



Grain Yield Increase – a Role for Genetic Modification?

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The challenge

There appears to be a general lack of awareness regarding the menace of continuing population growth and of the magnitude of the challenge of attaining food security in the forthcoming decades. The population equivalent of about one Germany (ca. 80 Mio) is currently being added to the planet annually, this unavoidably leading to a global human population of ca. 10 billion by 2050-70 (Gerland *et al.*, 2014). Competing demands for agricultural products for non-food purposes exacerbate the situation. There is increasing demand for cereal grain and soybean for use as feed in livestock production, especially in countries with rapid economic growth that is accompanied by dietary change like, for instance, in China (Hansen and Gale, 2015). Additionally, substantial land is devoted to extensive oil palm plantations to satisfy diverse industrial demands. Additional competition for starch and vegetable oil relates to biofuel production: bioethanol and biodiesel. These three key forces – population growth, animal feed production, chemical raw material/energy production – are driving demand for agricultural products to unprecedented levels: numerous studies have shown that feeding a more populated and more prosperous world will require an approximate doubling of agricultural production by 2050 (Tilman *et al.*, 2011).

Under the constraints of limited resources like arable land, water and fertilizers, the unpredictable conditions of global climate change and the notoriously low investment in agricultural R&D, achieving this doubling within only 30-40 years is one of THE challenges of the century. Further intensification of existing land use and further wild land clearing for agriculture appear as the most likely measures to be taken, thus dramatically exacerbating the environmental impact of agriculture with fatal consequences on terrestrial and marine ecosystems that are highly threatened already. The current global yield increases of the main crops are around 1% annually, resulting in predicted 2050 supply shortfalls of 67%, 42%, 38% and 55% of maize, rice, wheat and soybean, respectively (Ray *et al.*, 2013). In light of this, truly game-changing solutions are required. The unbiased consideration of all possible avenues is mandatory to achieve sustainable food security for the coming generations. Among these is modern plant science.

Possible contribution from plant science

Plant science has contributed to food security in the past. The Green Revolution of the 1960s, as the most shining example, consisted of a bundle of improvements in agricultural practices which incorporated novel semi-dwarf wheat and rice varieties as an essential component. Such plant types strongly increased the harvest index (the proportion of a crop that can be harvested). The discovery and its implementation were recognized with the award of the Nobel Peace Prize in 1970 to Dr. Norman Borlaug. The Green Revolution achieved an approximate yield duplication which was much needed at the time. It is a further duplication that is required today. The question simply is: can it be done again?

Modern Plant Science has dramatically increased scientific knowledge and tools over the past decades. Breeding techniques that are based on DNA markers, the identification of quantitative trait loci (QTLs) that control desired traits and their combination through marker-assisted backcrossing, the possibility of identifying genomic regions of interest by investigating entire genomes in genome-wide association studies (GWAS), the availability of fully sequenced genomes, the ease of introducing targeted mutations into selected genes through CRISPR-Cas9 etc. have altogether revolutionized plant breeding. But have all of these methodologies delivered any accepted general strategies related to yield increase?

Yield is a highly complex trait that incorporates a plethora of biological components. Yield depends on literally all of the numerous physiological processes involved in plant development from seed germination to flower setting and grain filling. Plant architecture is another important yield component. Moreover, interaction with the environment, such as the plant's capability of coping with different soils, making use of fertilizers, and withstanding abiotic stresses such as drought, heat and cold, all contribute to yield. The genetically encoded capability of being more or less susceptible to the attack of pathogenic viruses, bacteria fungi and insects (biotic

stresses) add to the long list of yield determinants. Consequently, yield gain can be viewed in terms of loss avoidance to attain the crop plant's yield potential (Evans and Fischer 1993), defined as the yield that can be attained under optimal, non-limiting and controlled growth conditions. Given the many determinants, it is not surprising that the numerous publications on the genetics of crop yield, and the numerous QTLs determined across crop plants cannot provide any unifying and game-changing idea. Rather the whole issue is represented as being highly complex and there is general acceptance that – in essence – there is no single most important gene capable of controlling yield. Much more work would be required to decipher the underlying highly complex genetic and biochemical network. But this requires time that is not available.

It is however still possible to countenance single gene solutions for yield increase. As examples I call on the semi-dwarf wheat and rice varieties of the Green Revolution mentioned above. At the time, classical breeding was employed, where breeders did not need to know the genes (alleles) they were assembling. With today's knowledge, it can be stated that the spectacular yield improvements achieved were – in fact – based on single genes!

