

## Assessing Threats Posed by Destructive Banana Pathogens

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### Abstract

**Significant production of many tropical crops occurs in areas where their most damaging diseases do not occur. The continued production of these crops depends on the ongoing exclusion of the causal agents. The long-range dissemination of plant pathogens can result from natural phenomena, such as hurricanes and trade winds, or human activities. Human-assisted dissemination is usually unintentional, but intentional movement also occurs. In response to terrorist attacks, there has been heightened interest in understanding and preventing biological threats to world agriculture. Devising means to prevent introduction and developing contingency plans in case of arrival of the thousands of diseases that threaten major and minor crops is not feasible. Even when these diseases affect a major crop, such as banana, limited resources indicate that only the most important pathogens could be addressed. A recently published model for pathogen threat assessment is discussed. It was developed to evaluate threats posed by the deliberate introduction of pathogens to the USA, but can also be used to assess the unintentional global movement of pathogens. How the model and its associated criteria could be used by banana specialists is demonstrated with representative threats from the major groups of pathogens: *Ralstonia solanacearum* phylotype IV (blood bacterial wilt), *Xanthomonas campestris* pv. *musacearum* (Xanthomonas wilt), tropical race 4 of *Fusarium oxysporum* f. sp. *cubense* (Fusarium wilt), *Mycosphaerella eumusae* (eumusae leaf spot), *Guignardia musae* (freckle), *Pratylenchus coffeae* (root-lesion nematode) and *Banana bunchy top virus* (bunchy top disease). Significant data gaps, as they relate to threat assessment, are discussed.**

### INTRODUCTION

Diseases have a major influence on where and to what extent many tropical crops are grown (Ploetz, 2007b). Many of the most dangerous diseases are host specific and have limited geographic distributions. Some of these diseases co-evolved with the host plant, whereas others are new-encounter diseases with which the crop has no evolutionary history.

The Enemy Release Hypothesis (ERH) indicates that biota are often most fit in new territories where they left behind destructive pests or pathogens (Hallett, 2006; Mitchell et al., 2006). Major production of many crops often occurs where their most damaging diseases do not occur (Ploetz, 2007b). The absence of a single or a few key pathogens is a pivotal reason for their productivity in new production areas. Well-known, tropical examples include Para rubber, *Hevea brasiliensis*, which is produced primarily in Southeast Asia where the South American leaf blight pathogen, *Microcyclus ulei*, is not

present, and cacao, *Theobroma cacao*, which is produced mainly in Africa and Asia where the pathogens that cause witches' broom, *Moniliophthora* (formerly *Crinipellis*) *perniciosa*, and frosty pod, *Moniliophthora rorei*, are not found (Ploetz, 2007a,b). The continued production of these crops depends upon the continued exclusion of the pivotal (most dangerous) pathogens, and failures to do so can be costly. For example, when the co-evolved rust pathogen, *Hemileia vastatrix*, was re-united with its coffee host in India and Sri Lanka, it caused the collapse of the coffee industries there, and resulted in the British becoming a nation of tea drinkers (Large, 2003). In this regard, banana is a vulnerable crop since it has been released in different production areas from several important pathogens.

## **LONG-DISTANCE DISPERSAL OF PLANT PATHOGENS**

Brown and Hovmøller (2002) distinguished two types of long-distance dispersal (LDD) of plant pathogens (defined as 500 km or more in their article). The first involved aerial, one-step invasions of new territories that resulted in dramatic, sometimes transcontinental, expansions of geographic ranges. These were recognised as rare events that had greater impacts on the large-scale distribution of pathogen populations than did the second, more typical dispersion event. The later events resulted in gradual dispersion of pathogens that expanded geographic ranges slowly and usually within continents. Brown and Hovmøller (2002) observed that the underlying mechanisms for both kinds of dispersion were often the same.

In this paper, two kinds of LDD are distinguished by the underlying mechanisms, rather than the rates of dispersion that are involved. The first involves natural phenomena, such as hurricanes and trade winds. These conditions can move particulate matter, such as pathogen propagules, great distances. This type of LDD is limited to pathogens that can survive extreme conditions in the upper atmosphere (e.g. desiccation, low temperatures and UV irradiation); i.e., those that produce resilient, melanised spores. The rust fungi provide the most frequent examples, for instance, *Puccinia melanocephala*, cause of sugarcane rust, and *H. vastatrix*, both of which were moved by trade winds from Africa to the Americas in the 1970s (McCook, 2006; Purdy et al. 1985), and *Phakopsora pachyrhizi*, cause of soybean rust, which apparently moved via Hurricane Ivan into the southern USA from South America in 2004 (Schneider et al., 2005).

