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Improved resistance to septoria in superior varieties

by

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1. ABSTRACT

Septoria tritici blotch has been the major disease of wheat in the UK for over two decades. It is the principal target for fungicides on wheat and the major target for resistance breeding. This project aimed to apply knowledge of the genetics of septoria to improve methods of selecting for resistance. This will help breeders to produce high-yielding, high-quality wheat varieties with good resistance to septoria. In turn, growing such varieties will promote cost-effective disease control in the UK's major arable crop.

A study of diversity in a large number of wheat varieties, using the technique of association genetics, found that many genes in UK cultivars make moderate contributions to septoria resistance. The introduction of some of these genes can be traced back to breeding programmes between 30 and 55 years ago which aimed to increase yield and improve resistance to other diseases. Research in this project and elsewhere has shown that all 21 chromosomes in wheat carry genes which increase resistance to septoria. This type of resistance is likely to be durable and its effect in controlling disease is unlikely to be eroded through evolution of the fungus that causes septoria. The results of the project imply that breeders can improve septoria resistance by using parental lines which have diverse pedigrees and therefore probably have different resistance genes, then selecting progeny which combine genes from both parents.

In the past, many breeders found it difficult to produce new wheat varieties which combined septoria resistance with high yield. This project showed that there is a yield penalty of septoria resistance. While it is unlikely that the negative relationship between yield and septoria resistance can be broken completely, breeders should be able to select varieties which have a balance of these and other traits appropriate to current market conditions. This is reflected in the fact that many high-yielding varieties on the current Recommended List now have moderately good resistance to septoria.

To continue the current trend towards improved septoria resistance in high-yielding varieties, breeders will need to make use of genetically diverse parental varieties, well-adapted to UK conditions. As agricultural practices develop and the climate changes, the profile of diseases on wheat and other crops is likely to vary. As with septoria, the use of association genetics to study a wide range of varieties, followed by genetic analysis to investigate the relationship of disease resistance to other traits, can be applied to new diseases. This will support the efforts of breeders to release high-yielding varieties in which diseases can be controlled effectively and economically.

2. KEY MESSAGES FOR LEVY PAYERS

- This project studied the genetics of resistance to septoria tritici blotch in UK wheat varieties, especially types of resistance which are likely to have durable value in controlling septoria.
- There is a wide range of genes for potentially durable resistance to septoria in varieties adapted to UK conditions, distributed over much of the wheat genome.
- Wheat breeders have made significant advances in recent years in producing a steady stream of varieties on the Recommended List with high yield and moderately good septoria resistance. They will be able to continue this trend by crossing parents which come from different lineages within the UK wheat pedigree and therefore probably have different resistance genes. They can then select progeny lines which have improved resistance because they combine desirable genes from both parents.
- Resistance to septoria tends to be associated with reduced yield. The yield penalty is not generally large but it can be high enough to make the most septoria-resistant wheat varieties uncompetitive at a time when effective fungicides are readily available.
- Genetic analysis has shown that at least some of the yield penalty of septoria resistance can be broken. Several genes increase septoria resistance but do not depress yield, or *vice-versa*. Breeders can use genes such as these to produce varieties that combine competitive high yields with the level of septoria resistance which will be required when new regulations restricting the use of pesticides are fully implemented in the late 2010's.
- Varieties with yields close to those of the market leaders and Recommended List ratings for septoria resistance of 6-8, indicating potentially durable resistance, will increasingly provide a cost-effective option for growing wheat in the UK.

3. ACKNOWLEDGEMENTS

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4. SUMMARY

4.1. Background

Septoria tritici blotch has consistently been the major disease of wheat in the UK for over two decades. It is the principal target for foliar fungicides applied to wheat and the major target for resistance breeding for the UK market and in most of western Europe. Until quite recently, it was feasible for farmers to choose to grow septoria-susceptible varieties and to protect them with systemic fungicides. The options for chemical control of septoria have become severely limited, however, by the emergence of insensitivity to strobilurin (QoI) fungicides during the early 2000s (Fraaije *et al.* 2005) and the recent evolution of reduced sensitivity to triazole fungicides (Fraaije *et al.* 2007). It is therefore increasingly important for farmers to have access to septoria-resistant wheat varieties with optimal quality and high yield.

