OpenPlant Fund Application Form

Title of Project
Identifying nutrient-status dependent elements regulating the wheat transcriptional response to neighbours

Primary contact for the team
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Team
Stéphanie Swarbreck, Department of Plant Sciences, University of Cambridge, ss2062@cam.ac.uk
Collect samples, and conduct analysis of root system architecture, analyse data

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Wheat genomics expertise, RNAseq analysis,

Summary
We propose to use RNAseq to investigate the wheat response to the presence of neighbour under low and high nutrient conditions, with the aim of identifying nutrient-status dependent regulators of the transcriptional response to neighbours.

Proposal
Our previous work has shown that wheat plants[1] grown under high nutrient conditions showed a clear response to the presence of a neighbour. Under those conditions, wheat lateral roots were shorter in the presence of a blackgrass (*Alopecurus myosuroides* L.) or *Brachypodium dystachion* (competing neighbours) compared to laterals from a wheat plant grown alone, this is largely driven by a higher proportion of laterals with a length < 0.5cm in the presence of a neighbour. However, under low nutrients conditions there was no significant neighbour effect on lateral roots length. This lead to the hypothesis that, wheat plants which are nutrient replete are more sensitive, or more likely to respond, to the presence of a neighbour, and that the nutrient status of the plants is affecting the response to neighbour. As an exploratory experiment, we propose to compare the transcriptome of lateral roots (controlled for size, i.e. lateral roots shorter than 0.5) from wheat plants grown under high (HN) vs. low nutrient (LN) conditions (similar to those used in our previous work), and identify genes that are differentially regulated. In addition, we will compare the lateral root transcriptome of plants grown in the presence (wbg) or absence (w1) of a neighbour, under low vs high nutrient conditions. Thus, we will have samples from four conditions: w1-HN, w1-LN, wbg-HN, wbg-LN.

We ask for funding for RNA extraction kits, library construction and sequencing for a minimum of three replicates per condition (a total of 12 samples). We will conduct an analysis of patterns of transcript abundance and group together transcripts that respond similarly. For example, it would be interesting to identify groups of transcripts that are down-regulated in the presence of a neighbour under HN conditions but not under LN conditions. Perhaps these transcripts share common regulators that relate to the nutrient status of the plant. Identifying nutrient-status dependent regulatory elements of the downstream response to the presence of neighbour would enable us to manipulate and re-program plants so that they are less sensitive to the presence of neighbour even under high nutrient conditions.

Benefits and outcomes
We believe that our project fits within the remit of OpenPlant as it would add new information from RNAseq to investigate the effect of a widespread weed (blackgrass) on wheat performance and bring

new information that would enable possible sustainable improvement to wheat production. All data produced will be made available to the wider public thus fitting with the philosophy of the OpenPlant initiative. Data will be made widely available through the wheat expression browser website http://www.wheat-expression.com/# This dataset will add information about wheat root transcriptome which is scarce, available datasets tend to originate from leaf or grain studies. In addition, within this project we aim to build connections between the Earlham Institute and the Department of Plant Sciences, University of Cambridge.

Sponsor for the research and cost centre
Prof. Howard Griffiths, Department of Plant Sciences, University of Cambridge, hg230@cam.ac.uk
I confirm that I have the full support of the sponsor listed above and that they can be added to the OpenPlant Fund mailing list to receive project updates (to which they can unsubscribe at any time).
Costcode: PDAG/351

Budget
RNA extraction kit (£282)
RNAseq for 12 samples including construction of cDNA libraries.
Costs towards HPC resources to support bioinformatic analysis.

1.	Finch, J. A. *et al.* **Wheat root length and not branching is altered in the presence of neighbours, including blackgrass.** *PLoS ONE* **12, e0178176–21 (2017).**