

CURRICULUM VITAE

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Specialisation:

Secondary cell wall molecular regulation, woody plants genomics and plant breeding

Research profile:

- regulation, at transcriptional and post-transcriptional levels, of secondary cell walls biosynthesis, in woody plants.
- study of molecular mechanisms associated with wood formation and adaptation of woody species
- post- transcriptional regulation by smallRNAs and epigenomic regulation
- Enhancement of ligno-cellulosic products for energy production
- Biodiversity studies of agroforestry systems for developed of sustainable production

International grants

Project no. FP7-KBBE-2011-5

Project title: *Promoting a functional and comparative understanding of the conifer genome- implementing applied aspects for more productive and adapted forests.*

Investigator. Duration: 2012-2016

Project no. P-KBBE/AGR-GPL/0001/2010

Project title: *TREEFORJOULES - Improving eucalypt and poplar wood properties for bioenergy.*

Principal Investigator (Portugal). Duration: 2011-2015

Project no. ERA-PG/0001/2006

Project title: *Genome-wide Analysis of Short RNAs as Modulators in Dehydration Stress - Tolerance Using tolerant and Genetic Model Systems*

Investigator. Duration: 2007-2010

Training

- 2002/2006 – Nova University of Lisbon, Lisbon, Portugal
- 2006/2007 – INRA-Biogeco, Bordeaux, France
- 2007/2009 – iBET – Instituto de Biologia Experimental e Tecnológica, Oeiras, Portugal
- 2014/2015 – iBET – Instituto de Biologia Experimental e Tecnológica, Oeiras, Portugal

International cooperation

- Laboratoire de Recherche en Sciences Végétales (LRSV), UMR CNRS/UPS, Toulouse, France, J. Grima-Pettenati. Molecular regulation of cell wall biosynthesis and their properties (*Eucalyptus* spp.).
- INRA-CNRGV, Toulouse, France, H. Bèrges. Development and analysis of BAC libraries in *Eucalyptus* spp. and *Quercus suber* (cork-oak).
- INRA-BIOGECO, Bordeaux, France. Post-transcriptional regulation by miRNAs in Pines (*Pinus* spp.).
- University of Orleans, Orleans France, S. Maury. Epigenomics of woody species.

- Plant Biotechnology Laboratory, ITQB-UNL /IBET, Oeiras, Portugal, S. Araújo & P. Fevereiro. Molecular regulation of stress responses in legumes.
- University of Pavia, Pavia, Italy, A. Balestrazzi. DNA damage repair and genotoxic stress response in plants.
- Universidad Politecnica de Madrid, Madrid, Spain, I. Allona. Gene expression regulation in woody species.

