

Octávio S. Paulo
Computational Biology and Population Genomics Group (CoBiG2)

Faculdade de Ciências, Universidade de Lisboa

octavio.paulo@fc.ul.pt

Gabinete 2.3.46A



Ciências
ULisboa

Faculdade
de Ciências
da Universidade
de Lisboa



Computational
Biology & Population
Genomics Group



Projeto de Tese de Mestrado I

UNIVERSIDADE DE LISBOA
FACULDADE DE CIÊNCIAS
DEPARTAMENTO DE BIOLOGIA ANIMAL



Recovery of cyanobacterial draft genomes from a metagenome dataset Applications to the detection of antibiotic resistance variants

Duarte Teomóteo Balata

Mestrado em Biologia Humana e Ambiente

Versão Provisória

Dissertação orientada por:
Professor Doutor Octávio Paulo e Doutora Elsa Dias

2.1 Cyanobacterial strains

Forty three cyanobacterial strains (Table S7.1), previously isolated from Portuguese surface freshwater reservoirs and wastewater treatment plants (Fig. 2.1), belonging to “Estela Sousa e Silva Algae Culture Collection” (Laboratory of Biology and Ecotoxicology, INSA, I.P., Lisbon, Portugal) (Paulino *et al.*, 2009) and “LEGE Culture Collection” (Laboratory of Ecotoxicology, Genomics and Evolution, CIIMAR, Porto, Portugal) (Martins *et al.*, 2010, 2011), respectively, were studied.







Figure 2.1: Map of freshwater sampling sites (39°23'59.5" N 8°13'28" O).

Projetos de Tese de Mestrado I

Abstract

The Role of Cyanobacteria in the Aquatic Resistome †

Tânia Rosado ¹, Duarte Balata ², Rani de la Rivière ^{1,3}, Vera Manageiro ^{4,5,6} , Dina Carpinteiro ⁷, Luís Vieira ⁷, Francisco Pina-Martins ² , Carina Menezes ¹, Octávio S. Paulo ², Manuela Caniça ^{4,5,6}  and Elsa Dias ^{1,5,6,*} 

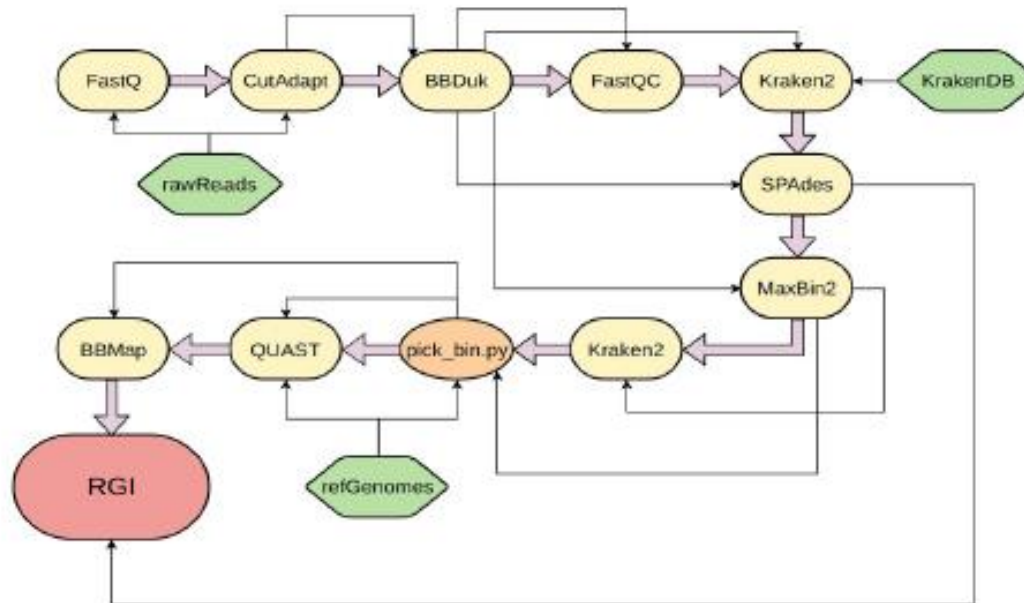


Figure 2.2: Flowchart of the custom GNU Make CyanoPipeline. Yellow shapes represent third party software. Green shapes represent the necessary pipeline input files. The orange shape represents a custom python script. The red shape denotes a browser tool that's not included in the pipeline, but used as the final step of the analysis. Thin arrows represent Input/ Output stream and large arrows represent the succession of software tools.