The overall purpose of the IMPRESSIV (IMProved RESistance to Septoria in Superior Varieties) project was to apply knowledge of the genetics of resistance to septoria to improve methods of selecting for resistance, thus helping breeders to produce high-yielding, high-quality varieties with good resistance to septoria and supporting cost-effective disease control in the UK's major arable crop.

At the time that IMPRESSIV began, many breeders were finding it difficult to produce new wheat varieties which combined high resistance to septoria with the high yield required for commercial success. A previous Sustainable Arable LINK project, *Breeding for Improved Resistance to Septoria Tritici* (BIRST, SA-LINK project LK0913), found evidence for an association between septoria resistance and reduced yield. This suggested that the difficulty in releasing high-yield, septoria-resistant wheat varieties may have resulted from a yield penalty of septoria resistance. An important aim of IMPRESSIV, therefore, was to test whether or not there is indeed a yield penalty, to understand its nature in more detail if it does exist, and to investigate the genetic relationship between septoria resistance and reduced yield so we could determine if the association between the two traits could be broken.

BIRST and previous work at the John Innes Centre had found that there are essentially two types of resistance to septoria in wheat varieties. Major-gene resistance is effective against some isolates of the septoria fungus, *Mycosphaerella graminicola*, but not others. It is controlled by single genes which each have a large effect. By contrast, partial resistance is not completely effective but it operates against all isolates of *M. graminicola*. The fact that fungi cannot evolve to overcome partial resistance (or at least do so very slowly) means that partial resistance is generally durable. Some individual genes for partial resistance to septoria had been identified before IMPRESSIV began but a large proportion of this type of resistance appeared to be

controlled by many genes with small effects, dispersed throughout the genome. A second aim of IMPRESSIV was to determine how effectively known genes for septoria resistance controlled the disease in the field.

The overall situation of two types of resistance to septoria, revealed by previous research at JIC and by other research groups is similar to that in other crop diseases, including powdery mildew and rusts of cereals. To support breeding for resistance, however, it is essential to have specific information about the genetics of each individual disease. A third aim of IMPRESSIV was to continue research on the genetics of resistance of septoria, focussing in particular on potential new sources of resistance which might be useful in breeding.

4.2. Association genetics of resistance

Part of the research in BIRST involved a study of field resistance to septoria in a large set of 226 wheat varieties which had either been on the NIAB Recommended List during the 1990s or were related to those varieties, mainly as progenitors. They included varieties dating back to the origin of scientific wheat breeding in the 1860s but the majority were from the period between 1970 and 1999. Two papers about this project reported the distribution of genes for septoria resistance in these varieties (Arraiano & Brown 2006) and variation in their susceptibility to septoria in field conditions (Arraiano *et al.* 2009).

Technical developments in molecular genetics, however, meant that further study of this material would make a substantial advance in achieving the goals of the IMPRESSIV project. A new method of screening the genome of wheat for molecular marker varieties, Diversity Array Technology (DArT, Akbari *et al.* 2006) was applied to the full set of 226 varieties, supplementing data on 98 varieties using an older type of DNA marker, simple sequence repeats (SSR), which had been obtained by BIRST. The data on markers and septoria were analysed by relating varieties' scores for susceptibility to septoria in the field to the inheritance of molecular markers through the history of UK wheat breeding. This technique is known as association genetics because it attempts to associate genetic variation in the distribution of DNA markers with phenotypic variation in a trait. It is widely used in human genetics and is becoming increasingly important in crop research (Rafalski 2010). The salient discoveries were as follows.

- Genes controlling septoria resistance were identified on 11 of the 21 chromosomes of wheat. Six of these had been detected by the previous analysis in BIRST.
- The DNA marker most strongly associated with variation in resistance to septoria was very close indeed to the location of a gene known to have a large effect on grain yield of wheat and on grain size in particular (Snape *et al.* 2007).
- Four of the most potent genes for susceptibility to septoria had all been introduced inadvertently into UK wheat germplasm. Two were introduced from a variety used to breed for rust resistance and yield in the 1950s, one from a variety used to increase yield in the 1960s and one in a source of eyespot resistance introduced in the 1980s.
- A gene especially effective against septoria was discovered in Pastiche, a variety identified previously as a good source of resistance (Arraiano *et al.* 2009).
- The introgression of two resistance genes into UK wheat varieties could be traced through two lineages. Some of the most resistant modern varieties have both these genes and lack certain genes which increase susceptibility.
- A further gene was found a “lost lineage”, a group of varieties from the 1980s which together constituted a source of resistance which had not been exploited subsequently in UK wheat breeding programmes.

