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NEW SOURCES OF GERMPLASM: LINES, TRANSGENES, AND BREEDERS

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INTRODUCTION

There have been many claims that plant breeding would be radically altered by genetic engineering and genetic erosion. There is little doubt that both will affect breeding procedures in the long term; their short term effects are probably minor. A more relevant and immediate concern is the lack of newly-trained Ph.D.s with hands-on experience in plant breeding. Neither public nor private institutions seem to have yet recognized this dilemma or its potential impact. Several important institutions that historically trained many plant breeders have all but abandoned plant breeding education. Fewer than a half-dozen maize breeding Ph.D.s are produced each year in the US and even fewer in Europe. Many administrators, private and public, have decided that the future of plant breeding lies in genomics, relying on claims that molecular genetics has revolutionized the time frame for product development. 'Seldom has it been pointed out that it is going to take as long to breed a molecular engineering gene into a successful cultivar as it takes for a natural gene' (Bingham, 1983, p. 223). Additionally, claims often suggest simple solutions to very complex problems ('Agricultural biotechnology is already having an impact' [on starvation!]; Theil, 2001). Such claims are often made with little knowledge of the problems of selecting germplasm, conducting multiple year/location performance trials, genotype x environment interactions or even the concept of epistasis - that an allele may have different effects in different genetic backgrounds. The surprising point is that these claims are often accepted at face value by upper management of seed companies whose breeders certainly know that the claims of quick solutions are highly unlikely to reach farmers' fields for well over a decade. 'The public must be cautioned that the simplest advances take, on average, 10 years from inception of breeding effort to placement on the farm in quantity' (Duvick, 1982, p. 583). All breeding organizations have experience with 'new' sources of germplasm and know that deployment is slow, difficult, but, on rare occasions, highly rewarding. With adequate long-term investment, however, new elite, germplasm can yield unique and productive hybrids. *The time needed to place a new transgene into a commercial hybrid is approximately the same as moving a new source of tropical germplasm into a commercial US hybrid.* The relative advantages and issues associated with the two approaches vary, but the relative financial costs are clearly very different.

PLANT BREEDING Ph.D.s

A recent survey by Wehner et. al. (2002) indicates that the trend in training new plant breeding Ph.D.s is down, with a total in all agronomic and horticultural crops being about 60 per year at the turn of the 21st century (Table 1). Note that many of these Ph.D.s are laboratory trained rather than field oriented (note the high numbers in Table 2 for Cornell, Wisconsin, and Minnesota, for example, all with very strong laboratory emphases). Currently, there are about a half-dozen open industrial positions in maize breeding and several public ones, and virtually no recent maize breeding graduates are available. All new positions in plant breeding essentially require cross-training - both classical genetics and plant breeding as well as basic molecular genetics. Once employed, application of molecular training is minimal for most Ph.D.s. engaged in field breeding.

TRANSGENE UTILIZATION

Bacillus thuringiensis (*Bt*) was used as an insecticide by the 1950s. The first gene encoding the *Bt* toxin was cloned by 1981 (Schnepf and Whiteley, 1981). *Bt* gene regulation was known by 1986 (Whiteley and Schnepf, 1986). *Bt* was transformed into maize in 1990 (Koziel et al., 1993). *Bt* hybrids were first sold in 1997. Because *Bt* was a well-known entity with a long history of use as an 'organic' insecticide, little (essentially no) toxicity and allergenicity testing were required for its initial use as a transgene. Even so, its transgenic use took 16 years. *Even with a cloned gene that was functionally well*

Table 1. US Ph.D.s in plant breeding from 1995 to 2000

	US	INTERNATIONAL	TOTAL
1995-1996	52	87	139
1997-1998	52	77	129
1999-2000	42	79	121
TOTAL	146	243	389

Table 2. US universities prominant in plant breeding Ph.D.s from 1995 to 2000.

	US	INTERNATIONAL	TOTAL
All Universities	146	243	389
Cornell	18	27	45
Wisconsin	22	16	38
North Carolina State	7	26	33
Nebraska	5	27	32
Minnesota	16	13	29
Texas A&M	9	18	27
Iowa State	13	12	25
Oregon State	4	16	20
Michigan State	10	8	18

characterized, with a gene product that had been studied, accepted, and used for decades, and with essentially no toxicity-testing and no proof-of-function needed, it still took over 10 years to get a product to market.

GERMPLASM UTILIZATION

In 1975, a small, all-tropical maize breeding project began at N.C. State. In 1990, NC296, a temperate-adapted, all-tropical line was released. NC296 has been used for production in at least 3 countries, including the U.S. Its development required 15 years. Its actual deployment took an additional 5 or so years.

While these events are not exactly comparable for several reasons, they are not unrepresentative of the minimum lengths of time needed for development and agronomic testing prior to sales. Obviously, training new plant breeding Ph.D.s is faster; provided the faculty, facilities, and budgets exist, none of which is assured in today's era of big bucks - and big claims - biotechnology.

INTEGRATION OF BREEDING WITH PLANT MOLECULAR BIOLOGY

Breeding progress continues to increase yield at a rate of 1% to 2% per year, with additional gains made for disease resistance, earlier maturity, improved standability, and improved production efficiency. This is best documented in maize, a crop that does not have the quality requirements that appear to restrict the annual yield gains in crops such as wheat. Vegetable crops show similar gains in yield and harvestability. Virtually all of this progress is due to the utilization of polygenic factors not readily handled by currently-available molecular procedures. Thus, there is likely to be little contribution of molecular genetics to routine breeding practices until this limitation is overcome.

Currently in place and in development are several simply-inherited qualitative traits such as *Bt*-insect control, several herbicide resistances, various virus resistances, and new sources of a passable equivalent of cytoplasmic male sterility.

What is actually needed by plant breeders? Traits that plant breeders can only manipulate with difficulty or traits that are currently unavailable. These include such obvious, but difficult, traits as drought tolerance, fungal-toxin (aflotoxins, fusomonins) resistance, salt tolerance, heat tolerance, and general environmental stability.

Basically, there is a 15-year lag time between gene discovery and seed sales to farmers. This time lag is roughly the same as the timeframe needed to incorporate a new germplasm source into a commercial product. It is unlikely that this lag can be reduced, but political events could effectively increase it, especially in Europe. Thus, any new developments in molecular genetics must promise a 20 - 30% improvement in yield or offer a useful, novel trait without reducing yield or they are unlikely to survive the 15+ year development curve.

In addition, some realism needs to accompany proposed modifications in seed characteristics. Clearly, there are benefits to be gained from eliminating unhealthy or quality-degrading oils from soybean or palm. It is far from clear that increasing oil or protein content in maize will be beneficial. No crop is an island unto itself. Food or rations containing oil or protein from legumes, starches from grains, and vitamins from vegetable crops probably make more economic sense than a maize crop with 10% oil, a completely balanced amino acid ratio, and additional vitamin Z. If there were no other problem with such a maize crop, there would soon develop some fungal species - probably one producing a toxin - that would find such maize to its liking.

Let's look at what is required to move a newly sequenced gene into a commercial product.

1. Promotor selection and testing.
2. Allele sequence modification.
3. Numerous transformation events.

4. Laboratory and greenhouse testing.
5. Backcrossing into elite lines.
6. Production of experimental hybrids or varieties.
7. 3 years of small-plot field trials at numerous sites.
8. 2 years of larger, "strip" trials at many locations.