Projetos de Tese de Mestrado II



Article

Understanding the Impact of Drought in *Coffea* Genotypes: Transcriptomic Analysis Supports a Common High Resilience to Moderate Water Deficit but a Genotype Dependent Sensitivity to Severe Water Deficit

Isabel Fernandes ^{1,†}, Isabel Marques ^{2,*†}, Octávio S. Paulo ^{1,†}, Dora Batista ¹, Fábio L. Fábio M. DaMatta ⁵, José C. Ramalho ^{2,4,*} and Ana I. Ribeiro-Barros ^{2,4,*}








International Journal of
Molecular Sciences



Article

Transcriptomic Leaf Profiling Reveals Differential Responses of the Two Most Traded Coffee Species to Elevated [CO₂]

Isabel Marques ^{1,2,*}, Isabel Fernandes ², Pedro H.C. David ², Octávio S. Paulo ², Luis F. Goulao ³, Ana S. Fortunato ⁴, Fernando C. Lidon ⁵, Fábio M. DaMatta ⁶, José C. Ramalho ^{1,5,*} and Ana I. Ribeiro-Barros ^{1,5,*}



International Journal of
Molecular Sciences



Article

A Transcriptomic Approach to Understanding the Combined Impacts of Supra-Optimal Temperatures and CO₂ Revealed Different Responses in the Polyploid *Coffea arabica* and Its Diploid Progenitor *C. canephora*

Isabel Marques ^{1,2,*}, Isabel Fernandes ², Octávio S. Paulo ², Fernando C. Lidon ³, Fábio M. DaMatta ⁴, José C. Ramalho ^{1,3,*} and Ana I. Ribeiro-Barros ^{1,3,*}

Projetos de Tese de Mestrado II

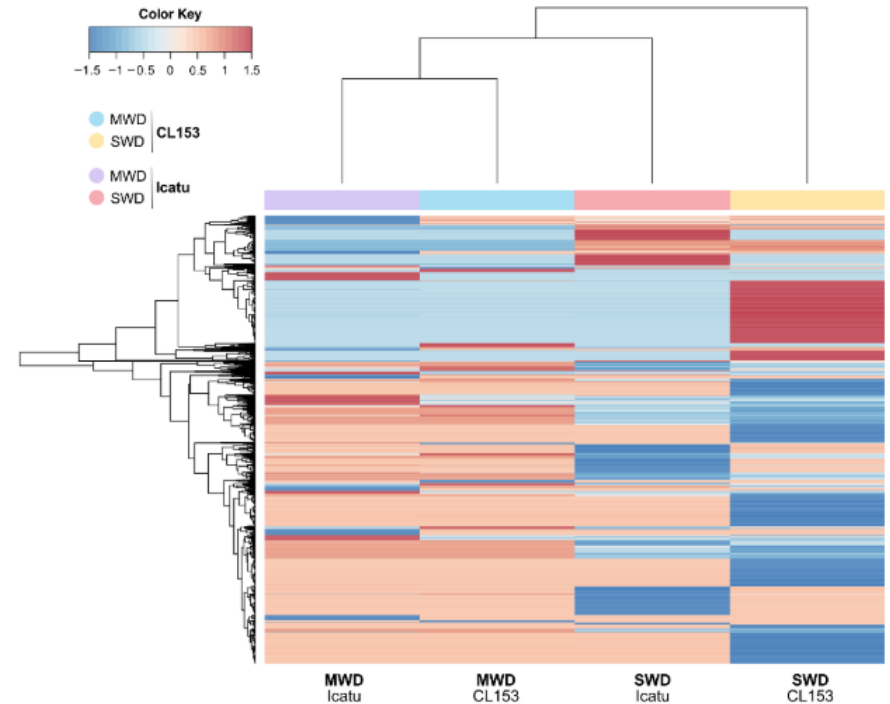
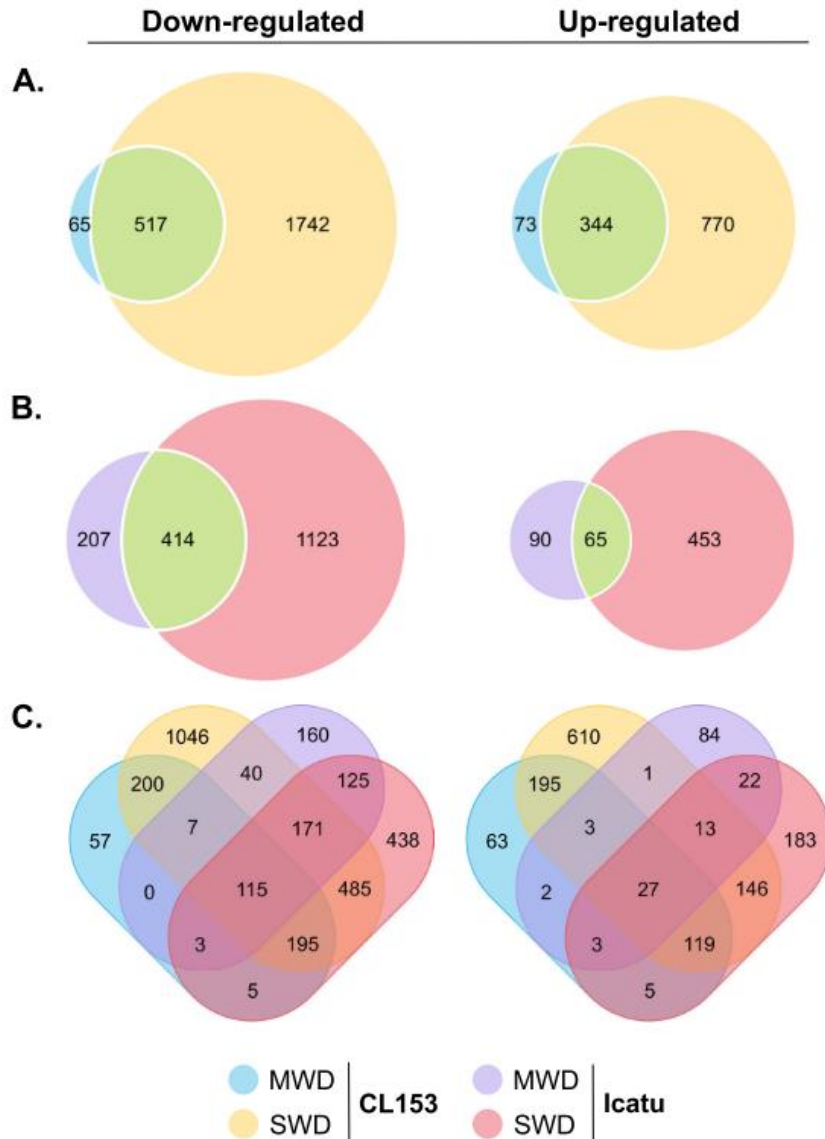
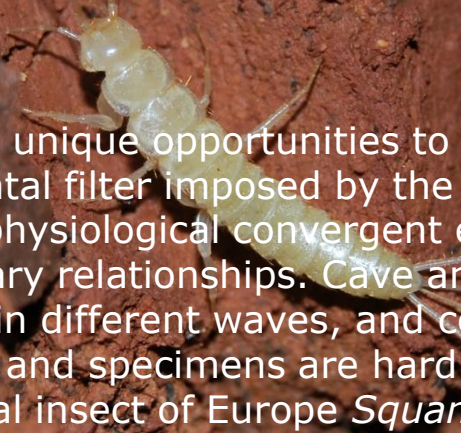


