

CURRICULUM VITAE

September 5, 2017

Name: David William Galbraith
Title: Professor, School of Plant Sciences and BIO5 Institute

Education: Cambridge University, England. B.A. Biochemistry, 1973.
Cambridge University, England. M.A., Biochemistry, 1976.
Cambridge University, England. Ph.D., Biochemistry, 1977.

Professional Experience

1976-78: N.A.T.O. Science Research Fellowship, Department of Biological Sciences, Stanford University.
1978-82: Assistant Professor, Section of Genetics, Molecular and Cellular Biology, School of Biological Sciences, University of Nebraska-Lincoln.
1982-1988: Associate Professor, Sections of Genetics, Molecular and Cellular Biology and of Molecular Plant Biology, School of Biological Sciences, University of Nebraska-Lincoln.
1989-present: Professor, Department/School of Plant Sciences, University of Arizona.
Member, Arizona Cancer Center.
2003-present: Professor, BIO5 Institute for Collaborative Bioscience.

Honors

Selected for Scholarship and College Prize, Jesus College, and to the Benn W. Levy Research Studentship, Department of Biochemistry, Cambridge University, 1973.
Selected for NATO Science Research Fellowship, 1976.
Plenary lecturer, Third Annual Conference of the French Association for Flow Cytometry, Gif-sur-Yvette, November 1986.
Invited participant in a D.O.E. sponsored workshop: Analysis of plant chromosomes and genomes, Los Alamos National Laboratory, November 1986.
Invited participant in a N.S.F. Interkingdom Workshop: Membrane Traffic and Recycling in Eukaryotes, Tampa, May 1988.
Invited instructor at an E.M.B.O. Practical Course: Flow cytometry and sorting in molecular biology, Cologne, August, 1988, September, 1989, and September, 1991.
Invited organizer and chair of a Concurrent Session on Plant Sciences at the XVth Congress of the International Society for Analytical Cytology, Asheville, South Carolina, March 1990.
Invited discussant at the Gordon Conferences (Plant Molecular Biology), Plymouth, June 1990.
Invited N.S.F. review team member, visiting Mexico City, Cuernavaca and Irapuato, July 1990.
Organizational Committee member, International Society for Plant Molecular Biology Congress, October 1991.
Invited plenary speaker, Rocky Mountain Cytometry Association Biennial Meeting, Vail, Colorado, October 1991.
Associate Editor, Cytometry, June 1992-present.
Invited organizer and chair of a Workshop Session on Other Life Forms at the XVII Congress of the International Society for Analytical Cytology, Colorado Springs, March 1993.
Invited instructor: Short Course in Plant Flow Cytometry, Casaccia, Rome, November 1994.
Invited organizer and chair of a Symposium Session on Analysis of Molecular and Cellular Interactions at the XVIII Congress of the International Society for Analytical Cytology, Rimini, Italy, April 1996.
Member, Scientific Advisory Committee of the International Society for Analytical Cytology, 1996-2002; 2008-present.
Chair, Scientific Advisory Committee of the International Society for Analytical Cytology, 2002-2004.

Member, Organizational Committee, XIX Congress of the International Society for Analytical Cytology, Colorado Springs, February 1998.

Invited instructor, Second International School And Conference on Flow and Image Cytometry, Jagiellonian University, Krakow, Poland, June 1998.

Invited instructor, Annual Royal Microscopical Society Flow Cytometry Course, Sheffield University, England, September 1998.

Invited instructor, Biennial Course in Flow Cytometry, Los Alamos National Laboratory (1999-2007), and University of New Mexico, Albuquerque (2009-current), June 1999, June 2001, June 2003, June 2005, June 2007, June 2009, June 2011, June 2013, June 2015.

College of Agriculture Research Faculty of the Year Award, October 1999.

Invited plenary speaker, Chips to Hits '99, Berkeley, November 1999.

Invited Frontiers plenary speaker, I.S.A.C. XX, Montpellier, France, May 2000.

Elected Councilor, International Society for Analytical Cytology, 2000-2004.

Invited plenary speaker, Brazil International Genome Conference, Agrados Reis, Brazil, March 2001.

Invited plenary speaker, Plant, Animal and Microbe Genomes X Conference, San Diego, January 2002.

Invited Cytomics plenary speaker, I.S.A.C. XXI, San Diego, May 2002.

Invited plenary speaker, 2nd Virtual Conference on Genomics and Bioinformatics, Washington, D.C., September 2002.

Invited plenary speaker, Queenstown Molecular Biology Meeting, Queenstown, New Zealand, September 2002.

Elected Fellow, American Association for the Advancement of Science, February 2003.

Invited plenary speaker, Maize Genetics meeting, Lake Geneva, March 2003.

Invited keynote speaker, 2nd National Congress in Analytical Cytology, Brno, Czech Republic, May 2003.

Invited plenary speaker, 1st International Cytomics Conference, Cardiff, Wales, May 2003.

Invited plenary speaker, S.E.B. Symposium, Durham, England, July 2003.

Founder Fellow, Arizona Arts, Sciences and Technology Academy, January 2004.

Invited plenary speaker, 1st Annual A.C.P.F.G. Research Symposium, Adelaide, Australia, October 2004.

Invited keynote speaker, Victorian Microarray Technology Consortium, Melbourne, Australia, May 2005.

Invited organizer and instructor, 1st Portuguese Microarray Workshop, The University of Trás-os-Montes and Alto Douro, Vila Real, Portugal, June 2005.

Invited instructor, Biennial National Flow Cytometry Course, Bowdoin College, Maine, June 2006, June 2008, June 2010, June 2012, June 2014.

Invited instructor, Second Plant Microarray Short Course, Boston, August 2006.

Invited keynote speaker, Annual Meeting of the Czech Society for Analytical Cytology, Brno, Czech Republic, June 2007.

Invited organizer and instructor, 2nd Portuguese Microarray Workshop, The University of Trás-os-Montes and Alto Douro, Vila Real, Portugal, October 2007.

Invited organizer and chair of a Workshop on Plant Genomics at the XXIV Congress of the International Society for Analytical Cytology, Budapest, Hungary, May 2008.

Invited keynote speaker, D.GfZ (German Cytometry Society) Annual Meeting, Leipzig, Germany, October 2009.

Invited keynote speaker, G.I.C. (Italian Cytometry Society) Annual Meeting, Ferrara, Italy, October 2009.

Invited keynote speaker, IVth International Congress in Flow Cytometry, Bogota, Colombia, May 2010.

Invited keynote speaker, Microbial Single Cell Genomics Workshop 2010, Bigelow Laboratory, Boothbay Harbor, Maine, September 2010.

Invited symposium speaker, CYTO 2011: XXVIth Congress of the International Society for Advancement of Cytometry, Baltimore, May 2011.

Invited keynote speaker, SUMMIT 2011: Inaugural meeting of the Southern California Flow Cytometry Association, Los Angeles, November 2011.

Invited keynote speaker - CellTech 2013 - Flow Cytometry, San Diego, January 2013.

Invited keynote speaker, Queensland Institute for Medical Research, July 2013.

Invited keynote speaker. PepTalk 2014, Palm Springs, January 2014.

Invited keynote speaker, SEFCIG Annual Meeting, Atlanta, March 2015.
Elected Secretary, International Society for Advancement of Cytometry, May 2016.
Appointed International Academic Master, 111 Program in Plant Stress Biology, at Henan University, Kaifeng, China, April, 2016.

Professional Affiliations

International Society for Advancement of Cytometry.
American Society of Plant Biologists.
American Association for the Advancement of Science.

Summary of Published Work

I have published 178 articles, reviews, and other scientific contributions, which are listed in order of appearance on pages 7-16. According to Clarivate Analytics-Web of Science, my publications have been cited 9,811 times, with a Hirsch-index of 48. Google Scholar indicates my publications have been cited 14,237 times, with a Hirsch-index of 57 and an i10 score of 127. My research contributions have been recognized nationally by my peers through election as Fellow of the American Association for the Advancement of Science in 2003, and by my local colleagues in the award of College of Agriculture Research Faculty of the Year in 1999.

I consider the following publications to be particularly important contributions to the field:

1. Galbraith, D.W., Harkins, K.R., Maddox, J.R., Ayres, N.M., Sharma, D.P., and Firoozabady, E. (1983). Rapid flow cytometric analysis of the cell cycle in intact plant tissues. *Science* 220:1049-1051.

This paper has been cited in Thompson-Reuters Web of Science 1197 times since publication, is still cited about 50 times each year; it now is the 12th most cited article to have been published in *Science* in 1983. It describes a break-through application of flow cytometry to higher plants, starting with gentle homogenization of plant tissues. The homogenates are then stained with a DNA-specific fluorochrome, and analyzed by flow cytometry. The nuclei present in the homogenates provide a signal proportional to their DNA contents. This allows a determination of DNA content, ploidy level, and cell cycle status. The method is in widespread use around the world, having major applications in molecular biology, agriculture, genetic engineering, ecology, systematics and taxonomy. The concept of homogenization of eukaryotic organisms, followed by flow cytometric analysis of these homogenates is now finding traction in the study of other living orders, including insects and mammals.

2. Birnbaum, K., Shasha, D.E., Wang, J.Y., Jung, J.W., Lambert, G.M., Galbraith, D.W., and Benfey, P.N. (2003). A gene expression map of the *Arabidopsis* root. *Science* 302:1956-1960.

This pioneering paper has been cited 748 times since publication. It describes a method for identifying and separating for study the different cell types found within the *Arabidopsis* root, and goes on to describe the global transcriptional activities of these different cell types. Identification of the different cells relies on the expression of GFP under the control of cell type-specific promoters; separating and purifying them involves use of methods, developed in the Galbraith laboratory, for preparation and sorting of protoplasts prepared from the roots of transgenic plants.

3. Kawasaki, S., Borchert, C., Deyholos, M., Wang, H., Brazille, S., Kawai, K., Galbraith, D.W., and Bohnert, H.J. (2001). Gene expression profiles during the initial phase of salt stress in rice (*Oryza sativa* L.). *Plant Cell* 13:889-906.

This paper has been cited 632 times. The microarrays and the microarray methods, developed and contributed by the Galbraith laboratory, were employed in a collaboration with the group of Hans Bohnert for the analysis of changes in gene expression induced by salt stress. This represents one of the first publications employing microarrays for analysis of plant gene expression. Importantly, it uncovered time-related changes in gene expression, indicating that plant responses to salt stress (and, by implication, any stress) must be considered as processes that change over time.

4. Ozturk, Z.N., Talamé, V., Deyholos, M., Michalowski, C.B., Galbraith, D.W., Gozukirmizi, N., Tuberosa, R., and Bohnert, H.J. (2002). Monitoring large-scale changes in transcript abundance in drought- and salt-stressed barley. *Plant Molecular Biology* 48:551-573.

Cited 388 times, this work continued the approach outlined in Reference [3] extending it to another important crop.

5. Zhang, X., Zhang, L., Dong, F., Gao J., Galbraith, D.W., and Song, C.-P. (2001). Hydrogen peroxide is involved in abscisic acid-induced stomatal closure in *Vicia faba*. *Plant Physiology* 126:1438-1448.

Cited 502 times, this publication identifies hydrogen peroxide as a key upstream signaling molecule linking the action of abscisic acid to the closing of stomates. This is highly relevant to an understanding of the molecular responses of plants to drought stress.

6. Galbraith, D.W., Harkins, K.R., and Knapp, S. (1991). Systemic endopolyploidy in *Arabidopsis thaliana*. *Plant Physiology* 96:985-989.

This paper has been cited 330 times since publication. This paper applied the technique described in Reference [1], above, to the model plant *Arabidopsis thaliana*. Surprisingly, all somatic cells within the organs of the plant, with the exception of the developing flowers, were found to exhibit a high degree of polysomaty. Successive rounds of endoreduplication, due to the onset of additional S-phase activity without an intervening mitosis, results in cells having 4C, 8C, 16C, 32C, and even 64C nuclei. Endoreduplication is developmentally-regulated. Importantly, the genome size for *Arabidopsis* was defined by this work as 0.32 pg/2C (about 157 Mbp), relevant to the process of whole-genome sequencing that was being initiated at the time of publication.

7. Sheen, J., Hwang, S., Niwa, Y., Kobayashi, H., and Galbraith, D.W. (1995). Green Fluorescent Protein as a new vital marker in plant cells. *Plant Journal* 8:777-784.

This paper has been cited 297 times, and is the first to demonstrate GFP expression in plants. It appeared less than two years after the original description, in *Science*, of GFP expression in bacteria and worms, for which work Marty Chalfie was awarded the Nobel Prize in 2008.

8. Bak, S., Tax, F.E., Feldmann, K.E., Galbraith, D.W., and Feyereisen, R. (2001). CYP83B1, a Cytochrome P450 at the metabolic branchpoint in auxin and indole glucosinolate biosynthesis in *Arabidopsis thaliana*. *Plant Cell* 13:101-111.

This paper has been cited 240 times. It was based on the use of microarrays to define candidate cytochrome P450 genes in terms of their patterns of gene expression. The *Arabidopsis* cytochrome P450 gene family remains particularly intractable in terms of assigning catalytic functions to its approximately 180 members. Methods such as these facilitate functional definition.

9. Grebenok, R.J., Pierson, E.A., Lambert, G.M., Gong, F.-C., Afonso, C.L., Haldeman-Cahill, R., Carrington, J.C., and Galbraith, D.W. (1997). Green-Fluorescent Protein fusions for efficient characterization of nuclear localization signals. *Plant Journal* 11:573-586.

Cited 165 times, this paper defined, for the first time, methods to characterize nuclear localization signals in plants, based on GFP targeting. It served as the basis for subsequent work defining cell type-specific gene expression based on nuclear polyA⁺ RNA information.

10. Johnston, J.S., Bennett, M.D., Rayburn, A.L., Galbraith, D.W., and Price, H.J. (1999). Reference standards for determination of DNA content of plant nuclei. *American Journal of Botany* 86:609-613.

Cited 186 times, this paper highlights the importance of defined plant reference standards for use in flow cytometric measurement of nuclear DNA contents, hence genome sizes. These standards are used worldwide.

11. Harkins, K.R., and Galbraith, D.W. (1984). Flow sorting and culture of plant protoplasts. *Physiologia Plantarum* 60:43-52.

This paper, which has been cited 45 times, reports the pioneering development of flow cytometry and cell sorting for the analysis and recovery of living plant protoplasts.

12. Afonso, C.L., Harkins, K.R., Thomas-Compton, M., Krejci, A., and Galbraith, D.W. (1985). Production of somatic hybrid plants through fluorescence-activated sorting of protoplasts. *Nature Biotechnology* 3:811-816.

Cited 37 times, this paper reports the first use of flow sorting to selectively isolate heterokaryons formed by fusion of protoplasts of different plant species, and their regeneration into somatic hybrid plants. This approach has been used by others to resynthesize *Brassica napus*, an important crop (canola).

13. Zhang, C.Q., Barthelson, R.A., Lambert, G.M., and Galbraith, D.W. (2008). Characterization of cell-specific gene expression through fluorescence-activated sorting of nuclei. *Plant Physiology* 147:30-40. PMID: 18354040.

This paper, cited 62 times, outlines a novel method for examining gene expression within specific cell types. It involves expression of a nuclear-targeted form of GFP, placing this expression under the control of cell-type specific promoters, and producing transgenic plants. These plants are then homogenized, and fluorescent nuclei isolated via flow sorting. Expression profiling is then done on microarrays using polyA⁺ RNA isolated from the sorted nuclei as targets. The genes identified as being phloem-companion cell specific show a high level of concordance with those identified via protoplast sorting [reference 2].

14. Gong, F.-C., Giddings, T.H., Meehl, J.B., Staehelin, L.A., and Galbraith, D.W. (1996). Z-membranes: artificial organelles for over-expressing recombinant integral membrane proteins. *Proceedings of the National Academy of Sciences U.S.A.* 93:2219-2223.

This paper describes the first example of how to engineer a novel intracellular organelle within a eukaryotic cell based on transgenic expression of a transmembrane protein, and outlines the probable mechanism for the formation of this organelle. It has been cited 32 times.

15. Bharathan, G., Lambert, G., and Galbraith, D.W. (1994). Nuclear DNA content of monocotyledons and related taxa. *American Journal of Botany* 81:381-386.

Cited 69 times, this paper was the first to systematically investigate genome sizes across different plant taxa, using flow cytometry. This detailed dataset laid to rest the misconception that monocotyledons in general have larger genomes than dicotyledons.