(If # 7 and # 8 are not done adequately, better have good lawyers or deep pockets, should the product not satisfy some segment of the public. Given the current US political and economic climate, even another case as innocuous as the Star-Link episode could lead to federal detention as a criminal, rather than merely a civil, offense).

9. Production of commercial quantities of seed.
10. Sale to farmers.

Costs of this range from as low as 5 million to in excess of 60 million US dollars. This compares to the generally accepted, approximate cost of development a useful new inbred line by conventional means of 1 million US dollars.

Thus, commercial development of a single gene is roughly 50 times as costly as the development of a commercial inbred by conventional breeding. While a very successful inbred might be used in 25% of the US hybrid seed sold (and additional seed sales in Europe and Asia), a very successful transgene might be used in 50% of the seeds sold, potentially reducing the relative cost to about 25X.

This is a formidable barrier, as *Bt* seems to have been sold at just about the break-even point for the farmer, at about 30% of seed cost. It is unlikely that any combination of transgenes now on the horizon could greatly increase this premium while farmers are selling maize for US $2/bushel. Thus, in maize, it appears that the potential transgenic premium for ALL transgenes is about 20 - 30% of total maize seed sales or about $45 million US dollars per year. Yet, several individual companies invested well over $100 million each in *Bt* development alone, and even today it is not completely clear who owns *Bt* in maize. Certainly, it is not the woman (Helen Whiteley) whose lifework laid the scientific groundwork for *Bt*'s use as a transgene - she died a few months before she would have almost certainly been elected to the National Academy of Sciences and received little recognition from the general public for her work.

Table 3. Steps generally necessary to complete before final yield trials can be conducted.

New Germplasm	Transgene
1. Choice of source	1. Discovery
2. F_1 cross	2. Modification
3. F_2	3. Efficacy testing
4. F_2S_1	4. Transformation of model species
5. F_2S_2	5. Construct comparison
6. F_2S_3	6. Maize transformation
7. F_2S_4	7. Backcross (BC_1 to BC_6-equivalent) into best lines

There are several factors often overlooked by those of us who are out to save the world. Perhaps foremost among them is that the world often doesn't want to be saved.

Vices seldom disappear.

Food preferences are hard to change (northern Asians prefer japonica rices, southern Asians like indica rices; neither are apt to accept "golden" rice very readily; few seem to like high lysine maize - despite its scientific success, it has largely been an economic failure).

Transgenes are effectively site mutations and generally carry slightly deleterious

effects (about 8% on average, if tobacco data can be extrapolated to

other crops - Wernsman, personal communication).

Interactions of transgenes with other loci of importance cannot be ignored. Epistasis exists.

What are the most serious barriers to integrating plant molecular biology with plant breeding?

1. Complete Ph.D. training in both plant breeding and molecular biology is not feasible. Both require almost 3 years of coursework plus apprenticeship, and no one advisor can cover both fields.
2. It is humanly impossible for a university professor to carry out both a creditable plant breeding program and a creditable molecular biology program. This would be true even if constant grant-writing were not job # 1.
3. Either molecularly-trained Ph.D.'s will have to postdoc with plant breeders - an unlikely scenario -
4. Or plant breeding Ph.D.s will have to post-doc in molecular labs - also unlikely as there is a severe shortage of plant breeding Ph.D.s, most of whom have full-time employment offers by the time they finish prelims.
5. More likely, plant breeding Ph.D.s will take some basic molecular genetics coursework and have some minimal lab experience.

In fact, any molecularly-engineered trait of clear economic use will be rapidly utilized by plant breeders. What is lacking at present is an array of useful transgenic traits. The easy and obvious ones have been implemented. At the moment, the pipeline of molecularly-engineered traits appears to be largely empty. (*Bt* for maize rootworms is still knocking about, but it has few companions). Indeed, the

question can be asked, does the pipeline exist or do we just have random bits of pipe strewn about, with rather little organization?

There is little doubt that plants (and animals) will be used to produce certain chemicals and pharmaceuticals, but this is apt to be on a horticultural scale, rather than a broad-based agricultural effort. There is considerable need for fungal and bacterial protection of crop plants *a la Bt* for certain lepidopterous insects. Worldwide, the greatest problem that needs to be solved for most food- and feed-crops is post-harvest protection against insects and vermin. That would solve far more problems than adding carotene to rice or lysine to maize.

It is simply untrue that a new transgenic can be routinely created, tested, and deployed within a decade (Goodman and Carson, 2000). Table 4 lists the procedures needed, prior to yield testing, for exotic- and transgene-containing lines, while Table 5 lists the times required for these steps and outlines additional procedures necessary prior to commercialization.

Table 4. Elapsed time prior to yield trials and minimum field-testing procedures.

New Germplasm	**Transgene**
7 seasons	Minimum = 7 seasons
What Remains?	
New Germplasm:	**Transgenic:**
Small plot trials	Experimental Use Filing
Strip trials	Small plot trials
Production	USDA/EPA/APHIS/FDA Clearances
Sales	Strip trials
	Production
	Sales

Minimum Agronomic Testing Required for Any New Line
(Standard, Exotic or Transgenic)

3 years of small plot trials, usually on several testers
2 years of strip tests, usually in hybrids with two or more lines

For especially promising materials, these may be compressed into 4 years of trials.

Table 5. Total time required before sales can safely begin.

New Germplasm:
12 Seasons, 9 of which must be summer.

Transgene:
16 Seasons, 6 of which must be summer.

Conclusion:
Both approaches require 10 years minimum, if no complications are encountered.

Only the naive would promise commercial production of hybrids containing a truly new transgene or a new source of exotic germplasm within a decade (Table 6). A more realistic assessment of the time from isolation and sequencing of a truly new, potentially useful transgene until it might realistically reach farmers' fields is about 15 years, **if** no unforeseen delays occur. Many of the reasons are listed in Table 4, which deals with the scientific procedures required; political and social problems may cause *much* additional delay. The current procedures have been nicely summarized by Feitshans (2000), but changes are very likely after the StarLink episode. Note that one more herbicide-resistance gene or one more *Bt* gene does not meet the definition of truly new.

Table 7 presents the relative costs for development of an exotic line vs. a transgenic line. For consistency, the following assumptions are made throughout this paper:

Nursery plots cost $20 each {regardless of season}.

Yield trial plots cost $10 each.

Strip trial plots cost $50 each.

Specific to Table 7, choice of exotic source was based on the cost of an expert consultant @ $2000/day for one week. The discovery cost of a truly-useful transgene was (greatly under-) estimated as a once-in-ten-year event by a $100,000/year postdoc or equivalent {salary & lab costs}. Modification costs were on the same basis for one year. Efficacy testing, transformation of model species, construct

Table 6. Why must a new transgene require more than a decade for deployment?

1. Gene product expression must be optimized
2. Multiple constructs must be developed, transformed, and tested (often in *E. coli*, tobacco or *Arabidopsis*).
3. Toxicity/allergen testing must be done.
4. Six seasons of backcrossing (the potential exists to reduce this to 3 by Marker Assisted Selection) to various elite lines must be completed, accompanied by performance trials of lines on a *per se* basis.
5. Various USDA/EPA/APHIS and perhaps FDA regulatory hurdles must be overcome. (Allow a minimum of 1 year, if non controversial; 5 years *minimum* otherwise - remember Star-Link).
6. If customer satisfaction is to be protected and legal liabilities minimized, standard and customary product testing must follow prior to sales. (This means 3 years of multiple-location, small plot trials of each potential transgenic hybrid and two years of widespread strip trials).

