

BOLSA DE INVESTIGAÇÃO (M/F)

Referência: PTDC/AGR-AAM/099577/2008

Título do Projecto: Study of the role and regulation of glutamine synthetase in *Medicago truncatula* seeds.

Código interno: PR192801

Está aberto concurso para recrutamento de um(a) bolseiro(a) de Investigação para colaborar no projecto acima referido, financiado pelo programa COMPETE - Programa Operacional Factores de Competitividade na sua componente FEDER e pelo orçamento da Fundação para a Ciência e a Tecnologia na sua componente OE.

A bolsa, em regime de exclusividade, terá a duração inicial de 1 ano, eventualmente renovável até três anos, com início previsto em 1 de Junho de 2010.

O valor mensal da bolsa será de € 745,00, pago por transferência bancária (preferencialmente).

Local de trabalho: IBMC - Instituto de Biologia Molecular e Celular (Grupo “Molecular Biology of Nitrogen Assimilation”)

Programa de trabalho: ver anexo.

Perfil pretendido:

Os candidatos devem ter o grau de licenciatura em Bioquímica, Ciências Biológicas ou afins, sendo dada preferência a quem tiver média de licenciatura igual ou superior a 14 valores e experiência na área.

O prazo para recepção de candidaturas decorre de 7 a 21 de Maio de 2010.

As propostas deverão incluir carta de motivação, CV e uma carta de referência e ser enviadas por correio electrónico para candidaturas@ibmc.up.pt com indicação do código interno (PR192801).

A contratação será regida pelo estipulado na legislação em vigor relativamente ao Estatuto de Bolseiro de Investigação Científica, nomeadamente a Lei 40/2004, de 18 Agosto, e o Regulamento de Bolsas de Investigação Científica do IBMC (www.ibmc.up.pt/fellowships.php).

“Study of the role and regulation of glutamine synthetase in *Medicago truncatula* seeds.”**Supervisor:**

Helena Carvalho

Project summary:

Nitrogen is the major nutrient limiting plant growth and crop yield. A major challenge of modern agriculture is to reduce the excessive input of nitrogen fertilisers and, at the same time, to improve grain quality without affecting yield. One way to achieve this goal is to improve plant nitrogen utilization efficiency (NUE). Glutamine synthetase (GS), occupies a central position in nitrogen assimilation and recycling and genetic evidence indicates that the reaction catalyzed by GS represents a key component of NUE and plant yield.

Legumes can obtain a significant part of their nitrogen from the atmosphere through a symbiotic interaction with nitrogen fixing bacteria. Perhaps due to this special source of nitrogen, legumes produce protein-rich seeds with a high nutritive value, representing a major source of nutrients for human and animal livestock diets. It is therefore extremely important to understand how nitrogen is assimilated and partitioned in legumes. We have previously done a considerable amount of work to understand how GS is regulated and how it regulates nitrogen metabolism, using the model legume *Medicago truncatula*. This plant is particularly well suited for the study of GS because it contains a very small GS gene family, consisting of only three members: MtGS1a and MtGS1b encoding cytosolic isoenzymes and MtGS2, encoding a plastid-located polypeptide. We investigated how the individual genes are differentially regulated, the sites of expression of each gene and gene products, the isoenzyme composition and distribution in different organs of the plant, posttranslational mechanisms of GS regulation and structural and biochemical determinants of the isoenzymes. Following the advances in *M. truncatula* genome sequencing, we have recently identified a new gene encoding a plastid located GS, which we found to be specifically expressed in the seeds and only during seed development. The accumulation of storage proteins in seeds, involves N-remobilization, a process in which glutamine synthetase is a key player. In spite of the importance of GS for seed metabolism and the mechanisms underlying protein reserve accumulation, it has been poorly investigated in seeds. This proposal aims at complementing our previous work by extending our knowledge on the contribution of GS for seed metabolism and in particular to the function and regulation of this novel seed specific GS gene.

In all plant species studied to date, including *M. truncatula*, the plastid located GS isoenzyme (GS2) has been reported as being encoded by a single nuclear gene. The existence of a second GS2 gene in the genome of *M. truncatula*, located in the same chromosome and not too distant from the first gene suggests a recent duplication event. Gene duplications provide opportunities for functional innovation and we postulate that the duplication of this gene occurred after legume speciation leading to a novel gene expression pattern (the seed) and novel product functions related to legume seed metabolism. During this project, we also propose to search for the existence of a second GS2 gene in closely related plant species and perform phylogenetic studies to estimate the time of the duplication event.

Our preliminary results revealed the existence of at least two alternatively spliced transcripts corresponding to this gene, exclusively expressed in the seeds and more specifically during seed development. These findings are extremely interesting because alternatively spliced transcripts may encode distinct proteins, expanding the coding capacity of genes. Seeds perform specific nitrogen metabolic pathways related to the production of storage compounds and grain legumes produce protein-rich seeds involving high requirement of nitrogen. It is conceivable that different proteins encoded by this novel GS2 gene are involved in different seed specific metabolic pathways, probably related to the accumulation of protein seed reserves. We also propose to investigate this aspect. Taken together the results obtained in the course of this project will provide novel and important information regarding the regulation of GS gene expression in plants, the evolution of GS genes and its implications for the metabolic processes occurring in the seed. Our findings together with the development of the genomic resources, and the recent advances that have been made towards understanding the metabolic control of seed filling in *M. truncatula*, could support attempts to engineer legume seed composition for added end user value.