ENGINEERING CROP PLANTS TOWARDS IMPROVED PRODUCTIVITY: 
THE CRUCIAL STEP OF TRANSLATIONAL RESEARCH

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ABSTRACT

Plant sciences have made enormous progress in recent years. There has been a 
dramatic increase in our genetic understanding of plants opening up huge opportunities to 
improve crop plants for the benefit of society. The socio-economic mega-trends of a 
steadily growing world population, growing wealth, need for alternative feedstocks and 
climate change demand substantial investments into agriculture. However, we have to 
recognize that the research pipeline which transfers new knowledge into improved crop 
varieties is not functioning effectively yet. One major reason for this imbalance between 
knowledge accumulation and implementation is the suboptimal link between the 
academic plant science community and the agro-biotech industry. Both sectors have 
expertise in specific fields of research, e.g. academia in basic mechanisms and enabling 
technologies, industry in field testing and high-throughput genomics. Innovation 
therefore requires “Public-Private-Partnerships” with fair “win-win” research projects. 
Agro-biotech companies need to integrate more efficiently new technologies into their 
R&D pipeline which is a lengthy multi-step process from discovery to elite event 
selection.

Because of the plethora of technologies emerging from basic plant research highly 
reproducible testing of large numbers of individual plants is crucial in the selection 
process of elite events which enter the process of product development. Experimental 
parameter at all levels, i.e. environmental factors, plant material choice and data 
evaluation processes, have to be thoroughly defined to ensure a robust evaluation pipeline. 
In such a pipeline reproducible non-destructive phenotyping is a key technology.

Within Bayer BioScience the rules and requirements of translational research 
have been increasingly implemented in recent years. Especially in research programs on 
complex agronomic traits like yield, stress tolerance and nutrient use efficiency 
worldwide partnerships with leading academic institutions have very much fostered R&D 
progress. Outstanding examples are the elimination of harvest loss due to pod shattering 
in oilseed rape by knocking-out some alleles of the “indehiscence” gene or the 
improvement of energy use efficiency in several crops by silencing or over-expressing 
genes encoding components of the plant’s energy household, e.g. the PARP gene (“poly-
ADP ribose-polymerase” (Figure 1.). In those plants in which the expression of energy 
household genes has been modified transcription profiling revealed altered ABA 
signaling resulting in yield stability and stress tolerance in suboptimal growing conditions 
(Vanderauwera et al. 2007). Also plants in which energy loss has been reduced by 
dimming the process of photorespiration show increased biomass production and 
exended root growth.
PARP – A Key Player in Plant Stress Responses

Abiotic stress

Fig. 1. PARP ("poly-ADP ribose-polymerase") is a key player in plant stress response. The silencing of PARP results in the alteration of ABA signaling and maintenance of energy homeostasis in stress conditions.

The measurement of energy use efficiency in self-crossed populations of double-haploid isogenic oilseed rape lines with high or low energy use efficiency has revealed that certain crop traits are significantly controlled by epigenetic mechanisms (Figure 2.).

Isogenic Lines May Display Different Phenotypes

Energy use efficiency
Energy use efficiency
Energy use efficiency
Energy use efficiency
Energy use efficiency
Energy use efficiency
Energy use efficiency

Fig.2. Measurements of energy use efficiency in populations of self-crossed double haploid isogenic lines have revealed the importance of the epigenotype for the productivity of crops.

The genetically identical lines differ in genome-wide DNA methylation and histone acetylation and thereby show clearly distinct gene expression patterns (Hauben et al. 2010). Because of the complexity of these genome-wide epigenetic variations only systems biology approaches will reveal the underlying molecular gene networks. First microarray analyses identified co-regulated networks for genes related to photosystem II and the mitochondrial respiration pathway, again pathways clearly involved in the plant’s energy household.

In conclusion: To meet the challenges facing agriculture now and in near future we need to raise agricultural productivity with the help of improved crop varieties, plant biotechnology and innovative crop protection solutions. We need an effective translation of discoveries in academia into crops by building stable, long lasting Public-Private-Partnerships. Robust phenotyping strategies in model plants and in crops are essential to develop crops with improved yield and stress tolerance. Targeting the plant’s energy metabolism is a promising strategy for improving productivity of our major crops.

LITERATURE CITED