Table 7. Relative costs of development of an exotic line vs. a transgenic line.

	EXOTIC	TRANSGENIC
Choice of Source/Discovery	14,000	1,000,000
Breeding/Modification	38,000	100,000
Efficacy Testing		50,000
Transformation of Model Species		50,000
Construct Comparisons		50,000
Maize Transformation		50,000
Backcrossing		1,200
TOTAL COSTS	**52,000**	**1,301,200**

comparisons, and maize transformation were estimated at six months each. It was assumed that 5 elite lines would be backcrossed, carrying two 'reps' as insurance for each line. Breeding development with the exotic was assumed to require 20 F_2 plots, 50 F_2S_1 plots, and 250 plots per year for subsequent breeding generations (S_2, S_3, S_4), as well as 5% of a breeder's effort for four years (4 x $5,000 = $20,000). The cost prior to yield trials is estimated to be over $1.3 million per transgene vs. about $52,000 for an exotic, a ratio of about 25X. An additional $150,000 would need to be allotted for the Experimental Use Filing and the EPA/APHIS/FDA clearances (and these latter costs are probably much under-estimated), raising the cost ratio to about 28X. Note that no attempt has been made to estimate the costs of administration, supervision, plant variety protection, patents, or costs of access to germplasm or licenses for genetic-engineering tools and procedures. All of these have costs and restrictions well beyond the scope of this discussion. Note that the only estimates available for the development of *Bt* for maize prior to its deployment are inferred from glittering generalities; on those bases, private industry invested over 150 million on *Bt*, mostly by Monsanto, Mycogen, and Novartis - still, that is a fraction of the average $500 million cost of a new human medicine (Zall, 2001). Maunder (personal communication) estimates the total research cost for *Bt* in maize and cotton to be $800 million, contrasting it to greenbug-resistance breeding in sorghum which cost $6 to 8 million; total initial acreage for greenbug-resistant sorghum was 4 million, while initial *Bt* acreage was only 1.6 million. Currently, estimated minimum cost-to-market for a transgene in tobacco (the most readily genetically engineered crop plant) is thought to be about 10 million US dollars (Wernsman, personal communication). These figures differ substantially from the customary figure of 1 million US dollars for total cost of a new, useful conventionally-bred maize inbred.

The costs in Table 7 do not cover all the ancillary costs included in such sweeping generalizations, but there clearly is a very different level of investment required for successful transgenic development than for germplasm development. Not the least of these is that germplasm development uses the same equipment, facilities, and analyses as does conventional breeding, so that new infrastructure costs are low. Not only are molecular biology costs high on a day-to-day basis, but the initial equipment/building costs are high, and the facilities themselves (and the Ph.D.s who use them) are often instantaneously out-of-date. Nor do the biotech costs in Table 7 cover the numerous (and increasing) indirect costs implicitly passed on to seed producers (Hoegemeyer, 2000).

Another factor that sometimes seems to be overlooked is the possibility that one person's once-in-10-years biotech discovery may trail someone else's equivalent discovery made in only 9 years. This is not so unlikely, because most biotech labs (just like most maize breeding organizations) are working on the same sorts of projects using very similar materials and techniques. There are several possible consequences of being second or third in the biotech discovery race; most are not pleasant. In the worst case, an organization may not even be able to use its own product. On the other hand, unique germplasm belongs to its developer, if the starting materials were legitimate. A new B73 x B37 derivative can be protected, despite its very public background; it need not even be patented or have Plant Variety Protection; contracts and trade secrets are usually sufficient.

The molecular biology costs in Table 7 are clearly underestimated in one very important way - the assumption that a post-doctoral equivalent will discover a highly useful new gene once in 10 years. If that were so, we would be swamped with new transgenes for there have been hundreds, if not thousands, of such researchers diligently searching for some applicable use for their skills for the past 25 years and our net result so far has been several *Bt*, herbicide-resistant, virus-resistant, and male-sterility transgenes. And thus far in maize, only *Bt* seems to have had much consequence. Thus, the discovery estimate is probably too low by a factor of at least 10, based on the ratio of plant molecular biology postdocs to transgenes in use or in early stages of field experimentation.

Is Marker-assisted Selection (MAS) an alternative to transgenics? Studies by Beavis (1994), Openshaw and Frascaroli (1998), and Bernardo (2001) strongly suggest that MAS is only effective under specific circumstances:

1. Few genes (perhaps as few as 5 - 10).

2. Large effects (on the order of 10%/locus).
3. High heritability (low heritability can work, but be prepared to gather lots of very good data).

The direct costs are often in the hundreds of thousands of US dollars per cross evaluated. For those who are interested in the discouraging details, see Goodman and Carson (2000). MAS is sometimes used to reduce the number of backcross generations needed to develop 'isogenic' recoveries of elite lines. Under ideal conditions (100+ markers, backcross populations of 1,000s), as few as 3 backcross generations may be needed, but be prepared for many additional field trials with the resulting backcross 'inbreds' and the expenditure of several hundred thousand extra US dollars per project.

There are few obvious cases where Marker-Assisted Selection is currently more efficient than phenotypic selection. Most such cases involve sporadic diseases that are not easy to study or not easy to study in the U.S. Several that qualify are common and southern rusts, maize streak virus from Africa, downy mildew from Asia, and Rio Quarto virus from Argentina. Under most circumstances, yield and traits such as drought-resistance would not qualify, due to low heritabilities and difficulties in acquiring adequate field data on early-generation segregates.

New sources of germplasm can provide yield increases and added protection against the largely unknown dangers of a too-narrow germplasm base. Tables 8, 9 and 10 list those 50%-tropical GEM materials that are competitive with commercial checks after two years of multiple location trials. These families clearly represent new sources of germplasm for the US. The GEM families that are tested from N.C. State are derived from elite, fully-tropical materials (either exceptional germplasm accessions, tropical hybrids, or tropical inbreds) crossed to elite, temperate, private inbreds provided by cooperating private companies. Virtually all companies with breeding programs of consequence participate. These "breeding crosses" are selfed and the resulting families are topcrossed (as S_1s, S_2s, or S_3s) to standard foundation-seed testers of the appropriate heterotic group. By testing in multiple environments, it is clear that some of the families tested are competitive, but several questions have yet to be seriously addressed by GEM:

1. Performance of topcrosses of S_1, S_2, and S_3 families (and hence selection of lines to advance) can be seriously affected by sample size used to generate the topcross family (Goodman, 2001).
2. Can inbred lines be selected directly from 50%-temperate/50%-tropical germplasm, when the tropical source represents germplasm accessions which have no history of inbreeding, hence no elimination of deleterious recessive alleles? How about 75%-temperate, 25%-tropical lines from these same sorts of populations? (The inbreds of the 1930s, derived from U.S. open-pollinated sources would never survive nursery selection today, and inbreds from never-before-selfed materials may have the same sorts of problems - for a summary see Crow, 1998).

