Phenotyping transpiration dynamics in real time: the key to mine the banana biodiversity for better water use efficiency?

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The quest for tolerant varieties: phenotyping at plant and cellular level.

Dr. Ir. Sebastien Carpentier
Growth characterization

AIM: characterize the diversity within edible Musa towards drought tolerance

- 32 cultivars (representatives of biodiversity)
- Mild osmotic stress treatment (5% PEG)
LIDAR
Area/growth
growth
Tissue damage

Cachaco

Mbwazirume
Cultivar growth ranking

Growth relative to reference

STRESS
5 % PEG

CONTROL
0 % PEG

Genome:
- Reference (ABB)
- AAA
- AAB
- ABB
- BB
- Reference (ABB)
What is the effect of mild osmotic stress?
Transpiration and stomatal behaviour

IR pictures
Temperature

Infrared
Temperature

17.44 °C

17.68 °C

20.18 °C

E Kissel
Kissel et al. 2015

- **EXPERIMENTS**

<table>
<thead>
<tr>
<th>days</th>
<th>drought</th>
<th>varieties</th>
</tr>
</thead>
<tbody>
<tr>
<td>165</td>
<td>mild + severe</td>
<td>4</td>
</tr>
<tr>
<td>157</td>
<td>mild + severe</td>
<td>6</td>
</tr>
<tr>
<td>135</td>
<td>mild</td>
<td>6</td>
</tr>
</tbody>
</table>

- **DROUGHT**

<table>
<thead>
<tr>
<th>Level</th>
<th>pF</th>
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<tbody>
<tr>
<td>control</td>
<td>1.8 - 2.1</td>
</tr>
<tr>
<td>mild</td>
<td>2.5 - 2.7</td>
</tr>
<tr>
<td>severe</td>
<td>2.8 - 3.1</td>
</tr>
</tbody>
</table>

- **VARIETIES**

<table>
<thead>
<tr>
<th>Varieties</th>
<th>Genome</th>
<th>Year</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yangambi Km5</td>
<td>AAA</td>
<td>x</td>
</tr>
<tr>
<td>Mbwazirume</td>
<td>AAAh</td>
<td>x</td>
</tr>
<tr>
<td>Mpologoma</td>
<td>AAAh</td>
<td>x</td>
</tr>
<tr>
<td>Sukali Ndizi</td>
<td>AAB</td>
<td>x</td>
</tr>
<tr>
<td>Kayinja</td>
<td>ABB</td>
<td>x</td>
</tr>
<tr>
<td>Cachaco</td>
<td>ABB</td>
<td>x</td>
</tr>
</tbody>
</table>
\[ \delta^{13}C = \left( \frac{\delta^{13}C_{\text{blad}}}{\delta^{13}C_{\text{atm}}} - 1 \right) \times 1000\% \]
$$m_{\text{plant}} = 0.0646 \times \text{area}$$

$$R^2 = 0.906$$

$$m_{\text{water}} = m_{\text{total}} - (m_{\text{dry}} + m_{\text{plant}} + m_{\text{pot}})$$
Hours averaged over days
HOUR*genotype; LS Means
Current effect: F(45, 120)=.63689, p=.95692
Effective hypothesis decomposition
Vertical bars denote 0.95 confidence intervals
Days at 13h

DAY; LS Means
Current effect: F(5, 40)=22,676, p=.00000
Effective hypothesis decomposition
Vertical bars denote 0.95 confidence intervals

DV_1

DAY
DAY*genotype; LS Means
Current effect: F(15, 40)=83500, p=63527
Effective hypothesis decomposition
Vertical bars denote 0.95 confidence intervals
Photosynthesis

![Box plot of $V_{c,max}$]

$V_{c,max}$ (μmol CO$_2$/m$^2$/s)

Categories:
- B
- A
- B

Legend:
- Black
- Orange
- Light Blue
- Blue
Stomatal conductance and photosynthesis
Ontologies

- Growth
- Stomatal behavior/photosynthesis
- Climate data!!!
Gene ontology enrichment

Energy
- Glycolysis
- Sucrose metabolism
- Glucose metabolism

AAA specific
Gene ontology enrichment

Energy
- Glycolysis
- Sucrose metabolism
- Glucose metabolism

Stress
- Response to oxidative stress
- Oxidation-reduction

7 (!) Peroxidases
Experimental set up: allele mining

Adapted from Keiichi Mochida and Kazuo Shinozaki 2010
The quest for tolerant varieties: the importance of integrating “omics” techniques to phenotyping

Michel Zivy, Stefanie Wienkoop, Jenny Renaut, Carla Pinheiro, Estelle Goulas and Sebastien Carpentier

The primary objective of crop breeding is to improve yield and/or harvest quality while minimizing inputs. Global climate change and the increase in world population are significant challenges for agriculture and call for further improvements to crops and the development of new tools for research. Significant progress has been made in the molecular and genetic analysis of model plants. However, is science generating false expectations? Are ‘omic techniques generating valuable information that can be translated into the field? The exploration of crop biodiversity and the correlation of cellular responses to stress tolerance at the plant level is currently a challenge. This viewpoint reviews concisely the problems one encounters when working on a crop and provides an outline of possible workflows when initiating cellular phenotyping via “-omic” techniques (transcriptomics, proteomics, metabolomics).

Keywords: proteomics, data integration and computational methods, phenotype, omics-technologies,
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