16. Harkins, K.R., Jefferson, R.A., Kavanagh, T.A., Bevan, M.W., and Galbraith, D.W. (1990). Expression of photosynthesis related gene fusions is restricted by cell type in transgenic plants and in transfected protoplasts. *Proceedings of the National Academy of Sciences U.S.A.* 87:816-820.

Cited 42 times, this was the first demonstration of cell type-specific transgenic gene expression in higher plants. In this case, it employed β -glucuronidase as the transgenic marker, light-regulated promoters as the sequences controlling transgene expression, and flow sorting based on the presence or absence of chlorophyll fluorescence to separate mesophyll and epidermal protoplasts for analysis. Importantly, it defined that protoplasts “remember” in the short term the transcriptional state of the tissue from which they are derived.

17. Zanetti, M.E., Chang, I.-F., Gong, F.C., Galbraith, D.W., and Bailey-Serres, J. (2005). Immunopurification of polyribosomal complexes of *Arabidopsis* for global analysis of gene expression. *Plant Physiology* 138:624-635.

This collaboration, which I formed and funded as lead P.I. on a N.S.F. plant genome grant, led to the development of a novel method for examining gene expression in a cell type-specific manner, in this case looking at transcripts associated with polyribosomes. Cited 122 times, this approach has now been adopted by others for use in mammalian systems.

18. Mustroph, A., Zanetti, M.E., Jang, C.J.H., Galbraith, D.W., Girke, T., and Bailey-Serres, J. (2009). Profiling translomes of discrete cell populations resolves altered cellular priorities during hypoxia in *Arabidopsis*. *Proceedings of the National Academy of Sciences U.S.A.* 106:18849-18854.

This extended the work of reference [17], allowing identification of the “translatome” and of the effects of hypoxia on translated messages. It has already been cited 236 times. It shows that focusing on transcription does not tell the whole story of gene expression, and some consideration of the translatability of cellular messages is also required.

19. Zhang, C.Q, Gong, F.C., Lambert, G.M., and Galbraith, D.W. (2005). Cell type-specific characterization of nuclear DNA contents within complex tissues and organs. *Plant Methods* 2005, 1:7 doi:10.1186/1746-4811-1-7. PMID: 16270943.

This paper, cited 54 times, outlines methods for analysis of the endoreduplication status within the different cell types found in the *Arabidopsis* root. Polysomaty (reference [6]) is cell type-specific, and this observation implies a linkage between operation of the cell cycle and differentiation of specific tissues.

20. Grindberg, R.V., Yee-Greenbaum, J.L., McConnell, M.J., Novotny, M., O’Shaughnessy, A.L., Lambert, G.M., Araúzo-Bravo, M.J., Lee, J., Fishman, M., Lin, X., Robbins, G.E., Lin, X., Venepally, P., Badger, J.H., Galbraith, D.W., Gage, F.H., and Lasken, R.S. (2013). RNA-Seq from single nuclei. *Proceedings of the National Academy of Sciences U.S.A.* 110:19802-19807.

This paper describes, for the first time, whole genome transcriptional analysis from the polyadenylated RNA extracted from a single eukaryotic nucleus. It promises to provide uniquely detailed information concerning gene expression within different cell types, and about the extent of stochasticity in gene expression. This will be extremely relevant to the analysis of differentiation, of the responses of organisms to biotic and abiotic stress, and of the initiation and progression of disease states. It has already been cited 37 times.

Cumulative List of Publications

1. Galbraith, D.W. (1977). Membranes of soybean callus. Ph.D. thesis. University of Cambridge. 214 pp.
2. Galbraith, D.W., and Northcote, D.H. (1977). The isolation of plasma membranes from protoplasts of soybean suspension cultures. *Journal of Cell Science* 24:295-310.
3. Galbraith, D.W., and Galbraith, J.E.C. (1979). A method for the identification of fusion of plant protoplasts derived from tissue cultures. *International Journal of Plant Physiology* 93:149-158.
4. Galbraith, D.W., and Mauch, T.J. (1980). Identification of fusion of plant protoplasts II. *International Journal of Plant Physiology* 98:129-140.
5. Galbraith, D.W., and Mauch, T.J. (1980). Somatic hybridization of higher plants. *What's New in Plant Physiology* 11:21-24.
6. Galbraith, D.W. (1981). Identification and sorting of plant heterokaryons. U. S. Dept. of Commerce Patent 4,300,310.
7. Galbraith, D.W., Mauch, T.J., and Shields, B.A. (1981). Analysis of the initial stages of plant protoplast development using 33258 Hoechst: reactivation of the cell cycle. *Physiologia Plantarum* 51:380-386.
8. Galbraith, D.W. (1981). Microfluorometric quantitation of cellulose biosynthesis by plant protoplasts using Calcofluor White. *Physiologia Plantarum* 53:111-116.
9. Galbraith, D.W., and Shields, B.A. (1982). The effects of inhibitors of cell wall synthesis on tobacco protoplast development. *Physiologia Plantarum* 55:25-30.
10. Galbraith, D.W., and Harkins, K.R. (1982). Cell sorting as a means for isolating somatic hybrids. In: *Plant Tissue Culture 1982* (A. Fujiwara, ed.) Maruzen Press, Tokyo, pp. 617-618.
11. Galbraith, D.W., Harkins, K.R., Maddox, J.R., Ayres, N.M., Sharma, D.P., and Firoozabady, E. (1983). Rapid flow cytometric analysis of the cell cycle in intact plant tissues. *Science* 220:1049-1051.
12. Sharma, D.P., Firoozabady, E., Ayres, N.M., and Galbraith, D.W. (1983). Improvement of anther culture in *Nicotiana*: media, culture conditions and flow cytometric determination of ploidy levels. *International Journal of Plant Physiology* 111:441-450.
13. Harkins, K.R., and Galbraith, D.W. (1984). Flow sorting and culture of plant protoplasts. *Physiologia Plantarum* 60:43-52.
14. Galbraith, D.W. (1984). Selection of hybrid cells by fluorescence-activated cell sorting. In: *Cell Culture and Somatic Cell Genetics of Plants* (I.K. Vasil, ed.) Academic Press, N. Y., pp. 433-447.
15. Galbraith, D.W. (1984). Flow cytometric analysis of the cell cycle in higher plants. In: *Cell Culture and Somatic Cell Genetics of Plants* (I.K. Vasil, ed.) Academic Press, N. Y., pp. 765-777.
16. Firoozabady, E., and Galbraith, D.W. (1984). Transformation of plant protoplasts by *Agrobacterium* does not require an intact plant cell wall. *Plant Cell, Tissue and Organ Culture* 3:175-188.
17. Galbraith, D.W., Afonso, C.L., and Harkins, K.R. (1984). Flow sorting and culture of protoplasts: Conditions for high-frequency recovery and growth of sorted protoplasts of suspension cultures of *Nicotiana*. *Plant Cell Reports* 3:151-155.
18. Afonso, C.L., Harkins, K.R., Thomas-Compton, M., Krejci, A., and Galbraith, D.W. (1985). Production of somatic hybrid plants through fluorescence-activated sorting of protoplasts. *Nature Biotechnology* 3:811-816.
19. Shoemaker, R.C., Couche, L., and Galbraith, D.W. (1986). Callus induction, somatic embryogenesis and plant regeneration in cotton (*Gossypium hirsutum* L.). *Plant Cell Reports* 3:178-181.
20. Harkins, K.R., and Galbraith, D.W. (1987). Factors governing the flow cytometric analysis and sorting of large biological particles. *Cytometry* 8:60-71.
21. Keeler, K.H., Kwankin, B., Barnes, P.W., and Galbraith, D.W. (1987). Polyploid polymorphism in big bluestem (*Andropogon gerardii* Vitman). *Genome* 29:374-379.
22. Shoemaker, R.C., Christofferson, S.E., and Galbraith, D.W. (1987). Storage protein accumulation patterns in somatic embryos of cotton (*Gossypium hirsutum* L.). *Plant Cell Reports* 6:12-15.
23. Meyer, D.J., Afonso, C.L., Harkins, K.R., and Galbraith, D.W. (1987). Analysis of plant plasma membrane antigens. In: *Plant Membranes: Structures, Function and Biogenesis* (C. J. Leaver, H. Sze, eds.). UCLA Symposia on Molecular and Cellular Biology, New Series, 63:123-140.

24. Galbraith, D.W., Harkins, K.R., and Jefferson, R.A. (1988). Flow cytometric characterization of the chlorophyll contents and size distributions of plant protoplasts. *Cytometry* 9:75-83.
25. Meyer, D.J., Afonso, C.L., and Galbraith, D.W. (1988). Isolation and characterization of monoclonal antibodies directed against plant plasma membrane and cell wall epitopes: Identification of a monoclonal antibody that recognizes extensin and analysis of the process of epitope biosynthesis in plant tissues and cell cultures. *Journal of Cell Biology* 107:163-175.
26. Galbraith, D.W. (1989). Flow cytometry and cell sorting: applications to higher plant systems. *International Review of Cytology* 116:165-227.
27. Galbraith, D.W. (1989). Flow cytometric analysis and sorting of somatic hybrid and transformed protoplasts. In: *Biotechnology in Agriculture and Forestry* Vol. 9, Plant Protoplasts and Genetic Engineering (Y.P.S. Bajaj, ed.). Springer-Verlag, New York, pp. 304-327.
28. Harkins, K.R., Jefferson, R.A., Kavanagh, T.A., Bevan, M.W., and Galbraith, D.W. (1990). Expression of photosynthesis-related gene fusions is restricted by cell-type in transgenic plants and in transfected protoplasts. *Proceedings of the National Academy of Sciences U.S.A.* 87:816-820.
29. Fox, M.H., and Galbraith, D.W. (1990). The application of flow cytometry and sorting to higher plant systems. In: *Flow Cytometry and Cell Sorting* (M.R. Melamed, T. Lindmo, M.L. Mendelsohn, eds.), John Wiley, N. Y.: pp. 633-650.
30. Galbraith, D.W. (1990). Isolation and flow cytometric characterization of plant protoplasts. In: *Methods in Flow Cytometry* (Z. Darzynkiewicz, H. Crissman, eds.), *Methods in Cell Biology* 33:527-547.
31. Galbraith, D.W. (1990). Flow cytometric analysis of plant genomes. In: *Methods in Flow Cytometry* (Z. Darzynkiewicz, H. Crissman, eds.), *Methods in Cell Biology* 33:549-562.
32. DeRocher, E.J., Harkins, K.R., Galbraith, D.W., and Bohnert, H.J. (1990). Developmentally-regulated systemic endopolyploidy in succulents with small genomes. *Science* 250:99-101.
33. Galbraith, D.W. (1991). Fluorescence-activated cell sorting of protoplasts and somatic hybrids. In: *Plant Tissue Culture Manual: Fundamentals and Applications* (J.M. Brevis, ed.), Kluwer Academic Publishers, Dordrecht, D5:1-19.
34. Galbraith, D.W., Harkins, K.R., and Knapp, S. (1991). Systemic endopolyploidy in *Arabidopsis thaliana*. *Plant Physiology* 96:985-989.
35. Galbraith, D.W., Zeiher, C.A., Harkins, K.R., and Afonso, C.L. (1992). Biosynthesis, processing and targeting of the G-protein of Vesicular Stomatitis Virus in tobacco protoplasts. *Planta* 186:324-336.
36. Galbraith, D.W. (1992). Large particle sorting. In: *Flow Cytometry and Cell Sorting* (A. Radbruch, ed.), Springer-Verlag, Berlin, pp. 189-204.
37. Bharathan, G., Lambert, G., and Galbraith, D.W. (1994). *American Journal of Botany* 81:381-386. Nuclear DNA content of monocotyledons and related taxa.
38. Galbraith, D.W. (1994). Flow cytometry and sorting of plant protoplasts and cells. In: *Methods in Flow Cytometry, Second Edition* (Z. Darzynkiewicz, H. Crissman, J.P. Robinson, eds.), *Methods in Cell Biology* 42: 539-561, Academic Press, San Diego.
39. Afonso, C.L., and Galbraith, D.W. (1994). The callus associated protein (CAP) gene of *Nicotiana tabacum*: Isolation, characterization, and evidence for possible function as a transcriptional factor. In *In Vitro Cell and Developmental Biology (Plants)* 30:44-54.
40. Zilmer, N.A., Rodriguez, J.J., Yopp, T.A., Lambert, G.M., and Galbraith, D.W. (1995). Flow cytometric analysis using digital signal processing. *Cytometry* 20:102-117.
41. Galbraith, D.W., Bohnert, H.J., and Bourque, D.P. (1995). *Methods in Plant Cell Biology* (part A) (editors). *Methods in Cell Biology* Volume 49, Academic Press.
42. Galbraith, D.W., Bourque, D.P., and Bohnert, H.J. (1995). *Methods in Plant Cell Biology* (part B) (editors). *Methods in Cell Biology* Volume 50, Academic Press.
43. Galbraith, D.W., Grebenok, R.J., Lambert, G.M., and Sheen, J. (1995). Flow cytometric analysis of transgene expression in higher plants: Green Fluorescent Protein. *Methods in Cell Biology* 50:3-12.
44. Sheen, J., Hwang, S., Niwa, Y., Kobayashi, H., and Galbraith, D.W. (1995). Green fluorescent protein as a new vital marker in plant cells. *Plant Journal* 8:777-784.

45. Godavarti, M., Rodriguez, J.J., Yopp, T.A., Lambert, G.M., and Galbraith, D.W. (1995). Neural network analysis of digital flow cytometric data. *Proceedings of the IEEE International Conference on Neural Networks* vol. 5 (Perth, Australia), Nov./Dec. 1995, pp. 2211-2216.
46. Galbraith, D.W., and Lambert, G.M. (1996). Advances in the flow cytometric characterization of plant cells and tissues. In: *Flow Cytometric Applications in Cell Culture* (M. Al-Rubeai and A. N. Emery, eds.), Marcel Dekker, New York, pp. 311-326.
47. Gong, F.-C., Giddings, T.H., Meehl, J.B., Staehelin, L.A., and Galbraith, D.W. (1996). Z-membranes: artificial organelles for over-expressing recombinant integral membrane proteins. *Proceedings of the National Academy of Sciences U.S.A.* 93:2219-2223.
48. Grebenok, R.J., Galbraith, D.W., Benveniste, I., and Feyereisen, R. (1996). Ecdysone 20-mono-oxygenase, a cytochrome P450 enzyme from spinach, *Spinacia oleracea*. *Phytochemistry* 42:927-933.
49. Godavarti M., Rodriguez, J.J., Yopp, T.A., Lambert, G.M., and Galbraith, D.W. (1996). Automated particle classification based on digital acquisition and analysis of flow cytometric pulse waveforms. *Cytometry* 24:330-339.
50. Grebenok, R.J., Pierson, E.A., Lambert, G.M., Gong, F.-C., Afonso, C.L., Haldeman-Cahill, R., Carrington, J.C., and Galbraith, D.W. (1997a). Green-Fluorescent Protein fusions for efficient characterization of nuclear localization signals. *Plant Journal* 11:573-586.
51. Shen, Z., Corbin, D.R., Greenplate, J.T., Grebenok, R.J., Galbraith, D.W., and Purcell, J.P. (1997). Studies on the mode of action of cholesterol oxidase on insect midgut membranes. *Archives of Insect Biochemistry and Physiology* 34:429-442.
52. Grebenok, R.J., Galbraith, D.W., and Della Penna, D. (1997b). Characterization of *Zea mays* endosperm C-24 sterol methyltransferase: one of two types of sterol methyltransferase in higher plants. *Plant Molecular Biology* 34:891-896.
53. Grebenok, R.J., Lambert, G.M., and Galbraith, D.W. (1997c). Characterization of the targeted nuclear accumulation of GFP within the cells of transgenic plants. *Plant Journal* 12:685-696.
54. Galbraith, D.W. (1998). Miniatis? *Trends in Plant Science* 3:157-158.
55. Galbraith, D.W., Dolezel, J., Lambert, G., and Macas, J. (1998). DNA and ploidy analyses in higher plants. *Current Protocols in Cytometry* (J.P. Robinson *et al.*, eds.), Wiley, New York, pp 7.6.1 - 7.6.22.
56. Schmelz, E.A., Grebenok, R.J., Galbraith, D.W., and Bowers W.S. (1998). Damage-induced accumulation of phytoecdysteroids in spinach: a rapid root response involving the octadecanoic acid pathway. *Journal of Chemical Ecology* 24:339-360.
57. Macas, J., Nouzova, M., and Galbraith, D.W. (1998). Adapting the Biomek 2000 Laboratory Automation Workstation for printing DNA microarrays. *BioTechniques* 25:106-110.
58. Galbraith, D.W., Anderson, M.T., and Herzenberg, L.A. (1998). Flow cytometric analysis and sorting of cells based on GFP accumulation. *Methods in Cell Biology* 58: 315-341.
59. Macas, J., Lambert, G.M., Dolezel, D., and Galbraith, D.W. (1998). NEST (Nuclear Expressed Sequence Tag) analysis: a novel means to study transcription through amplification of nuclear RNA. *Cytometry* 33:460-468.
60. Winkler, R.G., Frank, M.R., Galbraith, D.W., Feyereisen, R., and Feldmann, K.A. (1998). Systematic reverse genetics of Transfer-DNA-tagged lines of *Arabidopsis*: isolation of mutations in the cytochrome P450 gene superfamily. *Plant Physiology* 118:743-750.
61. Grebenok, R.J., Ohnmeiss, T.E., Yamamoto, A., Huntley, E.D., Galbraith, D.W., and Della Penna, D. (1998). Isolation and characterization of an *Arabidopsis thaliana* C-8,7 sterol isomerase: functional and structural similarities to mammalian C-8,7 sterol isomerase emopamil-binding protein. *Plant Molecular Biology* 38:807-815.
62. Galbraith, D.W., Herzenberg, L.A., and Anderson, M. (1999). Flow cytometric analysis of transgene expression in higher plants: Green Fluorescent Protein. *Methods in Enzymology* 320:296-315.
63. Johnston, J.S., Bennett, M.D., Rayburn, A.L., Galbraith, D.W., and Price, H.J. (1999). Reference standards for determination of DNA content of plant nuclei. *American Journal of Botany* 86:609-613.
64. Chytilova, E., Macas, J., and Galbraith, D.W. (1999). Green Fluorescent Protein targeted to the nucleus, a transgenic phenotype useful for studies in plant biology. *Annals of Botany* 83:645-654.