Publications

1. Kazana, V., Tsourgiannis L, Iakovoglou V., Stamatiou C., Alexandrov A., Araújo S., Bogdan S., Bozic G., Brus R., Bossinger G., Boutsimea A., Celepirovic N., Cvrcková H., Fladung M., Ivankovic M., Kazaklis A., Koutsona P., Luthar Z., Máchová P., Malá J, Mara K, Mataruga M, Moravcikova J, Paffetti D, **Paiva JAP**, Raptis D, Sanchez X, Sharry S, Salaj T, Šijacic-Nikolic M., Tel-Zur N, Tsvetkov I, Vettori C, Vidal N. (2016) Public attitudes towards the use of transgenic forest trees: a cross-country pilot survey. *iForest - Biogeosciences and Forestry* 0: 1220-1229. doi: 10.3832/ifer1441-008. **IF: 1.269**
2. Yu H, Soler M, Clemente HS, Mila I, **Paiva JAP**, Myburg AA, Bouzayen M, Grima-Pettenati J, Cassan-Wang H (2015) Comprehensive genome-wide analysis of the Aux/IAA gene family in *Eucalyptus*: evidence for the role of EgrIAA4 in wood formation. *Plant & Cell Physiology* 56: 700-14. doi: 10.1093/pcp/pcu215. **IF: 4.931**
3. Carocha V, Soler M, Hefer C, Cassan-Wang H, Fevereiro P, Myburg AA, **Paiva JAP**, Grima-Pettenati J (2015) Genome-wide analysis of the lignin toolbox of *Eucalyptus grandis*. *New Phytologist* 206 :1297-313. doi: 10.1111/nph.13313. **IF: 7.672**
4. Carvalho A, Graça C, Carocha, V, Pêra S, Lousada J, Lima-Brito J, **Paiva JAP*** (2015) An improved total RNA isolation from secondary tissues of woody species for coding and non coding gene expression analyses. *Wood Science and Technology* 49:647-658. doi: 10.1007/s00226-015-0709-9 [*corresponding autor]. **IF: 1.920**
5. Soler M, Camargo, Oliveira ELO, Carocha V, Cassan-Wang H, Savelli B, Hefer CA, **Paiva JAP**, Alexander AM, Grima-Pettenati J (2014) The *Eucalyptus grandis* R2R3-MYB transcription factor family: evidence for woody growth-related evolution and function. *New Phytologist* 206: 1364-77. doi: 10.1111/nph.13039. **IF: 7.672**
6. Myburg AA, Grattapaglia D, Tuskan JA, Hellsten U, Hayes RD, Grimwood J, Jenkins J, Lindquist E, Tice H, Bauer D, Goodstein DM, Dubchak I, Poliakov A, Mizrahi E, Kullar ARK, Hussey SG, Pinard D, van der Merwe K, Singh P, van Jaarsveld I, Silva-Junior OB, Togawa RC, Pappas MR., Faria DA., Sansaloni CP., Petroli CD., Yang X, Ranjan P., Tschaplinski TJ, Ye C-Y, Li T, Sterck L, Vanneste K, Murat F, Soler M, San Clemente H, Saidi N, Cassan-Wang H, Dunand C, Hefer CA, Bornberg-Bauer E, Kersting AR, Vining K, Amarasinghe V, Ranik M, Naithani M, Elser J, Boyd AE, Liston A, Spatafora JW, Dharmwardhana P, Raja R, Sullivan C, Romanel E, Alves-Ferreira M, Külheim C, Foley W, Carocha V, **Paiva J**, Kudrna D, Brommonschenkel SH, Pasquali G, Byrne M, Rigault P, Tibbits J, Antanas Spokevicius, Rebecca C. Jones, Steane DA, Vaillancourt RE, Potts BM, Joubert F, Barry K, Pappas G, Strauss S, Jaiswal P, Grima-Pettenati J, Salse J, Van de Peer Y, Rokhsar DS, Schmutz J (2014) The genome of *Eucalyptus grandis*. *Nature* 510: 356-362. doi:10.1038/nature13308. **IF: 41.456**
7. Pereira-Leal JB, Abreu IA, Alabaça CS, Almeida MA, Almeida P, Almeida T, Amorim MI, Araújo S, Azevedo H, Badia A, Batista D, Bohn A, Capote T, Carrasquinho I, Chaves I, Coelho AC, Costa MM, Costa R, Cravador A, Egas C, Faro C, Fortes AM, Fortunato AS,

- Gaspar MJ, Gonçalves S, Graça J, Horta M, Inácio V, Leitão LM, Lino-Neto T, Marum L, Matos J, Mendonça D, Miguel, A, Miguel CM, Morais-Cecílio L., Neves I, Nóbrega F, Oliveira MM, Oliveira R, Pais MS, **Paiva JAP**, Paulo OS, Pinheiro M, Raimundo JAP, Ramalho JC, Ribeiro AI, Ribeiro T, Rocheta M, Rodrigues AI, Rodrigues JC, Saibo NJM, Santos TE, Santos SM, Sá-Pereira P, Sebastiana M, Simões F, Sobral RS, Tavares R, Teixeira R, Varela C, Veloso MM, Ricardo CPP (2014) A comprehensive assessment of the transcriptome of cork oak (*Quercus suber*) through EST sequencing. *BMC Genomics* 15:371 doi:10.1186/1471-2164-15-371. **IF: 3.986**
8. Yu H, Soler M, Mila I, San Clemente H, Savelli B, Dunand C, **Paiva JAP**, Myburg AA, Bouzayen M, Grima-Pettenati J, Cassan-Wang H (2014) Genome-wide characterization and expression profiling of the AUXIN RESPONSE FACTOR (ARF) gene family in *Eucalyptus grandis*. *PLoS One* 9: e108906. doi: 10.1371/journal.pone.0108906. eCollection 2014. **IF=3.534**
 9. da Fonseca PGS, **Paiva JAP**, Almeida LGP, Vasconcelos ATR, Freitas AT (2013) Empirical assessment of sequencing errors for high throughput pyrosequencing data. *BMC Research Notes* 6:25 doi: 10.1186/1756-0500-6-25.
 10. Oliveira JS, Mendes ND, Carocha V, Graça C, **Paiva JA**, et al. (2013) A computational approach for MicroRNA identification in plants: combining genome-based predictions with RNA-Seq data. *J Data Mining Genomics Proteomics* 4:130. doi: 10.4172/2153-0602.1000130
 11. Carvalho A, **Paiva J**, Lousada JL and Lima-Brito J (2013). The transcriptomics of secondary growth and wood formation in Conifers. *Molecular Biology International*, 2013, Article ID 974324, 1-12. doi:10.1155/2013/974324
 12. Cassan-Wang H, Soler M, Yu H, Camargo ELO, Carocha V, Ladouce N, Savelli B, **Paiva JAP**, Leplé, JC, Grima-Pettenati J (2012) Reference genes for high-throughput quantitative RT-PCR analysis of gene expression in organs and tissues of *Eucalyptus* grown in various environmental condition. *Plant & Cell Physiology* 53: 2101-2116. doi:10.1093/pcp/pcs152. **IF: 4.931**
 13. Capitão C , **Paiva JAP**, Santos DM and Fevereiro P (2011) In *Medicago truncatula*, water deficit modulates the transcript accumulation of components of small RNA pathways. *BMC Plant Biology* 11:79. doi:10.1186/1471-2229-11-79. **IF: 3.813**
 14. **Paiva JAP**, Prat E, Vautrin S, Santos MD et al. (2011) Advancing *Eucalyptus* genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. *BMC Genomics* 12:137. doi: 10.1186/1471-2164-12-137. **IF: 3.986**
 15. Wang H, Soler M, Yu H, Camargo ELO, Clemente HS, Savelli B, Ladouce N, **Paiva J**, Grima-Pettenati J (2011) Master regulators of wood formation in *Eucalyptus*. *BMC Proceedings* 5(Suppl 7):P110 doi:10.1186/1753-6561-5-S7-P110
 16. **Paiva JAP***, Fevereiro P, Marques P, Rodrigues JC, Le Provost G, Plomion C, Grima-Pettenati J, Bouchez O, Klopp C, Berges H, Graça J (2011) Deciphering cork formation in *Quercus suber*. *BMC Proceedings* 5(Suppl 7):P172. doi:10.1186/1753-6561-5-S7-P172 [*Corresponding Author]
 17. **Paiva JAP***, Rodrigues JC, Fevereiro P, Neves L, Araújo C, Marques C, Freitas AT, Bergès H, Grima-Pettenati J (2011) Building up resources and knowledge to unravel transcriptomics dynamics underlying *Eucalyptus globulus* xylogenesis. *BMC Proceedings* 5(Suppl 7):052. Doi:10.1186/1753-6561-5-S7-052 [*Corresponding Author]
 18. Chaves I, Pinheiro C, **Paiva JAP**, Planchon S, Sergeant K, Renaut J, Graça JA , Costa G, Coelho AV, Ricardo CPP (2009). Proteomic evaluation of wound-healing processes in

