Chapter 1
Introduction

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Abstract Climate change, coupled with the effects of population growth, excessive consumption, and environmental degradation, represents a challenge to future food security around the globe. To meet this challenge will require integrated approaches across the food system and in many other areas. Plant breeding is a central component of this response and has the potential to drive progress towards sustainable intensification. To do so effectively will require the judicious deployment of genomic tools, including DNA sequencing, allied with the focused utilization of germplasm diversity and precision high-throughput phenotyping.

1.1 Impact of Climate Change

The consequences of anthropogenic climate change are now being seen and have been predicted with greater or lesser degrees of certainty into the future. Global mean temperatures are increasing and precipitation patterns changing. The challenges facing the world have been enunciated many times over the past decade and include the concept of facing a "perfect storm" (Beddington 2009) in which concerns over food and water security and climate change, driven in part by population growth and exacerbated by environmental pressures and a decline in ecosystem services become more severe by 2030 and beyond. Such predictions have become statements of the consensus of opinion.

Increased environmental variability, for example in terms of increased frequency of episodes of environmental stress outside the range associated with adaptation, will have ecological significance. For example, interannual temperature variability is predicted to increase by 100 % for Central Europe by 2071–2100; with

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winter rainfall increasing and summer rainfall decreasing (Schär et al. 2004). Whilst water deficit is referred to frequently as an outcome of climate change, episodes of intense rainfall leading to flooding now occur more regularly in many countries and are likely to increase in frequency bringing other major challenges to national economies. In addition, prolonged summer droughts due to climate change will increase soil compaction and as a consequence will later increase opportunities for surface flooding.

1.2 Challenges to Food Production

The concept of "sustainable intensification" or "getting more with less" has become equally prevalent over this same period: the need to increase the production and productivity of agricultural systems whilst simultaneously ameliorating their impact on biodiversity, soil quality, air, and water pollution. At the present time more than one billion people are undernourished or malnourished.

Although food production per se is only part of the total "food system" and therefore an increase in food production can only be part of the answer to the need to increase food security, it is nonetheless likely to be an important part. Again, breeding of new crop varieties is only part of the chain through which improved varieties are utilized by farmers; other factors include agronomy and the farm system, the seed system, extension agencies, private sector dealers and the wider involvement of input and market supply chains. However, genetic improvement is a cornerstone of agricultural development as a central means by which research in genetics and genomics is translated to impact on farmers' fields.

The major challenges include:

1. Developing crops with improved drought tolerance and enhanced water use efficiency (WUE)
2. Improving tolerance of saline soils
3. Tolerance of floods and related consequences of changes in rainfall patterns
4. Increasing nutrient use efficiency and reducing pollution of water and air
5. Enhancing yield and guarding against losses from biotic and abiotic stresses

Drought is an important environmental factor limiting the productivity of crops worldwide. Climate change models predict greater variability in rainfall patterns and increased periods of summer drought will affect many regions. The growing demand for crops exhibiting greater drought tolerance and water use efficiency is reflected in the increasing emphasis on selection of varieties better able to tolerate prolonged periods of water deficit.

Problems of soil salinity are a major constraint to crop development in many drier areas of the world. In 1980, in excess of 3×10^6 ha of arable land were considered saline. This area has more than doubled in the past two decades (Malhotra and Blake 2005) and it is estimated that salinity in soil affects about 7 % of the land's surface. For many regions, the design of salt-tolerant crops is considered a priority. Unfortunately, there are only a few naturally occurring salt-tolerant higher plant species. Rising sea-levels, and increased wind speeds both, a likely consequence of climate change, will also induce more instances of coastal flooding and increased salinity and desiccation stresses affecting particularly low-lying locations and coastal areas found typically in the UK and elsewhere.

Detailed studies have illustrated the importance of rooting depth and the vertical variability of root function on soil water uptake. They have also highlighted that the porosity of soil should not be considered a fixed parameter, but is actually under the influence of the vegetation (Macleod et al. 2007). Recently there have been a number of laboratory studies published, which describe how roots do change soil hydraulic properties (Macleod et al. 2007). The studies have demonstrated a change to the water release characteristics, which tend to be associated with an increased number of larger pores in the rhizosphere and an increase in water repellence. This follows from the observation that root activity tends to increase the number of large pores at the root–soil interface. The generation of soil structure by roots has been widely reported in the literature and there is evidence that this phenomenon is influenced by plant species.