65. Macas, J., Nouzova, M., and Galbraith, D.W. (1999). Adapting the Biomek 2000 Laboratory Automation Workstation for printing DNA microarrays. In: *Expression Genetics: accelerated and high-throughput methods*. BioTechniques Books, Update Series (M. McClelland and A.B. Pardee, eds.), Eaton Publishing, pp. 13-19.
66. Staehelin, L.A., Galbraith, D. W., and Giddings, T.H. (1999). Product and process for cellular protein segregation. U. S. Dept. of Commerce Patent 5,935,822.
67. Chytilova, E., Macas, J., Sliwinska, E., Rafelski, S., Lambert, G., and Galbraith, D.W. (2000). Nuclear dynamics in *Arabidopsis thaliana*. *Molecular Biology of the Cell* 11:2733-2741.
68. Galbraith, D.W., and Lucretti, S. (2000). Large particle sorting. In: *Flow Cytometry and Cell Sorting Second Edition*, (A. Radbruch, ed.), Springer-Verlag, Berlin, pp. 293-317.
69. Nouzová, M., Neumann, P., Navrátilová, A., Galbraith, D.W., and Macas, J. (2001). Microarray-based survey of repetitive genomic sequences in *Vicia* spp. *Plant Molecular Biology* 45:229-244.
70. Bak, S., Tax, F.E., Feldmann, K.E., Galbraith, D.W., and Feyereisen, R. (2001). CYP83B1, a Cytochrome P450 at the metabolic branchpoint in auxin and indole glucosinolate biosynthesis in *Arabidopsis thaliana*. *Plant Cell* 13:101-111.
71. Bohnert, H.J., Ayoubi, P., Borchert, C., Bressan, R.A., Burnap, R.L., Cushman, J.C., Cushman, M.A., Deyholos, M., Galbraith, D.W., Hasegawa, P.M., Jenks, M., Kawasaki, S., Koiwa, H., Kore-eda, S., Lee, B.H., Michalowski, C.B., Misawa, E., Nomura, M., Ozturk, N., Postier, B., Prade, R., Song, C.-P., Tanaka, Y., Wang H., and Zhu J.-K. (2001). A genomics approach towards salt stress tolerance. *Plant Physiology & Biochemistry* 39:1-17.
72. Kawasaki, S., Borchert, C., Deyholos, M., Wang, H., Brazille, S., Kawai, K., Galbraith, D.W., and Bohnert, H.J. (2001). Gene expression profiles during the initial phase of salt stress in rice (*Oryza sativa* L.). *Plant Cell* 13:889-906.
73. Bohnert, H.J., Kawasaki, S., Michalowski, C., Wang, H., Ozturk, N., Deyholos, M., and Galbraith, D. (2001). Isolation of candidate genes for tolerance to abiotic stresses. In: *Rice Genetics IV* (G.S. Khush, D.S. Brar, and B. Hardy, eds.) , Science Publisher Inc., New Hampshire, USA, pp. 345-363.
74. Deyholos, M.K., and Galbraith, D.W. (2001). High-Density DNA microarrays for gene expression analysis. *Cytometry* 43:229-238.
75. Galbraith, D.W., Macas, J., Pierson, E.A., Xu, W., and Nouzová, M. (2001). Printing DNA microarrays using the Biomek® Laboratory Automation Workstation. In: *DNA Arrays: Methods and Protocols* (J.B. Rampil, ed.). *Methods in Molecular Biology* 170:131-140.
76. Chytilova, E., Macas, J., Sliwinska E., Rafelski, S., Lambert, G., and Galbraith, D.W. (2001). Nuclear Dynamics in *Arabidopsis thaliana*. In: *GFP in Motion, volume II* (B. Ludin, ed.). CD-ROM, published by Trends in Cell Biology, Elsevier Press.
77. Xu, W., Bak, S., Decker, A., Paquette, S.M., Feyereisen, R., and Galbraith, D.W. (2001). Microarray-based analysis of gene expression in very large gene families: the Cytochrome P450 gene superfamily of *Arabidopsis thaliana*. *Gene* 272:61-74.
78. Zhang, X., Zhang, L., Dong, F., Gao J., Galbraith, D.W., and Song, C.-P. (2001). Hydrogen peroxide is involved in abscisic acid-induced stomatal closure in *Vicia faba*. *Plant Physiology* 126:1438-1448.
79. Xiong, L., Gong, Z., Rock, C.D., Subramanian, S., Guo, Y., Xu, W., Galbraith, D., and Zhu, J.-K. (2001). Modulation of abscisic acid sensitivity and biosynthesis by a Sm-like protein in *Arabidopsis*. *Developmental Cell* 1:771-781.
80. Staehelin, L.A., Galbraith, D. W., Giddings, T.H., and Cowan, C. (2002). Product and process for cellular protein segregation. U. S. Dept. of Commerce Patent 6,344,343.
81. Fernandes, J., Brendel, V., Gai, X., Lal, S., Chandler, V.L., Elumalai, R., Galbraith, D.W., Pierson, E., and Walbot, V. (2002). Comparison of RNA expression profiles based on maize EST frequency analysis and microarray hybridization. *Plant Physiology* 128:896-910.
82. Ozturk, Z.N., Talamé, V., Deyholos, M., Michalowski, C.B., Galbraith, D.W., Gozukirmizi, N., Tuberosa, R., and Bohnert, H.J. (2002). Monitoring large-scale changes in transcript abundance in drought- and salt-stressed barley. *Plant Molecular Biology* 48:551-573.
83. Sliwinska, E., and Galbraith, D.W. (2002). Factors affecting nuclear dynamics and Green Fluorescent Protein targeting to the nucleus in *Arabidopsis thaliana* roots. *Plant Science* 163:425-430.

84. Murthi, S., Sankaranarayanan, S., Xia, B., Rodríguez, J.J., and Galbraith, D.W. (2002). An improved data acquisition system for digital flow cytometry. *ISCAS 2002. IEEE International Symposium on Circuits and Systems* 1:669-672.
85. Galbraith, D.W. (2003). Global analysis of cell type-specific gene expression. *Comparative and Functional Genomics* 4:208-215.
86. Boyce, J.M., Knight, H., Deyholos, M., Openshaw, M., Galbraith, D.W., Warren, G., and Knight, M.R. (2003). The *sfr6* mutant of *Arabidopsis* is defective in transcriptional activation via CBF/DREB1 and DREB2 and shows sensitivity to osmotic stress. *Plant Journal* 34:395-406.
87. Postier, B.L., Wang, H.-L., Singh, A., Impson, L., Andrews, H.L., Klahn, J., Li, H., Risinger, G., Pesta, D., Deyholos, M., Galbraith, D.W., Sherman, L.A., and Burnap, R.L. (2003). The construction and use of bacterial DNA microarrays based on an optimized two-stage PCR strategy. *BMC Genomics* 2003, 4:23.
88. Wang, H., Kawai, K., Deyholos, M., Galbraith, D.W., and Bohnert, H.J. (2003). Temporal progression of gene expression responses to salt shock in maize roots. *Plant Molecular Biology* 52:873-891.
89. Birnbaum, K., Shasha, D.E., Wang, J.Y., Jung, J.W., Lambert, G.M., Galbraith, D.W., and Benfey, P.N. (2003). A gene expression map of the *Arabidopsis* root. *Science* 302:1956-1960.
90. Galbraith, D.W. (2004). Cytometry and plant sciences, a personal retrospective. *Cytometry* 58:37-44.
91. Galbraith, D.W., Elumalai, R., and Gong, F.-C. (2004). Integrative flow cytometric and microarray approaches for use in transcriptional profiling. *Methods in Molecular Biology* 263:259-279.
92. Meyers, B.C., Galbraith, D.W., Nelson, T., and Agrawal, V. (2004). Methods for transcriptional profiling in plants: be fruitful and replicate. *Plant Physiology* 135:637-652
93. Song, C-P., Guo, Y., Qiu, Q., Lambert, G., Galbraith, D.W., Jagendorf, A., and Zhu, J.-K. (2004). A probable Na⁺/H⁺ exchanger on the chloroplast envelope functions in pH homeostasis and chloroplast development in *Arabidopsis thaliana*. *Proc. Natl. Acad. Sci. U.S.A.* 101:10211-10216.
94. Inan, G., Zhang, H., Li, P., Wang, Z., Cao, Z., Zhang, C., Quist, T.M., Goodwin, S.M., Zhu, J., Shi, H., Damsz, B., Charbaji, T., Gong, Q., Ma, S., Fredricksen, M., Galbraith, D.W., Jenks, M.A., Rhodes, D., Hasegawa, P.M., Bohnert, H.J., Joly, R.J., Bressan, R.A., and Zhu, J.-K. (2004). Salt Cress (*Thellungiella halophila*): a halophyte and cryophyte *Arabidopsis* Relative Model System (ARMS) and its applicability to molecular genetic analyses of growth and development of extremophiles. *Plant Physiology* 135: 1718-1737.
95. Miyazaki, S., Fredricksen, M., Hollis, K.C., Poroyko, V., Shepley, D., Galbraith, D.W., Long, S.P., and Bohnert, H.J. (2004). Transcript expression profiles of *Arabidopsis thaliana* grown under controlled conditions and open-air elevated concentrations of CO₂ and of O₃. *Field Crops Research* 90:47-59.
96. Galbraith, D.W. (2004). Nuclear Dynamics in Higher Plants. In: *The Nuclear Envelope* (D. E. Evans, C.J. Hutchinson, and J.A Bryant, eds.), *SEB Symposium Series Volume 56*, Garland Science/BIOS Scientific Publishers, Abingdon, pp.217-228.
97. Galbraith, D.W. (2004). The rainbow of Fluorescent Proteins. *Methods in Cell Biology* 75:153-169.
98. Galbraith, D.W., and Bak, S. (2004). Functional Genomics of the Cytochrome P450 Gene Superfamily in *Arabidopsis thaliana*. In: *Plant Functional Genomics* (D. Leister, ed.), Haworth Press, Binghamton, New York, pp. 595-620.
99. Kristensen, C., Morant, M., Olsen, C.E., Galbraith, D.W., Lindberg-Møller, B., and Bak, S. (2005). Metabolic engineering of dhurrin in transgenic *Arabidopsis* plants with marginal inadvertent effects on the metabolome and transcriptome. *Proc. Natl. Acad. Sci. U.S.A.* 102:1779-1884.
100. Zanetti, M.E., Chang, I.-F., Gong, F.C., Galbraith, D.W., and Bailey-Serres, J. (2005). Immunopurification of polyribosomal complexes of *Arabidopsis* for global analysis of gene expression. *Plant Physiology* 138:624-635.
101. Birnbaum, K., Jung, J.W., Wang, J.Y., Lambert, G.M., Hirst, J.A., Galbraith, D.W., and Benfey, P.N. (2005). Cell-type specific expression profiling in plants using fluorescent reporter lines, protoplasting, and cell sorting. *Nature Methods* 2:1-5.
102. Murthi, S., Sankaranarayanan, S., Xia, B., Lambert, G.M., Rodríguez, J.J., and Galbraith, D.W. (2005). Performance analysis of a dual-buffer architecture for digital flow cytometry. *Cytometry* 66A:109-118.

103. Galbraith, D.W., Bartos, J., and Dolezel, J. (2005). Flow Cytometry and Cell Sorting in Plant Biotechnology. In: *Flow Cytometry in Biotechnology* (L.A. Sklar, ed.), Oxford University Press, New York, pp. 291-322.
104. Brown, J.K., Lambert, G.M., Ghanim, M., Czosnek, H., and Galbraith, D.W. (2005). Nuclear DNA content of the whitefly *Bemisia tabaci* (Aleyrodidae: Hemiptera) estimated by flow cytometry. *Bulletin of Entomological Research* 95:309-312. PMID: 16048678.
105. LaJeunesse, T.C., Lambert, G., Andersen, R.A., Coffroth, M.A., and Galbraith, D.W. (2005). *Symbiodinium* (Pyrrophyta) genome sizes (DNA content) are smallest among dinoflagellates. *Journal of Phycology* 41:880-886.
106. Zhang, C.Q., Gong, F.C., Lambert, G.M., and Galbraith, D.W. (2005). Cell type-specific characterization of nuclear DNA contents within complex tissues and organs. *Plant Methods* 2005, 1:7 doi:10.1186/1746-4811-1-7. PMID: 16270943.
107. Gardiner, J.M., Buell, C.R., Elumalai, R., Galbraith, D.W., Henderson, D.A., Iniguez, A.L., Kaeppler, S.M., Kim, J.J., Liu, J., Zheng, L., and Chandler, V.L. (2005). Design, production, and utilization of long oligonucleotide microarrays for expression analysis in maize. *Maydica* 50:425-435.
108. Ammiraju, J.S.S., Luo, M., Wang, W., Kudrna, D., Goicoechea, J.L., Mueller, C., Talag, J., Kim, H.R., Sisneros, N.B., Blackmon, B., Fang, E., Tomkins, J., Brar, D., MacKill, D., McCouch, S., Kurata, N., Lambert, G., Galbraith, D.W., Arumuganathan, K., Rao, K., Walling, J.G., Gill, N., SanMiguel, P., Soderlund, C., Jackson, S., and Wing, R.A. (2006). The *Oryza* Map Alignment Project (OMAP) bacterial artificial chromosome library resource: unveiling a new era in whole genome comparative genomics to study monocot plant evolution, development, and physiology. *Genome Research* 16:140-147.
109. Song, C-P., and Galbraith, D.W. (2006). AtSAP18, an orthologue of human SAP18, is involved in the regulation of salt stress and mediates transcriptional repression in *Arabidopsis*. *Plant Molecular Biology* 60:241-257. PMID: 16429262.
110. Galbraith, D.W., and Birnbaum, K. (2006). Global studies of cell type-specific gene expression in plants. *Annual Reviews of Plant Biology* 57:451-475.
111. Rangwala, S.H., Elumalai, R., Vanier, C., Ozkan, H., Galbraith, D.W., and Richards, E.J. (2006). Meiotically-stable natural epigenetic variation in *Sadhu*, a novel *Arabidopsis* retroposon. *P.L.o.S. Genetics* 2:270-281.
112. Barthelson, R.A., Sundareshan, P., Galbraith, D.W., and Woosley, R.L. (2006). Development of a comprehensive detection method for medicinal and toxic plant species. *American Journal of Botany* 93:566-574.
113. Ozkan, H., Tuna, M., and Galbraith, D.W. (2006). No DNA loss in autotetraploids of *Arabidopsis thaliana*. *Plant Breeding* 125:288-291.
114. Xiong, Z., Barthelson, R., Weng, Z., and Galbraith, D.W. (2006). Designing and testing of a Citrus tristeza virus resequencing microarray. *Proceedings of the XVI Conference of the International Organization of Citrus Virologists*, Monterrey, Nuevo León, México November 07-13, 2004.
115. Li, J., Li, X., Su, H., Chen, H., and Galbraith, D.W. (2006). A framework of integrating gene relations from heterogeneous data sources: an experiment on *Arabidopsis thaliana*. *Bioinformatics* 22:2037-2043. PMID: 16820427.
116. Galbraith, D.W. (2006). The daunting process of MIAME. *Nature* 444:31. PMID: 17080064.
117. Galbraith, D.W. (2006). Microarray analyses in higher plants. *OMICS: A Journal of Integrative Biology* 10:455-473. PMID: 17233557.
118. Galbraith, D.W. (2007). Protoplast analysis using flow cytometry and sorting. In: Dolezel, J., Greilhuber, J., Suda, J. (eds.): *Flow Cytometry with Plant Cells*, Wiley-VCH, pp. 231-250.
119. Galbraith, D.W. (2007). Analysis of plant gene expression using flow cytometry and sorting. In: Dolezel, J., Greilhuber, J., Suda, J. (eds.): *Flow Cytometry with Plant Cells*, Wiley-VCH, pp.405-422.
120. Agrawal, A., Cronin, J.P., Tonazzi, J.C., Goodyear, A. G., LeCompte, R.S., Hogan, M.E., Galbraith, D.W. (2007). High surface area substrates for microarrays and methods to make same. U. S. Dept. of Commerce Patent 7,195,872.

