Title
Marker-assisted selection in public breeding programs: The wheat experience

Journal
Crop Science, 44(6)

ISSN
0011-183X

Author
Dubcovsky, Jorge

Publication Date
2004-11-01

Peer reviewed

based on a common set of clones reveal modes of chromosomal evolution in potato and tomato. Genetics 120:1095–1103.
Celarier, R.P. 1956. Additional evidence for five as the basic chromosome number of the Andropogoneae. Rhodora 58:135–143.
Chase, M., M. Duvall, H. Hills, J. Conran, A. Cox., L. Eguiarte et al. 1995. Molecular systematics of Lilianae. p. 109–137. *In* P. Rudall et al. (ed.) Monocotyledons: Systematics and evolution. Royal Botanic Gardens, Kew.
Chase, M.W., D.E. Soltis, P.S. Soltis, P.J. Rudall, M.F. Fay, W.H. Hahn et al. 2000. Higher-level systematics of the monocotyledons: An assessment of current knowledge and a new classification. p. 3–16. *In* K.L. Wilson and S.A. Morrison (ed.) Monocots: Systematics and evolution Vol. 1. CSIRO, Melbourne, Australia.
Devos, K.M., and M.D. Gale. 2000. Genome relationships: The grass model in current research. Plant Cell 12:637–646.
Dunford, R.P., N. Kurata, D. Laurie, T. Money, Y. Minobe, and G. Moore. 1995. Conservation of fine-scale DNA marker order in the genomes of rice and the Triticeae. Nucleic Acids Res. 23:2724–2728.
Fay, M.F., P.J. Rudall, S. Sullivan, K.L. Stobart, A.Y. de Bruijn, G. Reeves, F. Qamaruz-Zaman, W-P. Hong, J. Joseph, W.J. Hahn, J.G. Conran, and M.W. Chase. 2000. Phylogenetic studies of Asparagales based on four plastid DNA regions. *In* K.L Wilson and D.A Morrison (ed.) Monocots: Systematics and evolution. CSIRO Publishing, Melbourne, Australia.
Goff, S.A., D. Ricke, T. Lan, G. Presting, R. Wang, M. Dunn et al. 2002. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). Science 296:92–100.
Gokce, A.F., and M.J. Havey. 2002. Linkage equilibrium among tightly linked RFLPs and the *Ms* locus in open-pollinated onion populations. J. Am. Soc. Hortic. Sci. 127:944–946.
Gokce, A.F., J. McCallum, Y. Sato, and M.J. Havey. 2002. Molecular tagging of the *Ms* locus in onion. J. Am. Soc. Hortic. Sci. 127:576–582.
Harushima, Y., M. Yano, A. Shomura, M. Sato, T. Shimano, Y. Kuboki et al. 1998. A high-density rice genetic linkage map with 2275 markers using a single F_2 population. Genetics 148:479–494.
Jones, R., and H. Rees. 1968. Nuclear DNA variation in *Allium.* Heredity 23:591–605.
King, J.J., J. Bradeen, O. Bark, J. McCallum, and M.J. Havey. 1998. A low-density genetic map of onion reveals a role for tandem duplication in the evolution of an extremely large diploid genome. Theor. Appl. Genet. 96:52–62.
Kole, C., P. Quijada, S. Michaels, R. Amasino, and T. Osborn. 2001. Evidence for homology of flowering-time genes VFR2 from *Brassica rapa* and FLC from *Arabidopsis thaliana.* Theor. Appl. Genet. 102:425–430.
Lagercrantz, U. 1998. Comparative mapping between *Arabidopsis thaliana* and *Brassica nigra* indicates that brassica genomes have evolved through extensive genome replication accompanied by chromosome fusions and frequent rearrangements. Genetics 150: 1217–1228.