The F_2S_2 entries from Tables 8, 9, and 10 should be released in the coming year. Those lines with fewer generations of inbreeding have been selfed and retested, often on a second tester. If F_2S_2 lines from those entries continue to be competitive with check hybrids, they will be released in the future.

It is important to note that not only the relative expense, but also the likelihood of success and the ultimate impacts must be weighed in plant breeding investments. It is often not clear that a new transgene is superior in ultimate impact to a potential new breeding source. Has the introduction of *Bt* been of equivalent historical importance to hybrid maize as the release of such important inbreds as Wf9, Oh43 or B73? (or FR1064 or LH185, for more recent examples).

The data in Tables 11 and 12 demonstrate quite clearly that an investment in "new" germplasm can have a substantial effect on productivity. It is possible that some of the yield advantages in Tables 11 and 12 for the temperate-adapted, tropical lines crossed onto commercial hybrids (relative to the commercial hybrids *per se*) resulted from plant height differences. The NC296, NC296A, and NC346 crosses with commercial hybrids averaged about 16 cm or 6 inches taller than the hybrids themselves. (In Table 13, the height differences were half those in Tables 11 and 12). On the other hand, the crosses all carried the Ga^S allele from the temperate-adapted, tropical inbreds, and could only accept a fraction of the pollen available in the yield-trial fields. In addition, the B73*Ht*.Mo17*Ht* x NC296 hybrid has been grown in strip trials, where height advantages are minimal, at Andrews, NC, by Ed and Keith Wood, who had noted its yield potential and gray leaf spot resistance. It out-yielded all the commercial and pre-commercial hybrids tested (Table 14), including several of those in Tables 11 and 12.

It should be emphasized that few breeding sources, tropical or temperate, present such clear-cut yield contributions as NC296 and NC346. Most US maize breeders would concur with Troyer (1999) that domestic elite x elite crosses are the foundation for all serious US maize breeding. Indeed, in most US maize breeding programs, 'foreign' breeding sources (including unfamiliar domestic sources) receive little attention and cursory testing.

Table 8. Best 50%-tropical GEM family topcrosses - Second year/2nd tester N.C. State 2001

PEDIGREE	YIELD Mt/ha	% H_2O	% EP	
EXC8 PE1 N16 F1S4 x LH132.195				
C001-003	10.1	18.8	93.9	(Cr1-044)
Check mean	9.7	19.0	91.9	
C.V.	13.0	5.4	10.0	18 Env.
DK687	10.2	18.6	93.8	
LH132.51	9.1	18.1	90.5	
LH200.62	10.0	19.1	89.8	
N8811	8.8	20.6	90.8	
P3165	9.6	21.0	95.5	
P32K61	10.1	18.1	93.2	
P33G26	9.7	17.5	86.5	
EXD1 DK212T DKXL380 N11 F2S2 x LH132.195				
1507-001	10.3	19.4	94.2	(7431-03)
Check mean	10.1	18.3	97.7	
C.V.	11.4	5.1	4.6	17 Env.
DK687	10.4	18.2	98.5	
LH132.51	9.6	17.5	95.9	
LH200.62	10.6	18.3	96.5	
N63-G7	9.6	15.3	99.3	
N8811	10.0	20.5	98.7	
P3165	9.7	20.4	96.8	
P32K61	10.8	17.7	98.7	
P33G26	9.8	16.9	98.0	
EXD3 DK888 S11b F1S1 x FR697.615				
1367-001	9.7	19.8	94.5	
Check mean	9.5	18.9	95.0	
C.V.	11.7	4.1	5.7	19 Env.
DK687	10.2	18.7	96.2	
DK697	10.2	20.0	94.0	
LH132.51	8.7	18.2	93.1	
LH200.62	9.5	19.3	95.4	
N63-G7	8.8	15.4	95.7	
N8811	9.2	20.9	92.5	
P3165	8.9	21.0	93.9	
P32K61	10.1	18.0	97.6	
P33G26	9.8	17.2	95.4	
EXD5 DK888 N11 F2S2 x LH132.195				
1776-001	10.1	22.4	95.4	(7451-27)
1778-002	10.2	21.7	95.7	(7451-27)
1780-001	10.5	21.3	93.3	(7451-27)
9365-001	10.3	20.1	94.2	(7451-22)
9366-005	10.0	20.5	99.5	(7451-22)
9367-001	10.4	20.5	95.9	(7451-22)
9367-003	10.1	20.3	97.7	(7451-22)
9367-005	10.0	20.2	99.1	(7451-22)
9375-001	10.3	21.5	97.6	(7451-27)
9378-001	10.1	21.3	98.5	(7451-27)
EXD5 DK888 N11 F2S2 x LH132.195				
9378-001	10.4	20.0	96.2	(7451-27)
Check mean	10.1	19.5	95.7	
C.V.	10.8	5.5	6.8	16 Env.
AS897	9.5	18.7	96.6	
DK687	10.2	19.2	97.7	
DK697	10.9	20.0	89.2	
LH132.51	9.1	18.7	96.9	
LH200.62	10.7	19.6	96.4	
N8811	9.8	21.8	95.7	
P3165	9.5	21.1	97.5	
P3223	10.8	18.5	96.9	
P32K61	10.5	18.5	93.7	
P33G26	10.2	17.8	97.2	

Checks used are listed just below C.V. values for each experiment.

N = Non-Stiff Stalk cross; S = Stiff Stalk cross.

Two-digit number following N or S is company code.