- potato (*Solanum tuberosum* L.) tuber tissue. *Proteomics* 9: 4154-4175. Doi: 10.1002/pmic.200700649. **IF: 3.807**
19. **Paiva JAP**, Garcés M, Alves A, Garnier-Géré P, Rodrigues JC, Lalanne C, Porcon S, Le Provost G, Silva-Perez D, Brach J, Frigerio J-M, Claverol S, Barré A, Fevereiro P, Plomion P (2008) Molecular and phenotypic profiling from the base to the crown in maritime pine wood-forming tissue. *New Phytologist* 178(2): 283-30. Doi:10.1111/j.1469-8137.2008.02379.x. **IF: 7.672**
20. **Paiva JAP**, Garnier-Géré PH, Rodrigues JC, Alves A, Santos S, Graça J, Le Provost G, Chaumeil P, da Silva-Perez D, Bosc A, Fevereiro P, Plomion C (2008) Phenotypic and molecular plasticity of maritime pine (*Pinus pinaster* Ait.) wood forming tissues along a growing season. *New Phytologist* 179: 1180-1194. Doi: 10.1111/j.1469-8137.2008.02536.x. **IF: 7.672**
21. Gaspar MJ, de-Lucas AI, González-Martínez SC, Alía R, **Paiva JAP**, Hidalgo E, Louzada L; Almeida H (2008) Use of molecular markers for estimating breeding parameters: a case study in a maritime pine progeny trial. *AL. Tree Genetics & Genomes* 5: 609-616. Doi: 10.1007/s11295-009-0213-1. **IF: 2.451**
22. Le Provost G, Herrera R, **Paiva JAP**, Cheumeil P, Salin F, Plomion C (2007) A micromethod for high throughput RNA extraction in forest trees. *Biological Research* 40: 291-297, ISSN 0716-9760
23. Gion J-M, Lalanne C, Le Provost G, Ferry-Dumazet H, **Paiva J**, Frigerio JM, Chaumeil P, Barré A, de Daruvar A, Brach J, Claverol S, Bonneau M, Plomion C (2004) The proteome of maritime pine wood forming tissue. *Proteomics* 5: 3731-3751 Doi: 10.1002/pmic.200401197. **IF: 3.807**
24. Le Provost G., **Paiva J.**, Pot D, Brach J., Plomion C (2003). Seasonal variation in transcript accumulation in wood forming tissues of maritime pine (*Pinus pinaster* Ait.) with emphasis on a cell wall glycine-rich Protein. *Planta* 217: 820-830. Doi: 10.1007/s00425-003-1051-2. **IF: 3.263**