR and partial nucleotide sequencing of the virus gene may determine the identity of the virus more precisely.

Present, the host range test is in progress.