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PLANT BREEDING AT THE ONSET OF THE 3RD MILLENIUM

INTRODUCTION

This paper focusses on the expectations and uncertainties commending on the future, considerations which are always open ended. How open may become clear when looking back to the last century, and asking which predictions one would have made 100 years ago. At that time the principles of classical plant breeding were just invented with the discovery of the Mendelian laws. Recombination, hybrid breeding or genomics were unknown words, showing how vague any statement is about the role of plant breeding at the onset of the third millenium. Classical and biotechnological breeding techniques rely on the production and use of variability followed by the selection of the better plant type.

Table 1
Yield of wild species of cereals (dt/ha) in areas of origin and yield development of cereals in Germany (altered from Geisler 1980).

Year	Wheat	Barley	Rye	Oats
8000 B.C. (wild species)	3	3	–	–
1300 – 1400	5	4	5	3
1500 – 1600	9	6	8	4
1800	10	8	9	6
1900	14	13	10	12
1950	26	24	22	22
1975	46	40	34	37
2000	73	58	49	46

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The big challenge of the scientific century just passed – more or less the life span of the Plant Breeding and Acclimatization Institute (IHAR) – was the discovery and the programmed use of the phenomenon of genetic recombination. Thus, the former simple selection was backed by recombination, and in parallel, breeding changed from traditional routes to a sophisticated industrialized process. It became possible to start the process of combination breeding in a scientific way and to predict the results of a logical crossing program. The yields increased dramatically (Table 1), a success causing today in parts of the world more a problem rather than admiration. To some extent plant breeders became victims of their success.

THE CLASSICAL BREEDING PROCESS

The speed of classical progress is different, guided by two main characteristics:

1. The fertilization system with a quicker development in inbreeders allowing pure line production, compared to a slower progress in outbreeders with population cultivars. (With the invention of hybrid breeding this problem of outbreeders was overcome.)
2. The immediate demands as, e.g., visible in oats (depending on the feed needs for horses).

Traits or genes up till the beginning of economic breeding projects part of nature owned by nobody, became a precious good sliding out of the public domain into the private sector. The breeding aims are identical: Yield, resistances, and quality (Table 2). The priority amongst them may change; presently the importance of quality is e.g. increasing while we do not emphasize yield but rather yield stability. This underlines already that a successful new variety has never to be better in only one trait; it is the result of the art to combine numerous useful genes in one genotype.

Since a higher plant contains 20000 to 30000 genes – showing the only relative value of a single gene, recombination is today and in the future the central process. Thus, the challenge in plant breeding is the optimal combination of many genes. Good luck, the “green thumb” of the breeder, are still important prerequisites for success in plant breeding. The question is whether increasing knowledge on the function of genetic material will help in offering reliable tools for a better combinations of the $\sim n^{20000}$ alleles (n = number of alleles per locus) in a better genome (Rommens and Kishore 2000). It should be stressed that even though there is a spectrum of new technologies, the present breeding progress documented by the annual licencing of better cultivars all over the world, is the result of classical breeding, and this will continue. Of course, progress in plant production demands also progress in agronomy, agrochemistry and breeding.

Table 2

Aims in modern breeding research with a priority of industrialized countries

Aims	Topics	Details
1. Improvement of quality	of primary compounds	starch sugars[1]
		fatts/oils[1]
		proteins[1]
	secondary metabolites	vitamines[1]
		aromas
		drugs
	new compounds	pharmaceuticals
		vaccines
2. Production of resistances	against diseases	viruses[1]
		bacteria[1]
		fungi
	against pests	insects[1]
	abiotic stress	shortage of water
		temperature
		salts
		gasses
	against herbicides[1]	
3. Yield improvements	increase of photosynthetic activity	
	increase in nutrient uptake efficiency	
	facilitating hybrid systems	
	better adaptation to temperature	
	improved metabolic transport	
4. Maintenance of biodiversity	in ecosystems	
	in variability of cultivars	
	in the genotypes	

Topics where an additional input from biotechnology is already a reality in existing cultivars are marked with [1]