A second kind of LDD involves human activity, and is a more common cause of intercontinental movement. Human-assisted events are usually not intentional, and there are examples involving banana. The unwitting movement of *Fusarium oxysporum* f. sp. *cubense* throughout the tropics in infected suckers is well known and is recognised as a key factor that led to the pathogen's wide dissemination and the ultimate collapse of the 'Gros Michel'-based export trades (Stover, 1962a). Likewise, the spread of *Mycosphaerella fijiensis* and *M. musicola* out of their Asian centre of origin was probably assisted by the movement of infected banana leaves that were used as packing materials, as well as the movement of banana germplasm by the breeding programs (Hayden et al. 2003; Rivas et al., 2004). Although Stover (1962b) hypothesised that *M. musicola* moved to Africa and the Caribbean via air-borne masses of ascospores, Hayden et al. (2003) showed with genetic data that this was unlikely. Parnell et al. (1998) indicated that ascospores of *M. fijiensis* were probably capable of moving no more than 200 km.

Plant pathogens are also moved intentionally by humans. The latter activities are usually clandestine and orchestrated by governmental programs (for example, the US Army anti-crop program and the USSR's KGB) (Whitby, 2002). Although the general

public is usually unaware of the scope and impact of such programs, in some cases intentional activities are publicised. A recent report from Brazil on the politically motivated movement of *Moniliophthora perniciosa* from Rondônia to Bahia is an uncommon example (Junior, 2006a,b). This act of bioterrorism in the late 1980s resulted in a precipitous decline in cacao production in Bahia, with the net result of reducing Brazil from the second to fifth most important cacao producer in the world (Ploetz, 2007b).

## **PATHOGEN RISK ASSESSMENT**

In response to 9/11, there has been heightened interest in understanding and preventing bioterrorist threats to world agriculture (Fletcher et al., 2006; Schaad et al., 2006). Clearly, devising tools for the intervention, and action plans for the arrival, of the thousands of diseases that threaten major and minor crops is not feasible. Even when these diseases affect a major crop such as banana, limited resources would allow only the most important pathogens to be addressed. Thus, an obvious question is: “How might these pathogens be identified?”

A recently published model for pathogen threat assessment (Schaad et al., 2006) is discussed below. It was developed to evaluate threats posed by the deliberate introduction of pathogens to the USA, but can also be used to assess the unintentional, global movement of pathogens. Use of the model is demonstrated with representative banana pathogens.

## **THE THREAT MODEL**

To understand better the relative threats that were posed by the introduction of exotic plant pathogens, the US Department of Agriculture, Agricultural Research Service (USDA, ARS) recently convened workshops at which subject matter experts (SMEs) were asked to develop a risk assessment model. The SMEs had expertise on different types of pathogens and diverse professional backgrounds, and the model was to be used to determine the relative importance of various pathogen threats to the USA.

The SME panel developed 17 criteria that they felt had the greatest influence on pathogen threat (Table 1). Based on its relative importance, a weight was assigned to, and used to obtain individual scores for, each criterion. The weighting criteria are unpublished, but were provided by N.W. Schaad for this paper. The weighted models were based on the analytical hierarchy process. It uses pairwise comparisons to place criteria in tiered categories, and has been used previously in strategic planning and risk assessment (Saaty, 1982). The sum of individual criteria scores for a pathogen were used by Schaad et al. (2006) to assess the threat it posed. Theoretically, a maximum-threat pathogen would have a total score of 100.

Although the paper that describes the model focused on pathogen threats to the USA (Schaad et al., 2006), it can also be used to assess global threats. Criteria 2, 8, 10 and 12 are associated with deliberate pathogen movement and were excluded in this assessment to examine accidental movement.

For the present paper, a representative list of important banana pathogens was evaluated. The chosen pathogens are global threats in that they have limited geographic distributions and pose significant threats to banana production in other regions. Two bacterial pathogens were included: the blood bacterial wilt pathogen, *Ralstonia solanacearum* phylotype IV, which is restricted to Indonesia (Fegan and Prior, 2006; Thwaites et al., 2000); and *Xanthomonas campestris* pv. *musacearum*, cause of

Xanthomonas wilt and restricted to East Africa (Aritua et al., 2008; Tushemereirwe et al., 2004). Three fungal pathogens were chosen: tropical race 4 of *Fusarium oxysporum* f. sp. *cubense* (TR4), which causes Fusarium wilt, has a wide host range and is generally restricted to Southeast Asia (Ploetz, 2006); *M. eumusae*, which causes eumusae leaf spot and has an unclear distribution in the eastern hemisphere (Crous et al., 2003); and *Guignardia musae*, which causes freckle, may be comprised of Bluggoe- and Cavendish-specialised strains and is restricted to Southeast Asia (Jones, 2000). One virus was chosen: *Banana bunchy top virus* (BBTV), the cause of bunchy top disease, is the most damaging virus of banana and, with the exception of the Hawaiian Islands, is restricted to the eastern hemisphere (Jones, 2000). Other damaging banana pathogens, such as *M. fijiensis* and *Radopholus similis*, were not assessed since they are already widely distributed.

## RESULTS

The model of Schaad et al. (2006) separated the evaluated banana pathogens into two groups (Table 2). Two pathogens posed a far lower risk than the others, and in this assessment appeared to be low risk: *G. musae* and *M. eumusae* had relatively low percentiles for both deliberate and accidental scenarios (scores less than 34). This was in stark contrast to the remaining pathogens that were analysed. Due to its lethal impact, persistence, wide host range and other serious attributes, TR4 appears to be most threatening, both as an accidental and bioterroristic threat (both scores over 80). Also posing significant, albeit lower, threats worldwide, were *R. solanacearum* phylotype IV, *X. campestris* pv. *musacearum* and BBTV.

