

Date: Sept 30, 2024

Subject: Letter of intent to collaborate with the ODFP

To whom it might concern:

I am pleased to confirm that the Oxidative Stress Signalling Group at the VIB-UGent Center for Plant Systems Biology is committed to establishing a collaboration with the Open Door Fellowship Program (ODFP), with myself serving as the Principal Investigator of the receiving group.

Upon successful recruitment, this collaboration will aim to support a female post-doctoral researcher within my team, fostering synergies in academic writing and the transfer of skills.

Sincerely,

Frank Van Breusegem



VIB-UGent Center for Plant Systems Biology
Ghent University
Technologiepark-Zwijnaarde 71 - 9052 Ghent - Belgium
Tel. +32(0)9 331 39 20
www.psb.ugent.be

Prof. Dr. Frank Van Breusegem

Frank.VanBreusegem@psb.vib-ugent.be

OPEN DOORS FELLOWSHIP PROGRAM- APPLICATION TEMPLATE FOR RECEIVING LABORATORIES IN BELGIUM

APPLICATION MODALITY A: This modality has been conceived for those research institutions in Belgium that are looking for new scientific partners in Africa, and that are willing to explore new joint research streams with their counterparts.

Objective: The application presented by the candidate ODFP fellow shall align with the scope and the requirements of open slots offered by the Belgian research laboratories and published on the ODFP web page.

The slots open slots offered by the Belgian research laboratories shall be published on the ODFP web page <https://ipbo.vib-ugent.be/en/belgian-research-groups-portal>

Information from the hosting institutions in Belgium

Contact details of a focal point	✉: frank.vanbreusegem@ugent.be ☎: 093313920
Name of the research or academic institution	Ghent University-VIB
Name of the research group	Oxidative Stress Signaling
Website of institution /research group	Van Breusegem Lab VIB Labs

Present the group's research line(s) and activities, including a list of commonly used technologies (e.g. *bioinformatics, genetic engineering, chromatography, sequencing, metabolomics, metagenomics*).

Reactive Oxygen Species (ROS), causing oxidative stress, were long considered as harmful by products of (diseased) metabolism. However, recently they have emerged as important regulators of plant stress responses. Perturbation in ROS production and/or scavenging are sensed by plant cells as a 'warning' message, and genetic programs leading to stress acclimation or cell death are switched on. Knowledge on regulatory events during ROS signal transduction is now only scratching the surface. Through combined top-down and bottom-up genomics and proteomics approaches we are dissecting the gene network governing ROS signal transduction in plants and **pinpoint genes that are potential candidates for innovative molecular breeding strategies to develop stress-tolerant crops**. Our current



project studying stress physiology uses genetic engineering, genomics, and bioinformatics to elucidate the fundamental cellular science behind drought stress.

Deciphering the molecular mechanisms underlying grass pea (*Lathyrus sativus*) water and oxidative stress resistance Because of its high resilience towards environmental stresses, grass pea (*Lathyrus sativus*) is a very promising crop in the climate change scenario and the anticipated advent of increasingly frequent water stress events (such as extreme drought and sudden waterlogging). However, there is a range of variability regarding this tolerance, which is barely understood.

The aim of this project is to unravel the genetic and molecular mechanisms underlying grass pea' water and oxidative stress response by screening a worldwide collection of germplasm and establish the potential role of this crop as a model for multiple abiotic stress resistance studies. A multidisciplinary approach has been employed, combining the phenotypic characterization of water stress responses with genome wide association studies (GWAS) using grass pea natural variation; as well as molecular and biochemical assessments related to the antioxidative landscape and transcriptomic data of a selection of tolerant and susceptible grass pea accessions. To our knowledge, such a comprehensive study of grass pea tolerance to both water deficit and waterlogging simultaneously has not yet been performed.

The project runs in collaboration with the lab of Maria Carlota Vaz at the ITQB NOVA institute in Lisbon (Portugal) <https://www.itqb.unl.pt/research/plant-sciences/plantx>

Describe the primary hard and soft skills desirable from the awarded ODFP fellow to deliver the task at hand.

Hard Skills

- (i) DNA and RNA extraction: the candidate should have prior knowledge on the techniques, as these will be used during a short training.
- (ii) Basic knowledge on PCR, transcriptomics, biochemistry and microscopy is required.
- (iii) Basics on bioinformatics (e.g. BLAST, databases, ...) and statistical analysis is important.