121. Galbraith, D.W. (2007). Silica breaks through in plants. *Nature Nanotechnology* 2:272-273. PMID: 18654282.
122. Kris, R.M., Felder, S., Deyholos, M., Lambert, G.M., Botros, I., Martel, R., Seligmann, B., and Galbraith, D.W. (2007). High-throughput, high-sensitivity analysis of gene expression in *Arabidopsis thaliana*. *Plant Physiology* 144:1256-1266. PMID: 17496109.
123. Weng, Z., Barthelson, R., Gowda, S., Hilf, M.E., Dawson, W.O., Galbraith, D.W., and Xiong, Z. (2007). Persistent infection and promiscuous recombination of multiple genotypes of an RNA virus within a single host generate extensive diversity. *P.L.o.S. ONE* 2(9): e917. doi:10.1371 / journal.pone.0000917.
124. Keilin, T., Pang, X., Venkateswari, J., Halaly, T., Crane, O., Ogradovitch, A., Sherman, A., Volpin, H., Galbraith, D.W., and Or, E. (2007). Digital expression profiling of a grape-bud EST collection leads to new insight into molecular events during grape-bud dormancy release. *Plant Science* 173: 446-457.
125. Barthelson, R.A., Lambert, G.M., Vanier, C., Lynch, R.M., and Galbraith, D.W. (2007). Comparison of the contributions of the nuclear and cytoplasmic compartments to global gene expression in human cells. *B.M.C. Genomics* 8:340. PMID: 17894886.
126. Pang, X., Halaly, T., Crane, O., Keilin, T., Keren, A., Ogradovitch, A., Galbraith, D., and Or, E. (2007). Involvement of calcium signaling in dormancy release of grape buds. *Journal of Experimental Botany* 58:3249-3262.
127. Noizet, M., Harrabi, F., Vijayalakshmi, M.A., Galbraith, D.W., Thomas, D., and Thomasset, B. (2008). Targeted protein accumulation promoted by auto-assembly and its recovery from plant cells. *Biotechnology Journal* 3:392-402.
128. Zhang, C.Q., Barthelson, R.A., Lambert, G.M., and Galbraith, D.W. (2008). Characterization of cell-specific gene expression through fluorescence-activated sorting of nuclei. *Plant Physiology* 147:30-40. PMID: 18354040.
129. Yuan, J.S., Galbraith, D.W., Dai, S.Y., Griffin, P., and Stewart, C.N., Jr. (2008). Plant Systems Biology comes of age. *Trends in Plant Sciences* 13:165-171.
130. Edwards, J.D., Sweeney, M., Janda, J., Gaikwad, A., Liu, B., Leung, H., and Galbraith, D.W. (2008). Development of a high-throughput, low-cost genotyping platform based on oligonucleotide microarrays, and its evaluation in rice. *Plant Methods* 2008, 4:13. PMID: 18510771.
131. Facella, P., Lopez, L., Carbone, F., Galbraith, D.W., Giuliano, G., and Perrotta, G. (2008). Global profiling of diurnal and circadian transcriptional oscillations in tomato and their modulation by cryptochrome photoreceptors. *P.L.o.S. ONE* 3(7): e2798. doi:10.1371/journal.pone.0002798.
132. Mathiason, K., He, D., Grimplet, J., Galbraith, D.W., Or, E., and Fennell, A. (2008). Transcript profiling in *Vitis riparia* during chilling requirement fulfillment reveals coordination of gene expression patterns with optimized bud break. *Functional and Integrative Genomics* 9:81-96.
133. Galbraith, D.W. (2009). Global expression profiling of the corn genome. In: *Molecular Genetic Approaches to Maize Improvement* (A.L. Kriz and B.A. Larkins, editors). *Biotechnology in Agriculture and Forestry*, volume 63: Springer-Verlag, Berlin, pp. 251-266.
134. Sliwiska, E., Pisarczyk, I., Pawlik, A., and Galbraith, D.W. (2009). Measuring genome size of desert plants using dry seeds. *Botany* 87:127-135.
135. Luo, Q., Köksul, F., Janda, J., Samanta, M.P., Stolc, V., Galbraith, D.W., and Rock, C.D. (2009). Evidence for antisense transcription associated with microRNA target mRNAs in *Arabidopsis*. *P.L.o.S. Genetics* 5(4): e1000457. doi:10.1371/journal.pgen.1000457.
136. Lee, T.-H., Kim, Y.-K., Pham, T.T.M., Song, S.I., Kim, J.-K., Kang, K.Y., An, G., Jung, K., Galbraith, D.W., Kim, M., Yoon, U.-H., and Nahm, B.H. (2009). RiceArrayNet: A database for correlating gene expression from transcriptome profiling, and its application to the analysis of co-expressed genes in rice. *Plant Physiology* 151:16-33.
137. Galbraith, D.W. (2009). Simultaneous flow cytometric quantification of plant nuclear DNA contents over the full range of described angiosperm 2C values. *Cytometry* 75A:692-698. PMID: 19565637.
138. Andrés, F., Galbraith, D.W., Talón, M., and Domingo, C. (2009). Analysis of a new allele of *SE5* sheds light on the role of phytochromes in photoperiodic flowering in rice. *Plant Physiology* 151:681-690.
139. Ophir, R., Pang, Z., Venkateswari, J., Halaly, T., Laveea, S., Galbraith, D., and Or, E. (2009). Gene-expression profiling of grape bud response to two alternative dormancy-release stimuli expose

- possible links between impaired mitochondrial activity, hypoxia, ethylene-ABA interplay and cell enlargement. *Plant Molecular Biology* 71:403-423.
140. Galbraith D.W. (2009). Flow cytometry and sorting of plant protoplasts and cells. In: *Essential Cytometry Methods* (Z. Darzynkiewicz, J.P. Robinson, and M. Roederer. Eds.). Elsevier.
 141. Galbraith D.W. (2009). The rainbow of Fluorescent Proteins. In: *Essential Cytometry Methods* (Z. Darzynkiewicz, J.P. Robinson, and M. Roederer. Eds.). Elsevier.
 142. Mustroph, A., Zanetti, M.E., Jang, C.J.H., Galbraith, D.W., Girke, T., and Bailey-Serres, J. (2009). Profiling transcriptomes of discrete cell populations resolves altered cellular priorities during hypoxia in *Arabidopsis*. *Proc. Natl. Acad. Sci. U.S.A.* 106:18849-18854.
 143. Barthelson R.A., Qaisar U., and Galbraith, D.W. (2010). Functional analysis of the *Gossypium arboreum* genome. *Plant Molecular Biology Reporter* doi: 10.1007/s11105-009-0157-5.
 144. Galbraith, D.W., and Edwards, J.D. (2010). Applications of microarrays for crop improvement: here, there, and everywhere. *BioScience* 60:337-348.
 145. Galbraith, D.W. (2010). Flow cytometry and fluorescence-activated cell sorting in plants: the past, present, and future. *Biomedica* 2010;30(Suppl.):65-70.
 146. Zárate, X., Henderson, D.C., Phillips, K.C., Lake, A.D., and Galbraith, D.W. (2010). Development of high-yield autofluorescent protein microarrays using hybrid cell-free expression with combined *Escherichia coli* S30 and wheat germ extracts. *Proteome Science* 2010, 8:32 doi:10.1186/1477-5956-8-32. PMID: 20546627.
 147. Oh, D.H., Dassanayake, M., Haas, J.S., Kropornika, A., Wright, C., Paino d'Urzo, M., Hong, H., Ali, S., Hernandez, A., Lambert, G., Inan, G., Galbraith, D.W., Bressan, R.A., Yun, D.J., Zhu, J.-K., Cheeseman, J.M., and Bohnert, H.J. (2010). Genome structures and halophyte-specific gene expression of the extremophile *Thellungiella parvula* in comparison to *Thellungiella salsuginea* (*T. halophila*) and *Arabidopsis thaliana*. *Plant Physiology* 154:1040-1052.
 148. Liu, Y., Zhu, X.Y., Zhang, S., Bernardo, M., Edwards, J.D., Galbraith, D.W., Leach, J., Zhang, G., Liu, B., and Leung, H. (2011). Dissecting quantitative resistance against blast using heterogeneous inbred families in rice. *Theoretical and Applied Genetics* 122:341-353.
 149. Galbraith, D.W., Janda, J., and Lambert, G.M. (2011). Multiparametric analysis, sorting, and transcriptional profiling of plant protoplasts and nuclei according to cell type. *Methods in Molecular Biology* 699:407-429.
 150. Krishnan, A.R., Sweeney, M., Vasic, J., Galbraith, D.W., and Vasic, B. (2011). Barcodes for DNA sequencing with guaranteed error correction capability. *Electronics Letters* 47:236-237.
 151. Bourzac, K.M., Rounseville, M.P., Zarate, X., Maddula, V.S.R.K., Henderson, D.C., Luckey, J., Seligmann, B., and Galbraith, D.W. (2011). A high-density quantitative nuclease protection microarray platform for high throughput analysis of gene expression. *Journal of Biotechnology* 154:68-75. PMID: 21504771.
 152. Kimzey, M.J., Zarate, X., Galbraith, D.W. and Lau, S.S. (2011). Optimizing microarray-based *in situ* transcription-translation of proteins for MALDI mass spectrometry. *Analytical Biochemistry* 414:282-286.
 153. Galbraith, D.W. (2011). Frontiers in Genomic Assay Technologies: the grand challenges in enabling data-intensive biological research. *Frontiers in Genetics* 2:26. doi:10.3389fgene.2011. 00026. PMID 22303322.
 154. Vasic, B., Ravanmehr, V., and Galbraith, D.W. (2011). Analysis and synthesis of boolean cell-cycle gene regulatory networks. *Proc. 2011 Information Theory and Applications Workshop, San Diego*.
 155. Galbraith, D.W., Bennetzen, J.L., Kellogg, E.A., Pires, J.C., and Soltis, P.S. (2011). The genomes of all angiosperms: a call for a coordinated global census. *Journal of Botany* Article 646198 doi:10.1155/2011/646198.
 156. Baisakh, N., Ramana Rao, M. V., Rajasekaran, K., Subudhi, P., Janda, J., Galbraith, D., Vanier, C. and Pereira, A. (2012). Enhanced salt stress tolerance of rice plants expressing a vacuolar H⁺-ATPase subunit c1 (*SaVHAc1*) gene from the halophyte grass *Spartina alterniflora* Löisel. *Plant Biotechnology Journal* 10:453-464.

157. Galbraith, D.W., Lambert, G.M., Lasken, R., and Grindberg, R.V. (2012). Method for Classification of Cells Based on Gene Expression. Provisional Patent Application filed with the U. S. Dept. of Commerce.
158. Zhang, C.Q., and Galbraith, D.W. (2012). RNA interference-mediated gene knockdown within specific cell types. *Plant Molecular Biology* 80:169-176. PMID: 22740284.
159. Galbraith, D.W. (2012). Flow Cytometry and Cell Sorting: the Next Generation (guest volume editor). *Methods* Volume 57.
160. Galbraith, D.W. (2012). Flow Cytometry and Cell Sorting: the Next Generation: Introduction. *Methods* 57:249-250.
161. Galbraith, D.W., and Lambert, G.M. (2012). High-throughput monitoring of plant nuclear DNA contents via flow cytometry. *Methods in Molecular Biology* 918:311-325.
162. Wang, Z., Hobson, N., Galindo, L., McDill, J., Hawkins, S., Neutelings, G., Datla, R., Lambert, G., Galbraith, D.W., Cullis, C., Wong, G.K.-S., Wang J., and Deyholos, M.K. (2012). The genome of flax (*L. usitatissimum*) assembled *de novo* from short shotgun sequence reads. *Plant Journal* 72:461-473.
163. Qin, J., Scheuring, C.F., Wei, G., Zhi, H., Zhang, M., Huang, J.J., Zhou, X., Galbraith, D.W., and Zhang, H.-B. (2013). Identification and characterization of a repertoire of genes differentially expressed in developing top ear shoots between a superior hybrid and its parental inbreds in *Zea mays* L. *Molecular Genetics and Genomics* 288:691-705.
164. Grindberg, R.V., Yee-Greenbaum, J.L., McConnell, M.J., Novotny, M., O' Shaughnessy, A.L., Lambert, G.M., Araúz-Bravo, M.J., Lee, J., Fishman, M., Lin, X., Robbins, G.E., Lin, X., Venepally, P., Badger, J.H., Galbraith, D.W., Gage, F.H., and Lasken, R.S. (2013). RNA-Seq from single nuclei. *Proceedings of the National Academy of Sciences U.S.A.* 110:19802-19807.
165. Galbraith, D.W. (2014). Flow cytometry and sorting in *Arabidopsis*. In: *Arabidopsis Protocols* (3rd edition; J.J.S. Serrano, ed.). *Methods in Molecular Biology* 1062:509-537.
166. Zarate, X., and Galbraith, D.W. (2014). A cell-free expression platform for production of protein microarrays. *Methods in Molecular Biology* 1118:297-307.
167. Galbraith, D.W. (2014). Endoreduplicative standards for calibration of flow cytometric C-value measurements. *Cytometry* 85A:368-374.
168. Chen, S.-C., Cannon, C.H., Kua, C.-S., Liu, J.J., and Galbraith, D.W. (2014). Genome size variation in the Fagaceae and its implications for trees. *Tree Genetics and Genomes* 10:977-988.
169. Mittal, A., Balasubramanian, R., Cao, J., Singh, P., Subramanian, S., Hicks, G., Nothnagel, E.A., Abidi, N., Janda, J., Galbraith, D.W., and Rock, C.D. (2014). *TOPOISOMERASE 6B* is involved in chromatin remodeling associated with hormone and environmental control of carbon partitioning, secondary metabolite and cell wall synthesis, and epidermal morphogenesis in *Arabidopsis*. *Journal of Experimental Botany* 65:4217-4239.
170. Galbraith, D.W. (2014). Challenges and solutions in cytometric measurements of non-mammalian species. *Cytometry* 85A:831-832. Galbraith, D.W. (2014). Challenges and solutions in cytometric measurements of non-mammalian species. *Cytometry* 85A:831-832.
171. Naivar, M.A., and Galbraith, D.W. (2015). Digital data acquisition and processing. *Current Protocols in Cytometry* 71:10.19.1-10.19.12. doi: 10.1002/0471142956.cy1019s71.
172. Galbraith, D.W. (2015). Redrawing the frontiers in the age of post-publication review. *Frontiers in Genetics*: doi: 10.3389/fgene.2015.00198.w
173. Cantu-Bustosa, J.E., Vargas-Cortez, T., Morones-Ramirez, J.R., Balderas-Renteria, I., Galbraith, D.W., McEvoy, M.M., and Zarate X. (2016). Expression and purification of recombinant proteins in *Escherichia coli* tagged with the metal-binding protein CusF. *Protein Expression and Purification* 121:61-65 doi: 10.1016/j.pep.2016.01.007.
174. Samadder, P., Weng, N., Doetschman, T.C., Heimark, R., and Galbraith, D.W. (2016). Flow cytometry and single nucleus sorting for Cre-based analysis of changes in transcriptional states. *Cytometry* 89: 430-442.
175. Canady, M., Clark, C., Smith, R., Larsen, C., Gutierrez, A., Janda, J., Galbraith, D.W., Blaszczyk, A.G., and Wozniak, E.M. (2016). How the novel biostimulant CYT14 influences nutrient uptake of common

- foliar nutritional supplements as evidenced by genomics and ICP analysis. *Acta Horticulturae* 1148:69-75. doi: 10.17660/ActaHortic.2016.1148.8
176. Blaszcak, A.G., Smith, R., Gutierrez, A., Galbraith, D.W., Janda, J., Vanier, C., and Wozniak, E.M. (2016). Molecular mechanism of action for the novel biostimulant CYT31 in plants exposed to drought stress. *Acta Horticulturae* 1148: 85-92. doi: 10.17660/ActaHortic.2016.1148.10
 177. Galbraith, D.W., Sliwiska, E., and Samadder, P. (2017). Nuclear Cytometry: Analysis of the patterns of DNA synthesis and transcription using flow cytometry, confocal microscopy, and RNA sequencing. *Flow Cytometry Protocols*, 4th edition (Hawley and Hawley, eds.). *Methods in Molecular Biology*: In Press.
 178. Nicolini, A.M., Toth, T.D., Kim, S., Mandel, A.M., Galbraith, D.W., and Yoon, J.-Y. (2017). Mie scatter and interfacial tension based real-time quantification of colloidal emulsion nucleic acid amplification. *Advanced Biosystems*: In Press.

