

Designação do Projeto	PATHOmics: Patogenómica da ferrugem do cafeeiro para descobrir mecanismos de virulência e marcadores de diagnóstico
Código do Projeto	LISBOA-01-0145-FEDER-029189
Objetivo Principal	Reforçar a investigação, o desenvolvimento tecnológico e a inovação
Região de Intervenção	Lisboa
Entidade Beneficiária	FCiências.ID – Associação para a Investigação e Desenvolvimento de Ciências; Instituto Superior de Agronomia
Data de Aprovação	14-05-2018
Data de Início	01-07-2018
Data de Conclusão	30-06-2022
Custo Total Elegível	239.911,10€
Apoio Financeiro da União Europeia	FEDER – 95.964,44€
Apoio Financeiro Público Nacional/ Regional	OE – 143.946,66€

Objetivos

A ocorrência de doenças fúngicas em plantas comercialmente importantes é uma das maiores ameaças para a produtividade e sustentabilidade das culturas agrícolas exploradas pelos seus produtos agroalimentares, dos quais dependem a sobrevivência e bem-estar da população mundial. Pelo que, o desenvolvimento de estratégias e ferramentas para o controlo e/ou combate de tais doenças, assegurando uma produção eficiente e de alta qualidade e visando a segurança alimentar, reveste-se da maior importância económico-social.

A proposta apresentada (PATHOmics) enquadra-se neste contexto pretendendo contribuir para o aumento da sustentabilidade de uma cultura de importância mundial, o café, a qual tem repercussões económicas de grande impacto no mercado global, em particular no espaço europeu. Em particular, este projeto propõe-se a gerar conhecimento científico sobre a virulência do agente patogénico e ferramentas moleculares que serão críticas para o delineamento de novas e eficazes práticas de

controlo e monitorização da principal doença fúngicas do cafeeiro. Embora o cafeeiro seja uma cultura tropical, em Portugal, as várias atividades da indústria transformadora ligadas ao setor Agroalimentar “Café e chá” têm grande relevância, tendo apresentado nos últimos anos uma produtividade superior à média europeia. Por outro lado, a investigação que se desenvolve em Portugal sobre as doenças do cafeeiro há mais de 60 anos tem sido alvo de reconhecimento internacional, projetando Portugal na linha da frente nesta área científica e promovendo a cooperação internacional. Pelo que, o desenvolvimento da presente proposta terá potencialmente um impacto relevante a vários níveis.

Atividades

- 1 - Sequencing and generation of a reference genome for *H. vastatrix*
- 2 - Genomic analyses for probing marker/loci related with rust virulence
- 3 - Transcriptomic analyses for identification of race-specific candidate genes for virulence
- 4 - Validation of genetic and functional markers

Resultados Atingidos

This project contributed to the increase of knowledge and data on the worldwide population genetic differentiation, drivers of genetic diversity, virulence divergence and adaptive evolution of the coffee pathogen, *Hemileia vastatrix*, providing relevant information with implications for disease control. The main objectives proposed by this project were overall achieved, regardless several constraints and drawbacks experienced during the project's development. Results of high significance were obtained, of which the following are highlighted:

- 1) Production of an unprecedented amount of genomic and transcriptomic data simultaneously for different *H. vastatrix* isolates, allowing to directly address the genomic and functional variation that gives rise to different pathotypes, which were made publicly available
- 2) Release of a chromosome-level reference genome of *H. vastatrix*, including a complete circularized 171 kb sequence of the mitochondrial genome, as a high-quality resource for advancing knowledge on the complex coffee rust pathogen.
- 3) Genetic structuring was found for the first time in *H. vastatrix*'s populations within the group infecting *C. arabica* and interspecific hybrids (the most epidemiological relevant group in cultivated coffee). Strong evidence is provided that local adaptation driven by coffee hosts has a fundamental role in shaping population structure,



suggesting that events of convergent evolution may happen in geographical distant regions cultivating the same coffee genotypes. These findings have strong implications for resistance breeding and disease control measures, since different strategies may be required to slow down pathotype evolution.

4) A large number of pathotype-specific transcripts were identified providing ground to understand the molecular basis of virulence divergence. Although many species-specific genes may account for the complex virulence of *H. vastatrix*, as a high proportion of hypothetical or no-match proteins are found, differences in pathotypes could be mainly due to transcription of different isoforms from the same gene, probably due to alternative splicing. Within these, candidate effectors were identified. On the other hand, pathotype-specific expression profiles were also evident.

5) Retrotransposons stood out as probably having a very relevant functional role in host-adaptation with evidence overall provided by both genomic and transcriptomic data. Moreover, high retrotransposon activity was detected, suggesting that they could be a strong generator of genetic diversity.

7) SNPs associated with genetic lineages and genes/transcript isoforms exclusively or differentially expressed among pathotypes were identified as putative candidate markers for pathotype/lineage discrimination, which are in a final stage of validation and testing for screening. In the future, these may be implemented as discriminatory tools in survey programs to monitor disease.

A website was created (<https://sites.google.com/view/pathomics>) compiling all data, resources and information generated by the project, and making it available to the scientific community and the public in general. It includes a description of the project, the project's team, the outputs (comprising publications, communications, advanced training, public databases), and outreach activities.