It is good luck that new tools arose when the number of breeding aims and the need to produce more food from less land increased (Fig. 1). One powerful tool, biotechnology, is such an additional piece in the mosaic for crop production, recently increasingly coupled with sustainability, which aims according to the Rio Conference: economic prosperity, social security and ecological stability. However, biotechnology and genomics are an addition to classical techniques only, and will never replace them. Thus, a prerequisite for a successful modern plant breeding industry is the continuation with classical breeding allowing merchandising of biodiversity. It can be foreseen, however, that ultimately genomics will speed up and alter agricultural research and breeding resulting in a chain from a single isolated gene, via cell research, single phenotypes

and cultivars, processed crops, trade to the consumer, incorporating breeding as one process of agrobusiness.

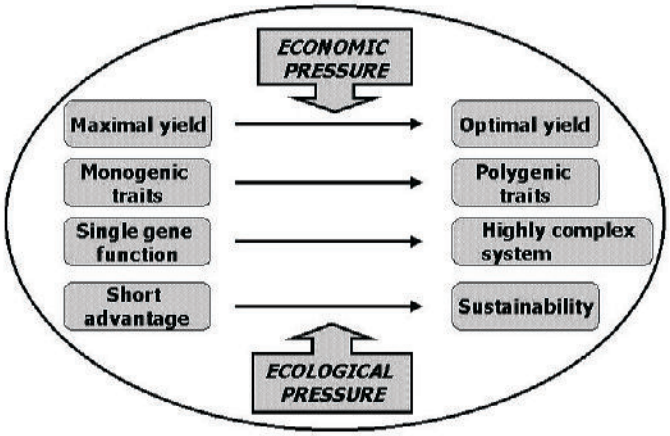

Fig. 1 Changing needs in breeding goals due to economic and ecological pressure

GENERAL CONSIDERATIONS IN USING NEW TOOLS

The expectations for the new millennium rely on further steady progress of the classical techniques but increasingly we expect new developments from processes summarized as biotechnology. There is as much hope as there is skepticism concerning the future contribution of biotechnology and its most advanced part: gene transfer. Biotechnology needs both tools, tissue culture and genomics and even genomics rely on tissue culture steps. The production of the first transgenic cultivars being now in the market was driven by available technical possibilities. The structural analysis and subsequently the functional gene analysis was much faster in bacteria, and in consequence it was easier to transfer genes identified in viruses and bacteria than those from higher plants. Now heavy research is going on in the functional analysis of higher plants to identifying enzymes, the field of proteomics. As soon as its regulation and the metabolisms is under control, the area of metanomics, an efficient improvement of existing cultivars will be the result, particularly in characters also of interest to the consumer with the consequence of an easier acceptance of new products. The possibility of converting our descriptive research field to a constructive one, using genomics, proteomics and metanomics increases the value of the genetic resources of higher plants as the principle source for desired genetic information.

Normally, selection is performed in the classical process at the whole plant level under field conditions. If clear markers or selection systems,

as e.g. selection against toxic compounds exist, the cell and tissue culture part of biotechnology might be helpful to achieve specific quality characteristics. Biotechnology allows to transfer this process into the test tube uncoupling it from the natural environmental variability. Since the environment can modify the desired characters, the reliability increased by transferring the selection process into the greenhouse or to the petri dish. This gain in reproducibility is, however, counterbalanced by the increased artificiality. So it is necessary to have at least a final field test after any biotechnological selection. The increased artificiality is probably one reason, why numerous lines or clones selected at the cell level, did not express this character under field conditions (Wenzel and Foroughi 1993). For future considerations *in vitro* selection is not a general way to go; there may be exceptions where this procedure pays but not too much should be invested into this ambiguous approach.

QUALITY

One of the key issues for farmers engaged in food production today is the difficult concept of quality, which is thought of as the sum total of physical characteristics embodied in the product. Shannon (1996) differentiates four categories of quality issue facing the producer and the customers: fitness for purpose, diet and health, safety and hygiene, and ethics and perceptions. At present the scientific community is not equipped to deal with the complicated situation of understanding the nutritional needs but first steps are done in the direction of functional foods, thus making breeding for quality a central goal.