4.3. Genetics of durable resistance

In plant diseases in general (Brown & Hovmøller 2002), including septoria (Cowger *et al.* 2000), major-gene resistance can be overcome by mutation in the pathogen in a matter of a few years, so it only has a temporary benefit in crop varieties. Partial resistance, though less effective, is generally durable. Study of the panel of 226 wheat varieties in BIRST showed that many wheat varieties in the UK have moderate to high levels of partial resistance to septoria. The association genetic analysis done in IMPRESSIV postulated the existence of numerous genes controlling this form of resistance, distributed throughout the wheat genome. There therefore appears to be a rich source of genes for durable resistance in wheat germplasm used in breeding programmes for the UK.

For reasons relating to the assumptions which underpin the statistical analysis, all predictions of gene locations made by association genetics in crop plants must be regarded as tentative. Research to test the predictions about the locations of partial resistance genes formed an important part of the work in IMPRESSIV. In the course of this research, some additional partial resistance genes were also found.

The research used crosses of wheat varieties in which variation in septoria resistance among the progeny lines was related to the presence of DNA markers on a genetic map. Some of the crosses used in IMPRESSIV were made or developed during the project while others were provided by colleagues at the John Innes Centre or by companies participating in the project. These are the main findings of this part of the project.

- In a cross of Pastiche with Torfrida, a gene controlling a large proportion of partial resistance was detected in Pastiche. This gene was in the same location as one predicted by the association genetics analysis using the DArT markers added to the existing dataset by IMPRESSIV. While it is not straightforward to quantify the effect of genes for partial resistance to disease, the results indicate that if plants with the Torfrida gene had an average of 10% septoria on their flag leaves, those with the Pastiche gene would have an average of 6%. The Pastiche gene would evidently make a useful contribution to disease control but would not be sufficient on its own.
- The cross of Spark x Rialto has been studied extensively for yield and environmental adaptation (Snape *et al.* 2007). In this population, there was an association between partial resistance and the presence of the major resistance gene *Stb6* on chromosome 3A of Rialto, supporting a hypothesis arising from BIRST (Arraiano *et al.* 2009). It is quite a large effect; if plants with the Spark gene had an average of 10% septoria on flag leaves, the Rialto gene would reduce disease to an average of 5%.
- In the same cross, susceptibility to septoria was also associated with a gene in Rialto which reduces the final height of the plant. The effect of increased plant height on disease escape is well known (van Beuningen & Kohli 1990, Arraiano *et al.* 2009) because there is a lower rate of spread of spores borne by rain splash from lower leaves to upper leaves in taller plants. Here, while shorter plants tended to have less septoria in general, those with the gene which reduced height had more disease even allowing for the fact that they were shorter. In plants in which the flag leaves were 65cm from the ground, if those with the Rialto (short) gene had 10% septoria, those with the Spark (tall) gene would be predicted to have 4% disease.

- Flame and Longbow are close to the extremes of resistance and susceptibility respectively among UK wheat varieties. In a cross of these two varieties, Flame was found to carry a gene for partial resistance in the same location as that predicted by association genetics to have the greatest effect on septoria. This would reduce disease from 10% in plants with the Longbow gene to 5% in those with the Flame gene. Like Rialto, Flame has *Stb6* on chromosome 3A but in the cross with Longbow, this gene had a comparatively weak association with disease in the field.
- A cross of Xi19 x Solstice was contributed to the project by Groupe Limagrain. This population was generated by a LINK project on 'Identification of genetic markers for lodging resistance in wheat', led by Dr Pete Berry of ADAS. Xi19 was found to have genes which increase resistance on three chromosomes while Solstice to have one. Association genetics predicted the presence of the septoria-resistance gene in Solstice and one of those in Xi19 although neither of these varieties was included in the association genetic study.
- In all the crosses studied, a large proportion of variation between the progeny lines could not be explained by the genes identified using DNA marker maps. This implies that there are many genes which collectively control a large fraction of variation in resistance to septoria but which individually have small effects and are scattered throughout the wheat genome.
- One of the objectives of IMPRESSIV was to test whether major-gene resistance controls septoria in the field. BIRST found that *Stb6* on chromosome 3A was associated with reduced levels of septoria in field trials (Arraiano *et al.* 2009) but this does not seem to be a benefit of major resistance genes in general. Resistance was associated with *Stb6* in Rialto in the cross with Spark while a partial resistance gene was located close to but not at the position of *Stb6* in a cross of Senat and Savannah (Eriksen *et al.*, 2003). In Flame x Longbow, *Stb6* had a weak association with resistance. There was no evidence for an association of other specific resistance genes with reduced septoria in field conditions.