Liu, F., X. Cui, H. Horner, H. Weiner, and P. Schnable. 2001. Mitochondrial adehyde dhydrogenase activity is required for male fertility in maize. Plant Cell 13:1063–1078.
Maughan, P., M. Saghai-Maroof, and G. Buss. 1996. Molecular-marker analysis of seed weight: Genomic location, gene action, and evidence for orthologous evolution among three legume species. Theor. Appl. Genet. 93:574–579.
Michaels, S., and R. Amasino. 1999. Flowering locus C encodes a novel MADS-domain protein that acts as a repressor of flowering. Plant Cell 11:949–956.
Mozo, T., S. Fischer, H. Shizuya, and T. Altmann. 1998. Construction and characterization of the IGF *Arabidopsis* BAC library. Mol. Gen. Genet. 258:562–570.
Ori, D., R. Fritsch, and P. Hanelt. 1998. Evolution of genome size in *Allium* (Alliaceae). Plant Syst. Evol. 210:57–86.
Parkin, I., D. Lydiate, and M. Trick. 2002. Assessing the level of collinearity between *Arabidopsis thaliana* and *Brassica napus* for *A. thaliana* chromosome 5. Genome 45:356–366.
Paterson, A., Y. Lin, Z. Li, K. Schertz, J. Doebley, S. Pinson, S. Liu, J. Stansel, and J. Irvine. 1995. Convergent domestication of cereal crops by independent mutations at corresponding genetic loci. Science 269:1714–1718.
Ranjekar, P.K., D. Pallotta, and J. Lafontaine. 1978. Analysis of plant genomes. V. Comparative study of molecular properties of DNAs of seven *Allium* species. Biochem. Genet. 16:957–970.
Sasaki, T., J. Song, Y. Koga-Ban, E. Matsui, F. Fang, H. Higo et al. 1994. Toward cataloguing all rice genes: Large-scale sequencing of randomly chosen rice cDNAs from a callus cDNA library. Plant J. 6:615–624.
Seki, M., M. Narusaka, A. Kamiya, J. Ishida, M. Satou, T. Sakurai et al. 2002. Functional annotation of a full-length *Arabidopsis* cDNA collection. Science 296:141–145.
Stack, S.M., and D.E. Comings. 1979. The chromosomes and DNA of *Allium cepa.* Chromosoma 70:161–181.
Tanksley, S.D., M. Ganal, J. Prince, M. de Vicente, M. Bonierbale, P. Brown et al. 1992. High density molecular linkage maps of the tomato and potato genomes. Genetics 132:1141–1160.
Till, B., S. Reynolds, E. Greene, C. Codomo, L. Enns, J. Johnson et al. 2003. Large-scale discovery of induced point mutations with high-throughput TILLING. Genome Res. 13:524–530.
Young, J., P. Krysan, and M. Sussman. 2001. Efficient screening of *Arabidopsis* T-DNA insertion lines using degenerate primers. Plant Physiol. 125:513–518.
Yu, J., S. Hu, J. Wang, G. Wong, S. Li, B. Liu et al. 2002. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). Science 296:79–92.
Zhang, H.B., S. Choi, S.S. Woo, Z. Li, and R.A. Wing. 1996. Construction and characterization of two rice bacterial artificial chromosome libraries from the parents of a permanent recombinant inbred mapping population. Mol. Breed. 2:11–24.
Zhao, Q., Y. Zhang, Z. Cheng, M. Chen, S. Wang, Q. Feng et al. 2002. A fine physical map of the rice chromosome 4. Genome Res. 12:817–823.