Table 3

Some examples for the improvement of quality characteristics by gene transfer.

Transformed plant (example)	New quality	Foreign gene	Gene source
Potato	Biodegradable plastics		*Alcaligenes*
	Cyclodextrine	Cyclodextrin transferase	*Klebsiella*
	Increased cytochrom	Cytochrom oxidase	*Arabidopsis*
	Carbohydrates	Glucose–pyrophosphorylase	*E.coli or yeast*
	Serum albumine		*Homo sapiens*
Alfalfa	Improved protein	Chicken albumine	Chicken
Rape seed	More lauric acid	Lauric thioesterase	*Umbellularia*
	More stearic acid	Antisense desaturase	*Brassica*
	Encephaline	Chimeric gene	*Man / mouse*
Rice	Vitamine A	Carotine genes	*Narcissus*
	Allergene minus	Antisense	Rice
Barley	Heat–stable ß–amylase	Antisense	Barley

Strong emphasis has been placed on the main storage products, starch, oils, and proteins. One example for success in improving this quality, is the breakthrough of classical approaches in breeding of glucosinolate and erucic acid free rape seed (Röbbelen 1995). Due to a rather simple genetic bases and a very efficient selection system working on single seeds, the breeding process was very fast. In rape seed also via gene transfer substantial progress has been achieved, e.g. by transformation of ACP–thioestrases from *Umbellularia, Cuphea* and *Carthamus* as well as antisense desaturases altering the length of the fatty acids between C8 and C18 (Töpfer and Martini 1998). For starch its composition out of amylose and amylopectine could be altered by gene technology. For the processing industries, this saves an expensive separation step. Modifications of the aminoacid composition of proteins of plants were an aim in plant breeding since long. Particularly in mutation breeding programs, lysine rich cereals were of interest. Now the biotechnological production of higher amounts of essential amino acids in plants is possible. For extensive agricultural systems the idea to vaccinate animals via feeding is realistic. It should not be too difficult to incorporate genes which will produce chemicals active as a vaccine directly in the plant. Such approaches might be of interest under the economical and the ecological aspect. In Table 3 several possible modifications of plant quality are summarized.

RESISTANCES

Of particular interest for the ecological stability are genes giving resistance to biotic and abiotic stress. The incorporation of such genes is the most effective, economical and prophylactic means of plant protection. In the area of abiotic stress resistance the strategy is to influence physiological parameters or secondary products. Production of plants resistant to heat, frost or draught followed for quite a while mutation breeding procedures – actually with very limited success. In such mutants and natural occurring stress resistant genotypes often very similar proteins were detected. These similarities give hope for a more general basis of the different stresses.

Increase in genetical resistance is fast when the resistance is monogenic. For more complex resistances, oligo– or polygenic ones, the selection process needs rather large populations and several repetitions. For producing a new variety it would be ideal just to add to a superior cultivar one or a few missing traits. Although this can be achieved in principle by classical approaches, the big advantage is that with transfer procedures the existing optimized genotype is not destroyed by meiotic segregation during the necessary recombination processes. For gene transfer in principle the transfer procedures work, and thus today the crucial problems are no longer whether gene transfer will work but rather to isolate the responsible gene.

For the most important pathogens, the fungi, up till now progress in applying molecular procedures is rather slow. As a first central step in the direction of identifying resistance genes, a rapidly increasing number of monogenic, race specific genes showing a gene for gene interaction have been mapped (e.g. Wenzel 1998). Besides the race specific genes, an increasing number of quantitatively inherited genes (QTLs) are localized (Lübberstedt *et al.* 2001). One strategy for the isolation of disease resistance genes exploits the observation that many resistance genes isolated in one plant species share similar sequences or represent members of comprehensive and wide spread gene families (Bent 1996), allowing increasingly an *in silico* analysis via bioinformatics (review Thümmler and Wenzel 2000).

