INCORPORATING ENVIRONMENT AND PREDICTA-B PATHOGEN LEVELS TO IMPROVE DISEASE PREDICTION IN WESTERN AUSTRALIA

G.J. Poole\textsuperscript{a}, M. Harries\textsuperscript{b}, D. Hübner\textsuperscript{b}, M. Miyan\textsuperscript{b}, W. McLeod\textsuperscript{b}, and A. McKay\textsuperscript{a}

\textsuperscript{a} SARDI, Urbrae, SA. Email: Grant.Poole@sa.gov.au
\textsuperscript{b} Dept. of Agriculture and Food Western Australia, Geraldton and Perth, WA.

ABSTRACT: PreDicta-B is a soil-based DNA assay that detects and quantifies soil-borne pathogen levels prior to planting of grain crops. Disease is a result of the interaction between pathogen levels, host, and the environment. In the past, predictions of environment were not included in predictions of risk categories from the DNA test. In 2010 and 2011 surveys were conducted in Western Australia to assess several variables including soil-borne levels of the pathogens *Rhizoctonia solani* (AG8), *Gaumannomyces graminis* var *tritici*, *Bipolaris sorokiniana*, *Fusarium pseudograminearum*, *F. culmorum*, *Pratylenchus neglectus*, *P. thornei* and *P. teres*. Initial correlations between soil DNA levels of the pathogen and in-crop disease assessments were weak, so the effects of environment (temperature, precipitation and soil) were investigated and found to have a significant effect on in-crop root disease levels. A model that utilizes a logistical regression of environmental parameters with soil DNA and in-crop disease levels was developed for all of the aforementioned soil-pathogens and will be applied to future data sets to validate the model. This model will be used to develop regional soil-borne disease risk categories to enable researchers to better understand the role of environment in root disease complexes in the field and for growers to make more informed management decisions.

INTRODUCTION

Several soil-based pathogen DNA assays (as used in PreDicta-B) have been developed and shown reasonably reliable correlations between DNA levels and various root disease levels based on controlled environment bio-assays (2). However, pathogen and in-crop disease level relationships were not very strong under field survey conditions in Western Australia (WA) in 2010 and 2011. Previous studies to refine soil disease risk categories with take-all have shown that it is useful to express disease risk in a probability based logistical regression approach (1). In this paper we explore the use of a logistical regression approach through incorporating environmental variables into the pathogen and host relationship in order to refine risk categories for PreDicta-B.

MATERIALS AND METHODS

Paddocks sown to wheat were selected and sampled in 2010 extending from Geraldton in the north to Pingelly and Corrigin in the south. From the 143 paddocks, 115 and 50 in 2010 and 2011, respectively, had reliable data that were included in the analysis (165 total over two years). From each paddock, a 1 ha focus area was sampled for PreDicta-B pre-sow and post-harvest, additionally 40 plants were collected during cereal anthesis and scored to provide disease incidence for each of the 5 cereal diseases (Table 1) and overall disease severity was rated on a scale of 0 to 5 (5=high disease). Data included in the statistical analyses were disease incidence, severity, and soil DNA (PreDicta-B). Environmental data were obtained from the Bureau of Meteorology website (www.bom.gov.au) for 11 WA weather stations and assigned to individual paddock locations. A logistical regression was conducted between disease, soil DNA, and environmental parameters.

RESULTS AND DISCUSSION

Logistical regression showed that environmental factors interacted to varying degrees with pre-sow pathogen DNA on the incidence of five root diseases (Figure 1). There were significant environmental effects over both years for all root diseases. Soil DNA levels were the most stable across years for *Pratylenchus neglectus* and *Bipolaris*, but the least for *Rhizoctonia* and Take-all. Soil DNA levels were most strongly associated with *Rhizoctonia* and *Bipolaris* (Common root rot) incidence. Overall disease severity was significantly associated with five soil-borne pathogen incidences measured (Table 1). When environment was regressed against disease incidence and pathogen soil DNA levels (log DNA from 1 to 3) for *Rhizoctonia*, the probability of incidence ranged from 25% to 50% in locations characterized by high temperature and low rainfall, while it was 10% to 35% when environment was not considered. This information will be useful to growers to use PreDicta-B results to make better informed decisions. These results have given researchers an idea of how the pathogen DNA levels, the environment and crop disease actually interact under field conditions over a broad geographic area.

Table 1. Summary statistics of the percent (%) fields with soil DNA detected as well as correlation (r-values) across years, incidence versus soil DNA, and incidence versus disease severity (n=165 paddocks over 2010 and 2011).

<table>
<thead>
<tr>
<th>Disease Incidence</th>
<th>% Fields$^a$</th>
<th>Soil DNA$^c$</th>
<th>Disease Severity$^d$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Year$^b$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rhizoctonia</td>
<td>21</td>
<td>0.29</td>
<td>0.54</td>
</tr>
<tr>
<td>Take-all</td>
<td>27</td>
<td>0.30</td>
<td>0.05</td>
</tr>
<tr>
<td>F. neglectus</td>
<td>34</td>
<td>0.88</td>
<td>0.01</td>
</tr>
<tr>
<td>B. sorokiniana</td>
<td>44</td>
<td>0.62</td>
<td>0.38</td>
</tr>
<tr>
<td>Crown rot</td>
<td>17</td>
<td>0.45</td>
<td>-0.08</td>
</tr>
</tbody>
</table>

$^a$ % Fields with detectable soil DNA levels (PreDicta-B).

$^b$ Correlations (r-values) across years for each pathogen.

$^c$ Correlations (r-values) of disease incidence vs. soil DNA.

$^d$ Correlations (r-values) of disease incidence vs. severity.

Figure 1. Probability of *Rhizoctonia* in-crop disease incidence with increasing levels of soil DNA (log scale) in a high temperature and low rainfall environment with a sandy soil.

REFERENCES