Marker-Assisted Selection in Public Breeding Programs: The Wheat Experience

Jorge Dubcovsky*

It has been suggested that the recent progress in the area of plant molecular biology and plant genomics have the potential to initiate a new Green Revolution. However, these discoveries need to be implemented in new cultivars to realize that potential. The controversy about transgenic crops has delayed the incorporation of alien genes into plants and significantly increased the cost to develop and release transgenic crops. These costs are usually beyond the resources of public breeding programs and, therefore, are not currently used in most cultivated plants.

Fortunately, biotechnology has provided additional tools that do not require the use of transgenic crops to revolutionize plant breeding. Progress in molecular genetics has resulted in the development of DNA tags, which can be used in marker-assisted selection (MAS) strategies for cultivar development (Paterson et al., 1991). These

Dep. of Agronomy & Range Science, Univ. of California, One Shields Ave., Davis, CA 95616. Received 23 July 2003. *Corresponding author (jdubcovsky@ucdavis.edu).

Abbreviations: BAC, bacterial artificial chromosome; MAS, marker-assisted selection; SNP, single nucleotide polymorphism.

molecular markers can be used as chromosome landmarks to facilitate the selection of chromosome segments including useful agronomic traits during the breeding process. These markers are particularly useful for incorporating genes that are highly affected by the environment, genes for resistance to diseases that cannot be easily screened for, and to accumulate multiple genes for resistance to specific pathogens and pests within the same cultivar, a process called gene pyramiding. An additional advantage of the incorporation of MAS into breeding programs is that very different types of traits, e.g. a disease resistance gene or a gene to increase grain protein content, can be manipulated using the same technology. Dekkers and Hospital (2002) have recently reviewed some of the potential limitations of MAS strategies, and concluded that the use of MAS will be determined by the economic benefit relative to conventional selection.

The alleles that are incorporated by MAS are generally present within the gene pool of a particular crop and are transferred by meiotic chromosome recombination. One of the positive aspects of this approach is that these genes reside at their natural chromosomal locations, thereby minimizing the possibility of gene silencing. Another important aspect of cultivars developed by MAS is that they are not transgenic and therefore, do not face the public resistance against transgenic crops.

The MAS strategy is a way to capitalize on available markers and to incorporate valuable traits into elite lines that are suitable for cultivar release. In addition, release of these MAS-improved cultivars is an efficient way of demonstrating the power of these technologies to the public. However, limited funding for implementation efforts had delayed the incorporation of these powerful technologies into most public breeding programs.

Wheat Breeding in the USA: A Public Effort

Wheat (*Triticum aestivum* L.) is a self-pollinating species and therefore, growers can save seed from one harvest for the next year. This has reduced the profitability of wheat breeding for the private sector and has resulted in the continuous existence of a large, vibrant public sector involved in cultivar development. For example, the total number of cereal crop breeders in the USA in the last census was 893, with 80% being in the private sector and 20% being in the public sector (Frey, 1996). In wheat, approximately 60% of the breeders were in the public sector. By comparison, only 7% of the corn breeders were in the public sector. Public investments in wheat breeding during the past century have resulted in the development of the majority of cultivars grown by U.S. farmers. State agricultural colleges and experimental stations, USDA, or CIMMYT developed approximately 60% of the cultivars released in the USA during the 20th century. In addition, a high percentage of the area of wheat production in the USA is attributed to publicly developed cultivars (KS 62%, ND 64%, WA 88%, NE 90%) (NASS, 2001).

Fuglie et al. (1996) found a typical range of 40 to 60% return on public research investment, with public wheat breeding consistently at the top of this range. In addition, nine out of the 10 interspecific translocations involving the introgression of novel genes into cultivated germplasm that significantly affected U.S. wheat production were developed in public plant breeding programs (Mercado et al., 1996). These data provide convincing support of the broad impact of public wheat breeding efforts both in cultivar development and in germplasm enhancement.

Public wheat-breeding programs are typically supported by wheat grower associations. However, low wheat prices in the past years have resulted in a reduction of resources available to the U.S. wheat growers and a shrinking of resources for research and development in new technologies. This situation was aggravated by a limited investment of federal funding agencies during the 1990s in implementation grants for public wheat breeding programs. This limited investment in practical applications is difficult to understand in light of the large investment made by the same funding agencies in wheat molecular genetics and wheat genomics.

During the last 10 yr, public researchers constructed detailed wheat genetic maps including more than 3000 molecular markers and physical maps including more than 16 000 loci (http://wheat.pw.usda.gov/NSF/; verified 2 July 2004). In addition to mapping, U.S. federal agencies have funded the sequencing of more than 105 000 wheat ESTs, the construction of wheat Bacterial Artificial Chromosome (BAC) libraries (Cenci et al., 2003; Lijavetzky et al., 1999), the assembly of BACs into physical maps (http://wheat.pw.usda.gov/PhysicalMapping/; verified 2 July 2004), and the sequencing of large segments of wheat DNA (SanMiguel et al., 2002). These powerful genomic resources have started to yield the first successful positional cloning efforts in wheat (Faris et al., 2003; Feuillet et al., 2003; Huang et al., 2003; Yahiaoui et al., 2004; Yan et al., 2003; Yan et al., 2004). Cloning of agronomically important genes has made possible to develop "perfect markers," based directly on the allelic variation responsible for the differences in the trait. Examples of perfect markers in wheat include the glutenin genes for gluten strength (Anderson et al., 1989), the waxy genes for starch properties (Briney et al., 1998), the puroindoline genes for hardness (Beecher et al., 2002), the vernalization genes for vernalization requirement (Yan et al., 2003; Yan et al., 2004), the *Rht* genes for semi-dwarf habit (Peng et al., 1999), and the *Lr10* and *Lr21* genes for leaf rust resistance (Feuillet et al., 2003; Huang et al., 2003). Wheat researchers have also developed closely linked molecular markers to yet unidentified genes with positive effects on quality characteristics and resistance to fungi, viruses, and insects (reviewed by Dubcovsky et al., 2000; Anderson, 2000).