PEDIGREE	YIELD Mt/ha	% H_2O	% EP	
EXD7 DKXL380 N11 F2S2 x LH132.195				
1930-002	10.0	18.8	97.5	(7541-15)
Check mean	10.1	18.7	95.1	
C.V.	11.4	4.8	7.7	17 Env.
DK687	10.5	18.6	97.0	
LH132.51	9.6	17.8	90.2	
LH200.62	10.5	18.6	93.9	
N8811	9.7	21.1	98.2	
P3165	9.4	20.5	91.4	
P3223	10.3	17.6	90.3	
P32K61	10.9	17.8	97.9	
P33G26	10.1	17.2	99.2	
EXE4 CHIS740 S14 F1S2 x FR697.615				
161-7W97	10.0	20.6	94.1	
362-6C98	9.7	19.4	95.1	
Check mean	9.7	19.3	94.4	
C.V.	12.5	5.0	5.1	14 Env.
AS897	9.0	18.4	93.2	
DK679	10.5	19.7	95.0	
DK687	9.8	19.0	94.3	
DK689	10.0	19.7	93.7	
DK697	10.2	20.0	94.3	
LH132.51	8.8	18.3	95.8	
LH200.62	10.3	19.3	95.6	
N8811	9.3	21.6	92.2	
P3165	8.7	21.1	92.6	
P31G98	11.4	18.4	95.2	
P3223	10.2	18.6	95.1	
P32K61	9.5	18.4	94.3	
Uniform Tests of Better F2S3 Bulks, Several Testers				
EX67 Best F2S3 Bulks x NC258.OH43E				
B2283-01	11.3	18.7	97.8	DKXL380 S11
AS897	10.7	16.9	91.2	
DK687	10.6	17.9	98.4	
DK697	13.5	19.6	98.3	
LH132.51	10.9	16.4	89.8	
LH200.62	12.3	18.3	97.8	
P3165	10.4	20.8	97.6	
P3223	12.5	17.1	94.5	
P32K61	11.1	17.6	99.7	
Check mean	11.5	18.0	95.8	
C.V.	11.1	4.5	7.8	(7 locations)
EX68 Best F2S3 Bulks x FR697.615 or LH132.195				
B2120-01	10.9	21.1	97.6	DK888 S11
B2143-02	10.6	19.2	98.6	DK888 S11
B2283-01	10.5	18.9	98.1	DKXL380 S11
BCr1-044	11.0	18.9	100.0	PE1 N16
EX68 Best F2S3 Bulks x FR697.615 or LH132.195				
DK687	11.0	18.8	99.5	
LH132.51	9.8	18.0	95.7	
P3165	10.1	21.0	99.6	
P32K61	10.8	17.9	100.0	
Check mean	10.4	18.9	98.7	
C.V.	10.8	5.1	6.5	(9 locations)
EX69 Best F2S3 Bulks x LH287, LH200, or LH244				
B2011-01	11.4	17.8	97.9	SE32 S17 x LH287
B2088-01	11.1	18.2	97.6	DK212T S11 x LH287
B2111-01	10.7	18.8	97.6	DK212T S11 x LH287
B2116-02	11.4	19.3	97.2	DK212T S11 x LH287
B2120-01	12.3	20.2	94.7	DK888 S11 x LH287
B2121-04	11.4	20.3	98.7	DK888 S11 x LH287
B2127-01	11.0	19.0	97.1	DK888 S11 x LH287
B2131-01	11.1	20.7	93.8	DK888 S11 x LH287
B2143-02	11.8	18.8	98.1	DK888 S11 x LH287
B2146-01	11.2	21.0	96.2	DK888 S11 x LH287
B2152-02	11.2	18.8	95.8	DK888 S11 x LH287
B2152-03	11.3	19.1	89.8	DK888 S11 x LH287
B2226-02	11.7	16.9	95.1	XL370A S11 x LH287
B2282-01	10.6	19.0	98.7	XL380 S11 x LH287
B2283-01	11.5	18.8	96.4	XL380 S11 x LH287
BCr1-705	10.8	17.6	98.6	PE1 N16 x LH244
BCr1-044	10.7	17.9	97.3	PE1 N16 x LH200
DK687	11.0	18.9	99.2	
LH132.5	10.1	18.5	91.2	
LH200.62	11.6	19.2	99.6	
P3165	10.4	20.8	98.6	
P32K61	10.4	18.0	97.2	
Check mean	10.7	19.0	97.1	
C.V.	11.1	4.7	8.4	(9 locations)

Table 9. Best GEM F2S3 Bulks Topcrossed onto Several Testers - 2001 Data, N.C. State

Entry	YIELD	H_2O	EP	YIELD	H_2O	EP	YIELD	H_2O	EP	YIELD	H_2O	EP	YIELD	H_2O	EP	Source
	NC258 x OH43E Tester			FR697 x FR615 Tester			LH287 Tester			LH185Bt Tester			LS Means Across Tester			
B2011-01	10.0	18.0	98.2	10.0	18.5	93.6	11.4	17.8	97.9	13.3	20.1	100.0	11.2	18.6	97.4	SE32 S17
B2084-02	10.5	17.9	99.2	10.5	18.0	95.6	11.0	17.6	92.9	12.4	18.6	100.0	11.1	18.0	96.9	DK212T S11
B2086-01	10.5	19.9	97.2	9.7	20.6	91.9	9.6	19.5	93.6	12.8	20.5	100.0	10.6	20.1	95.7	DK212T S11
B2088-01	10.1	18.8	96.1	10.3	18.7	95.3	11.1	18.2	97.6	12.6	19.2	100.0	11.0	18.7	97.2	DK212T S11
B2089-01	9.5	18.4	96.6	10.0	18.9	97.9	10.1	18.6	94.5	12.3	19.5	100.0	10.5	18.8	97.2	DK212T S11
B2109-01	9.6	18.6	94.0	9.5	19.1	97.2	11.0	19.6	90.9	11.1	19.6	92.7	10.3	19.2	93.7	DK212T S11
B2111-01	10.4	18.3	92.1	10.2	19.7	97.0	10.7	18.8	97.6	11.8	19.3	100.0	10.8	19.0	96.7	DK212T S11
B2112-02	10.3	18.2	98.2	9.2	18.7	93.9	10.5	18.4	94.6	11.2	18.6	100.0	10.3	18.5	96.7	DK212T S11
B2116-02	9.8	19.0	98.1	9.7	19.4	98.0	11.4	19.3	97.2	11.6	19.6	100.0	10.6	19.3	98.3	DK212T S11
B2120-01	11.1	20.5	96.2	10.8	21.1	97.6	12.3	20.2	94.7	13.6	20.7	97.7	12.0	20.6	96.5	DK888 S11
B2121-04	10.8	20.2	97.9	8.9	21.3	96.6	11.4	20.3	98.7	13.2	20.5	100.0	11.1	20.6	98.3	DK888 S11
B2127-01	10.1	18.8	90.9	9.9	19.0	97.8	11.0	19.0	97.1	12.8	20.2	85.2	10.9	19.3	92.7	DK888 S11
B2131-01	9.4	20.2	97.0	9.7	21.5	98.4	11.1	20.7	93.8	13.5	20.5	99.7	10.9	20.7	97.2	DK888 S11
B2132-03	10.6	19.0	95.9	9.7	19.9	99.0	11.2	19.5	85.9	11.9	20.7	100.0	10.9	19.8	95.2	DK888 S11
B2142-01	10.3	19.3	100.0	9.4	19.8	98.7	11.0	19.6	91.0	11.8	19.7	100.0	10.6	19.6	97.4	DK888 S11
B2143-02	10.5	18.8	96.5	10.6	19.2	98.6	11.8	18.8	98.1	12.3	20.1	100.0	11.3	19.3	98.3	DK888 S11
B2146-01	9.7	21.2	97.5	10.0	22.0	95.1	11.2	21.0	96.2	13.3	20.8	99.5	11.1	21.3	97.1	DK888 S11
B2150-01	10.7	20.2	96.7	9.9	20.2	92.9	10.6	19.8	94.8	12.0	21.2	99.5	10.9	20.3	96.0	DK888 S11
B2152-02	10.3	18.6	91.8	10.1	19.0	96.4	11.2	18.8	95.8	12.0	19.6	100.0	10.9	19.0	96.0	DK888 S11
B2152-03	10.6	17.9	94.2	10.3	18.4	95.8	11.3	19.1	89.8	11.7	19.5	99.8	11.0	18.7	94.9	DK888 S11
B2156-02	.	.	.	9.8	19.6	95.1	10.3	19.7	97.1	11.1	20.1	99.5	10.2	19.7	97.0	DK888 S11
B2201-01	10.2	18.4	97.1	9.7	18.9	94.6	10.8	18.0	93.0	12.1	18.9	99.8	10.7	18.5	96.1	DKB830 S11
B2226-02	10.7	18.2	88.1	9.9	18.5	90.9	11.7	16.9	95.1	12.8	18.9	100.0	11.2	18.1	93.5	XL370A S11
B2228-03	10.2	18.9	95.0	10.5	18.6	95.0	10.5	18.5	95.7	11.7	19.3	99.0	10.7	18.8	96.2	XL370A S11
B2250-01	10.5	18.0	95.4	10.0	18.2	99.2	10.7	17.3	90.3	11.6	19.0	100.0	10.7	18.1	96.2	XL370A S11
B2250-02	10.4	18.0	99.7	10.0	17.9	99.4	10.7	17.2	96.3	11.2	18.5	100.0	10.6	17.9	98.9	XL370A S11
B2253-01	9.7	17.1	97.9	9.6	18.9	95.2	10.0	17.1	94.8	12.0	19.1	99.5	10.3	18.1	96.9	XL370A S11
B2258-03	9.3	18.1	97.8	9.7	18.2	99.4	9.9	17.8	98.8	10.4	19.1	100.0	9.8	18.3	99.0	XL380 S11
B2282-01	10.2	18.8	98.6	10.1	19.5	99.8	10.6	19.0	98.7	12.3	20.0	100.0	10.8	19.3	99.3	XL380 S11
B2283-01	11.3	18.7	97.8	10.5	18.9	98.1	11.5	18.8	96.4	12.9	20.0	99.3	11.6	19.1	97.9	XL380 S11
BCr1-044	11.3	18.2	97.8	10.3	18.0	96.8	10.2	18.0	94.9	10.7	17.9	97.3	11.0	18.2	97.6	PE1 N16
BCr1-181	10.5	19.7	95.6	9.4	19.5	99.0	10.4	19.5	98.2	.	.	.	10.5	19.7	98.4	PE1 N16
BCr1-239	9.2	19.0	97.6	9.6	19.0	99.7	10.1	18.1	99.8	9.4	18.7	99.6	9.9	18.9	100.1	PE1 N16
BCr1-705	10.2	18.4	94.3	9.8	17.8	95.6	10.8	17.6	98.6	.	.	.	10.7	18.1	96.9	PE1 N16
AS897	10.7	16.9	91.2	.	.	.	.	.	.	.	.	.	11.2	17.3	91.9	
DK687	10.6	17.9	98.4	11.0	18.8	99.5	11.0	18.9	99.2	.	.	.	11.3	18.7	99.8	
DK697	13.5	19.6	98.3	.	.	.	.	.	.	.	.	.	13.0	20.0	99.0	
LH132.51	10.9	16.4	89.8	9.8	18.0	95.7	10.1	18.5	91.2	.	.	.	10.7	17.8	93.0	
LH200.62	12.3	18.3	97.8	.	.	.	11.6	19.2	99.6	.	.	.	12.2	19.1	99.8	
P3165	10.4	20.8	97.6	10.1	21.0	99.6	10.4	20.8	98.6	.	.	.	10.8	21.0	99.4	
P3223	12.5	17.1	94.5	.	.	.	.	.	.	.	.	.	13.0	17.4	95.2	
P32K61	11.1	17.6	99.7	10.8	17.9	100.0	10.4	18.0	97.2	.	.	.	11.2	18.0	99.8	
1064.185Bt	.	.	.	.	.	.	.	.	.	10.6	18.3	100.0	9.3	17.7	97.6	
198.185Bt	.	.	.	.	.	.	.	.	.	10.8	17.6	100.0	9.4	17.1	97.6	
200.185Bt	.	.	.	.	.	.	.	.	.	11.7	21.1	100.0	10.3	20.6	97.6	
CHECK MEAN	11.5	18.0	95.8	10.4	18.9	98.7	10.7	19.0	97.12	11.0	19.0	100.0	11.1	18.7	97.7	
C.V.	11.1	4.5	7.8	10.8	5.1	6.5	11.1	4.8	8.4	8.8	3.6	4.0	4.6	2.2	2.6	
	7 Locations			9 Locations			9 Locations			6 Locations						