The main overall conclusion of this part of the project is that there are many genes in varieties relevant to UK wheat breeding which make moderate contributions to partial, probably durable resistance to septoria. These genes are distributed throughout the wheat genome. In principle, breeders could improve septoria resistance by choosing parental lines which have diverse pedigrees and therefore probably have different resistance genes. They could then select progeny which have better resistance than either parent, mostly likely because they combine resistance genes from both parental lineages. In addition, a breeder can accumulate genes for partial

resistance over a few generations by selecting resistant lines in field trials, even if the individual genes have effects which are too small to be estimated by standard genetic techniques.

4.4. Further research on genetics of resistance

Knowledge of the genetics of disease resistance can help people involved in plant breeding and variety recommendation to understand whether the resistance of varieties may be durable or is likely to be overcome by a simple mutation in the pathogen. The latter situation often happens when a variety carries a new gene conferring complete resistance to rust or mildew become susceptible after a very few years (Brown & Hovmøller 2002), as indicated by Recommended List ratings for these diseases. We therefore continued research on the genetics of resistance in UK wheat varieties, though not to the same extent as in the earlier BIRST project.

Heines 110 is an important progenitor in the UK wheat pedigree and is in the parentage of most winter varieties. We located a gene in this line which confers resistance to one of our collection of *M. graminicola* isolates. Pathology and genetic data indicated that it is clearly different from two other genes which are also located on the same chromosome. A resistance gene was identified in Robigus, close to the location of a known major gene; further analysis, including additional crosses, will be required to determine the relationship between the gene in Robigus and the other gene. We also identified two spring wheat varieties, Early Hybrid II and Wembley, as previously unknown sources of resistance; research to identify and locate their resistance genes is in progress.

IMPRESSIV provided the breeders involved in the project with a list of major genes and important partial resistance genes in varieties released in north-western Europe between 2000 and 2007. This information supplemented the existing list of genes in pre-2000 varieties (Arraiano & Brown 2006) and included genes identified by BIRST.

Plant materials generated in IMPRESSIV will be useful for future research on genetics of resistance to septoria, including fundamental studies of the disease and applied work on improving resistance in high-yielding varieties. We developed pairs of near-isogenic lines for most of the known major resistance genes. Within each pair, the two lines are genetically almost identical except that they differ in alleles (different forms of a gene) controlling resistance or susceptibility to particular isolates of the septoria pathogen. We are now using material developed in IMPRESSIV, coupled with recent advances in DNA marker technology, to develop large sets of near-isogenic lines for detailed study of the two most important resistance genes in the variety Flame. One of these genes is especially interesting because it is the most widespread septoria-resistance gene in wheat breeding worldwide, including the UK, and appears not to be associated with a yield penalty, while the other gene is interesting for exactly the opposite reason, that several lines of evidence

indicate that it does depress yield. Another gene of particular interest is the important partial resistance gene in Pastiche.

4.5. Yield penalty of septoria resistance

The association genetic analysis in BIRST, extended by IMPRESSIV, showed that while both yield and septoria resistance had advanced during the 1980s and 1990s, selection for yield had inhibited selection for resistance. This implied that less progress had been made in improving septoria resistance than would have been possible had not yield been regarded as the more important trait in breeding. A group of related varieties, however, had better septoria resistance than would be predicted from their yields while analysis of the association of individual markers with the yield penalty of resistance showed that one of the most potent genes for septoria resistance was not associated with reduced yield. This pointed to an important conclusion, that some genes for septoria resistance might be associated with a yield penalty while others might not. If confirmed, it would indicate a strategy of breeding septoria-resistant, high-yielding varieties: both traits could be combined by using genetically diverse parents and selecting for each trait in the progeny in independent trials. Breeders could accelerate the release of such varieties by using parents known to have genes which increase resistance but do not depress yield or *vice-versa*.

We analysed the genetic relationship between yield and septoria resistance in several crosses, attempting to cover as many of the partial resistance genes predicted by association genetics as possible. All this research involved separate trials of the two traits; yield was measured in trials in which disease was eliminated or minimised by fungicides while septoria was scored in trials in which the disease was allowed to develop naturally. Where appropriate, rust was controlled with a QoI (strobilurin) and mildew with Talius or Flexity. The following are the key conclusions.