Summary of Invited Seminars and Presentations

Global interest in my work by the scientific community is highlighted by a total of 310 invited verbal presentations at scholarly meetings, seminars, training programs and workshops. Many of these presentations have been at international events and locations, and include multiple Plenary and Keynote invitations.

Invited Seminars and Presentations

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|-----|---------------|--|
| 1. | February 1977 | Carnegie Institution, Division of Plant Biology, Stanford University. |
| 2. | March 1977 | School of Biological Sciences, University of Nebraska-Lincoln. |
| 3. | June 1980 | Division of Biological Sciences, University of Kansas, Lawrence. |
| 4. | February 1982 | Department of Biology, University of Nebraska-Omaha. |
| 5. | March 1982 | Advanced Genetic Sciences, Manhattan, Kansas. |
| 6. | July 1982 | Fifth International Congress of Plant Tissue and Cell Culture, Lake Yamanaka, Japan. |
| 7. | July 1982 | Iwata Tobacco Experiment Station, Iwata, Japan. |
| 8. | July 1982 | Dept. of Agricultural Chemistry, Kyoto University, Japan. |
| 9. | July 1982 | Phytogen, Inc., Pasadena. |
| 10. | August 1982 | University Genetics Co., Norwalk. |
| 11. | November 1982 | University of Nebraska Medical Center, Dept. of Biochemistry, Omaha. |
| 12. | January 1983 | Dept. of Botany, North Carolina State University, Raleigh. |
| 13. | January 1983 | 15 th Miami Winter Symposium, Miami. |
| 14. | January 1983 | First Plant Molecular Biology Association Conference, Miami. |
| 15. | January 1983 | Dept. of Biology, Florida State University, Tallahassee. |
| 16. | May 1983 | Dept. of Botany and Plant Pathology, University of California, Riverside. |
| 17. | August 1983 | Sixth International Protoplast Symposium, Basel, Switzerland. |
| 18. | October 1983 | School of Biological Sciences, University of Nebraska-Lincoln. |
| 19. | January 1984 | 3M Corporation, St. Paul. |
| 20. | January 1984 | Dept. of Botany, University of Wisconsin-Madison. |
| 21. | January 1984 | Agrigenetics, Madison. |
| 22. | June 1984 | Tissue Culture Association Annual Meeting, Houston. |
| 23. | May 1985 | Dept. of Biology, University of Manchester Institute of Science and Technology. |
| 24. | May 1985 | Dept. of Biology, Northeast London Polytechnic. |
| 25. | June 1985 | Gordon Conference (Plant Tissue Culture), Plymouth. |
| 26. | November 1985 | First International Congress of Plant Molecular Biology, Savannah. |
| 27. | November 1985 | Department of Biometry and Plant Breeding, Cornell University. |

28. November 1985 Dept. of Horticulture, Purdue University.
29. June 1986 N.S.F.-Japan Workshop in Plant Biotechnology, Honolulu.
30. June 1986 Dept. of Biology, University of Hawaii.
31. August 1986 VIth International Congress of Plant Tissue and Cell Culture, Minneapolis.
32. November 1986 Dept. of Plant Sciences, University of Arizona, Tucson, Arizona.
33. November 1986 Los Alamos National Laboratory.
34. November 1986 C.N.R.S. Gif-sur-Yvette, France.
35. November 1986 E.N.E.A.-C.E.A., Casaccia, Rome.
36. November 1986 Plant Breeding Institute, Cambridge, England.
37. January 1987 Dept. of Radiation Biology, Colorado State University, Fort Collins.
38. February 1987 UCLA Conference on Plant Membranes, Park City.
39. April 1987 Graduate Student seminar series, University of Kansas, Lawrence.
40. August 1987 XIII Congress, International Society for Analytical Cytology (I.S.A.C.), Cambridge, England.
41. December 1987 Dept. of Plant Sciences, University of Arizona, Tucson, Arizona.
42. April 1988 Dept. of Biology, Texas A&M University, College Station.
43. May 1988 N.S.F. Inter-kingdom Workshop on Targeting in Eukaryotic Systems, Tampa.
44. May 1988 Biotechnology Program, University of Florida, Gainesville.
45. June 1988 Coulter Corporation, New York.
46. September 1988 E.M.B.O. Course, University of Cologne, West Germany.
47. September 1988 XIV I.S.A.C. Congress, Breckenridge, Colorado.
48. October 1988 Nebraska Criminal Defense Attorneys Association, Omaha.
49. August 1989 Annual Meeting of the American Chemical Society, Miami.
50. September 1989 E.M.B.O. Course, University of Cologne, West Germany.
51. January 1990 ENEA-CEA, Casaccia, Rome.
52. June 1990 Gordon Conference, Andover.
53. December 1990 Salk Institute, La Jolla.
54. February 1991 Dept. Radiation Oncology, University of Arizona Tucson, Arizona.
55. September 1991 E.M.B.O. Course, University of Cologne, West Germany.
56. September 1991 XVI I.S.A.C. Congress, Bergen, Norway.
57. October 1991 Rocky Mountain Cytometry Association Biennial Meeting, Vail.
58. January 1992 Zynaxis, Inc., Philadelphia.
59. February 1992 Biotechnology Program, Oregon State University, Corvallis.
60. February 1992 Molecular Probes, Inc., Eugene.
61. February 1992 Dept. of Radiation Biology, Colorado State University, Fort Collins.
62. March 1992 Dept. of Biology, Arizona State University, Tempe.
63. April 1992 U.S.D.A. Western Regional Research Center, Albany.
64. November 1993 Cell and Molecular Biology Program, Colorado State University, Fort Collins.
65. February 1994 Dept. Anatomy, University of Arizona, Tucson, Arizona.
66. June 1994 Smith-Kline-Beecham PLC, London, England.
67. June 1994 Dept. of Biological Sciences, Oxford Brookes University, England.
68. June 1994 Dept. of Chemical Engineering, University of Birmingham, England.
69. July 1994 Scottish Crop Research Institute, Dundee. Scotland.
70. November 1994 Noble Foundation, Ardmore, Oklahoma.
71. November 1994 ENEA-CEA, Casaccia, Rome, Italy.
72. November 1994 Biotechnology Program, University of Nebraska-Lincoln.
73. June 1995 Dept. of Biological Sciences, Warwick University, England.
74. June 1995 Dept. of Biology, De Montfort University, Leicester, England.
75. July 1995 Dept. of Biology, University of Oregon, Eugene.

76. November 1995 Monsanto Corporation, St. Louis, Missouri.
77. April 1996 XVIIIth I.S.A.C. Congress, Rimini, Italy.
78. April 1996 CNR, Milan, Italy.
79. May 1996 Ceregen, St. Louis, Missouri.
80. August 1996 Czech Academy of Sciences, Olomouc, Czech Republic.
81. August 1996 Czech Academy of Sciences, Ceske Budejovice, Czech Republic.
82. October 1996 Pioneer Hi-Bred, Johnston, Iowa.
83. December 1996 Sanger Center, Cambridge, England.
84. December 1996 Carnegie Institution, Stanford University, California.
85. April 1997 Dept. of Biology, University of Pennsylvania, Philadelphia.
86. April 1997 Biotechnology Program, Pennsylvania State University, State College.
87. July 1997 Technical University of Compiègne, France.
88. September 1997 Royal Botanical Gardens, Kew, England.
89. October 1997 International GFP Conference, New Brunswick, New Jersey.
90. October 1997 Plant Biology Program, Rutgers University, New Jersey.
91. January 1998 Biotechnology Program, Oregon State University, Corvallis.
92. February 1998 XIXth I.S.A.C. Congress, Colorado Springs.
93. May 1998 Scripps Research Institute, La Jolla, California.
94. June 1998 Czech Academy of Sciences, Olomouc, Czech Republic.
95. June 1998 Jagiellonian University, Krakow, Poland.
96. June 1998 Optical Biology Center, University of California, Irvine.
97. July 1998 C.N.R.S. Institute for Plant Molecular Biology, Strasbourg, France.
98. July 1998 IVth International Symposium on P450 Biodiversity, Strasbourg, France.
99. July 1998 Cornell University, Ithaca, New York.
100. September 1998 Annual Royal Microscopical Society Flow Cytometry Course, Sheffield University, England.
101. September 1998 Quantum Biotech, La Jolla, California.
102. November 1998 A.S.P.P. West Regional Symposium, San Francisco.
103. December 1998 North Carolina Biotechnology Center, Research Triangle Park, North Carolina.
104. January 1999 Third Kananaskis Tumor Heterogeneity Meeting, Calgary, Canada.
105. February 1999 U.S.D.A.-ARS, Plum Island, New York.
106. March 1999 Dept. of Biological Sciences, Durham University, Durham, England.
107. March 1999 Dept. of Plant Pathology, University of Arizona, Tucson, Arizona.
108. March 1999 Purdue University, Plant Biology Seminar Program, West Lafayette, Indiana.
109. April 1999 University of Washington, Dept. of Botany, Seattle, Washington.
110. April 1999 University of Minnesota, Dept. of Plant Biology, St. Paul, Minnesota.
111. May 1999 IInd International GFP Conference, San Diego, California.
112. June 1999 Annual Course in Flow Cytometry, Los Alamos National Laboratory, Los Alamos, New Mexico.
113. July 1999 U.T.C. Compiègne, France.
114. August 1999 C.I.P., Lima, Peru.
115. September 1999 Epicyte Pharmaceuticals, San Diego, California.
116. September 1999 Novartis Agriculture Discovery Institute, San Diego, California.
117. September 1999 University of Nebraska-Lincoln. Lincoln, Nebraska.
118. September 1999 Dept. of Physiology, University of Arizona, Tucson, Arizona.
119. November 1999 Chips to Hits '99, Berkeley, California.
120. February 2000 BioRad, Hercules, California.
121. March 2000 Society for Experimental Biology, Exeter, England.
122. April 2000 New Mexico State University, Las Cruces, New Mexico.
123. May 2000 KeyGene, Wageningen, Holland.

124. May 2000 XXth I.S.A.C. Congress, Montpellier, France.
125. May 2000 I.N.R.A., Montpellier, France.
126. June 2000 New York University, New York.
127. July 2000 Vth International Symposium on P450 Biodiversity, Elsinore, Denmark.
128. August 2000 E.M.B.O. Course, Uppsala, Sweden.
129. August 2000 Agricultural University of Uppsala, Sweden.
130. August 2000 Miltenyi Biotec, GmbH, Bergisch Gladbach, Germany.
131. October 2000 Stratagene Inc., La Jolla, California.
132. October 2000 The Salk Institute, La Jolla, California.
133. October 2000 Ceres Inc., Malibu, California.
134. November 2000 Los Alamos National Laboratory, Los Alamos, New Mexico.
135. November 2000 University of New Mexico, Albuquerque, New Mexico.
136. December 2000 John Innes Institute, Norwich, England.
137. December 2000 Cambridge University, England.
138. December 2000 Oxford University, England.
139. January 2001 Agilent, Palo Alto, California.
140. January 2001 BASF, Inc., Raleigh, North Carolina.
141. February 2001 Biomath Program, University of Arizona, Tucson, Arizona.
142. February 2001 Biomedical Engineering Program, University of Arizona, Tucson, Arizona.
143. March 2001 Brazil International Genome Conference, Agram dos Reis, Brazil.
144. March 2001 Synergen, Brasilia, Brazil.
145. March 2001 EMBRAPA, Sete Lagoas, Brazil.
146. April 2001 University of Arkansas, Little Rock, Arkansas.
147. May 2001 Royal Botanical Gardens, Kew, England.
148. June 2001 Los Alamos National Laboratory, Los Alamos, New Mexico.
149. September 2001 Genetics Program, University of Arizona, Tucson, Arizona.
150. October 2001 Dept. of Plant Biology, Arizona State University, Tempe, Arizona.
151. November 2001 GeneMachines, San Carlos, California.
152. January 2002 Breault Research, Tucson, Arizona.
153. January 2002 G.T.E.C., Tucson, Arizona.
154. January 2002 Xth Plant, Animal and Microbial Genome meeting, San Diego, California (plenary speaker).
155. April 2002 Stowers Institute for Medical Research, Kansas City, Kansas.
156. April 2002 Iowa State University, Ames, Iowa.
157. April 2002 Macalester College, St. Paul, Minnesota.
158. May 2002 XXIst I.S.A.C. Congress, San Diego, California (plenary speaker).
159. July 2002 Annual Meeting of the American Phytopathological Society, Milwaukee.
160. September 2002 Queenstown Molecular Biology Meeting, Queenstown, New Zealand.
161. September 2002 HortResearch, Auckland, New Zealand.
162. September 2002 Second Virtual Conference on Genomics and Bioinformatics, Washington, D.C.
163. September 2002 N.S.F. Annual Plant Genome Grantee meeting, Washington D.C.
164. November 2002 Annual Meeting of the Crop Science Society of America, Indianapolis, Indiana.
165. January 2003 XIth Plant & Animal Genome conference, San Diego, California.
166. March 2003 Duke University, Department of Biology, North Carolina.
167. April 2003 Texas A&M University, Genetics Program, College Station, Texas.
168. May 2003 1st International Cytomics Conference, Wales (keynote speaker).
169. May 2003 2nd Annual Meeting of the Czech Society for Analytical Cytology, Brno, Czech Republic (keynote speaker).
170. June 2003 Workshop on redox regulation in plants, Washington University, St. Louis, Missouri.