Although water stress is the most intensively researched physical stress to root growth, field data show that it may not always be the most critical. Various physical stresses may act in combination to limit root elongation. Hypoxia, water stress, and mechanical impedance to root growth will change with the water content of the soil and their relative importance will depend upon the degree of soil compaction.

Many of the world's ecosystems are characterized either by suboptimal nutrient availability, ion toxicities, or both (Lynch and St Clair 2004) and the majority of world agriculture is conducted with low fertility inputs on soils with poor availability of P and other nutrients. Whilst inherent nutrient use efficiencies may increase under elevated CO_2 (Drake et al. 1997), potential gains in net primary productivity may be limited by nutrient availability and/or uptake, both of which may be affected in contradictory ways, depending on the climate variable considered. The reduction in transpiration by C_3 plants under elevated CO_2 may reduce transpiration-driven mass flow of (mobile) nutrients such as Ca to roots. Conversely, the increased C allocation to below-ground processes, including root biomass, may have a positive impact on productivity depending on nutrient availability. The poor understanding of how many aspects of root morphology and function, including root architecture and exudation, are likely to respond to climate change means that the identification and selection of adaptive traits remains difficult. Furthermore, traits conferring adaptation to one stress may incur negative "trade-offs" with respect to other stresses (Lynch and St Clair 2004). This is particularly so for root adaptations. For example, low P induces alterations in root architecture that enhance top soil foraging (Lynch and Brown 2001), but may consequently result in greater susceptibility to drought stress (Ho et al. 2004). Likewise, increased specific root length may result in decreased root life-span (Eissenstat 1997).

Prioritization of breeding objectives is complicated by the gaps in our understanding of the range and magnitude of adaptations likely to be required as the impacts of climate change become more acute.

1.3 Promise of Genomics and Breeding

In recent years considerable gains have been made in our understanding of plant genome organization and gene expression. In large part this has been achieved through the study of "model species," i.e., species in which genetics and genomics are more tractable than in many crop plants. The best known and most developed of these models is *Arabidopsis thaliana*, the DNA sequence of which was published in 2000. Subsequently, a number of different model species have been developed and the number of crop species (e.g., rice, soybean) with sequenced genomes has also increased.

Progress in developing the resources, tools, and approaches to allow the more rapid development of improved crops has been significant in the last decade. These include not only genomics, transcriptomics, and metabolomics but also noninvasive dynamic high-throughput phenotyping (phenomics) and novel approaches to germplasm characterization and population development. At the heart of germplasm improvement are genetic resources, their collection, characterization, and utilization. Genetic resources offer a vast reservoir of important novel traits and allelic variation for traits. Increasingly genomics tools are being brought to bear on the variation collected in genebanks (McCouch et al. 2012). New approaches to selection are required to take full advantage of the pace at which new genomic knowledge is being acquired.

A range of genomics tools are now available in those species, which have been the subject of most study, particularly in maize but now increasingly in rice and other cereals. Progress in wheat has been slow due to the limited extent of genetic variation in the crop and its hexaploid nature but next-generation sequencing (NGS) approaches are changing this rapidly (Berkman et al. 2012). Genome sequencing with ever-increasing speed and reducing costs brings with it the potential for "genotyping by sequencing" which when allied with sophisticated statistical approaches is likely to allow the potential of genomewide selection (GWS) to be realized more effectively (Heffner et al. 2009).

Of course a major modern tool for the improvement of specific traits is genetic engineering. To date the importance of this technology has been widespread for a few traits in a small number of crops. Clearly genetic engineering has proven to be a controversial topic in some parts of the world and has engendered much debate ranging well beyond technical issues. However, the importance of regulation and intellectual property is pervasive in the area of modern plant breeding and not restricted to genetic engineering).

Modern breeding in both its genomics and phenomics components is increasingly data-rich. The role and importance of bioinformatics in integrating these data and converting them to usable knowledge has been emphasized greatly over the past 10–20 years and is now being reflected increasingly in public sector and commercial programs throughout the world.

There is an urgent need for increased public sector resources to be dedicated to the development of new varieties of crops for the tropics and subtropics. Genetic improvement approaches could be complemented by research to explore the potential of introduced species and ecotypes and allied with modeling of climate change scenarios to facilitate breeding targeted to the needs of regions most affected.

