



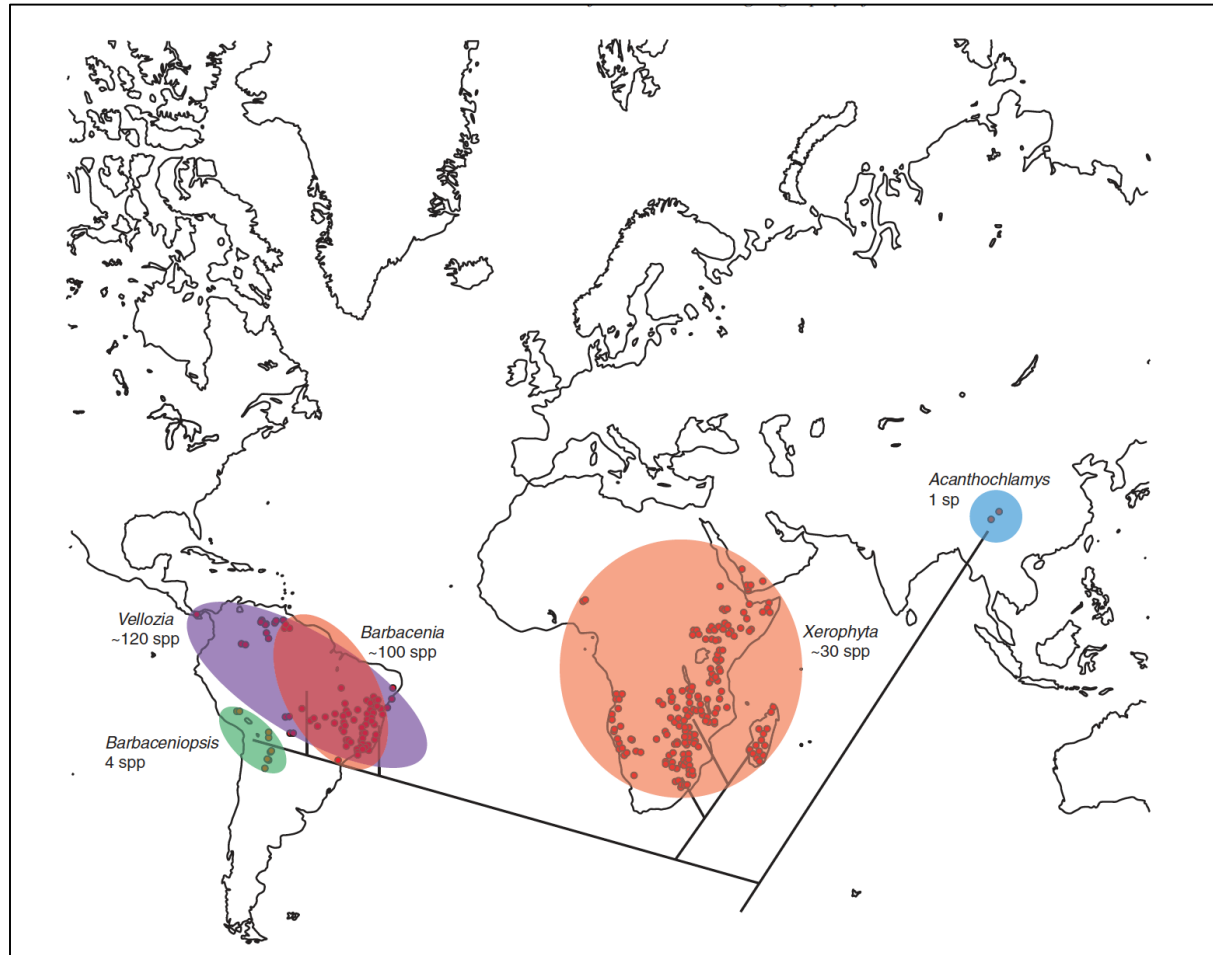
# Velloziaceae genomics and the Lactad-Unicamp as an EBP node