171. June 2003 Biennial National Flow Cytometry Course, Los Alamos, New Mexico.
172. July 2003 SEB Symposium, Durham, England (keynote speaker).
173. September 2003 NSF Annual Plant Genome Grantee meeting, Washington D.C.
174. December 2003 University of Illinois, Department of Crop Sciences, Urbana-Champaign, Illinois.
175. January 2004 XIIth Plant & Animal Genome Conference, San Diego, California.
176. March 2004 University of Washington, Department of Biology, Seattle, Washington.
177. April 2004 Crop Functional Genomics 2004, Jeju, South Korea.
178. April 2004 Seoul National University, Seoul, South Korea.
179. May 2004 XXIInd I.S.A.C. Congress, Montpellier, France.
180. October, 2004 1st Plant Functional Genomics Conference, Barossa, Australia (plenary speaker).
181. October, 2004 University of Queensland, Brisbane, Australia.
182. January 2005 XIIIth Plant & Animal Genome Conference, San Diego, California.
183. March 2005 Czech Academy of Sciences, Olomouc, Czech Republic.
184. April 2005 Carleton College, Minnesota.
185. May 2005 Victorian Microarray Technology Consortium, Melbourne, Australia (keynote speaker).
186. June 2005 First Portuguese National Microarray Workshop, Vila Real, Portugal (organizer and presenter).
187. June 2005 U.S.D.A. N.R.I. Annual Grantee Meeting, Little Rock, Arkansas.
188. June 2005 Biennial National Flow Cytometry Course, Los Alamos, New Mexico.
189. June 2005 Pacific Northwest Conference, Richland, Washington.
190. August 2005 Insightful Corporation, Seattle, Washington.
191. September 2005 NSF Annual Plant Genome Grantee Meeting, Washington D.C.
192. November 2005 International Rice Research Institute, Los Baños, The Philippines.
193. November 2005 US-AID Linkage Program Meeting, Manila, The Philippines.
194. January 2006 XIVth Plant & Animal Genome Conference, San Diego, California.
195. January 2006 C.N.R.S./I.N.R.A. Evry, Paris, France.
196. February 2006 U.S.D.A. N.R.I. Annual Grantee Meeting, Woodlands, Texas.
197. March 2006 Oregon Health Sciences Center, Portland, Oregon.
198. April 2006 University of Nevada, Las Vegas, Nevada.
199. June 2006 C.S.I.R.O., Canberra, Australia.
200. June 2006 Biennial National Flow Cytometry Course, Bowdoin College, Maine.
201. August 2006 Second Plant Microarray Short Course On Design and Analysis of Plant Microarray Experimentation, Boston, Massachusetts (plenary speaker).
202. August 2006 Gordon Conference, Mt. Holyoke College, Massachusetts.
203. October 2006 Fourth International Rice Functional Genomics Conference, Montpellier, France.
204. January 2007 XVth Plant & Animal Genome Conference, San Diego, California.
205. January 2007 University of Arizona Biomedical Engineering Program, Tucson, Arizona.
206. May 2007 Science Foundation Arizona, Tempe, Arizona.
207. May 2007 Guangdong Academy of Agricultural Sciences, Guangzhou, China.
208. May 2007 Huazhong Agricultural University, Wuhan, China.
209. May 2007 Chinese Agricultural University, Beijing, China.
210. June 2007 Biennial National Flow Cytometry Course, Los Alamos, New Mexico.
211. June 2007 University of Colorado, Boulder, Colorado.
212. June 2007 Annual Meeting of the Czech Society for Analytical Cytology, Brno, Czech Republic (keynote speaker).
213. June 2007 Czech Academy of Sciences, Olomouc, Czech Republic.
214. July 2007 Max Planck Institute, Golm, Germany.
215. September 2007 Ceres, Inc., Thousand Oaks, California.

216. September 2007 Pioneer Hi-Bred, Ames, Iowa.
217. September 2007 University of Nebraska-Lincoln, Biotechnology Program, Lincoln, Nebraska.
218. October 2007 University of Arizona, Interdisciplinary Graduate Program in Genetics, Tucson, Arizona.
219. October 2007 Second Portuguese National Microarray Workshop, Vila Real, Portugal (organizer and presenter).
220. October 2007 Fifth International Rice Functional Genomics Conference, Tsukuba, Japan.
221. November 2007 University of Missouri, IPG Program, Columbia, Missouri.
222. November 2007 University of Tennessee, Knoxville, Tennessee.
223. November 2007 Oak Ridge National Laboratory, Oak Ridge, Tennessee.
224. January 2008 XVIth Plant & Animal Genome Conference, San Diego, California.
225. January 2008 BIO5 Institute, University of Arizona, Tucson, Arizona.
226. March 2008 Department of Plant Systems Biology, Ghent University, Belgium.
227. May 2008 XXIVth I.S.A.C. Congress, Budapest, Hungary.
228. May 2008 Royal Botanical Gardens, Kew, England.
229. June 2008 Biennial National Flow Cytometry Course, Bowdoin College, Maine.
230. September 2008 SUNY Stony Brook, New York.
231. November 2008 Vidar Systems Corporation, Herndon, Virginia.
232. January 2009 XVIIth Plant & Animal Genome Conference, San Diego, California.
233. February 2009 CENICAFE, Chinchina, Colombia.
234. February 2009 2nd Annual Meeting of the Indian Cytometry Society, Bhubaneswar, India (plenary speaker).
235. February 2009 National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi, India.
236. February 2009 Delhi University, New Delhi, India.
237. February 2009 International Symposium on Recent Developments in Molecular Technologies, Panjab University, Chandigarh, India (plenary speaker).
238. April 2009 XXXIVth Annual Meeting of the Portuguese Genetics Society, Lisbon (keynote speaker).
239. June 2009 Biennial National Flow Cytometry Course, Albuquerque, New Mexico.
240. September 2009 2nd Biennial Flow Cytometry Conference, Food Research Institute, Norwich, England.
241. October 2009 Max Planck Institute, Tuebingen, Germany.
242. October 2009 19th Annual Meeting of the German Society for Cytometry, Leipzig, Germany (keynote speaker).
243. October 2009 G.I.C. (Italian Cytometry Society) Annual Meeting, Ferrara, Italy (keynote speaker).
244. October 2009 E.N.E.A. Casaccia, Rome, Italy.
245. October 2009 Donald Danforth Center, St. Louis, Missouri.
246. November 2009 Xishuangbanna Tropical Botanical Garden, China.
247. December 2009 University of Massachusetts, Amherst, Massachusetts.
248. January 2010 XVIIIth Plant & Animal Genome Conference, San Diego, California.
249. May 2010 SAGE Bionetworks, Seattle, Washington.
250. May 2010 XXVth I.S.A.C. Congress, Seattle, Washington.
251. May 2010 Cenicafe, Manizales, Colombia.
252. May 2010 IVth International Congress in Flow Cytometry, Bogota, Colombia (plenary speaker).
253. June 2010 Biennial National Flow Cytometry Course, Bowdoin College, Maine.
254. July 2010 Association for Tropical Biology and Conservation workshop, Bali, Indonesia.

255. September 2010 Microbial Single Cell Genomics Workshop 2010, Bigelow Laboratory, Boothbay Harbor, Maine, (plenary speaker).
256. October 2010 Massachusetts General Hospital, Boston, Massachusetts.
257. January 2011 XIXth Plant & Animal Genome Conference, San Diego, California.
258. February 2011 University of Liverpool, England.
259. February 2011 Czech Academy of Sciences, Olomouc, Czech Republic.
260. April 2011 Biomath Program, University of Arizona, Tucson, Arizona.
261. May 2011 CYTO 2011: XXVIth Congress of the International Society for Advancement of Cytometry, Baltimore, Maryland (plenary speaker).
262. June 2011 Stem Cell Institute, University of California, Irvine, California.
263. June 2011 Biennial National Flow Cytometry Course, Albuquerque, New Mexico.
264. June 2011 Chinese Agricultural University, Beijing, China.
265. June 2011 Workshop on Tropical Biodiversity and Genomics, Xishuangbanna Tropical Botanical Gardens, China (plenary speaker).
266. June 2011 Hong Kong University, China.
267. June 2011 Beijing Genomics Institute, Shenzhen, China.
268. July 2011 Western New York Flow Cytometry Group, Rochester, New York.
269. July 2011 University of Rochester, Rochester, New York.
270. October 2011 University of Toronto, Canada.
271. November 2011 SUMMIT2011: Inaugural meeting of the Southern California Flow Cytometry Association, Los Angeles, California (plenary speaker).
272. January 2012 XXth Plant & Animal Genome Conference, San Diego, California.
273. February 2012 Genetic Engineering News Webinar.
274. April 2012 Biotechniques Webinar.
275. June 2012 Biennial National Flow Cytometry Course, Bowdoin College, Maine.
276. June 2012 Regeneron, Inc., White Plains, New York.
277. July 2012 Royal Botanic Gardens, Kew, London, England.
278. July 2012 Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria.
279. September 2012 A.L.A.R.C., Maricopa, Arizona.
280. September 2012 Dept. of Chemistry and Biochemistry, University of Arizona, Tucson, Arizona.
281. November 2012 DowAgrosciences, Inc., Indianapolis, Indiana.
282. December 2012 Institute on Science for Global Policy, Tucson.
283. January 2013 FloCyte Associates Workshop, San Diego, California.
284. January 2013 CellTech 2013 - Flow Cytometry, San Diego, California (keynote speaker).
285. March 2013 North Carolina State University, Raleigh, North Carolina.
286. March 2013 FloCyte Associates Workshop, University of North Carolina, Chapel Hill, North Carolina.
287. June 2013 Biennial National Flow Cytometry Course, Albuquerque, New Mexico.
288. July 2013 Queensland Flow Cytometry Workshop, Queensland Institute of Medical Research, Brisbane, Australia.
289. July 2013 University of Queensland, Brisbane, Australia.
290. August 2013 Arizona Biological and Biomedical Sciences Program, Tucson, Arizona.
291. November, 2013 Arizona Cancer Bioimaging Program, Tucson, Arizona.
292. January 2014 XXIInd Plant & Animal Genome Conference, San Diego, California.
293. January 2014 PepTalk 2014, Palm Springs, California (keynote speaker).
294. May 2014 Institute of Plant Sciences, Volcani Center, Beit Dagan, Israel.
295. May 2014 Department of Plant Sciences, Weizmann Institute of Science, Rehovot, Israel.
296. May 2014 CYTO2014, Fort Lauderdale, Florida.
297. June 2014 Biennial National Flow Cytometry Course, Bowdoin College, Maine.

298. October 2014 SELECTBIO Advances in Plant Genomics online conference.
299. December 2014 Symposium & Workshop IARI (Indian Agricultural Research Institute), New Delhi, India.
300. December 2014 Symposium Punjab Agricultural University, Ludhiana, India.
301. December 2014 Symposium FACSAcademy, Jamia Hamdard University, New Delhi, India.
302. December 2014 Symposium, School of Life Sciences, University of Hyderabad, India.
303. December 2014 Symposium & Workshop, Calcutta University, India.
304. December 2014 Department of Botany, Delhi University, New Delhi.
305. January 2015 XXIIIrd Plant and Animal Genome Conference, San Diego, California.
306. March 2015 SEFCIG Meeting, Atlanta.
307. June 2015 Biennial National Flow Cytometry Course, Albuquerque, New Mexico.
308. June 2015 CYTO2015, Glasgow, Scotland.
309. September 2015 3rd Plant Genomics Congress USA, St Louis, Missouri.
310. January 2016 XXIVth Plant and Animal Genome Meeting, San Diego, California.
311. April 2016 Department of Biology, University of South Carolina.
312. April 2016 Department of Biochemistry, Oklahoma State University.
313. June 2016 Biennial National Flow Cytometry Course, Bowdoin College, Maine.
314. February 2017 U.S.D.A.-A.L.A.R.C., Maricopa, Arizona.
315. March 2017 2nd Annual A.B.R.C. Research Conference, U.A.-C.O.M., Phoenix, Arizona.
316. April 2017 Institute for Plant Stress Biology, Henan University, Kaifeng, China.
317. June 2017 CYTO2017, Boston, Massachusetts.
318. June 2017 Biennial National Flow Cytometry Course, Albuquerque, New Mexico.
319. July 2017 Becton Dickinson/Biocompare Webinar.

Summary of Extramural Grant Activity

I have been continuously funded from extramural sources since 1979. Total funds received as P.I. or co-P.I. amount to \$43,837,839, with \$42,062,193 accruing whilst employed at the University of Arizona. Direct expenditures through Galbraith accounts in the School of Plant Sciences and in BIO5 are about 54% of this amount. I have received funding from federal agencies including N.S.F., D.O.D., U.S.D.A., D.O.E., N.I.H. (three Institutes), C.D.C., and B.A.R.D., international agencies such as N.A.T.O., the International Rice Research Institute, and the Human Frontiers Science Program, state funding from Science Foundation Arizona, the Arizona Department of Health, and the Nebraska Soybean Distribution, Utilization, and Marketing Board., and industry funding from Agrigenetics, Inc., and University Genetics, Inc. I am currently funded by N.S.F., U.S.D.A.-B.A.R.D., and the Arizona Department of Health. I have two funding applications under evaluation at D.O.D., and one at N.S.F.

These grants have supported projects that ranged from individual investigator-initiated activities, to large-scale collaborative research programs involving investigators within sister academic and research institutions both across the U.S.A. and internationally. I have been P.I. for several large national and international collaborations.

In addition to running the competitively funded projects described above, I have had considerable administrative experience gained from operating a not-for-profit microarray facility within the School of Plant Sciences. As mentioned previously, I pioneered the use of microarrays for plants, as a part of several grant proposals funded by NSF, and was able to further develop this activity into a microarray production, distribution, and education program at the University of Arizona. Since FY03-FY11, my group collectively printed and distributed approximately 60,000 DNA microarrays to the research community world-wide,

the revolving accounts processed \$1,770,408 in revenue, and I designed and offered eleven week-long workshops in microarray technologies in Tucson and three at international locations.

I have been active in interactions with industry, through consulting (Agrigenetics, Monsanto, Accuri (Becton Dickinson), Ventana Medical Systems, High Throughput Genomics, and Chromocell; I served on the Scientific Advisory Board of Accuri before this company was purchased by Becton-Dickinson), grant mechanisms (SBIR funding), patents, and publications. Particularly noteworthy was a large, recently-completed project funded by Science Foundation Arizona. This project translated improved technology developed at the UA to the private sector, with a resultant return on investment (in terms of further funding received by the private sector partnership) in the amount of ~\$24M, with HTG subsequently going public with an IPO in 2015. This is recognized as a major example of the way research at the UA can facilitate development of biotechnology companies in the Tucson area.

Listing of Extramural Funding

February, 1979: U.S.D.A. Competitive Grants Program in Biological Stress. Grant amount \$35,000. Funding period 9/79-8/82.

November, 1979: N.S.F. Biological Instrumentation Program. Purchase of Flow Cytometer - Cell Sorter. Grant amount \$130,000.

January, 1980: U.S.D.A. Competitive Grants Program in Genetic Mechanisms for Crop Improvement. Grant amount \$50,000. Funding period 9/80-8/82.

February, 1980: N.S.F. I.S.E.P. Biology of Cells Laboratory. Grant amount \$39,846.

October, 1981: University Genetics. Grant amount \$100,800. Funding period 1/82-12/82.

October, 1981: N.I.H. (Co-P.I. with S. Schuster and D. Wylie). Grant amount \$245,000. Funding period 9/82-8/85.

November, 1982: Agrigenetics Research Associates. Grant amount \$410,000. Funding period 2/83-1/88.

December, 1982: U.S.D.A. Competitive Grants Program in Biological Stress. Grant amount \$70,000. Funding period 9/83-8/85.

January, 1984: Nebraska Soybean Distribution, Utilization and Marketing Board. (co-P.I. with J. Specht). Grant amount \$90,000. Funding period 6/84-5/87.

November, 1984: D.O.E. Division of Basic Energy Research. Grant amount \$230,000. Funding period 5/85-5/88.

June, 1984: N.S.F. Developmental Biology Program. Grant amount \$250,000. Funding period 3/85-2/88.

November, 1984: N.S.F. Biological Instrumentation Program. Grant amount \$125,000. Funding period 10/85-9/87.

January, 1987: N.S.F. Biological Instrumentation Program. Project Title: Techniques of flow cytometric analysis. Grant amount: \$298,180. Funding period 11/87-10/90.

May, 1988: D.O.E. Division of Basic Energy Research. Project Title: Controls of the plant endomembrane-secretory pathway. Grant amount: \$243,000. Funding period 6/88-5/91.

February, 1989: D.O.E. Research Instrumentation Program. Project Title: Purchase of cell sorters. Grant amount: \$256,000. Funding period 2/89-1/90.

June, 1989: U.S.D.A. Competitive grants program. Project Title: Modeling effects of UV-B irradiation. Grant amount: \$150,000 (Hans Bohnert, co-P.I.). Funding period: 10/89-9/92.

April, 1992: N.S.F. Instrumentation / Instrument Development Program. Project Title: Flow cytometry: digital processing of molecular information. Grant amount: \$420,000 (J. Rodriguez, T. Yopp, co-P.I.s). Funding period: 4/92-9/95.

August, 1992: N.S.F. Cell Biology Program. Project Title: Molecular dissection of the plant golgi: a heterologous approach. Grant amount: \$88,000. Funding period: 8/92-1/95.

October, 1992: D.O.E./N.S.F./U.S.D.A. Joint Program on Collaborative Research in Plant Biology (E. Bernays, P.I., K. Feldmann, co-P.I.). Project Title: Interdisciplinary Research Training Group on Plant-Insect Interactions. Grant amount: \$1,300,000. Funding period: 10/92-9/97.