In many cases breeders seek improvements in yield and yield per unit of input. However, factors limiting yield are many and various and often these factors must be addressed directly in targeted approaches.

A major focus should be placed on water to develop climate-resilient crop varieties. Drought stress, water use efficiency, and root characteristics are important for interactions with soil including effects on flooding propensity.

Phenotypic selection for improved drought tolerance, or for yield under drought stress conditions, is widely accepted as difficult. Episodes of drought stress in natural environments are highly variable in their timing, duration, and severity, making it difficult to identify traits that confer a predictable advantage across stress environments (Passioura 1996). Direct selection for drought tolerance has been carried out in the field and indirect methods have also been used, but success has been limited. Where insufficient genetic variation is available to achieve any significant improvements in drought resistance from within a species, increasingly new allelic variants are being sought from wild relatives adapted to drier environments.

Many genes involved in plant adaptations to drought stress and desiccation-tolerance also confer improved salinity tolerance. New sources of salt tolerance are required as are more efficient techniques for identifying salt-tolerant germplasm so that new genes for salt tolerance can be introduced into crop cultivars. The mechanisms of salt tolerance remain poorly understood, despite salinity being studied in a range of glycophytic and halophytic plants. It is associated with a range of physiological adaptations, including ion compartmentation and the production of compatible solutes. Salt-tolerant plants may use vacuolar sodium storage and synthesize organic osmotic protectants including carbohydrates such as trehalose and fructans, and protein protectors such as glycine betaine and various compounds capable of scavenging reactive oxygen species like superoxide dismutase and glutathione peroxidase (Malhotra and Blake 2005). For legumes, an important consideration is the impact of salt on symbiotic nitrogen fixation. Free-living rhizobia are frequently more salt tolerant than their host, although the symbiotic process itself is sensitive to salinity. The transfer of gene(s) for salt tolerance into wheat following hybridization with the related (salt tolerant) species *Thinopyrum bessarabicum* (King et al. 1997) demonstrates the potential of introgression as a breeders' tool for transferring salt tolerance from wild into a crop species.

Water use efficiency, defined as the ratio between plant (usually shoot) production and transpiration is one measure of the ability of a plant to perform well under incipient drought. This can also be defined as the yield of product/water consumed. Condon et al. (2004) identified three key processes that can be exploited in breeding for higher water-use efficiency (1) moving more of the available water through the crop rather than it being wasted as evaporation from the soil surface or drainage beyond the root zone or being left behind in the root zone at harvest; (2) acquiring more carbon (biomass) in exchange for the water transpired by the crop; (3) partitioning more of the achieved biomass into the harvested product. These processes are not independent and targeting specific traits to improve one of the processes may have detrimental effects on the other two. Direct evaluation of WUE, which requires precise measurement of individual plant growth and water consumption, is not feasible in the field, making selection for WUE difficult within a breeding program. However, carbon isotope discrimination provides a robust, if indirect, method of identifying variation in WUE and is increasingly used in breeding programs (Rytter 2005).

In considering climate change adaptation and mitigation we need to remember that food security depends on more than arable and horticultural agriculture. Grasslands cover about 70 % of the world's agricultural area. They have a crucial role in terms of food production and in the delivery of ecosystem services such as water supplies, biodiversity, and carbon sequestration. For a number of years the potential importance of legumes in many agroecosystems, but also the limited extent to which this potential has been realized, has been recognized. Legumes do not just contribute in terms of food, feed, and fertility but are also important as fuel wood and with respect to carbon sequestration. However, their key attribute and a major reason why they are so important for the future of world agriculture is the nitrogen-fixing symbioses they form with nodulating bacteria. Genetic and genomic tools have been applied powerfully in recent years to understand the control of the legume–rhizobia interaction utilizing model legumes particularly *Medicago truncatula* and *Lotus japonicus* and the great challenge is to deploy this information in the improvement of the major grain and forage legumes. The importance of roots and root traits (size, architecture, interactions with soil, exudation etc.) has long been recognized but progress has been slow. However, genomics approaches allied to the development of noninvasive dynamic imaging techniques capable of phenotyping root traits brings significant new opportunities.

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