Figure 3. Clustered heat maps and dendrograms of the normalized log₂ fold change (FC) visualizing the expression of significant (FDR < 0.01) treatment-specific differentially expressed genes (DEGs) considering the effect of moderate water deficit (MWD) and severe water deficit (SWD) conditions compared to well-watered plants (WW) in *Coffea arabica* cv. Icatu (Icatu) and *C. canephora* cv. Conilon Clone CL153 (CL153) plants. Values were scaled by row using Z-scores. Hot colors represent up-regulated DEGs, and cold colors represent down-regulated DEGs. Column color labels represent water treatments (colors of treatments follow Figure 1).

Projetos de Tese de Mestrado III

Em co-orientação com a Prof. Ana Sofia Reboleira

Phylogenetics and Phylogeography of cave-dwelling arthropods



Subterranean ecosystems provide unique opportunities to answer eco-evolutionary questions. The strong environmental filter imposed by the lack of light and resource scarcity lead to dramatic morphophysiological convergent evolution in subterranean animals, often masking evolutionary relationships. Cave animals are the result of multiple colonizations of the underground in different waves, and consequent adaptation. Populations are presumably small and specimens are hard to thrive. This work will study the largest subterranean terrestrial insect of Europe *Squamatinia algharbica* (Insects: Zygentoma), endemic from caves of the Algarve. A large set of specimens from different populations with morphometric significant differences are available for sequencing. The main objective is to understand population genetics, and consequently gene flow and habitat fragmentation. This species is threatened by human activities, has reduced geographical distribution and is confined to the underground, therefore, the results of this project will also contribute to develop more effective conservation measures to this species and by extension to Portuguese endemic fauna.