The most efficient way to develop a positive synergistic effect between the large research investments in wheat genomics and the growers' investment in public wheat breeding is to fund implementation research projects. The MAS programs are good examples of implementation projects that have the potential to facilitate the transfer of valuable genes identified in basic research programs into public wheat varieties.

MASwheat: A Public MAS Program

The wheat public research sector has a long tradition of collaborative projects that were initiated at the begin-

ning of the 1990s by the International Triticeae Mapping Initiative. Large multi-laboratory projects continued later in the USA under the funding of the NSF-Plant Genome Initiative (http://wheat.pw.usda.gov/NSF/; verified 2 July 2004). Many of the collaborators of these projects were wheat breeders, facilitating the integration of basic and applied wheat researchers. This integrated research community and the availability of the results from previous research efforts in marker development were instrumental in developing a successful proposal for MAS in wheat.

Wheat researchers and breeders from 12 public programs across the USA organized a national wheat MAS consortium (MASwheat) that was funded by the USDA Initiative for the Future of Agriculture and Food Systems (2001–2004). The MASwheat project structure is similar to the Australian National Wheat Molecular Marker Program (NWMMP) implemented in 1996. The main objective of both projects is to empower the breeders by implementing MAS capacities within each of the existing public breeding programs. This strategy has been successful in closing the funding gap between the development of genomic tools and the public investment in cultivar development, and in transferring the value of genomic research to the wheat growers' fields.

The MASwheat project is committed to transfer new developments in wheat genomics and biotechnology to U.S. wheat production through marker-assisted selection. Available molecular markers are being used to transfer 22 resistance genes to fungi, viruses, and insects; and 21 gene variants related to bread, pasta, and noodle quality into 75 different recurrent parents (34 whites, 33 reds and 8 durums). Eighty MAS projects have been already completed and additional 350 backcrossing programs are currently being advanced in average two generations a year by MAS.

All the information and protocols used in the MASwheat project are publicly available through the project WEB site (http://maswheat.ucdavis.edu; verified 2 July 2004). The collaborative nature of the project and the public access to the information was lauded in a recent article in *Nature* focused on the current difficulties of public breeding programs (Knight, 2003). The numerous presentations in growers' meetings, field days and symposiums by the members of the MASwheat consortium are also improving the public understanding of the potential benefits of biotechnology.

Conclusions

Marker technologies are continuously evolving. The development of 96-well DNA extraction protocols and high-throughput genotyping equipment resulted in substantial reduction of MAS costs. A new generation of molecular markers based on the detection of single nucleotide polymorphisms (SNP) promises high-throughput assays at relatively low costs, along with the potential for high levels of multiplexing. Implementation of this multiplexing technology in plant improvement strategies can provide cost-effective tools for selection of multiple traits in breeding populations.

The challenge for the public plant breeders and for the federal funding agencies will be to generate the integrated proposals and necessary funding to continue the actual MAS programs and to incorporate new marker technologies.

One important aspect of the new genomic revolution is that most of the information is publicly available. Therefore, competitiveness will not be determined by access to the information but by the speed in which these technologies are incorporated into the breeding programs. This represents both a challenge and a fantastic opportunity for the public breeding programs that have the expertise to utilize successfully MAS technologies.

ACKNOWLEDGMENTS

The authors acknowledge financial support from USDA-IFAFS competitive grant 2001-04462. The first author thanks J. Anderson, B.S. Gill, S. Kianian, N. Lapitan, J. Sherman, and M.A. Soria for a critical review of this article.

REFERENCES

Anderson, J.A. 2000. Marker-assisted selection of disease resistance genes in wheat. p. 71–84. *In* M.M. Kohli and M. Francis. (ed.) Application of biotechnologies to wheat breeding. CIMMYT-INIA.