Soft Skills

Related to soft skills & competencies, the fellow should have excellent communication (verbal and written) in English, interpersonal communication, self-management, teamwork, and problem-solving.

Indicate the short and long-term outputs and synergies the PI in Belgium would like to see arising from this collaboration.

Expected Short-term synergies	Expected Long-term synergies
-------------------------------	------------------------------



• Protocols and genetic materials development • At least one joint publication • Exchange of expertise • Exchange of staff and students	• Growing and sampling of different Lathyrus accessions in Africa for experiments under local conditions. • Establishment of joint field experiments to assess performance under local conditions in Africa. • Development of at least one joint project research proposal.
--	---

Summarise (between 400 - 800 words approx.) the research project(s) or activities where the ODFP fellow would contribute with her/their research.

Statement of the problem: Because of its high resilience towards environmental stresses, grass pea (*Lathyrus sativus*) is a very promising crop in the climate change scenario and the anticipated advent of increasingly frequent water stress events (such as extreme drought and sudden waterlogging) However, there is a range of variability regarding this tolerance, which is barely understood.

Broad Objectives: This project aims to understand grass pea responds to water deficit and waterlogging stress. The project will provide the expertise in transcriptomics (UGent), biochemical analysis of anti-oxidants, and genome editing of model plants as well as *Lathyrus*.

The main objectives from this collaboration under the Open Doors Fellowship Program are to:

1. Biochemical profiling of small molecule antioxidants and enzymatic antioxidants.
2. Validation of identified genetic markers associated with water deficit and waterlogging tolerance to use in future marker assisted selection (MAS).
- 3: Validation of candidate genes (both from GWAS and transcriptomics) in experimental model systems (*Arabidopsis*)
4. Initiate cloning, gene editing and transformations (transient or stable) of the validated and promising candidates in *Lathyrus*.
- 5: Identify signaling pathways associated with water stress resilience of *Lathyrus* accessions.

Perspectives: The generated knowledge will be useful to develop new molecular tools for grass pea breeding and generate fundamental knowledge that may as well be translated to other related legume species. This will be essential to ease the development and release of new smart legume varieties, better prepared to durably face the increasingly frequent stress events and to be implemented in an African context.



Are there additional resources relevant to the work/project related to the short research stay (e.g. articles, videos, project documents and summaries, repositories) that would help the fellow have a wider background of the intended project? If so, please list them below.

- Improving oxidative stress resilience in plants. Kerchev PI, Van Breusegem F. Plant J. 2021. doi: 10.1111/tpj.15493.
- Reactive oxygen species and organellar signaling. Phua SY, De Smet B, Remacle C, Chan KX, Van Breusegem F. J Exp Bot. 2021. 72, 5807-5824. doi: 10.1093/jxb/erab218.
- Genome sequencing and assembly of Lathyrus sativus—A nutrient-rich hardy legume crop. Rajarammohan S, Kaur L, Verma A, Singh D, Mantri S, Roy J K, Sharma TR, Pareek A, Kandoth P K. 2023. Scientific Data. 10, 1–9.
- Contemporary proteomic strategies for cysteine redoxome profiling. Willems P, Van Breusegem F, Huang J. Plant Physiol. 2021. 186, 110-124. doi: 10.1093/plphys/kiaa074.
- Grass pea (Lathyrus sativus) interesting panoply of mechanisms to cope with contrasting water stress conditions – a controlled study of sub populational differences in a worldwide collection of accessions. Sanches M, Sampaio AM, Araújo S, van Eeuwijk F, Van Breusegem F, Vaz Patto MC. 2024. Agricultural Water Management. 292, 108664.
- A chromosome-scale reference genome of grasspea (Lathyrus sativus). Vigouroux M, Novák P, Oliveira LC, Santos C, Cheema J, Wouters RHM, Paajanen P, Vickers M, Koblížková A, Vaz Patto MC, Macas J, Steuernagel B, Martin C, Emmrich PMF. Nture. 2024. 11:1035 <https://doi.org/10.1038/s41597-024-03868-y>.
- Website Maria Carlota Vaz Patto Lab <https://www.itqb.unl.pt/labs/plantx/welcome>

To complete this application, **an official letter from the Principal Investigator of the Belgian receiving group confirming the collaboration with the ODFP should be sent together with this form duly filled.**

Applications must be submitted electronically to IPBO@vib-ugent.be (The application form must be named as follows: **"ODFP_ModalityA_name of research group"**). Please, send the application form and supporting letter as a **single PDF file**.