**BBSRC MIBTP Studentship Project**

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| **Project Title** | Understanding male fertility: gene control networks in plant gametogenesis and crop fertility |
| **Project Summary** | |
| Plant fertility is vitally dependent upon sexual reproduction and the differentiation of the male (sperm) and female (egg) gametes. Despite the importance of this process for future food security we have limited knowledge of the underlying mechanisms.    This research project aims to uncover the genetic control of plant gamete development and the evolution of gene networks that determine plant and crop fertility. Our research has identified a key regulatory hub in plant sperm cell development that involves the *Arabidopsis thaliana* transcription factor DUO1. This protein is widely conserved in important food crops such as maize, wheat, rice and tomato and forms a regulatory module with its target protein DAZ1 (a zinc finger transcription factor) (Borg et al., 2014). An exciting recent discovery is that this module is ancient and is even needed for sperm development in early land plants, such as mosses and liverworts (Higo et al., 2018).    **Project aims & description**  This project will explore the conservation and mechanisms by which the DUO1-DAZ1 module coordinates cell proliferation with sperm differentiation. Studies of gene function will involve crop species including tomato and maize, as well as early land plant models. Genetic and molecular analyses will be combined with comparative transcriptome studies to uncover co-expression and co-function gene networks. This will help to uncover novel plant fertility genes of potential value. Overall, the project seeks to establish how gene function and evolution has shaped the fertility of some of our important food crops, starting from their earliest origins.    From an applied perspective, the research is also expected to deliver novel information and tools of value in plant breeding applications such as hybrid seed production and the control of gene flow.    **Possible timeline**  Year 1.Identify germline targets of the DUO1-DAZ1 module based on bioinformatic analysis of transcriptome data; construct novel germlinemutants using gene editing technology.  Year 2.Use genetic and molecular methods toanalyse germline mutants; establish *in vitro/in vivo* DNA binding assays for DAZ1.  Year 3.Devise and test network model for the contribution of DUO1-DAZ1-targets to male germline development; analyse gene function by gene-editing and manipulation of protein function.  Techniques that will be undertaken during the project:   * Targeted manipulation of gene expression and protein function (eg. CRISPR/Cas9) * Advanced light microscopy and image analysis (eg. confocal laser scanning) * Comparative transcriptome analysis (microarray & RNA-seq data) * Co-expression and co-function network analysis * Transient gene expression assays and quantitative analysis (qRT-PCR)   BBSRC Strategic Research Priority: Understanding the Rules of Life - Plant Science  Sustainable Agriculture and Food – Plant and Crop Science | |
| **References** | |
| Borg, M., *et al.* (2011) The R2R3 MYB transcription factor DUO1 activates a male germline-specific regulon essential for sperm cell differentiation in *Arabidopsis*. *Plant Cell* 23:1-16.  Borg, M., *et al*.  (2014). An EAR-dependent regulatory module promotes male germ cell division and sperm fertility in *Arabidopsis*. *The Plant Cell* 26:1-17.  Brownfield, L., *et al.* (2009) A plant germ cell-specific integrator of cell cycle progression and sperm specification *PLOS Genetics* 5: e1000430.  Berger, F. and Twell, D. (2011) Germline specification and function in plants. *Annual Review of Plant Biology* 62:461-484.  Higo *et al*., (2018) Transcription factor DUO1 generated by neo-functionalization is associated with evolution of sperm differentiation in plants. *Nature Communications*9, 5283. | |