In plants biological processes such as growth or defense against biotic or abiotic stress are mediated by distinct programs of differential gene expression. The molecular structure of simple monogenic characters is increasingly understood (Young 2000). For disease resistances (fungi, bacteria and viruses) most genes code for a limited number of similar proteins involved in the signal transduction chain with transmembrane activity (leucine rich repeats, e.g., Meyers *et al*. 2000), another hint for a functional and local similarity is given; in addition these genes are arranged in gene clusters (Meyers *et al.* 2000). The identification of the subset of genes differentially expressed under certain growth conditions will facilitate the breeding of resistant crops. To steadily identify low abundance transcripts, which often code for important regulatory proteins like receptor proteins, enzymes involved in signal transduction or transcription factors, an enrichment procedure for such transcripts has to be applied. A number of enrichment techniques have been described of which representational difference analysis (RDA) has the ability to efficiently reduce the number of constitutively and abundantly expressed genes (Hubank and Schatz 1994). To gain comprehensive insight into gene function rapidly, subtracted cDNA libraries enriched for differentially and rarely expressed genes can be prepared by using suppression subtraction hybridization (SSH). In addition, SSH has the potential to facilitate the identification of genes which may not be detected by high–density expression profiling.

MARKER AIDED SELECTION

The availability of recombinant DNA techniques together with advances in molecular biology and cell culture provides access to a refined understanding of the genome. A systematic molecular analysis of the structure and function of plant genomes will be essential for future developments in plant science and its applied wing: breeding. The increasing amount of information about the DNA documented in molecular marker collections and in dense gene maps together with an excellent bioinformation system allows increasingly calculations about

the structure and function of genes. Particularly under the aspect of synteny comparisons will be possible, probably elucidating common principles. The identification of gene function will result in the identifi–cation of candidate genes which can be used for the improvement of crop plants, e.g. in breeding for resistance to biotic and abiotic stress. Tools helping to improving selection are of great immediate importance. And thus DNA probes, can be used as markers for the identification of genes responsible for traits of interest. Presently the most powerful applica–tion of such identified genes and molecular markers is opened up by marker aided selection (MAS). Such an identification of resistance genes needs, however, always the coupling with a dificile analysis of the genome of the corresponding pathogen. This is of particular importance when uniform monogenic traits are used. Coupled to uniformity is al–ways the danger of the rapid selection of new virulences in the pathogen populations. The epidemiology of the corresponding pathogens has to be monitored very carefully (Felsenstein 1995). Today, also for the descrip–tion of the ecotypes of the pathogens DNA–markers can be used.

Mapping monogenic traits is easier than mapping oligo– or polygenic ones, however, crops exist which have a more complex genome like the hexaploid wheat. Chromosomal location of markers is an essential step for genotyping. For *Triticum aestivum* "Chinese Spring" Huang *et al.* (2000a) used 256 primer combinations with the AFLP technique in nulli–tetrasomic stocks. The chromosome and arm assignment of AFLP markers provided a valuable tool for anchoring unknown linkage groups in chromosomes from experimental wheat crosses involving gene bank samples. Similar approaches were applied for mapping the *Pm 24* locus by bulked segregant analysis in an F_2 progeny from the cross Chinese Spring (susceptible to powdery mildew) × Chiyacao (resistant). An allele of a microsatellite locus located *2.4cM* from *Pm24* was shown to be diag–nostic and therefore potentially useful for pyramiding two or more genes for powdery mildew resistance in a single genotype (Huang *et al.* 2000b). Integration of molecular markers indicated that *Pm17* lies between the *Lr 26* and *Sec–1* locus, with both resistance genes allocated distally to the *Sec 1* locus in the satellite of the 1RS arm (Hsam *et al.* 2000). Using this information it was possible to combine three Pm genes in one line which is now under variety test, hoping that such a pyramided resis–tance will be more durable (Wenzel *et al.* 2001).

Most of such probes are only detecting monogenic traits. An increas–ing interest exists, elaborating probes form oligo– or polygenic charac–ters. A clear reproducible correlation between probes and polygenic, quantitative traits (QTLs) would result in a tremendous improvement of breeding programs.