- In a cross of the varieties Senat and Savannah, Eriksen *et al.* (2003) mapped genes for partial resistance to septoria on four chromosomes. The association genetics study detected genes at or near all these locations. Seed of this population was contributed to the project by Sejet Plant Breeding, allowing us to study yield, individual components of yield and other traits related to the development of plants and grain in a series of field trials. The relationship between septoria and yield varied from trial to trial, indicating that the yield penalty of resistance is affected by the environment. Over all the trials, septoria resistance was consistently associated with smaller grains, as measured by thousand grain weight, and with a larger number of grains, measured by ears m^{-2} or grains m^{-2} . The net effect on yield, however, was variable; for example, septoria-resistant lines tended to yield less on average than susceptible lines in one trial in Denmark but to yield more in another trial at the same site the following year.

- The most potent septoria-resistance gene in Senat was associated with a reduction in grain size in a trial in England but increased grain number in a trial in Denmark, once again indicating the effect of the environment on correlations between septoria and traits related to yield. Another resistance gene, by contrast, was not associated with yield or any component of yield.
- Environmental conditions had a dramatic effect on the yield penalty of septoria resistance in the Spark x Rialto population. Data on yield and yield components in this population was made available from a previous project at the John Innes Centre, in which 12 yield trials had been held at diverse locations in northern Europe at which disease was controlled by fungicides (Snape *et al.* 2007). We ran a separate series of field trials for septoria. The lines which were most susceptible to septoria had the highest yields and thousand-grain weights at fertile field trial sites, where the average yield was high. Conversely, the same septoria-susceptible lines had the lowest yields and smallest grain at low-yielding sites.
- A striking conclusion from the Spark x Rialto population was that none of the identified genes for septoria resistance were associated with a yield penalty. Likewise, in Senat x Savannah, the associations detected between resistance genes and yield components only accounted for part of the correlation between resistance and reduced yield. This implies that most of the correlation between the two traits is due to the combined effect of minor genes which individually each have only a small effect on septoria.
- By contrast, the resistance gene in Pastiche was associated with a yield *increase* of 0.2 t ha⁻¹ compared to Torfrida. This might be because Torfrida has a segment of chromosome from a wild grass which includes several genes affecting the performance of wheat in UK conditions, including one which reduces yield and another which increases susceptibility to septoria.
- In the Xi19 x Solstice population, the septoria resistance gene from Solstice was also linked to a gene for increased yield. The effects on both traits were quite small, just above the limit of detection.

There are three important conclusions from this part of the project. One is that, in general, there is a yield penalty of septoria resistance. Some of this yield penalty can be attributed to particular genes for septoria resistance but much of it cannot, implying that there are genes dispersed throughout the genome of wheat which not only have minor effects on septoria resistance but also have minor effects on depressing yield. The net effect is that if breeders select only for yield and

ignore septoria, they will inevitably produce septoria-susceptible varieties. Equally, if they select too strongly for septoria resistance, they will not be able to maximise yield.

The second conclusion, however, is that some genes deviate from the negative relationship between septoria resistance and yield. There are three pieces of evidence to support this claim. One is that in the association genetic analysis, a few varieties have much better resistance to septoria than would be predicted from their yield and that the analysis predicts the existence of at least one gene which makes an important contribution to resistance but does not affect yield. Unfortunately, plant populations suitable for testing the effect of this gene on the relationship between septoria and yield were not available for use in this project. The second piece of evidence is the association between resistance genes in Pastiche and Solstice with increased yield, although we do not know if both effects are caused by the same gene in each case or are separate effects of genes closely linked in the wheat genome. Thirdly, in all four populations in which resistance and yield were both studied, there was not a perfect correlation between septoria resistance and the yield penalty, once the effects of individually identified genes were taken into account. This means that breeders can select varieties which have high yield but at least moderate septoria resistance, as has in fact happened in the varieties on the current Recommended List. This has largely been made possible through the skill of breeders in designing efficient methods of selection for each trait.

Finally, the costs of resistance can be modified and even reversed by the environment, as shown in the Spark x Rialto population, and the nature of the costs can vary from one place to another, as shown by the Senat x Savannah population. Unfortunately, it appears that the greatest costs of resistance are expressed in the highest-yielding environments. A tendency for the highest-yielding varieties to be the most susceptible to septoria will constrain the extent to which yields can be maximised in future wheat varieties for the UK and for western Europe in general.