Anderson, O.D., F.C. Greene, R.E. Yip, N.G. Halford, P.R. Shewry, and J.M. Malpica-Romero. 1989. Nucleotide sequences of the two high-molecular-weight glutenin genes from the D genome of hexaploid wheat, *Triticum aestivum* L. cv. Cheyenne. Nucleic Acid Res. 17:461–462.

Beecher, B., A. Bettge, E. Smidansky, and M.J. Giroux. 2002. Expression of wild-type pinB sequence in transgenic wheat complements a hard phenotype. Theor. Appl. Genet. 105:870–877.

Briney, A., R. Wilson, R.H. Potter, I. Barclay, G. Crosbie, R. Appels et al. 1998. A PCR-based marker for selection of starch and potential noodle quality in wheat. Mol. Breed. 4:427–433.

Cenci, A., N. Chantret, K. Xy, Y. Gu, O.D. Anderson, T. Fahima et al. 2003. Construction and characterization of a half million clones: Bacterial Artificial Chromosome (BAC) library of durum wheat. Theor. Appl. Genet. 107:931–939.

Dekkers, J.C.M., and F. Hospital. 2002. The use of molecular genetics in the improvement of agricultural populations. Nat. Rev. Genet. 3:22–32.

Dubcovsky, J., G. Tranquilli, D. Lijavetzky, I.A. Khan, A.R. Schlatter, and M.M. Manifesto. 2000. Advances in molecular markers for bread making quality. p. 57–70. *In* M.M. Kohli and M. Francis (ed.) Application of biotechnologies to wheat breeding. CIMMYT-INIA.

Faris, J.D., J.P. Fellers, S.A. Brooks, and B.S. Gill. 2003. A BAC contig spanning the major domestication locus Q in wheat and identification of a candidate gene. Genetics 164:311–321.

Feuillet, C., S. Travella, N. Stein, L. Albar, A. Nublat, and B. Keller. 2003. Map-based isolation of the leaf rust disease resistance gene Lr10 from the hexaploid wheat (*Triticum aestivum* L.) genome. Proc. Natl. Acad. Sci. USA 100:15253–15258.

Frey, K.J. 1996. National Plant Breeding Study-1. Human and financial resources devoted to plant breeding research and development in the United States in 1994. Special Report 98. Iowa State University. Iowa Agriculture and Home Economics Experiment Station, Ames.

Fuglie, K.O., K.N. Ballenger, K. Day, C. Klotz, M. Ollinger, J. Reilly et al. 1996. Agricultural research and development: Public and private investments under alternative markets and institutions 735. USDA, Economic Research Service, Washington, DC.

Huang, L., S.A. Brooks, W.L. Li, J.P. Fellers, H.N. Trick, and B.S. Gill. 2003. Map-based cloning of leaf rust resistance gene *Lr21* from the large and polyploid genome of bread wheat. Genetics 164: 655–664.

Knight, J. 2003. Crop improvement: A dying breed. Nature 421:568–570.

Lijavetzky, D., G. Muzzi, T. Wicker, B. Keller, R. Wing, and J. Dubcovsky. 1999. Construction and characterization of a bacterial artificial chromosome (BAC) library for the A genome of wheat. Genome 42:1176–1182.

Mercado, L.A., E. Souza, and K.D. Kephart. 1996. Origin and diversity of North American hard spring wheats. Theor. Appl. Genet. 93: 593–599.

NASS. 2001. National Agricultural Statistics Service, State Offices. [Online] http://www.usda.gov/nass/sso-rpts.htm; verified 2 July 2004.
Paterson, A.H., S.D. Tanksley, and M.E. Sorrells. 1991. DNA markers in plant improvement. Adv. Agron. 46:39–90.
Peng, J.R., D.E. Richards, N.M. Hartley, G.P. Murphy, K.M. Devos, J.E. Flintham et al. 1999. 'Green revolution' genes encode mutant gibberellin response modulators. Nature 400:256–261.
SanMiguel, P., W. Ramakrishna, J.L. Bennetzen, C.S. Busso, and J. Dubcovsky. 2002. Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5A. Funct. Integr. Genom. 2:70–80.
Yahiaoui, N., P. Srichumpa, R. Dudler, and B. Keller. 2004. Genome analysis at different ploidy levels allows cloning of the powdery mildew resistance gene Pm3b from hexaploid wheat. Plant J. 37: 528–538.
Yan, L., A. Loukoianov, G. Tranquilli, M. Helguera, T. Fahima, and J. Dubcovsky. 2003. Positional cloning of wheat vernalization gene *VRN1*. Proc. Natl. Acad. Sci. USA 100:6263–6268.
Yan, L., A. Loukoianov, G. Tranquilli, A. Blechl, I.A. Khan, W. Ramakrishna et al. 2004. The wheat *VRN2* gene is a flowering repressor down-regulated by vernalization. Science 303:1640–1644.