QTL

Recently the available genome data on QTL were analysed, to find out whether they are randomly distributed over the genome, or whether clusters exist (Lübberstedt *et al*. 2001). Since resistance genes often build clusters, it might be possible that in QTL clusters at least several quantitative loci are close or very close to qualitative ones and form functional units, comparable with the operon structure in microorganisms. Such an information simplifies the task to find qualitative and quantitative loci responsible for disease resistance and give additional hints about the basis of complex gene functions. It further would have consequences for plant breeding: To recombine tightly linked alleles demands large populations and very tightly linked markers. A successful combination will result, however, in a very powerful complex character. Otherwise – randomly distributed genes – may be combined easily but their stability is lower. For barley the data evaluation suggests such clustering of resistance genes with QTLs (Fig. 2). While for maize the situation points in a different direction. Thus in barley, the localization of gene clusters might be conserved across species and allows transfer of information by use of syntenic relationships.

Random distribution of QRL as indicated for maize would require genome–wide approaches such as QTL mapping or expression profiling for QRL identification. Markers need to be developed for a larger number of genome regions compared to clustered QRL. Combination of favourable QRL alleles should, however, be comparatively easier.

A detailed understanding of relationship between genomic organisation and function of QTL requires complete sequence information as well as detailed functional studies using new approaches like genomics, proteomics and metanomics. For large–genome grasses accumulation of these data can be expected for the next 1 – 2 decades. This general question on the relationship of genome organisation and the function of genetic material will become even more complex for traits like yield.

YIELD IMPROVEMENTS

The final and most economic aim in crop production is yield, a polygenic trait. To select and produce cultivars combining several polygenic traits is the most difficult part of plant breeding. The strategy of hybrid production offers a way to combine at least complex characteristics from two parents. This is true for sexual hybrids as well as for somatic cell fusion products in vegetatively propagated crops like potato. Presently, no strategies exist, however, to transfer QTLs via gene technology. The combination of complex characters became possible by somatic hybridization. Particularly, in vegetatively propagated crops cell fusion is the most efficient way to combine not only qualitatively inher–

Chr.	BINs[a]															
	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16
1(7H)	*Ml(2) Sr, Nb*	*Fs*	*Sb Fs(2)*	*Rh, Sb*	*Ml*		*Ml, Nb Ls*			*Ml*	*BYDV*					
2(2H)			*Lr(2) Ls*	*Lr, Nb Ls*	*Nb, Lr Fs*						*Fs*		*Ml*		*Ml, Rh Fs*	
3(3H)		*Bls, Nb Fs(2)*				*Nb, Fs*		*Bls*	*Nb*			*Nb*	*Nb, Fs Yr*		*Rh*	*Fs, Rh*
4(4H)	*Ls*	*BYDV*		*Fs(2)*	*Ml, Nb*	*Ml(2) Nb(2)*	*Lr*	*Ml, Sr Rh, Nb Fs*		*Ml, Yr(2)*	*BYDV*					
5(5H)		*Ml Yr(2)*	*Ml*	*Ml*		*Sb, Fs*	*Ml, Sb*	*Nb*	*BYDV*			*Fs(2)*				
6(6H)		*Ml*		*Yr*		*Ml, Lr Rh Nb(3)*	*Nb*	*Fs(2)*								
7(5H)			*Ml, Fs*	*Ml(2) Fs, Nb*	*Ml*		*Yr*		*Yr*	*Lr, Nb*	*Ml*	*Ml*	*Ml*		*Ml(2)*	

Fig. 2. Distribution of disease resistance QTLs in the barley genome subdivided by the BIN method (Kleinhofs *et al.* 1998).
[a] White BINs contain no major genes, grey ones only one, and black BINs contain at least three genes responsible for resistance. The resistances mapped are against: *Erysiphe graminis (Ml); Puccinia hordei (Lr); P. graminis (Sr); P. striiformis (Yr); Rhynchosporium secalis (Rh); Pyrenophora teres (Nb) Py.graminea (Ls); Cochliobolus sativus (Sb)* and *Fusarium sp* (Fs) (Lübberstedt *et al.* 2001)

ited traits but also quantitative ones. This works already in potato, where besides virus resistances (Thach *et al.* 1993) also more complex traits as the non–monogenic resistance to *Phytophthora* could be combined in somatic hybrids (Möllers *et al.* 1994).