Isabel R. Gerhardt, UMiP GenClima

Workshop Biodiversity and Biobank, Fapesp

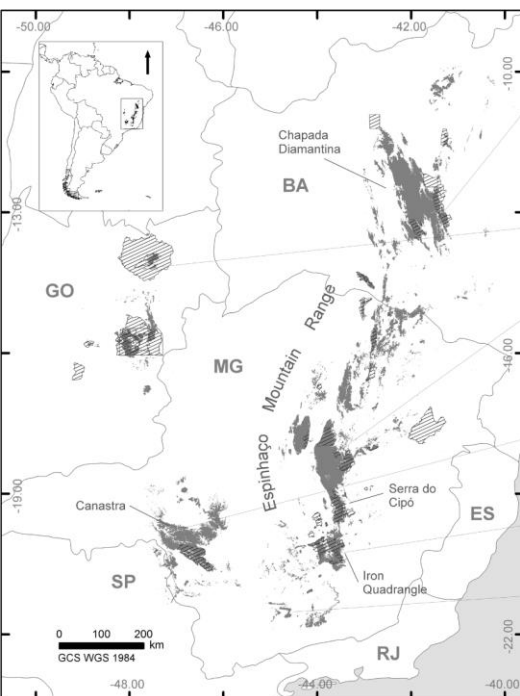
August 16, 2017

# Velloziaceae geographical distribution



Mello-Silva et al., Annals of Botany 108: 87–102, 2011.

# Velloziaceae cope with campos rupestres harsh environment



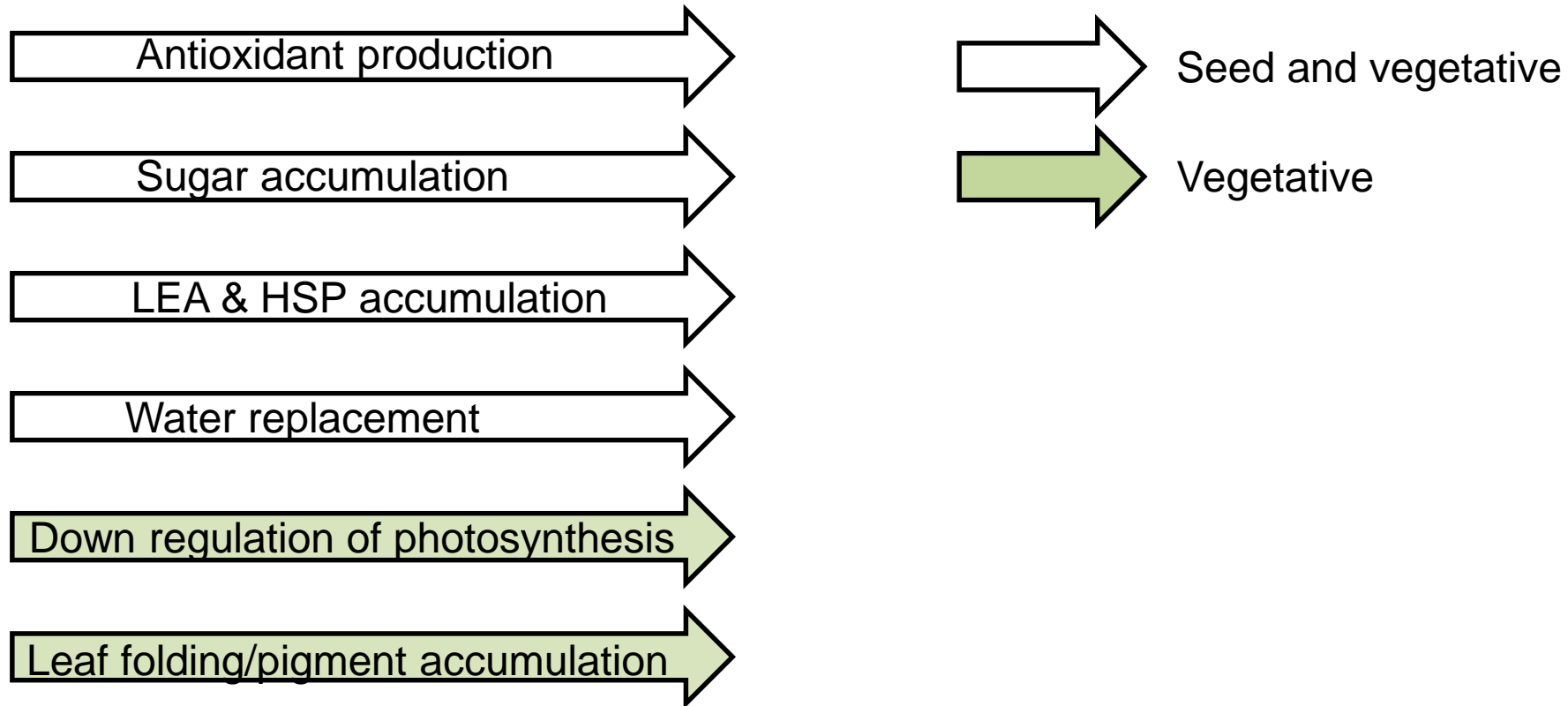
Silveira et al., Plant Soil, 2015

Photo: Rafael S. C. Souza



Velloziaceae are the largest family of desiccation tolerant angiosperms

# The evolution of desiccation tolerance and responses of seeds and vegetative tissues to water loss



Adapted from Farrant & Moore, *Curr Opin Plant Biol* 14:340–345, 2011



Vellozia nivea



Vellozia intermedia

## Functional Ecology



*Functional Ecology* 2015, **29**, 1499–1512

doi: 10.1111/1365-2435.12462

### Carbon assimilation and habitat segregation in resurrection plants: a comparison between desiccation- and non-desiccation-tolerant species of Neotropical Velloziaceae (Pandanales)

