Diversity of *Fusarium oxysporum* f.sp. *cubence* isolated from local banana cultivars in Indonesia













Fusarium wilt, known as Panama disease, is one of the major constraints in banana production. The disease is caused by the soil-born fungus *Fusarium oxysporum* f.sp. *cubense* (*Foc*) and has devastated banana plantations in almost every banana-growing country. A new strain of *Foc*, commonly known as Tropical Race 4 (TR4), was first detected in Taiwan and disseminated throughout SE Asia since the 1990s and was recently reported in Jordan, Mozambique, Oman, Pakistan and Lebanon. Indonesia is the center of origin for both wild and cultivated bananas that likely have co-evolved with *Foc*, hence we hypothesize a wide *Foc* diversity throughout the country. We have recently established a comprehensive collection of 114 *Foc* isolates from three main islands of Indonesia: Java, Kalimantan and Sumatera. We isolated *Foc* from the vascular tissue of banana plants showing wilting symptoms. As a preliminary result we morphologically and molecularly characterized – using specific diagnostics - the obtained collection. Around 65% of the isolates belong to TR4. Further extension of the collection and htp-genotyping will enable us to describe the *Foc* landscape in Indonesia.



Objectives

We aim to explore the genetic diversity of *Foc* from different banana cultivars, in its center of origin, Indonesia, in order to understand the genetic bases of its pathogenicity.

Methodology

- Collections were conducted on three main Indonesian islands: Java, Kalimantan and Sumatra.
- Fungi were isolated from the pseudostem of banana plants, having fusarium wilt symptoms, onto KOMADA agar medium.
- PCR based diagnostic tools (Dita *et al.*, 2010) were used to detect TR4 among the *Foc* isolates.
- Translation elongation factor 1a (*TEF-1*a) and RNA polymerase II second largest subunit (*rpb2*) were used to assess the phylogenetic structure within the *Foc* population collected.

Conclusions

- Our collection currently comprises 114 *Foc* isolates from ~25 banana cultivars, 65% of the isolates are TR4.
- Using *TEF-1*a and *rpb2* sequence data, we confirmed that the obtained isolates belong to *Foc*.
- Phylogenetic inference support the view that *Foc* has a high level of genetic diversity in Indonesia, form where it originates.



Results





Figure 2. A. Sampling sites of Foc collections in Java, Kalimantan and Sumatera islands. **B.** Fusarium wilting symptoms: yellowing of the leaf margins of older leaves, collapse of the leaves at the petiole. **C.** Internal Fusarium wilt symptom: discoloration on pseudostem. **D.** *Foc* isolated from infected banana grown *in vitro*.

Table 1. Host of Banana host cultivars of obtained Foc isolates

Location	Banana cultivars				
	Local name	Popular name	International name	Ploidy	Genome
	Pisang Ayam	Pisang Barangan	Lakatan	3x	AAA
	P. Wak	P. Awak	Awak	3x	ABB
	P. Abe	P. Kepok	Saba	3x	ABB
Sumatra	P. Talon	P. Raja	Raja	3x	AAB
	P. Barangan	P. Barangan	Lakatan	3x	AAA
	P. Tanduk Bawen	P. Tanduk		3x	AAB
	P. Mas	P. Mas	Sucrier	2x	AA
	P. Nyaru/ Selasih	P. Udang	Red, Rojo, Morado	3x	AAA
	P. Sanggar/ Manurun/ Nipah	P. Kepok	Saba	3x	ABB
	P. Awak/ Pulau Pinang	P. Awak	Awak	3x	ABB
	P. Ambon	P. Ambon hijau	Cavendish	3x	AAA
	P. Susu	P. Raja Sereh	Silk, Manzana	3x	AAB
Kalimantan	P. Hawa	P. Awak	Awak	3x	ABB
	P. Gelobok	P. Awak	Awak	3x	ABB
	P. Talas	P. Talas		2x	AA
	P. Selendang			3x	AAA
	Dwarf cavendish	P. Kapal	Dwarf cavendish	3x	AAA
	P. Raja	P. Raja Buluh	Raja	3x	AAB
	P. Kepok	P. Kepok	Saba	3x	ABB
	P. Mas Kirana	P. Mas Kirana	Sucrier	3x	AA
	P. Embuk			3x	AAB
	P. Kongkong			3x	AAA
	P. Susu	P. Raja Sereh	Silk	3x	AAB
	P. Glintung				
	P. Ambon	P. Ambon Kuning	Gros Michel	3x	AAA
	P. Ambon Lumut	P. Ambon Hijau	Cavendish	3x	AAA
Java	Cau Langadai	P. Siem		3x	ABB
	Cau Apu	P. Siem		4x	ABBB
	P. Jimbluk	P. Siem Jumbo		4x	ABBB
	P. Uli	P. Uli		2x	AA
	P. Raja Nangka	P. Nangka	Laknau	3x	AAA
	P. Cavendish	P. Ambon hijau	Cavendish	3x	AAA
	P. Kepok Pipik	P. Kepok Putih		3x	ABB
	P. Raja	P. Raja Buluh	Raja	3x	AAB
	P. Jarum			2x	AA

Figure 1. Maximum Likelihood tree obtained from the combined sequence data sets of TEF-1a and *rpb2*. Red colour indicates TR4. Bootstrap support values indicated at the nodes.

Wageningen UR, Plant Science Group
 P.O. Box 16, 6700 AA Wageningen
 Contact: nani.maryanimartawi@wur.nl
 T + 31 (0)317 7476149, M +31 (0)6 45191144
 www.wageningenUR.nl/ www.panamadisease.org

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