In a somatic hybrid population even transgressions were found to both sides: Less resistant as well as higher resistant to this fungus. Additionally, cell fusion was a successful procedure to rapidly incorporate cytoplasmic factors. Thus, gene combination does not hold true only for the genes of the nuclear genome but also for the plasmon (Lössl *et al.* 1999). Plastids may belong to different groups and thus different genome/plastome combinations can be selected after fusion. In the mitochondria this effect is even higher, since recombination and mixing of the mt–genomes take place. Some recombinations are better yielding than hybrids with the parental mitochondria. This possibility of the production of new cytoplasms is not restricted to vegetatively propagated plants; somatic hybridisation offers this approach in the future also for sexually propagated crops.

The somatic fusion allowed in the presence of nearly isogenic nuclear genomes the estimation of the contribution of mt genomes to starch production. Evaluation of cytoplasmic types lead to the conclusion that in starch content the types from non tuberosum *Solanum* species have a significant advantage to the tuberosum type cytoplasm.. In somatic hybrids an interaction between starch content and different mt–plastid combinations could be found. During the *in vitro* phase a selection for optimised organellar segregation took place (Lössl *et al*. 2000).

BIODIVERSITY

The more successful a newly bred cultivar expands, the less other cultivars can keep their areas. Moreover, leading cultivars are often closely related. A narrowing of the genetic basis is expected. Actually, uniformity is an essential prerequisite for registering a cultivar at seed boards. To check whether the fear of increased loss of biodiversity by this higher breeding speed is correct, in our institut Benedikte Hatz compared by the use of molecular markers the gene basis of more than 200 accessions of barley. Using 50 DNA–probes in a wide range of different barley varieties, land races and lines reaching from wild varieties till cultivars, she could demonstrate that although phenotypic variability is lost, the genotypic variability is not narrowed. Comparing the similarity of the DNA composition by measuring genetic distances, it became evident that newer and older types do not form any clear–cut genetic clusters. The danger that genetic variability is lost due to the selection process is not as large as anticipated.

SOME ADDITIONAL BREEDING AIMS

Speaking about the future, some additional topics should be mentioned, where modern plant breeding might contribute to the improvement of abiotic parameters. The physiological and genetical control of day length as well as genes involved in the vernalization process are increasingly understood. Getting possibilities in hand, to gear these processes, e.g. by increasing the efficiency of temperature dependent enzymes in countries with cold climates and doing the opposite in countries with hot climates will surely result in tremendous increase in plant production. A similar effect will be opened up by circumventing the day length dependence for many developmental processes of flowers or fruits. A further system for yield improvement will be the transfer of those genes responsible for the C3 or C4 carbohydrate cycle. Particularly for the warmer climates of tropical and subtropical countries such an alteration from the C3 to the C4 circle would pay with a striking yield increase. Of course also other improvements of the photosynthetic activity will help. Work along this line is in progress by altering the photosensory perception and signal transduction via modified phytochrome B contents (Quail *et al.* 1995).

Plants always interact with soil ions and microorganisms. One central goal in breeding is: selection of low input varieties by improving the metabolic transport processes, and uptake of water and solved minerals. This uptake is partly an active one which is assumed to be under genetical control. After an understanding of the responsible processes it should become possible to influence this system positively by means of combination breeding and gene transfer.

CONCLUSIONS

Table 4 summarizes the different goals and techniques mentioned in this article. It is demonstrated where advantages over the classical process are expected and to what extent. Such an evaluation is of particular importance when assuming that investments into biotechnology should be driven by demands and needs rather that by the available technology. Since we have to admit, however, that the coming up of technologies – the invention and discoveries – cannot be planned. Thus biotechnology is one option which will help to improve crop protection and thus making yields more secure.

