Plant genomics – a way forward?

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ABSTRACT

Diseases of plants cause significant losses in crop yield and quality. Plants contain a battery of genes whose role is to prevent pathogens invading. Their effective use in crop plants is very important in crop production and especially in chemical free cropping systems. Such genes are introduced into crop varieties by plant breeding. The new science of genomics may enable scientists to recognise all the resistance genes present in a plant. This will eventually allow plant breeders to more precisely and rapidly select useful resistant plants in their breeding programmes. Furthermore, genomics could enable effective deployment of these genes in cropping systems, so providing more durable resistance.

INTRODUCTION

Disease is a major threat to consistent crop production world-wide. Approximately 8000 different fungi alone cause diseases in plants and when bacteria and viruses are added to the picture it is clear that crop plants are under constant attack by disease. Such threats can be manifest to the human population both in terms of hunger, poverty and social change. During one week in the summer of 1846 almost the entire potato crop of Ireland was destroyed. This was caused by an epidemic of potato late blight (*Phytopthora infestans*) a fungal like organism. At the time the potato was a staple food of the poor and nearly one million people died in the Great Famine and an additional one and a half million people emigrated to other countries. Another example of the devastating effects of fungal disease is that of *Plasmopora viticola* which causes downy mildew disease in grapes. This disease was brought to Europe from America on infected vines during the late 1870s. As a consequence the French wine industry was nearly wiped out. By chance in Bordeaux a mixture of lime and copper sulphate was sprayed on some vines to prevent theft of grapes on the side of roads. Miraculously these plants were disease free and the first chemical fungicide (Bordeaux Mixture), still in extensive use today, had been discovered.

However, another process has been occurring ever since mankind started cultivating plants. This process is the use of plant genes that prevent diseases from attacking. Initially this was a serendipitous process by which people would select seed from disease free plants to grow in their fields the following year. Clearly those plants that could resist the local diseases would produce more seed and would represent a larger proportion of the following year's crop. Hence, over time a population of resistant plants would be developed. However, the risk of the arrival of a new pathogen as described above would always be present. Equally, the level of resistance would always be limited to that specified by genes present in the local plant populations. Also, if a disease was not present in any given year no "natural" selection pressure would be applied and, hence, resistance could be lost by drift. This would, therefore, contribute to the limitation in overall yield and quality of the plants and plant products produced for human consumption.

With the development of modern genetic science initiated by the Czech abbot Gregor Mendel, a new understanding of the mechanisms of resistance in plants evolved. A series of experiments revealed that plants carried genes that prevented specific pathogen isolates (or races) from attacking plants carrying them. With this knowledge it became possible to screen plants for resistance to disease and use them in breeding programmes in which disease resistance was one of the crop characters that could be selected for. Such "artificial" selection pressure maintains resistance genes in the plant population, which is one of the main differences between varieties produced by plant breeding and land races. Hence, highly bred varieties of crops plants were produced that could resist prevalent races of disease present in defined geographical areas.

However, there were several problems with this genetically based approach to producing disease resistant crops. The number of resistance genes present in the crop "gene pool" is limited. As there are lots of pathogen isolates present new isolates are selected that overcome the resistance. Hence, it has become necessary to find new genes in wild relatives of the crop types. These new resistance genes can be introduced into the crop plant by crossing. However, because the wild species have poor quality characteristics, it is necessary to carry out several generations of back-crossing to the variety in order to obtain a plant with all the characteristics of the original crop but with the new resistance gene. This process has two main drawbacks: it is slow often taking 10 - 15 years to introduce a new gene and it is costly because many offspring have to be screened in disease tests to determine if they have retained the new resistance gene in the crossing procedure. Furthermore, this process would have to be repeated for each crop type in which the resistance is required. In addition, the large hectarages of a particular variety that are grown offers a new environment in which a disease variant that can overcome the resistance can thrive. Hence, single resistance genes are often only effective in preventing disease for a few years. Then a new resistance needs to be found and introduced, this is often called the 'boom-bust' cycle.

Currently, genetic resistance is used extensively in agriculture but it is supplemented by the use of chemical fungicides, etc. in situations where no genetic resistance is available in crop varieties. This has proven to be very successful in maintaining production of food on a global scale. However, there are situations, such as that of organic growers, where the use of chemical fungicides is not an option. In such a situation crop production will be highly dependent of the judicial management of genetic resources. This management can take several forms, to which I shall return later, which will all be dependant on the availability of a range of disease resistance genes and their effective use in crop varieties. The new science of genomics may offer new opportunities to rapidly develop disease resistant crops in which resistance is more durable.

WHAT IS GENOMICS?