## DISCUSSION

Diseases have a major influence on where and to what extent many tropical crops are grown. In many cases, the most important production areas for a given crop are areas in which its significant pathogens do not occur (Ploetz, 2007b).

The ERH describes the powerful impact enemy release can have on the fecundity and vigour of plants (Ploetz, 2007b). Implied in the ERH is the potential for collapsed production of crop plants if they are united with their damaging pathogens. The current impact of the TR4 epidemic in Southeast Asia on Cavendish monocultures is a case in point (Ploetz, 2006).

The risk model that was developed by Schaad et al. (2006) and utilised in the present study allowed an objective classification of global threats that are posed by six important banana pathogens. There was a clear separation of these pathogens into low and high risk categories, and based on these results, TR4, *R. solanacearum* phylotype IV, *X. campestris* pv. *musacearum* and BBTV pose the greatest threats to sustainable banana production worldwide. Activities to monitor their distribution and spread, as well as the development of contingency plans for their arrival in other areas, should be given high priorities.

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## Tables

Table 1. Criteria developed by Schaad et al. (2006) to rate threats from deliberate plant pathogen introductions.

Pathogen properties
<ol style="list-style-type: none"><li>1. Pathogen survives easily for long periods under field conditions</li><li>2. Pathogen produces toxin or other compound in planta that is toxic to animals and/or humans</li><li>3. Pathogen is easily manipulated genetically (Deliberate)</li><li>4. Pathogen affects multiple hosts</li><li>5. Pathogen is easily disseminated or transmitted in nature</li><li>6. Disease(s) caused by pathogen affect(s) yield</li><li>7. Virulence of pathogen is high</li></ol>
Production and dissemination
<ol style="list-style-type: none"><li>8. Pathogen is easily fermented or grown (Deliberate)</li><li>9. Pathogen is easily introduced, establishment does not depend upon weather conditions</li><li>10. Pathogen is seed-transmitted and breeder and/or production seed is produced abroad (Deliberate)</li></ol>
Detection
<ol style="list-style-type: none"><li>11. Pathogen is difficult to detect or latent</li><li>12. Attributes of pathogen make it difficult to trace (Deliberate)</li></ol>
Disease management
<ol style="list-style-type: none"><li>13. Effective chemical measures are not available</li><li>14. Resistance against the disease is poor or not available</li></ol>
Impact
<ol style="list-style-type: none"><li>15. Presence of pathogen would result in a negative psychological impact</li><li>16. Pathogen is of quarantine significance and affects trade</li><li>17. Presence of pathogen or product could greatly affect economics</li></ol>

Table 2. Threat assessment for the deliberate and (accidental) movement of representative pathogens of banana

Pathogen <sup>b</sup>	Criteria <sup>a</sup>																	Deliberate (accidental) threat <sup>d</sup>
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	
<i>Ralstonia solanacearum</i> phylotype IV	H	L	H	L	M	H	H	H	H	L	H	L	H	H	M	H	H	81.3 (72.6)
<i>Xanthomonas campestris</i> pv. <i>musacearum</i>	M	L	H	L	M	H	H	H	H	L	H	L	H	H	M	M	H	67.3 (66.7)
<i>Fusarium oxysporum</i> f. sp. <i>cubense</i> TR4	H	L	M	L	H	H	H	H	H	L	H	L	H	M	H	H	H	86.4 (80.7)
<i>Mycosphaerella eumusae</i>	M	L	M	L	H	M	M	L	M	L	H	H	L	M	L	L	L	31.7 (27.5)
<i>Guignardia musae</i>	M	L	M	L	H	M	M	M	M	L	M	H	L	M	L	L	L	33.3 (26.9)
<i>Banana bunchy top virus</i>	L	L	H	L	H	H	H	L	H	L	H	M	H	H	H	M	M	76.2 (73.3)

<sup>a</sup>Criteria are described in Table 1.

<sup>b</sup>Taxa are representatives of the major taxonomic groups of banana pathogens that have restricted geographic ranges (i.e. threaten noninfested areas). Pathogens (and the diseases they cause) are: *R. solanacearum* phylotype IV (blood disease); *X. vasicola* pv. *musacearum* (*Xanthomonas* wilt), *F. oxysporum* f. sp. *cubense* TR4 of (*Fusarium* wilt); *M. eumusae* (*eumusae* leaf spot); *G. musae* (*freckle*); *Banana bunchy top virus* (*Banana bunchy top disease*).

<sup>c</sup>A weighted scoring system was used to determine the relative threat posed by the different pathogens. Absolute scores (Low, Medium and High) were multiplied by a relative weight assigned to each criterion based on its relative importance, as determined by an expert panel listed in Schaad et al. (2006).

<sup>d</sup>A maximum total score of 100 (= most threatening) is possible for deliberate movement (score calculations for deliberate and accidental movement are described in text). Criteria that are associated with deliberate pathogen movement, 2, 8, 10 and 12, were excluded from accidental movement assessments.