Table 10. Best 50%-Tropical GEM F2S2 Families from 2000 with Alternate Testers - 2001 Data, N.C. State

	LH244 Tester			LH195 Tester			LS Means Across Testers			
7 Locations Entry	YIELD Mt/ha	% H_2O	% EP	YIELD Mt/ha	% H_2O	% EP	YIELD Mt/ha	% H_2O	% EP	
9111-4	10.0	21.2	86.4	10.4	22.0	96.7	10.2	21.6	91.6	SCRGP3 N14
9131-4	11.4	21.2	92.4	11.3	22.4	88.0	11.4	21.9	90.6	SCRGP3 N14
9244-1	10.5	20.0	92.6	9.3	21.5	98.0	9.9	20.8	95.3	DK212T N11
9353-1	11.9	21.5	93.0	10.7	22.9	97.6	11.3	22.2	95.3	DK888 N11
9509-2	.	.	.	10.2	22.6	98.7	10.5	22.1	96.9	XL370A N11
9527-1	10.7	20.7	89.9	9.5	22.1	95.7	10.1	21.4	92.8	XL380 N11
9531-2	10.5	20.8	94.9	10.2	21.6	96.7	10.4	21.2	95.8	XL380 N11
9532-2	10.3	21.1	89.3	10.0	21.8	92.4	10.1	21.5	90.9	XL380 N11
	LH283 Tester									
1415-1	9.9	21.7	93.4	.	.	.	9.9	21.7	93.4	DK888 S11
1415-6	10.3	23.1	91.1	.	.	.	10.3	23.1	91.1	DK888 S11
P31G98	12.2	20.8	98.6	12.2	20.8	98.6	12.2	20.8	98.6	
P33G26	10.7	20.4	97.4	10.6	20.4	97.4	10.7	20.4	97.4	
P33P66	11.4	20.6	93.7	11.4	20.6	93.7	11.4	20.6	93.7	
Check mean	11.5	20.6	96.6	11.5	20.6	96.6	11.5	20.6	96.6	
C.V.	12.4	5.1	9.1	11.6	3.9	8.7	4.4	1.1	3.6	

Best 50%-Tropical F2S2 Families from 2000 with LH185Bt as tester

6 Locations Pedigree	YIELD Mt/ha	% H_2O	% EP	
1415-1	12.6	20.9	100.0	DK888 S11
1415-6	12.8	22.6	96.7	DK888 S11
FR1064.LH185Bt	10.6	18.3	100.0	
LH198.LH185Bt	10.8	17.6	100.0	
LH200Bt.LH262	11.7	21.1	100.0	
Check mean	11.0	19.0	100.0	
C.V.	11.7	4.7	3.7	

Table 11. NC296A topcrosses vs. commercial hybrids. 3 Yr., 8 Env.

	Commercial Hybrid			NC296A x Commercial-Hybrid Cross		
	YIELD Mt/ha	% H_2O	% EP	YIELD Mt/ha	% H_2O	% EP
B73*Ht*.Mo17*Ht*	7.5	16.1	92	9.5	18.0	83
Dekalb 689	8.8	18.0	91	8.2	19.3	82
LH132 x LH82	7.1	16.8	97	9.1	18.0	89
NK N8727	9.1	18.7	95	9.8	19.8	90
Pioneer 3140	8.8	18.0	97	8.4	19.8	89
Pioneer 3162	8.8	18.8	97	9.2	20.0	89
Pioneer 3165	8.9	19.8	89	9.1	20.8	83
Pioneer 3379	7.8	15.8	97	9.2	18.0	89
Pioneer 3394	8.6	16.4	98	9.7	17.8	90
Average	8.2	17.5	95	9.2	19.1	87
LSD.05(EntxEnv)	0.7	0.7	8	0.7	0.7	8
C.V.%(EntxEnv)	8	4	9	8	4	9

% EP = Percent erect plants at harvest.