Suzana Alcantara<sup>\*1,2</sup>, Renato de Mello-Silva<sup>1</sup>, Grazielle S. Teodoro<sup>3</sup>, Kamila Drequeceler<sup>1</sup>, David D. Ackerly<sup>2</sup> and Rafael S. Oliveira<sup>3</sup>

Vellozia spp. has contrasting strategies to cope with drought stress





# Genome size estimation and sequencing approaches

- Diploid ( $2n=16$ )  
(Melo et al., 1997)
- Flow cytometry
  - *Vellozia nivea* genome size: ~315 Mbp
  - *Vellozia intermedia* genome size: ~340 Mbp



# Genome size estimation and sequencing approaches

- Genome features
  - gene families
  - regulatory sequences
  - clusters of desiccation-associated genes
- Highly contiguous genome assemblies
- PacBio Sequel Platform at Arizona Genomics Institute
- 70X coverage
- Chromatin proximity ligation data

# Genome size estimation and sequencing approaches



RNA-Seq



## What is LaCTAD?

- An initiative of UNICAMP supported by FAPESP through the Multi-User Equipment Program.
- Mission: provide the Brazilian scientific community with new advanced technologies in genomics, proteomics, cell biology and bioinformatics.



## LaCTAD - Services

### Genomics

- Sanger
- Next-generation

### Cell biology

- Confocal microscopy
- Multiplex immunoassay
- Flow cytometry

### Proteomics

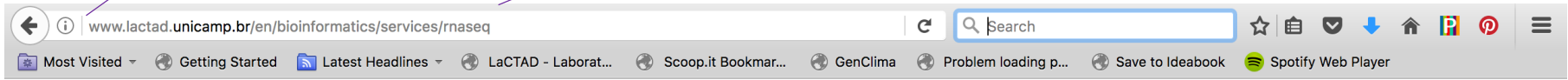
- Protein purification
- Microcalorimetry
- Mass spectrometry analysis  
(protein sequencing and  
identification)

### Bioinformatics

- DNA-Seq/RNA-Seq analysis
- Exome analysis
- Microarray analysis
- Small RNA identification
- Metagenome analysis



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The LaCTAD

Cell Biology

Genomics

Proteomics

Bioinformatics



- Small RNA Analysis
- Metagenomics Analysis
- Exome Analysis
- DNA-Seq
- RNA-Seq**

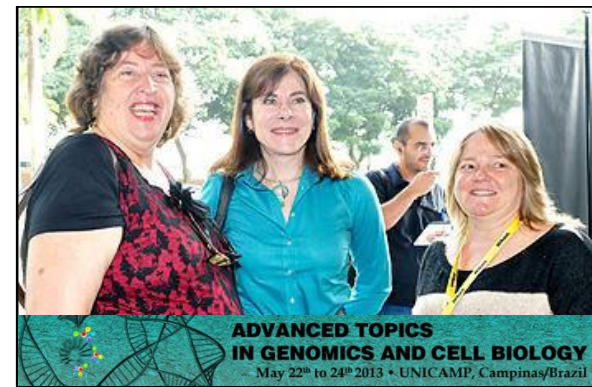
## RNA-SEQ

[Service Request](#)