4.6. Disease escape

In addition to the yield penalty of resistance, another cost of breeding varieties with reduced levels of septoria is less-than-ideal plant structure and development. Disease escape traits such as tallness and late flowering reduce the spread of splash-borne spores but do not alter the susceptibility of individual leaves to infection. In taller plants, there is a lower frequency of raindrops carrying spores being splashed upwards from lower to higher leaves, while in later-flowering varieties there is less time for disease to become established on flag leaves (van Beuningen & Kohli 1990, Arraiano *et al.* 2009).

While study of disease escape was not an objective of IMPRESSIV, the project produced further evidence that escape traits reduce septoria levels. This means it is not possible to optimise height, flowering time and septoria control simultaneously, so breeders need to make compromises among these traits in their varieties.

Plant height was negatively associated with levels of septoria, with the highest average levels of disease in the shortest lines, in all the crosses studied except Xi19 x Solstice. In the latter case, the lack of a relationship between height and septoria was probably because there was comparatively little variation in height among the progeny lines. Both varieties have the *Rht-D1b* semi-dwarfing gene and presumably differ in few minor genes affecting plant height.

4.7. Outlook for research on wheat disease resistance

This project generated a large amount of material and information relevant to breeding for septoria resistance and yield UK wheat varieties. Further genetic analysis is required to determine if the yield penalty associated with some resistance genes is an effect of those gene themselves or of closely linked genes. Research on some of the more important resistance genes is currently in progress at the John Innes Centre.

The effect of environmental variation on the penalty of resistance in terms of yield and individual yield components is intriguing and poorly characterised. Knowing which environmental factors minimise these penalties might help in the development of systems of crop management to maximise yield and minimise the cost of disease control in UK wheat crops.

IMPRESSIV found that association genetics is a fairly reliable method of identifying genes controlling complex traits in wheat. Most of the septoria resistance genes predicted in our work have been confirmed, either in this project or in research in other institutions (Eriksen *et al.* 2003, Risser *et al.* 2011, Kelm *et al.* 2011). Association genetics is now being used to study four important diseases of wheat (yellow rust, brown rust, mildew and septoria) in a new LINK project, *Wheat Association Genetics for Trait Analysis and Improved Lineages* (WAGTAIL), in which NIAB, JIC and eight wheat breeding companies are participating, including all those involved in IMPRESSIV.

4.8. Outlook for wheat breeding

The results of IMPRESSIV, including the genetics of partial resistance to septoria and the yield penalty of resistance, indicate a strategy of breeding for several complex traits simultaneously. Genetic diversity plays an important role in breeding for multiple traits. In plant breeding in general, one way of advancing a trait is by transgressive segregation. Parents of crosses can be chosen from diverse lineages which are likely to have different genes that improve the trait. Progeny with better values of the trait than either parent can then be selected, presumably because they combine favourable genes from both parents.

Advancing several traits simultaneously is more challenging. In relation to yield and septoria resistance, the key point is that the two traits are correlated but the correlation is imperfect. The two traits (or indeed several traits) can be selected in separate trials and breeders can aim for varieties with an optimal balance between them. The fact that the environment can modify and even reverse the yield penalty implies that trials must be done in conditions similar to those of farms in the UK. The emphasis placed on either trait will depend on market conditions; as the new pesticide regulations take full effect, it may be necessary to increase selection for disease resistance while maintaining yield as high as possible. Genetic diversity among plant material well-adapted to UK conditions is crucial. Having access to a wide range of genes gives breeders a high chance of breaking the relationship between a positive trait and a negative one. While new genes may be introduced from varieties which are poorly adapted to UK conditions or even from wild grasses related to wheat, breeders should be cautious about relying too heavily on such material. Research on several crosses in IMPRESSIV has shown that this generates a substantial risk of introducing undesirable genes along with beneficial ones. In practice, there is so much diversity in genes for partial, probably durable resistance to septoria tritici in UK wheat varieties that there should be no need to use poorly-adapted varieties or wild wheat species to improve resistance.

In summary, we are optimistic that in future, UK wheat breeders will be able to continue producing varieties with good resistance to septoria as regularly as they do now. This will be essential for UK farming to cope with new regulations on the marketing and use of pesticides from the late 2010's onwards and with increasing insensitivity to major groups of fungicides.

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