August 1993; U.S. Department of Agriculture N.R.I.C.G.P. Project Title: Targeting to the inner nuclear membrane; information from a plant viral glycoprotein Grant amount: \$110,000. Funding period: 8/93-7/95.

March, 1995: D.O.E. Research Instrumentation Program. Project Title: Purchase of confocal microscope. Grant amount: \$220,000. Funding period: 1996.

August, 1995: N.S.F. (J. Dolezel, co-P.I.). Project Title: Flow karyotyping and sorting of translocations in maize. Grant amount: \$38,498. Funding period: 1995-1998.

January, 1996: N.S.F. Instrumentation / Instrument Development Program. Project Title: Flow cytometry: digital processing of molecular information. Grant amount: \$50,000 (J. Rodriguez, co-P.I.). Funding period: 1/96-12/96.

November, 1996: U.S.D.A./N.R.I.C.G.P. Plant Genome Program. Novel techniques for gene characterization in higher plants. Grant amount: \$243,574. Funding period: 11/96-10/99.

February, 1997: NSF Instrumentation/Instrument Development Program (J. Rodriguez, and J. Sasian, co-P.I.s). Project Title: Flow cytometry: digital processing of molecular information. Grant amount: \$548,046. Funding period: 2/97-1/00.

February, 1997: Department of the Army (H. Bohnert, V. Chandler, R. Feyereisen, K. Feldmann, B. Larkins, co-P.I.s). Project Title: Molecular analysis of the structure and function of plant genomes. Grant amount: \$273,640. Funding period: 2/97-2/98.

May, 1997: NSF Joint Program on Collaborative Research in Plant Biology (D. Galbraith, K. Feldmann, G. Thompson, R. Feyereisen, J. Hildebrand, co-P.I.s). Project Title: Interdisciplinary Research Training Group on Plant-Insect Interactions. Grant amount: \$850,000. Funding period: 5/97-4/02.

May, 1997: U.S.D.A.-N.R.I.C.G.P. (Plant Genome; K. Feldmann, R. Feyereisen, co-P.I.'s). Project Title: Systematic reverse genetics of the P450 superfamily in *Arabidopsis*. Grant amount: \$350,000. Grant period: 1997-1999.

September, 1998: N.S.F. (V. Walbot, P.I., Chandler, Galbraith, Larkins, and others Co-P.I.s). Project Title: Maize gene discovery, sequencing and phenotypic analysis. Grant amount: \$12,604,901. Grant period: 1998-2003.

September, 1998: N.S.F. (H. Bohnert, P.I., Zhu, Galbraith, and others Co-PI's). Project Title: Genomics of stress tolerance. Grant amount: \$8,464,171. Grant period: 1998-2002.

October, 1998: N.I.H. (J. Rodriguez, co-P.I.). Project Title: Wavelet analysis of flow cytometric data. Grant amount: \$221,087. Grant period: 1998-2001.

August, 1999: Human Frontiers Program (K. Feldmann, P.I., D. Galbraith and others, Co-P.I.s). Project Title: Systematic reverse genetics of the P450 superfamily in *Arabidopsis*. Grant amount: \$600,000. Grant period: 1999-2003.

October, 1999: Agency: N.S.F. (D. Galbraith, P.I., B. Larkins, G. Thompson, H. Bohnert, Co-P.I.s). Project Title: Two-photon confocal microscope for biological imaging in plants. Grant amount: \$334,500. Grant period: 1999-2002.

June, 2000: Agency: N.S.F. (D. Galbraith, P.I., V. Chandler, R. Feyereisen, H. Bohnert, Co-PI's). Project Title: Acquisition of equipment for high-throughput Genomics Studies. Grant amount: \$532,000. Grant period: 2000-2003.

April, 2002: Agency: N.S.F. (D. Galbraith, PI, J. Dolezel, Co-PI). Project Title: Microarray-based analysis of plant genome structure. Grant amount: \$40,040. Grant period: 2002-2004.

October, 2002: Agency: N.S.F. (D. Galbraith, PI, J. Bailey-Serres, Co-PI). Project Title: Technology Development: Novel techniques for discovery of patterns of gene regulation within complex eukaryotic tissues. Grant amount: \$626,227. Grant period: 2002-2005.

November, 2002: Agency B.A.R.D. (D. Galbraith, E. Orr, Co-P.I.'s). Project Title: Exploring mechanisms involved in grape bud dormancy. Grant amount: \$157,401. Grant period: 2002-2005.

July, 2003: Agency N.I.H. (H. Brooks, PI, D. Galbraith, co-PI). Project Title: Targeting nuclei for renal cell specific gene analysis. Grant amount: \$295,790. Grant period: 2003-2005.

July, 2003: Agency P.H.S.-C.D.C. (R. Woosley, PI, D. Galbraith, co-PI). Project Title: DNA microarrays as a method to detect the contamination of foods. \$96,314. Grant period: 2003-2004.

August, 2003: Agency: U.S.D.A. (Z. Xiong, PI, D. Galbraith, co-P.I.). Project Title: Genome typing of citrus tristeza virus using oligonucleotide microarrays. Grant amount: \$169,000. Grant period: 2003-2005.

October 2003: Agency: N.S.F. (V. Chandler, P.I., D. Galbraith, and others Co-P.I.s). Project Title: Microarray resources for maize research. Grant amount: \$3,658,458. Grant period: 2003-2006.

April 2004: Agency N.S.F. (D. Galbraith, P.I., P. Haynes, co-P.I.). Project Title: Global analysis of the nuclear proteome. Grant amount: \$100,000. Grant period: 2004-2005.

June 2004: Agency: N.I.H. (D. Galbraith, P.I., R. Lynch, co-P.I.). Project Title: Functional genomics of nuclei. Grant amount: \$376,250. Grant period: 2004-2006.

November 2004: Agency: U.S.D.A.-N.R.I. (D. Galbraith, P.I., H. Leung, Manila, co-P.I.). Project Title: Microarray-based QTL mapping in rice. Grant amount: \$765,462. Grant period: 2004-2007.

May 2005: Agency N.S.F. (D. Galbraith, P.I., P. Haynes, S. Lau, D. Gang, co-P.I.s). Project Title: VCA: Self-assembling Protein Microarrays: Development of a Universal Resource for the Plant Research Community. Grant amount: \$1,674,110. Grant period 2005-2007.

July 2005: Agency: U.S.D.A. (C. Rock, Texas Tech, P.I., D. Galbraith, co-P.I.). Project Title: Functional Genomics of ABI1-like protein phosphatases and ABI3-like transcription factors by transcriptome profiling of maize protoplasts. Grant amount: \$100,000. Grant period: 2005-2007.

August 2005: Agency: N.S.F. (D. Gang, P.I., D. Galbraith, R. Wing, co-P.I.s). Project Title: Acquisition of instrumentation for -omics research at the University of Arizona. Grant amount: \$192,350. Grant period: 2005-2008.

September 2005: Agency: U.S.D.A. (Z. Xiong, P.I., D. Galbraith co-P.I.). Project Title: Genome typing of citrus tristeza virus using oligonucleotide microarrays. Grant amount: \$205,667. Grant period: 2005-2007.

December 2006: Agency: I.R.R.I. (D. Galbraith, P.I.). Project Title: Accelerated development of advanced rice genetic resources through whole-genome selection. Grant amount: \$60,000. Grant period: 2006-2008.

June 2007: Agency: Science Foundation Arizona (D. Galbraith, P.I., B. Seligmann, co-P.I.). Project Title: Center for Chemical Genomics and Translational Research. Grant amount: \$3,846,092. Grant period: 2007-2011.

September 2008: Agency: N.S.F. (B. Vasic, P.I., M. Marcellin, D.W. Galbraith, co-P.I.s). Project Title: TF08: Error correction algorithms for DNA repair: inference, analysis, and intervention. Grant amount: \$300,000. Grant period: 2008-2012.

August 2009: Agency: N.I.H. (B. Seligmann, P.I., D.W. Galbraith, co-P.I.). Project Title: miRNA HD array platform (S.B.I.R.). Grant amount: \$220,999. Grant period: 2009-2011.

June 2012: Agency: N.I.H. (T. Doetschman, co-P.I.). Project Title: Cell-specific analysis of transcription and epigenomic status in PDAC. Grant amount: \$371,000. Grant period: 2012-2014.

August 2013: Agency: U.S.D.A. B.A.R.D. (E. Or, P.I.). Project Title: characterization and manipulation of primary components potentially involved in ABA-mediated repression of grape bud dormancy release and in its removal. Grant amount: \$300,000. Grant period: 2013-2016.

October 2014: Agency: Arizona Department of Health Services, Arizona Biomedical Research Commission. Project Title: Identification of Changes in Gene Expression at the Earliest Stages of Prostate Oncogenesis. Grant amount \$100,000. Grant period: 2015-2016.

December 2014: Agency: N.S.F. (J-Y Yoon, co-P.I.). Project Title: DOTS-qPCR: a handheld, rapid molecular diagnostic tool for Ebola. Grant amount \$211,436.00. Grant period: 2015-2016.

Description of Research Interests

My research career has centered on the study of higher plants at the cellular and subcellular level, employing maize, *Arabidopsis thaliana*, maize, rice and, to a lesser extent, barley, ice plant and tobacco, to address a series of specific questions in plant biology. These are presented in detail below. In our work, we employ a variety of modern experimental techniques, including those of plant tissue, cell and protoplast culture, plant cell and molecular biology, and molecular biology of other systems (yeast, *E. coli*). My work most closely identifies with systems biology, and is based on a long term interest in the development of

novel techniques and instrumentation of analytical cell biology. This includes flow cytometry and cell sorting, confocal microscopy, marker gene technologies, microarrays, and Next Generation DNA sequencing. For this work, we employ a wide variety of different plant, animal, and microbial species, with recent funding being used in applying our methods to address specific problems in cancer biology.

A. Characterization of Global Gene Expression in Eukaryotic Organisms. Most eukaryotic organisms are multicellular, and the individual tissues of these organisms comprise a variety of different cell types. A central question of relevance to all aspects of cellular and organismal biology concerns relating the information content of the genome to the phenotypes displayed by these different cell types. Using the reductionist approach, one strategy is to identify the different cell types within these tissues, to devise methods to separate these cells in purified states, and to apply techniques to characterize global patterns of gene expression within these cells. Our idea has been to devise a method of fluorescence labeling of individual cell types, and to employ flow cytometry and cell sorting for enrichment purposes, and DNA microarrays and, more recently, NextGen sequencing for global gene expression analysis. In that higher plants typically comprise complex interspersions of cell types linked by rigid cell walls, we have had to devise novel means for flow cytometry and sorting of plant derived components.

Over the years, my initial research contributions to the scientific community have centered around the twin technologies of flow cytometry and cell sorting. My group has been heavily involved in the development of these techniques for use with higher plant cells, and we have been extending our work to include development of instrumentation and methods applicable to all cell types.

My interest in flow cytometry developed in response to the question as to how to devise simple methods for the rapid selection of somatic hybrids formed by fusion of protoplasts. We subsequently developed a complete technology, involving fluorescent labeling, cell sorting and protoplast regeneration, that permitted the recovery of large numbers of somatic hybrid plants (Afonso *et al.*, 1985); these methods were patented by the University of Nebraska (Galbraith, 1982). Devising methods for flow analysis and sorting of plant cells and protoplasts required considerable retooling of existing commercial instrumentation, since plant protoplasts are typically considerably larger and more-fragile than animal cells (Harkins and Galbraith, 1987; Galbraith *et al.*, 1988). Whilst developing these methods, my laboratory was able to show that flow cytometry could be employed for the rapid analysis of nuclear DNA contents in higher plants (Galbraith *et al.*, 1983), and the simple techniques that we developed are now in use world-wide for plant breeding purposes, particularly ploidy verification, and we further showed how these could be used for studies of speciation (Keeler *et al.*, 1987), systematics (Bharathan *et al.*, 1994), and standardization (Johnston *et al.*, 1999). Most recently (Galbraith, 2009), I have shown how new generations of portable flow cytometers might be used for rapid characterization of genome sizes for all angiosperms, and with others have proposed as systematic global inventory of the flowering plants before inevitable extinction due to anthropogenic activities (Galbraith *et al.*, 2011).

In adapting flow cytometric instrumentation for use with higher plants, the various limitations inherent to current commercial instruments became apparent. One of the most important of these involves the electronic configuration employed for data collection and analysis; in brief, this is as follows. When cells pass through the focused light source within a flow cytometer, the resultant fluorescence and light-scatter signals are converted into voltage-versus-time waveforms through the action of photomultipliers. These waveforms are passed to dedicated analog circuits, which produce separate voltage values proportional to three features of the waveforms, the pulse height, pulse area, and the pulse width. These values are then digitized and accumulated as frequency distributions in the digital domain using conventional microcomputers. The effect of analog processing is that most of the information contained within the pulse shapes is lost, apart from pulse height, area, and width. We have therefore been devising novel hardware and software data acquisition systems, employing recent advances in digital pulse processing, to recover information about pulse shapes (Zilmer *et al.*, 1995). This involves capturing the pulse waveforms at the point of detection, using flash analog-to-digital converters operating at 20-40 MHz. The data sets

corresponding to the waveforms are then fed into a digital pulse processing system and feature values are computed, or the pulses are directly employed for neural network classification (Godavarti *et al.*, 1995). The types of features that are computed include higher-order waveform descriptors such as skew, kurtosis, and Fourier Transform, as well as the conventional values for pulse height, area, and width. Further development of the digital data acquisition system involved design and implementation of a double-buffering system for pulse digitization and processing (Murthi *et al.*, 2005). With further increases in the computation capacity and processing speed of integrated circuits, we are now exploring adapting the digital data acquisition hardware for interfacing with commercial cell sorters to allow real-time sorting based on pulse shape analysis. This should allow us to determine whether these new features can provide additional power to discriminate between different cell types, particularly normal and cancer cells.

Flow cytometry and cell sorting relies on the presence of fluorescence within cells as a source of optical signals used for analysis. This has led to my interest in developing molecular methods, based on flow cytometry, for use in cell, molecular, and developmental biology. In particular, the aim has been to employ flow cytometry and cell sorting to allow a comprehensive description of the patterns of gene expression within specific cell types. This required the purification of the various different types of cells contained within eukaryotic tissues, and the preparation of cell-specific cDNA libraries from these cells. To use flow cytometry for this purpose, we require cell type-specific fluorescent labels. In early work, we demonstrated that it was possible to raise surface-specific antibodies using monoclonal procedures (Meyer *et al.*, 1988), and we explored transgenic expression of surface glycoproteins from animal viruses with some promise (Galbraith *et al.*, 1992). An alternative, and very successful, approach involved the expression of intracellular marker proteins in transgenic plants and transfected protoplasts, followed by histochemical and fluorometric detection of these proteins.

The first of these markers was the *E. coli* enzyme β -glucuronidase which we employed to demonstrate, in transgenic tobacco, the cell-specific gene expression of transcriptional gene fusions in which the GUS coding sequence was placed under the transcriptional regulation of promoters from a ribulose biphosphate carboxylase/oxygenase small subunit gene or from a chlorophyll a,b-binding protein gene (Harkins *et al.*, 1990). This work employed cell sorting to separate protoplasts from mesophyll and epidermis, followed by analysis of transgene expression in the sorted cells. We were further able to demonstrate cell-specific patterns of gene expression were preserved in protoplasts isolated from these tissues in wild-type plants, and subsequently transfected with these constructs. This important result argues that protoplasts can be used to report gene expression in the tissues from which they have been prepared (this point is elaborated below). In this work, analysis of GUS expression involved a fluorometric assay, which required lysis of the protoplasts. We spent some time attempting to devise substrate/product pairs that would permit quantitative measurement of GUS activities *in vivo* using flow cytometry. However, chemical and biochemical constraints appear to limit the suitability of the GUS system for *in vivo* applications in flow cytometry. Consequently, we turned our attention to other gene expression systems, notably that of Green Fluorescent Protein (GFP) from *Aequorea victoria*.

GFP is the archetype of a class of proteins having the unique property to form a fluorophore as a sole function of the primary sequence of the protein. Other researchers had established, in 1994, that expression of the GFP coding region could be achieved in a variety of eukaryotic cell-types, including *Coenorhabditis elegans* and *Drosophila melanogaster*, and that expression results in an obvious green fluorescence within the cytoplasm. We were amongst the first to demonstrate the expression of GFP within higher plant cells, through transfection of tobacco and maize leaf protoplasts with recombinant constructions. Importantly, we were also able to employ the flow cytometer to detect and sort protoplasts according to GFP fluorescence *in vivo* (Galbraith *et al.*, 1995; Sheen *et al.*, 1995).