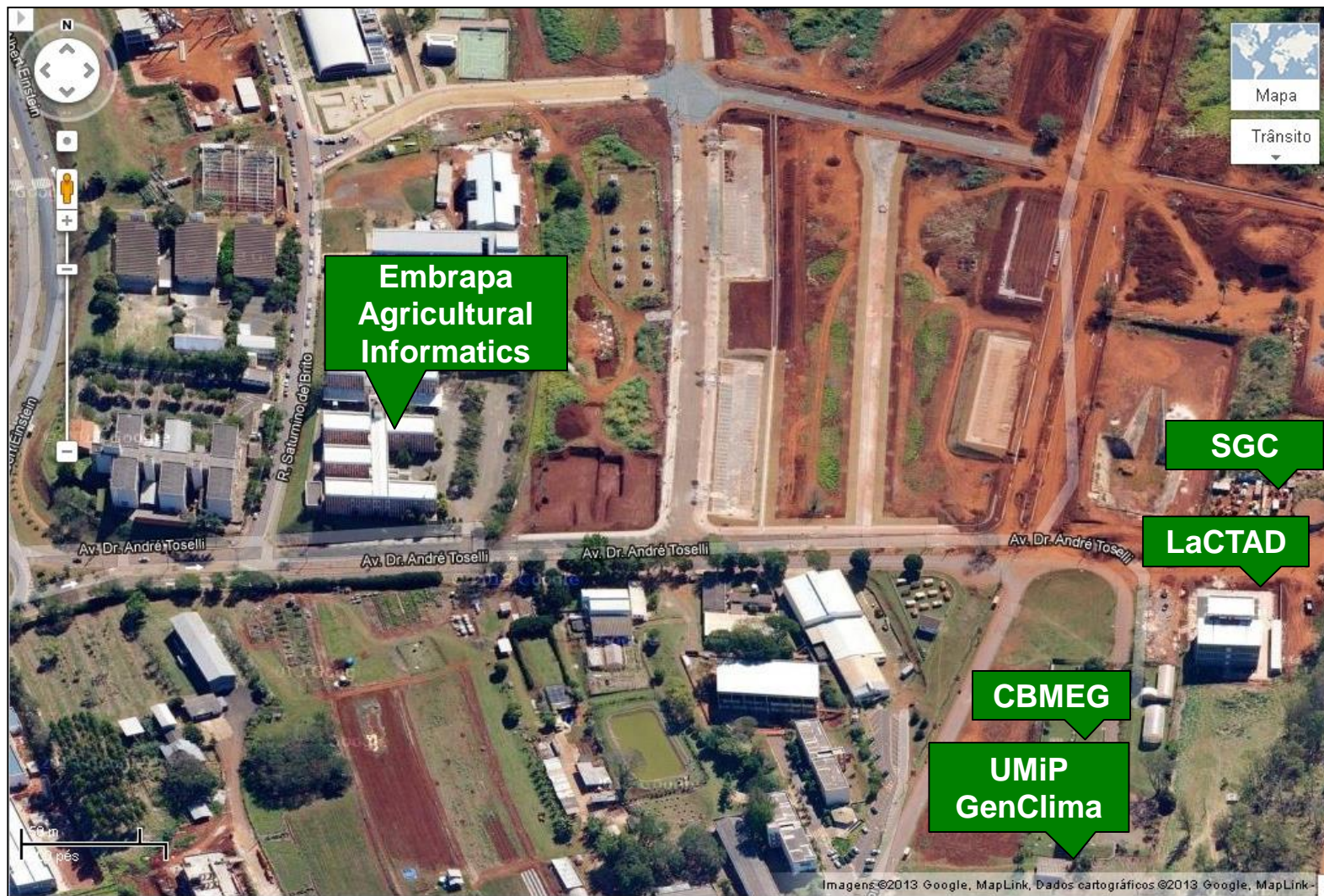
- De novo transcriptome assembly
- Mapping reads onto reference sequence
- Differential Gene Expression Analysis
- Functional Annotation of Transcriptome

## LaCTAD in numbers

- 359 researchers assisted from 14 Brazilian states
- 12.83 terabases of sequence data
- 15 courses offered
- Service acknowledged in 25 articles



# LaCTAD as an EBP node



# Unravelling microbial communities associated with Velloziaceae at JGI



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## Our Projects

Home > Our Projects > Approved User Proposals > Approved Proposals FY17

### Small-Scale Microbial/Metagenome

PI	Affiliation	Project Description
Alvarez-Cohen, Lisa	University of California, Berkeley	Unraveling functional dynamics and regulation crucial for the stability of an anaerobic ammonium oxidizing (anammox) community via community metatranscriptomics and 16S rRNA
McMahon, Katherine	University of Wisconsin-Madison	Reference Genomes for Freshwater Bacteria - Alpha- and Beta-Proteobacteria
Müller, Henry	Graz University of Technology (Austria)	Elucidating the relevance of DNA methylation of strain-specific plant-microbe interactions
Oliveira, Rafael	State University of Campinas (Brazil)	Unravelling microbial communities associated with native plant species from P-impooverished soils of a global biodiversity hotspot
Pan, Chongle	Oak Ridge National Laboratory	Multi-cycle Selection of Sorghum Microbiomes for Biological Nitrogen Fixation

*Vellozia epidendroides* x *Barbacenia macrantha*





# Acknowledgments

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