NC296A, a temperate adapted, all-tropical inbred was derived from Pioneer X105A x H5 from the Rockefeller program. This trial demonstrated that a tropical source could increase yields, even of elite hybrids, chosen to represent both high response and stress resistant types. Adapted from Goodman and Carson (2000).

Table 12. NC296 type topcrosses vs. Commercial Hybrids. 1995 96: Clayton, Lewiston, Plymouth (not '96), NC

	Commercial			X NC296			X NC346		
Hybrid	YIELD Mt/ha	% H_2O	% EP	YIELD Mt/ha	% H_2O	% EP	YIELD Mt/ha	% H_2O	% EP
B73*Ht*.Mo17*Ht*	6.8	16.6	68	8.2	18.4	81	8.2	18.1	80
DeKalb 743	7.9	19.5	78	8.3	19.6	80	8.5	19.4	83
NK N8727	8.4	19.1	86	8.8	19.4	87	8.4	19.5	84
Pioneer 3245	8.6	17.8	84	9.3	18.8	86	9.1	18.9	83
Pioneer 3394	8.1	16.5	92	8.5	17.7	82	8.8	18.2	84
Pioneer3283W	7.3	17.5	86	7.9	18.1	84	8.0	18.5	84
Pioneer3287W	7.1	18.3	81	8.0	18.8	77	7.6	18.7	81
Average:	7.7	17.9	82	8.4	18.7	82	8.4	18.8	83
DeKalb 689	7.6	18.1	78		*Various*				
LH132 x LH51	7.7	17.3	84		*Additional*				
Pioneer 3085	8.1	19.7	66		*Check*				
Pioneer 3165	8.1	19.9	74		*Hybrids*				
LSD .05	0.8	0.7	11		(Entry x Env.)				
C. V. %	8	3	11		(Entry x Env.)				

% EP = Percent erect plants at harvest.
Adapted from Goodman and Carson (2000).

Table 13. Topcrosses (with LH132.LH51) of 2nd cycle, all-tropical lines derived from NC296 crosses. Years 1997 -1999: Clayton, Lewiston, Plymouth, NC Year 1997 only: Sandhills, NC

Pedigree		Yield Mt/Ha	% H_2O	% EP	Ear HT	Tassel Days
101-12-2-1.296	1443-1	7.7	17.7	71	109	75
NC296.NC298	1445-2	7.5	18.9	70	113	79
NC296.NC304	1457-3	7.5	18.3	73	106	76
NC296.NC304	1469-1	7.9	19.1	72	113	76
Dekalb 689		7.4	17.8	70	108	77
LH132 x LH51		7.1	16.8	74	100	74
Pioneer 3165		6.9	20.5	57	106	78
LSD .05 (ENTRY x ENV)		0.6	0.7	8	6	3
C.V.% (ENTRY x ENV)		9	4	13	7	2

% EP = Percent erect plants at harvest.

Table 14. Strip trial comparison of an NC296 cross. Andrews, NC 1992.

Hybrid	YIELD Mt/Ha	% H_2O
B73*Ht*.Mo17*Ht* x NC296	11.3	20.7
Pioneer Brand 3156	10.9	18.9
Pioneer Expt. X1811	10.0	17.9
Ciba 4742	9.9	22.3
Pioneer Brand 3085	9.5	21.9
Pioneer Brand 3215	9.3	19.6
Pioneer Brand 3163	9.2	15.4
Pioneer Brand 3140	8.9	17.3
Pioneer Brand 3245	8.7	16.9
Ciba 4671	8.6	17.2
Pioneer Brand 3154	8.4	19.8
Funk's G-4680	7.3	18.7
Pioneer Brand 3146	7.0	15.9
LSD (.05)	2.5	1.6
C.V.	8.8	2.9

Given the extensive transgenic-backcrossing efforts that are currently underway almost everywhere within industry, coupled with the concurrent reductions in conventional breeding (and even sales) efforts (particularly long-term introgression programs), there may well be a new reliance on public breeding for novel germplasm in the future. Tables 15 - 18 suggest that efforts to produce 50%-tropical inbreds for use in the US can be successful, both as measured by grain yield and by grain moisture at harvest. It is unlikely that commercial breeders, who lack the tenure-protection system prevalent in the public sector, would be willing to devote a very substantial portion of their breeding efforts to such work. Simmonds (1993) noted the lack of emphasis devoted to *incorporation* of exotic germplasm, the use of it in high percentages within breeding stocks (as is the case for the materials listed Tables 11 to 18). He contrasted *incorporation* to the more common *introgression*, the use of exotic germplasm in low percentages, usually by backcrossing, often for disease- or insect-resistance. Materials such as those in Tables 8 to 10, particularly families originating from germplasm accessions, will probably be used for introgression via backcrossing by private breeders.

In any case, useful, unique germplasm currently is clearly undervalued relative to novel gene constructs, when a hybrid with a single transgene receives a 25%+ price-premium.

Table 15. NC258.NC296, 50%-tropical inbred derivatives crossed to FR992.FR1064 as tester. 1996 - 1998, Clayton, Lewiston, and Plymouth (not 1996), N.C.

Pedigree	Yield t/ha	% H_2O	% EP	Ear HT	Tassel Days
NC386 992-1	7.4	18.2	85	93	74
NC402 985-1	7.5	17.9	73	97	75
NC404 1013-3	7.8	18.3	74	101	73
8075-e/ 5524-1	7.4	18.0	80	91	73
8076-a/ 992-3	7.5	17.6	77	97	74
8076-a/ 992-5	7.3	17.9	83	91	73
8080-c/ 1013-2	7.8	18.2	77	104	73
DeKalb 689	7.5	16.7	64	104	75
LH132 x LH51	6.9	15.6	80	98	74
Pioneer 3165	7.4	19.3	59	106	77
LSD.05(ENTxENV)	0.6	0.5	7	6	1
C.V.% (ENTxENV)	7	3	10	6	1

% EP = Percent erect plants at harvest.

Table 16. TROPHY, all-tropical, low-moisture selections x NC268, a Stiff-Stalk tester. 1996- 1998, Clayton, Lewiston, and Plymouth (not 1996), N.C.

Pedigree	Yield t/ha	% H_2O	% EP	Ear HT	Tassel Days
NC356 x NC268	7.6	19.5	83	116	77
NC358 x NC268	7.6	19.0	77	104	73
NC390 x NC268	7.8	19.4	79	118	77
NC392 x NC268	8.2	18.1	73	116	75
NC394 x NC268	7.9	18.6	78	101	74
DeKalb 689	7.9	17.8	68	105	75
LH132 x LH51	7.5	16.2	84	98	73
Pioneer 3165	8.0	20.0	58	104	77
LSD.05(ENTxENV)	0.6	0.7	10	6	1
C.V.% (ENTxENV)	8	4	13	6	1

% EP = Percent erect plants at harvest.

Table 17. P105.A155 x NC262, 50%-tropical inbred derivatives crossed to LH195 as tester. 1993 - 1995, Clayton, Lewiston (not 1993), and Plymouth, N.C.

