Screening techniques for sweet potato drought tolerance

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ARC-Roodeplaat, Pretoria, South Africa
Introduction

• CIP – ARC collaboration (2009-2012)
• Methods for screening – fast, reliable?
• Identify parameter/s early growth stage
Plant physiology

• Use mechanisms to adapt to environment
• Identify mechanisms, survival, enhance
• Lack of knowledge, 75% yield lost – environmental impact
Plant physiology

• Tolerance – high metabolism (mild stress) reduced activity (severe stress)
• Avoidance – reduction in metabolic activity, dormant state, exposure to stress
Morphology

- apical shoot
- flower
- inflorescence
- nodes
- internode
- main stem
- secondary stem
- pencil roots
- fibrous roots
- storage roots
Plant physiology
Leaf cross section

- stoma (opening for gas exchange)
- waxy cuticle
- mesophyll (photosynthetic cells)
- air space
- guard cell
- carbon dioxide
- oxygen
- guard cells
- upper epidermis
- palisade mesophyll
- spongy mesophyll
- vein (vascular bundle)
- lower epidermis
- waxy cuticle
Materials and Methods

Choice of methods?
Choice of locations?
Trial set up

- different locations – focus ARC-Roodeplaat
- 4, 8, 35 genotypes
- 100%, 60%, 30% treatments
Treatments
Water management
Methodology
Leaf material

- Harvest before sunrise – steady state
- Keep cold – enzymes labile
Antioxidants

Reductase – produce NADP accept e from PS I
Dismutase – neutralize O radical
Peroxidase – disposes of hydrogen peroxide
Free Proline

• Stabilize membrane structure
• Maintain osmotic balance
Chlorophyll content measurement
LA measurement
Stem length
Relative water content

\[ RWC(\%) = \frac{FW-DW}{TW-DW} \times 100 \]
Stomatal conductance
C$^{13}$ discrimination analysis

- 98% atm CO$_2$ is C12
- Rubisco preference for 12C
- During drought 13C↔12C ratio ↑ more positive as conductance ↓: Leads to $\Delta$ ↓
- Possible relation $\Delta$ to $g_s$, $\Delta$ to t/ha, $\Delta$ to WUE
C13 determination
Yield
Carotenoid
Results
Pearson Correlation Analysis

Matrix

(-)
(+)

[Image]
### Correlation (4 genotypes)

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Correlation with yield

A

\[ r^2 = 0.429 \]

B

\[ r^2 = 0.257 \]

C

\[ r^2 = 0.509 \]
Correlation (35 genotypes)

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Correlation (35 genotypes)
## Correlation (8 genotypes)

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Correlation (8 genotypes)
Conclusion

- 14 repeatable correlations
- Correlations between early/late parameters
Conclusion

- Correlation between $\Delta$ and t/ha not very strong – better with more genotypes more repeats?
- Large variation measurements: ie. stomatal conductance, chlorophyll content – could become smaller with more repeats
NIRS calibration

NIRS (Near-InfraRed Spectroscopy) is the technique of using a sample's NIR absorbance characteristics to predict parameters of interest. NIR is a region of the Electromagnetic spectrum. Click the chart below to enlarge the graphic.

NIRS exploits the fact that many natural products absorb NIR radiation at specific regions or wavelengths. Specifically, N-H, O-H and C-H bonds are strongly absorbed by NIR radiation, with other molecular bonds less so. Thus, samples high in proteins (many N-H bonds) will absorb more in the amine (N-H) bond regions than samples low in protein. Samples high in moisture and or / sugars will have higher adsorptions in regions associated with hydroxyl (OH) bonds. A sample's NIR spectrum will be a composite of all the absorbances from all of the molecular bonds in the sample.
NIRS calibration

A simplified diagram:

To create a calibration, samples are chosen which are representative to the samples that will be analyzed. There may be as few as 60 samples or there could be several thousand. These samples are analyzed in the NIR, and the spectra stored. The samples are then sent to have the reference analysis performed on them. These are termed calibration samples. We will use 60 sample analyzed for protein content and scanned on a NIRSystems model 5000 for this example.

When the samples come back, the spectroscopist has:
60 sample spectra consisting of 700 datapoints (1100 - 2500 nm)
60 sample reference data consisting of protein content values

To create a calibration, a mathematical relationship can be established between these two sets of data. This relationship can then be used to predict the parameter value in unknown samples.
Recommendations

• More repeats for screening difference between genotypes
• 100% treatment - too much water – difference to 60% small
Thank you