Since the advent of molecular Biology, during the last thirty years, steady progress has been made in the identification of many genes involved in processes such as flowering, nutrition and disease resistance. However, these studies have often been narrowly focussed on one or more genes, as the available technologies limited our ability to work with more complex situations. Fundamental to that limitation was our ability to decode the sequence of

information present in DNA, the chemical in which the genetic information in genes is constructed. In recent years this has changed dramatically. First for bacteria and viruses, then for humans and now for plants the complete sequence of the genetic material, or genome, has been decoded. This information has allowed us to analyse genes on a whole genome scale instead of one at a time. Hence, the science of genomics has been born.

During the last decade several disease resistance genes have been isolated from plants. Interestingly they appear to have a conserved structure throughout the plant kingdom. Hence, with the sequencing of the genome of the model plant Arabidopsis (thale cress) it has been possible to identify all the genes in a single plant that have the potential to be disease resistance genes. This small weed may have at least 120 such disease resistance genes. Not only can we now potentially recognise all the disease resistance genes in the plant, but we also know their exact location on the chromosomes and in relation to other genes. In the near term it is this positional information that could prove to be very useful for the production of new resistant varieties.

However, genomics not only gives us positional information but also allows us to study how all the genes in a plant are responding to stress, such as being attacked by a plant pathogen. When the environment of a plant changes it responds by turning some genes "off" and others ""on". Using advanced robotic techniques, all the genes in an organism can be placed on a glass slide, making a so-called gene chip or micro-array. Plants are then exposed to a stress and the messenger RNA molecules, that are produced by those genes that are turned "on" in response to the stress, are isolated. These are then labelled with fluorescent dyes and exposed to the gene chip. Genes that are being expressed will then fluoresce. By comparing samples isolated from stressed and non-stressed plants in this way it is possible to analyse how a plant is responding to a pathogen on a genomic scale. This will allow us to understand the integration of plant processes that lead to a resistance response and enable plants to resist pathogen attack. The final goal of such analyses is an integration of all plant processes so that we can select those plants that are best suited to the environments in which we require them to produce crops. The practical application of this type of process is more long term. However, it may be essential to the understanding of complex traits that are dependent on the joint expression of many genes. Such traits are called quantitative traits (QTs) and the position on the chromosome where a gene responsible is located (a locus) is called a quantitative trait locus (QTL).

HOW TO USE THE NEW INFORMATION

A major limitation in the use of resistance genes is the speed with which genes can be introduced from new plant sources. The genomic approaches will allow plant breeders to know the precise location of every disease resistance gene in their crop. This is not a trivial exercise but once achieved will be an invaluable resource of information. Plant breeders will have available for the first time the sequence of every resistance gene. This will allow them to follow two possible strategies to produce disease resistant crops. The first route would be to isolate the genes and use them to directly introduce resistance into desirable crop types using genetic modification, currently not an option for organics. However, the second route will allow many genes to be recombined into new and useful

combinations. The DNA sequences can be used as marker information for traditional plant breeding crosses. For instance, if you have a DNA marker that allows you to detect the presence of a particular resistance gene then a plant breeder would be able to screen directly for offspring that contain the gene. This will allow the breeder to discard all those that lack the gene without carrying out any pathology tests. This could be done at the seedling stage so eliminating the costly process of growing large plants and maintenance of the appropriate pathogen isolates. But this would not be limited to a single gene. Potentially, such a screening could be carried out for many genes and unique and desirable combinations of genes identified in seedlings. This could greatly aid the plant breeding process.

Having located the active genes the next challenge will be their effective deployment. Here there are several possible routes. In order to minimise the likelihood of a disease epidemic it is necessary to manage the deployment of effective resistance genes such that there is variety in the sources of resistance being used at any one time. This could be achieved by ensuring that neighbouring crops carry different resistance genes. However, this can be difficult to manage on a national scale. Alternatively, the genomic approach could allow for the pyramiding of many resistance genes into single varieties. This would make it less likely that any one disease could spread effectively. Another possibility is the idea of a single variety where the only genetic difference between plants is their resistance gene complement, such varieties have been called multi-lines. This would allow resistance gene variation within a field making it difficult for an individual pathogen to overcome all resistance in the crop. This could potentially be achieved by very complex plant selection during breeding using many DNA markers. However, is probably only realistic through a genetic modification approach.

Finally, it should become possible to integrate disease control measures to produce a 'resistant crop' phenotype. It is possible to imagine combining single gene resistances in plants that show quantitative partial resistance phenotypes, perhaps producing more durable resistance. Furthermore, other control measures such as biological control and management practices could be combined with genetics to prevent disease.

CONCLUSION

The new genomic sciences allow us to analyse plant gene function in ways and on a scale that was unimaginable only a few years ago. In the near term it will allow us to follow many genes in plant breeding and allow us to select for plant lines with the required genetic make up much more efficiently than in the past. Further into the future, genomics will reveal the interaction between the many genes present in plants that work together to produce required crop characteristics. Combinations of appropriate genes could then be compiled into varieties using very precise plant breeding techniques.

From: Powell et al. (eds), *UK Organic Research 2002: Proceedings of the COR Conference, 26-28th March 2002, Aberystwyth*, pp. 307-310.