Before starting such biotechnological breeding activities, it should be checked, however, carefully whether it is cheaper, and/or faster, securer, more durable or not less sustainable than classical approaches. It would probably be a waste of time and money, if it is used just because it is more fashionable. If the use is done in the right manner, it is expected that the incorporation of biotechnology and in particular of DNA technologies will be the most efficient way to combine economic and ecologi–

Table 4.

Summary of biotechnological techniques and a subjective calculation on their expenses and advantages compared with the classical approach

Goal	Procedure					
	Classic	Rapid propagation	Somatic fusion	Haploids	Marker selection	Gene transfer
Quality	++	+++	++	++	+++	+++
			Resistance			
–disease	+++	+++	++	++	+++	++
–pest	+	+ –	+ –	+ –	+ –	+++
–stress	++	+ –	+ –	+ –	+ –	+
–herbicide	+ –	+ –	+ –	+ –	+ –	+++
			Yield			
–temperature	–	–	–	–	+	++
–hybrids	+++	–	++	+ –	+ –	+
–C3–C4	–	–	–	–	–	+
–low input	+ –	+ –	+ –	+ –	+	+ –

cal aims. Even the most intelligent approach may fail when regulations restrict this development; it will also fail, however, when light–minded strategies create problems which are difficult to overcome. Thus, it is necessary that world wide adopted regulations for the release of bio–technological modified plants are accepted. When making such regula–tions one should keep in mind, that classical breeding combines by chance in an unpredictable way two complete genomes while gene transfer works with identified DNA–pieces. The reproduction of all thinkable ecological problems into biotechnological procedures is, how–ever, not an intelligent way to go. To understand more and more how genetics and biology work, to direct in an anthropocentric manner its direction – particularly under the aspect of sustainability – is the big–gest challenge at the onset of the 3rd Millennium. Due to the high costs which have to be invested for isolation and due to the rule that precious things have their price, patenting is a fair way for protection. Anyone keeping patented gene collections should, however, be obliged to give licences. A clever usage of genes in gene banks is one of the best paying strategies to win the battle against stress, pests and diseases.

Uncovering genes and their structure and function relies also on good classical genetics and phenotypic characterizations. A fruitful coopera–tion between classical and molecular genetics is the way to go. All suc–cessful crop varieties are selected for specific traits, but up till now without knowing their exact molecular function. Since this strategy has already been quite successful, it can be expected that after understand–ing, e.g., the gene function of resistance genes, man has for the first time the chance, to be more efficient in plant protection than the concurring trial and error approach of pathogens.

Only by new ideas the natural evolution can be turned into an anthropocentric direction that helps man to survive. This was and is the motivation for today's and forthcoming plant breeding. With increasing understanding of the genetic basis of breeding – and the most advanced one is the combination of genomics, proteomics and metanomics – genetic resources harbouring such genes are gaining more and more importance. Probably each new cultivar will be polished with several transgenes. This means, however, that the vast majority of the genes will still be brought together by recombination and consequently progress in plant breeding in the new Millennium demands both a powerful classical program and progress in genomics (Fig. 3).

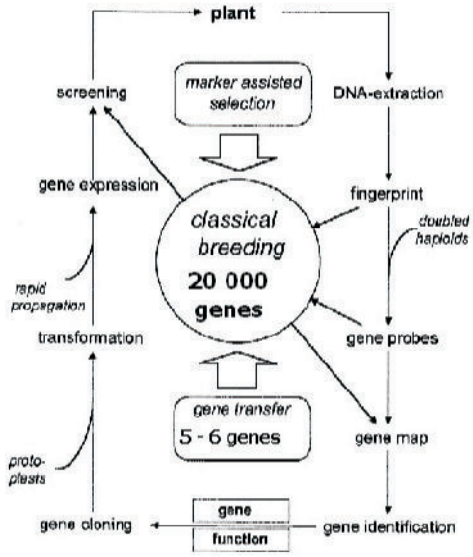

Fig. 3 Combination of classical approaches and new molecular techniques; only a useful combination will bring success

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