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Linking genes to field performance: adventures in sulfur research

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The development of widespread sulfur deficiency in crops became evident in the 1980’s and 90’s. It is well documented that this arose due to reduced aerial inputs due to decreased pollution as well as the use of low S fertilizer formulations. Negative impacts were seen on high S-requiring crops such as *Brassica napus* (oilseed rape, colza, canola) and also for cereals such as wheat. Both yield and quality were affected, and for example a detrimental impact of S deficiency on the content of S-rich storage proteins of wheat, which are essential for dough rheology, was observed (Zhao et al. 1999). In addition, low S availability has substantial impacts on uptake and accumulation of Se and Mo, which may have substantial implications for nutritional quality (Shinmachi et al. 2010; Stroud et al. 2010). Many studies demonstrated that remedial application of S fertilizers successfully restored yield and quality parameters. One area of importance was accurate diagnosis (Blake-Kalff et al. 2000; Blake-Kalff et al. 2001). Remediation of crop S deficiencies was a recent success story in relation to applied plant nutrition studies coupled with appropriate agronomy.

More fundamental studies have focused on the sulfur uptake and assimilatory pathways and their regulation as a paradigm for plant and indeed crop responses to mineral nutrition (Hawkesford and De Kok 2006). The rationale for such studies is a genetic solution for producing crops with increased efficiency for uptake and utilization of S, or for reduced physiological requirements for S. The most significant advances at the molecular level have been achieved using the model plant Arabidopsis thaliana, although such studies have more recently been extended into a number of crops including rice, wheat and Brassica, aided by rapid recent advances in resources for genomics in these crops (Buchner et al. 2004). Achievements over the past 20 years have resulted in the elucidation of molecular aspects of uptake and assimilation pathways, the existence of large multigene families, with isoforms having defined roles, pathways for regulation and inter connections with a range of metabolic pathways and physiological responses. A suggestion that manipulation of feedback mechanisms which restrict uptake could enable luxury uptake during time of plenty (immediately following fertilizer applications) and subsequent effective internal management of this reserve S, could ensure the most effective use of fertilizer applied S. A wide range of roles and requirements for adequate S-nutritional status have been established indicating little opportunity for decreasing crop S demands. One exception has been in identifying prospects for improving effective remobilization of S within the plant particularly, between senescing and newly developing organs (Blake-Kalff et al. 1998; Dubousset et al. 2009). Brassica species have proved to be a useful model for understanding physiological aspects of regulation, having a high S requirement and being particularly amenable to experimental manipulation of S sources for growth (Aghajanzadeh et al. 2016; Hawkesford and De Kok 2006).

Recent developments in high resolution crop monitoring and phenotyping offer opportunities to closely monitor impacts of S nutrition on crop growth and development, and hence performance in the field. As well as being able to follow crop establishment and determine yield components, opportunities exist to monitor subtle effect of fertilizer on developmental processes such as flowering or other physiological factors such as resistance to stress. Application of an automated field phenotyping platform to monitor crop performance at Rothamsted Research will be presented.

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