These so-called “green revolution genes” (see Hedden, 2003, for review) act on the pathway of the gibberellins, phytohormones controlling stem elongation. In rice, the responsible mutation affects the activity of GA 20-oxidase, an enzyme that catalyzes in the gibberellin biosynthetic pathway the conversion of a precursor molecule into the biologically active phytohormone. Semi-dwarf rice lines thus produce insufficient for normal stem elongation. In wheat, the gene affected is involved in the mode of action of gibberellin. Here, a signaling pathway leads from a gibberellin receptor to gibberellin-dependent gene expression and consequently, to stem elongation. In this pathway, the so-called DELLA proteins play a major role. Mutations in the wheat DELLA encoding genetic locus *Rht-1* cause partial insensitivity to gibberellin and reduced stem elongation. Thus, semi-dwarf wheat is partially “blind” for this phytohormone and does not respond sufficiently to the perfectly available phytohormone.

Transgenic single gene approaches to yield improvement

Transgenic solutions have already contributed substantially to yield improvement in terms of loss avoidance. They are essentially based on single gene types. Besides herbicide tolerant crops relying on bacterial herbicide-tolerant gene products that represent enzymes in important plant biochemical pathways or enzymes that inactivate the herbicide, there are the *Bacillus thuringiensis* insecticidal *cry* gene products that have revolutionized agriculture in many, but not all areas of the world (ISAAA 2016). As by 2016, the global area of biotech crops amounted to 185 million hectares with an approximately equal distribution between developing and industrial countries. These well-known biotech crops rank among the fastest adopted crop technologies in the world.

However, unlike loss avoidance to approximate the yield potential of a crop plant, other novel discoveries point to the possibility of increasing the maximum possible yield of crop plants (the potential yield), i.e. of increasing the physiological capacity to “produce more”. Some selected very recent examples shall be given.

The transformation of maize with the gene termed *PLASTOCHRON1* encoding a cytochrome P450 enzyme was shown to very significantly increase biomass and grain yield in maize, evidently by prolonging the proliferative phase of cells. The improvements were found in an inbred as well as in a panel of hybrids in the field (Sun *et al.*, 2017).

By increasing the effectiveness of photosynthetic dark reactions through expression of a gene from *Brachypodium* encoding the Calvin-Benson cycle enzyme sedoheptulose-1,7-bisphosphatase (SBPase), wheat grain yields could be increased by 30-40% in the greenhouse (Driever *et al.*, 2017).

A barley regulatory gene (SUSIBA2, a transcription factor), when transformed into rice under the control of a seed-specific promoter leads to the formation of longer panicles accommodating more filled grains together leading to a yield increase (expressed as g seed per plant) of +30% (Su *et al.*, 2015). The field-tested technology used confers a shift of carbon flux favoring the allocation of photosynthesis assimilates to above ground biomass, including seeds. Consequently, root exudates, the carbon source of methanogenic bacteria, are reduced. This leads to an up-to 10-fold reduction in the emission of the greenhouse gas methane. Rice paddies are the largest anthropogenic methane source with annual emissions of 25-100 million tons.

Fan *et al.* (2015) were able to increase rice yields by +40% in the field by expressing a gene coding for a variant of a nitrate transporter.

Own work (to be published) is based on the transformation of Golden Rice with an anti-apoptotic gene from *Arabidopsis*, *BAG4*, that is capable of attenuating a genetic program termed programmed cell death. We have found consistent yield increases over multiple generations in the greenhouse caused by larger and more grains on longer panicles, altogether giving a yield gain of +30%.

These examples are surprising: first by the diversity of the targeted biological processes, thus signaling a vast potential for yield improvement with single transgenes. Second, the magnitude of yield increases of 30-40% across all of these approaches is stunning, potentially a quantum leap, considering that a consistent increase of 3-5% per annum in the field would represent a more than welcome major achievement.

Discoveries have been made: what next?

These examples represent work done at public sector research institutions where scientists enjoy much room for curiosity- and hypothesis-driven work, with a high likeliness for serendipitous discoveries. In private sector research, the particular capacity is in turning discoveries into “useful” technologies. In the current regulatory environment, the costs for developing a transgenic crop plant from proof-of principle to the point where approval is granted and beyond, is in the tens of millions (Kalaitzandonakes *et al.*, 2007; Qaim, 2009), let alone the costs and capacities required for efficacy testing, marketing, and distribution. A typical public sector research grant is in the range of only a (very) few hundreds of thousands, maximally. Even conducting field trials or seeking IP protection – both necessary requirements to elicit the interest of industrial partners to cooperate – frequently represent unsurmountable hurdles. In this light, the published examples although potentially groundbreaking, of highest quality and holding great promise for the game-changing solutions required to achieve food security, run an equally great risk of remaining only interesting research results. The paths for developing GM crops, driven by political agendas, is cemented today and practicable for companies only. Can we really afford to reject from practical exploitation of such tax-payer funded discovery and knowledge? It is high time for a change. Opportunities can no longer be wasted in the light of the challenges ahead. Better funding and more capacity building in agricultural R&D can be a reasonable start.

“You better start swimming or you sink like a stone, for the times they are changing”(Bob Dylan, Nobel Prize in Literature Laureate, 2016.)

Citations

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