Pedigree	Yield t/ha	% H_2O	% EP	Ear HT	Tassel Days	So[1] Rst.
NC360	8.6	18.0	100	107	76	5.4
NC362	8.4	16.8	99	117	76	4.3
NC364	8.6	17.5	99	112	74	5.3
NC380	8.4	17.7	98	124	76	8.0
DeKalb 689	8.6	17.5	97	115	75	4.4
LH132.LH51	7.8	16.8	99	106	72	3.8
NC258.LH195	8.2	19.3	98	105	76	4.3
NC262.LH195	8.2	17.6	97	99	73	4.4
Pioneer3165	8.4	19.1	94	112	77	3.5
LSD.05	0.5	0.4	2	5	1	1.1
C.V.%	5	3	2	4	1	11

% EP = Percent erect plants at harvest.
[1] So. Rst = Southern Rust, scored on a 9 = no disease,1 = dead scale.

Table 18. P105.A155 x NC262, 50%-tropical inbred derivatives crossed to FR992.FR1064 as tester. 1996 - 1998, Clayton, Lewiston, and Plymouth (not 1996), N.C.

Pedigree	Yield t/ha	% H_2O	% EP	HT Ear	(cm) PLT.	Days to Tassel
NC360 921-1	7.9	17.0	81	91	271	72
NC382 914-4	7.3	16.4	93	101	255	73
NC384 925-1	7.6	16.6	88	85	254	71
NC418 914-1	7.4	16.6	91	99	253	73
NC420 202-1	7.4	17.2	86	94	265	72
192-1 911-3	7.3	16.5	87	102	271	73
194-1 914-2	7.5	16.6	91	103	261	74
DeKalb 689	7.3	17.6	83	100	260	74
LH132 x LH51	7.0	16.1	92	94	259	72
Pioneer 3165	7.3	19.8	68	103	259	76
LSD .05 (ENTxENV)	0.5	0.5	8	7	11	2
C. V. % (ENTxENV)	7	3	9	7	4	1

% EP = Percent erect plants at harvest.

Assuming 10,000 consequential genes in maize, a farmer currently pays about 8/10 of a cent per gene in a bag of hybrid seed, but $30 US for the *Bt* transgene, a factor of 3,000+ times more for a gene that:

1. Has exhibited the highest genotype x environmental interaction of anything except *cms*T, green-snap, or high-oil 'topcrosses'.
2. Results in a net income loss almost as often as a gain, when compared to conventional hybrids [USDA-ERS, 2000; National Center for Food and Agricultural Policy (Ferber, 1999)]

There will soon be even more-useful *Bt*s with better resistance to earworms (and subsequently to fungal toxins) and rootworms, but the price-factor for transgenes woefully under-values unique, traditional germplasm. Since the cost of transgenic breeding is at least 25X the current cost of conventional breeding, yet the cost to farmers for a transgene is about 3,000X more than for a normal gene, it appears that *Bt* is overvalued by at least a factor of 100. Thus, a more rational cost of *Bt* might be about $0.30 US per seed bag, rather than a $30 US premium. Such a price imbalance is even more pronounced when the added costs to the seed producers are considered (Hoegemeyer, 2000), and when the price received by the farmer is low, as it is at present. It becomes even less defensible when a transgenic crop must effectively be sold at a discount.

Once the euphoria over the promise of transgenics fades, the closing of so many quality breeding programs, the loss of valuable sales staff, and the centralization of decision-making at company headquarters (often by folks only remotely connected to breeding) are almost certain to be regarded as tragic. There are few good investments that are more long-term than rational plant breeding. Repeated studies have shown that very high returns on investment are available from expenditures on breeding and germplasm utilization (Ruttan and Sundquist, 1983), but the returns are not the instantaneous sort favored by the 5-year funding plans currently in vogue. *The usefulness of a breeding program is probably more dependent on continuity than ingenuity.* The probability of great success by any one breeder is small, but the odds of success of a group of reasonably competent breeders working independently and continuously is high. At present, the evidence that these same rules apply to biotechnology is almost non-existent.

In the plant biotech world, luck and legal maneuvering play a much larger role than in breeding. The fates of many of the major players remain uncertain, but some of them seem to be floating upward toward a 'belly-up' position.

GENOMICS WILL REVOLUTIONIZE BREEDING

For plants, genomics is essentially the simultaneous quantitative genetics of potential transgenes. Plant genomics is modeled after the human genome project. The purpose of the human genome project is basically to seek cures for human diseases.

Plant breeders are interested in major genes for disease control, but do have some skepticism about their durability, even when derived from alien species. Many, if not most, plant breeders are also doubtful that medical-type remedies, suitable for people, are economically viable for most major crops.

This is no trivial matter; despite many promises that discoveries in human genomics would lead to human disease cures, and despite massive investments (compared to plant biotechnology), there are very few current success stories.

EXOTIC GERMPLASM WILL IMPROVE BREEDING PROGRAMS

There is no substitute for continuous, intelligent, independent breeding programs. The three things most important for a successful breeding program are:

1. A good, patient, and observant breeder.
2. A consistently-funded, **continuous** program.
3. Access to quality testing facilities.

The best material, of any sort, will not substitute for a well-run, stable, continuous program. If a program lacks continuity, only purloined or purchased breeding (or the equivalent) will succeed. A common 'equivalent' is selfing a competitor's hybrid, but that still leaves a program 10 years behind the competitor's breeding. Stability of management goals is probably no less important to transgenic than to conventional breeding. Five-year plans, mergers, and spinoffs have serious deleterious effects on long-term research projects, which all types of plant breeding (both traditional and molecular) are. New germplasm, however valuable, cannot substitute for continuity.

Plagiarizing N.W. Simmonds (1991), we can add MAS, genomics, and possibly even transgenics to the bandwagons we have known. These include (but are certainly not restricted to):

induced polyploids
haploids
mutations
overdominance
genetic variances
harvest index
high-lysine
small tassels
nitrogen fixation
nitrate reductase
somaclonal variation
bracytic dwarfs
leafy hybrids
precision agriculture
high-oil topcrosses
ag chemical/seed synergy

Simmonds' observations merit repeating even after more than a decade, "The bandwagon, as it applies to plant breeding, is expensive and damaging. Resources are being diverted from doing genuinely useful jobs to the pursuit of trendy irrelevance; biotechnology is, I think, accelerating the collapse of proper agricultural research. A thoughtful watch on events and prudent adoption of such usable bits as become available would have been a much wiser response."

CONCLUSIONS

Significant improvements in maize hybrids using exotics and genetic engineering are both likely. If we are to feed the world's growing population without obliterating marginal lands, substantial improvements had better be certain. Both procedures require roughly the same length of time, if there are no surprises. At present, transgenes are greatly overvalued. Unique, useful germplasm is greatly undervalued. Current emphasis on transgenic backcrossing has already resulted in reductions in traditional breeding. These reductions have been most heavily felt in the area of improvements to the germplasm base. Destruction of continuity has been the worst side effect of multiple seed-company mergers.

Academic emphases on molecular biology has resulted in a current lack of young, field-trained plant breeders and greatly reduced public participation in current breeding of several major crops, particularly maize, soybeans, cotton, and sorghum. Given the current financial crises that are affecting most states and land-grant institutions, it is likely that industrial endowments will be needed to revive public breeding programs and the education of new breeders in the US.

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