Crop Plant Genome Sequence: What Is It Good For?

Robert A. Martienssen*

With the commitment of resources from USDA-IFAFS and NSF Plant Genome Program, it is likely that sequencing of plant genomes will be a major activity in the next few years. Nonetheless, the value of these sequences is still a matter of debate, leading to concerns that priorities need to be carefully evaluated, not just in research but also in education. It is worth therefore revisiting the largest genome project attempted so far—the human genome project—and the doubts raised at the beginning of what seemed to be an unimaginably difficult undertaking at the time.

The Human Genome Project

At the outset of the human genome project in the mid-1980s, there was heated debate over the merits of a project scheduled to take 15 to 20 yr and to cost in excess of $3000 million. Arguments against the enormous undertaking ranged from scientific, to economic, ethical, and educational. It was argued that conventional biomedical research would have to be abandoned to fund the project; that graduate education would take a back seat as students were trained in sequencing and little else; and that the sequence of our genes would breach our inalienable right to privacy. Finally, there was an underlying conviction that the human genome sequence would be of little scientific value compared to the outrageous cost.

In the event, the human genome project was completed in less than 10 yr, and cost the U.S. taxpayer less than $500 million. Technological advances halved the anticipated costs year after year, following "Moore's Law," which predicted comparable increases in computer speed and memory over the same time period. It is projected that, by the end of this decade, an entire human genome will cost less than $10 000 to sequence.

Scientifically, the human genome project is already revolutionizing our understanding of sporadic and inherited diseases, including cancer, Alzheimer's, autism, and many more. It can be argued that the first drugs designed on the basis of gene discovery were inhibitors of the novel protease found in the genome of HIV, drugs which have radically improved the prognosis for AIDS (Anon., 1996). Now that the genomes of microbes and viruses are known, as well as their human hosts, drugs that uniquely target pathogens will follow this example in large numbers.

With respect to education, the genome project raised a new generation of biologist as much at home with a computer algorithm as with a pipette, and has greatly raised the profile of biomedical sciences at campuses around the world. While the debate concerning genetic privacy has widened considerably since the sequence was announced, forensic applications have overturned hundreds of convictions and have made the "grave of the unknown soldier" a thing of the past (Williamson and Duncan, 2002).

Plant Genome Sequencing

What lessons are there to be learned from this experience for crop plant genomics and plant breeding? As with animals, model genomes (nematode, fly) have been sequenced first (*Arabidopsis* and rice, *Oryza sativa* L.). However, now that they have been completed and their impact is being felt in basic research, should we go on and sequence major crops such as maize (*Zea mays* L.), soybean [*Glycine max* (L.) Merr.], wheat (*Triticum aestivum* L.), cotton (*Gossypium* spp.), and trees? Much of the debate over crop plant genomics echoes the debate surrounding the human genome project 15 yr ago. However, while the model plant genomes have transformed basic plant biology in much the same way as animal genomes have, there are major differences between crop plant genomics and the human genome project.

For one thing, human genome research contributes to biomedical research and development, a trillion dollar activity worldwide. Crop plant genome research also underlies enormously important industries in food, feed, energy, and fiber, but here the analogy ends. First, several species must be targeted to cover agriculturally important plants, rather than one genome in the case of biomedical research. Second, the seed industry operates on far lower margins than the pharmaceutical industry, and has raised public concerns over food safety and security. Finally, the genetic information available to plant breeders is usually thought to be far less extensive than the vast array of epidemiological data collected by the biomedical community, making the sequence less useful. Each of these arguments is certainly valid, but just as plant breeders embraced the vision of genetics

Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724. Received 23 July 2003. *Corresponding author (martiens@cshl.org).