Taken together, these results pointed the way towards the selective isolation of different cell types according to gene expression, this being done by placing transgenic GFP expression under the control of promoters whose activities are cell type-specific. The conceptually simplest approach is to then make

protoplasts from the transgenic plants and flow sort those protoplasts expressing GFP. In collaboration with the laboratory of Dr. Philip Benfey, this approach was taken and was highly successful in identifying lists of genes whose expression is coordinated within specific root cells (Birnbaum *et al.*, 2003, 2005). However, this left unresolved the question as to whether it would be always possible to prepare protoplasts from any type of plant tissue, and whether the process of protoplast preparation might disturb patterns of cell type-specific gene expression. We therefore combined three research threads, one derived from the flow analysis of nuclei isolated from intact plant tissues (Galbraith *et al.*, 1983), the second from the analysis of a novel tobacco gene involved in transcriptional regulation (Afonso *et al.*, 1994), and the third from the identification of polyadenylated RNA within intact nuclei (see below), with the idea of flow sorting nuclei, labeled with GFP in a cell type-specific manner, and then using these sorted nuclei as sources of transcripts for global analysis of gene expression. Our first attempts to produce cell type-specific labeling of nuclei in transgenic plants employed an oligopeptide domain from the tobacco transcription factor which has the properties of a nuclear localization signal (NLS), which we showed could efficiently target GUS to the nucleus of higher plant cells. We combined this NLS into chimeric constructs comprising the complete GFP coding sequence linked translationally to that of GUS. This molecule was efficiently expressed within transfected protoplasts and transgenic plants, and strictly localized to the nucleus (Grebek *et al.*, 1997a, 1997b). An offshoot of this work has involved the extensive use of confocal microscopy for the examination of transgenic plants containing fluorescent nuclei. This work uncovered unusual and unsuspected patterns of nuclear movement and fragmentation within *Arabidopsis* root hairs (Chytilova *et al.*, 1999, 2000; Sliwinska *et al.*, 2002). A drawback of this approach was that nuclear GFP fluorescence was not retained within the nuclei after their release by homogenization of the transgenic tissue. Our second attempts, which successfully resolved this issue, involved producing transgenic plants expressing GFP as a histone fusion (Zhang *et al.*, 2004, 2008). Thence we were able to flow sort GFP⁺ nuclei from specific cell types and characterize gene expression within phloem companion cells via analysis of nuclear polyA⁺ RNA (Zhang *et al.*, 2008). Importantly, the results obtained from nuclear sorting closely paralleled those obtained from protoplast sorting, which argues that nuclear polyA⁺ RNA levels are a very useful proxy for total cellular polyA⁺ RNA levels. We have shown the same holds for mammalian cell lines (Barthelson *et al.*, 2007).

The concept of employing nuclei as sources of transcriptional information was developed in my laboratory in 1997 (Macas *et al.*, 1997). This method for characterization of global gene expression through analysis of the polyadenylated RNA contained in nuclei, which we termed NEST (Nuclear Expressed Sequence Tag) analysis, involved a modified form of AFLP analysis, converting transcripts into 3' cDNA fragments, which were then separated on polyacrylamide gels prior to sequencing. Our more recent work employed DNA microarrays and RNA-seq for characterization of nuclear polyadenylated transcript levels and sequences (see below). Most recently, we have found that we can perform global transcript analysis on the polyA⁺ RNA contained within a single nucleus (Grindberg *et al.*, 2013), and this opens the door to examination of transcriptional bursting and stochastic events in gene expression, as well as to the general concept of agnostic cell type characterization (i.e. identifying different cell types in the absence of specific markers through generalized clustering of expression patterns derived from analysis of single cells or nuclei). This should revolutionize our understanding of the regulation of gene expression in specific cell types and during disease onset and progression.

The advantage of studying nuclei over cells, when considering complex multicellular organs, can be generalized beyond plants. Thus, separating organs having complex interspersions of cell types into single cell suspensions can be difficult if not impossible for such organs as the C.N.S. Chopping mammalian organs to release nuclei rapidly and conveniently releases the nuclei, arresting transcription at the point of homogenization. We believe this approach has much to offer the research community. For example, my laboratory was funded by N.I.H. to characterize early events in pancreatic ductal adenocarcinoma through producing a genetically engineered mouse model in which expression of nuclear histone-GFP is coordinated within the developing pancreas with expression of a K-Ras oncogene, using a Cre-lox modulated gene expression system. This mouse line is currently being employed to probe early molecular events in prostate oncogenesis.

As an alternative way to examine gene expression, my laboratory, in collaboration with Dr. Julia Bailey-Serres at U.C. Riverside, also developed a convenient and accurate way to measure translation activities in specific cell types. This involved transgenic expression of an epitope-tagged ribosomal protein (L16) under the control of cell type-specific promoters. Total polyribosomes are then prepared from homogenates and employed for immunoprecipitation (Zanetti *et al.*, 2005; Mustroph *et al.*, 2009).

B. High-throughput Methods for Analysis of Gene Expression. During the period spanning 1995-2011, DNA microarrays emerged as an extremely popular means for the analysis of global gene expression. Starting in 1997, we actively developed microarray technologies for use in higher plants, first through conversion of an existing laboratory automation workstation (the Biomek 2000) to print arrays, and subsequently through acquisition of one of the first commercial microarray printer (a GeneMachines Omnigrd 100) and further high capacity microarray printers (the Omnigrd 300 and the Genetix ArrayMax). Our initial work examined the distribution of repetitive DNA elements within different species in the genus *Vicia* (Nouzova *et al.*, 2001). Over the period of 2002-2012, we established a central facility for printing oligonucleotide based microarrays, ultimately producing approximately 60,000 microarrays which were distributed to the academic scientific community. These arrays included the plant species *Arabidopsis thaliana*, *Zea mays*, *Solanum lycopersicum*, and *Oryza sativa*, and we also deployed our printing capacity to produce microarrays for the bovine and pig research communities. At the same time, we established a microarray scanning and hybridization service, and instituted annual five-day workshops to train researchers in microarray use. During the period 2002-2011, we ran 11 workshops, with an additional three at international locations, and trained approximately 450 scientists in microarray use. Recent publications from my laboratory have described the development and use of self-assembling protein microarrays (Zárate *et al.*, 2010; Kimzey *et al.*, 2011; Zárate and Galbraith, 2013).

C. Collaborative Research Activities. I have a consistent track record of highly collaborative research activities, exemplified by numerous grants beyond those already described. Some highlights include: (a) Maize Gene Discovery. This project, funded by the NSF Plant Genome Program, was an inter-university collaboration headed up by Stanford. Its goal was the characterization of all expressed genes within the important crop plant maize (*Zea mays*), which was done through EST sequencing at Stanford, contig assembly at Iowa State University, and EST amplification and printing as microarrays in my laboratory. The microarrays were the first generation of those provided to the global academic community as a cost-recovery service. We characterized these microarrays in terms of performance in transcript level estimation (Fernandez *et al.*, 2002). (b) Biology of Plant Stress. This project, also funded by the NSF Plant Genome Program, represented another inter-university collaboration. Its goal was an understanding of all plant genes whose expression is modulated by salt, osmotic, and cold stress. My contribution has been the production of microarrays from cDNAs of *Arabidopsis thaliana*, rice, maize, barley, and ice-plant (a natural halophyte), which were employed to monitor global changes in gene expression following imposition of stresses (Kawasaki *et al.*, 2001; Ozturk *et al.*, 2002; Wang *et al.*, 2003). These studies also provide insight into the pathways that are activated during stress responses, as well as identifying novel genes in these responses. Application of NEST analysis has, in turn, led to the implication of chromatin remodeling complexes in salt stress responses (Song and Galbraith, 2006). (c) Characterization of the Cytochrome P450 Gene Superfamily. This project, funded by the Human Frontier Science Program, was directed at understanding the function of the 286 individual members of the cytochrome P450 gene superfamily of *Arabidopsis thaliana*. It employed a combination of directed knockouts and DNA microarray analysis to assign function. Knockouts were done using T-DNA mediated insertion (Winkler *et al.*, 1998), and screening for identification of specific mutants involves PCR analysis of pooled genomic DNAs. A relatively small proportion (5-10%) of knockouts displays obvious phenotypes. We assigned functions to a limited number of genes (see, for example, Bak *et al.*, 2001). Microarray-based analyses were employed to systematically evaluate the degree of cross-hybridization between closely-related gene sequences (Xu *et al.*, 2001). (d) Plant Chromosome Sorting. In human, flow cytometry and sorting techniques have allowed the purification of most of the individual chromosomes to a high degree of purity. In higher plants, similar

work is limited by technical considerations as well as the fact that for many genomes, the individual chromosomes differ little, if at all, in size. My laboratory has a long history of collaboration with Dr. Jaroslav Dolezel of the Czech Academy of Sciences in Olomouc, centered around the use of flow sorting for the purification of individual plant chromosomes. (e) Signal transduction in grape bud dormancy. I have had a long and productive collaboration with Dr. Etti Or (Volcani Institute, Israel) funded by grants from the U.S.D.A. B.A.R.D. program in which we have explored changes in gene expression accompanying bud break in *Vitis vinifera*, with the aim of defining molecular targets for biotechnological modification (Keilin *et al.*, 2007; Mathiason *et al.*, 2008, Ophir *et al.*, 2009). The driving force behind this work relates to global climate change, since in the absence of a chilling period, bud-break in grape cannot be achieved, and chemicals currently used as alternatives for stimulating bud-break are being phased out, due to their toxicity. (f) Hand-held diagnostics for viral diseases. In response to the Ebola outbreak, I assembled a collaborative team with Dr. Jeon-Yool Yoon (University of Arizona, Department of Agricultural Biosystems Engineering) to design, fabricate, and evaluate a hand-held device for detection of pathogenic agents. This was subsequently funded by N.S.F. under their RAPID grants program.

D. Industry Outreach including SBIR and Patent Activities. I have been involved as a co-P.I. in three funded applications for SBIR funding with local Tucson firms, two from N.S.F. and one from N.I.H.. The first project, with High Throughput Genomics, Inc. (H.T.G.) and which progressed to Phase II, involved development of a novel multiplexed nuclease protection assay (NPA) for characterizing mRNA abundances within plant tissues (Kris *et al.*, 2007). The second project, with E.N.K.I. Technologies, Inc., aimed to construct novel substrates for microarray printing. The third leveraged the NPA assay for high density analysis of microRNAs. In addition, I hold four patents from the U.S. Dept. of Commerce, with two provisional patents currently filed. A further, major program with H.T.G., which was supported by Science Foundation Arizona, led to the development of a high density NPA for transcriptional profiling (Kris *et al.*, 2011). This assay has been commercialized and has led to a considerable economic impact in Tucson, due to expansion of the activities of H.T.G. within the biomedical assay sector (to the tune of ~\$25M).

E. Training Programs. In 1992, I submitted a proposal for research training in Plant-Insect Interactions in response to a N.S.F./D.O.E./U.S.D.A. Triagency Call for Proposals. This ten-year project focused on the molecular analysis of the ways that herbivorous insects interact with their host plants. My laboratory was involved in the analysis of phytosterol biosynthesis and metabolism, based on the observation that insects require dietary sterols. Insects further display feeding preferences; thus, plants containing undesirable sterols (for example, sterols containing a Δ^7 double bond, such as spinasterol, the major phytosterol in spinach) are recognized and avoided. This suggested that it might be feasible to deter insect herbivory within crop species through manipulation of endogenous sterol profiles. Prior to our work, a reasonable amount of information was available concerning the biochemistry of phytosterol biosynthesis. However, very little was known about the molecular biology of the genes encoding the enzymes involved in the pathway. To identify plant genes, we employed functional complementation of existing yeast sterol biosynthesis mutants via screening plant cDNAs placed within yeast expression vectors. We were able to clone Arabidopsis genes encoding sterol C24 methyl transferase and sterol C5 reductase (Grebenok *et al.*, 1997b; Grebenok *et al.*, 1998). Parallel studies characterized cytochrome P450 enzymes involved in sterol biosynthesis (Grebenok *et al.*, 1996), defined the responses of plants to insect herbivory (Schmelz *et al.*, 1998), and explored the mode of action of cholesterol oxidase on insect midgut membranes (Shen *et al.*, 1997).

Research Personnel Supervised

Over the last 25 years, I have directed the research of 23 postdoctoral research associates, 12 MS students, 5 PhD students, and 10 technicians. Over 100 undergraduates have worked in my laboratory. Of this latter group, three subsequently obtained Fulbright Scholarships to perform research in European laboratories. Of all persons passing through my laboratory and that are my co-authors, thirteen are tenure-track or tenured professors.

Summary of Teaching Activities

I have taught regularly as a component of my faculty appointments at the University of Nebraska Lincoln and subsequently at the University of Arizona. My appointment at the University of Nebraska-Lincoln was within the College of Arts and Sciences, the largest educational unit at the University. Within this College, the School of Biological Sciences was responsible for the major proportion of student credit-hour production. Therefore, all faculty members within the School had extensive teaching responsibilities.

My faculty appointment at the University of Arizona is within the College of Agriculture and Life Sciences. This College includes the Agricultural Experiment Station and, as part of the Land Grant system, has a bipartite assignment of teaching and research. My FTE appointment is 80% research and 20% teaching.

Both universities follow the semester system, the academic year comprising two 15-week semesters.

At the University of Nebraska, I team-taught Introductory Biology to Majors (freshman level; typical enrollment >250 students), had sole responsibility for a Junior/Senior level Cell Biology class (I developed this new course, which grew to an enrollment of ~60 students when I left the university, and had an associated laboratory that I developed with N.S.F. ISEP funding). I also regularly offered graduate level courses in Membrane Biology, and in Flow Cytometry, with both classes enrolling 6-10 students. I was responsible for independent research projects carried out in my laboratory, for undergraduate honors theses, and for various seminar courses at the graduate level.

At the University of Arizona, I have taught at all levels, including Introductory Plant Biology for non-majors (enrollment >150), the Freshman Colloquium in Plant Sciences (enrollment 20), the Honors Freshman Colloquium (enrollment 20), Cell Biology for seniors majoring in biology (enrollment 300), Plant Physiology (seniors majoring in Plant Sciences/and introductory level graduate students; enrollment ~25), Plant Biochemistry for seniors (enrollment 25), and Introduction to the Plant Sciences (an intro. level graduate course). My signature course is Methods in Cell Biology and Genomics, offered at the introductory graduate level. This enrolls ~15 students, drawn broadly from across the different colleges at the University of Arizona. I am responsible for supervising independent research projects in my laboratory, for undergraduate honors theses, and for various graduate seminar courses. I also organized some exploratory courses, notably an early (1995-96) internet-based course ("Learning and the Internet Environment") aimed at graduating seniors.

The University of Nebraska-Lincoln

Undergraduate Teaching (*indicates team-taught)

Fall Semester	1978-79	B.S. 295	Cell Biology
Spring Semester	1978-79	B.S. 106	Intro. Biol. Sciences*
Fall Semester	1979-80	B.S. 350	Cell Biology
		B.S. 498	Probl. Biol. Sciences
Spring Semester	1979-80	B.S. 498	Probl. Biol. Sciences
	1979-80	B.S. 399H	Honors Thesis
Fall Semester	1980-81	B.S. 350	Cell Biology
		B.S. 498	Probl. Biol. Sciences
Spring Semester	1980-81	B.S. 106	Intro. Biol. Sciences*
		B.S. 399H	Honors Thesis
Fall Semester	1981-82	B.S. 350	Cell Biology
		B.S. 498	Probl. Biol. Sciences
Spring Semester	1981-82	B.S. 498	Probl. Biol. Sciences

Fall Semester	1982-83	B.S. 350	Cell Biology
		B.S. 350	Cell Biology Lab.
Spring Semester	1982-83	B.S. 106	Intro. Biol. Sciences*
		B.S. 498	Probl. Biol. Sciences
Fall Semester	1983-84	B.S. 350	Cell Biology
		B.S. 350	Cell Biology Lab.
		B.S. 498	Probl. Biol. Sciences
Spring Semester	1983-84	B.S. 498	Probl. Biol. Sciences
Fall Semester	1984-85	B.S. 350	Cell Biology
		B.S. 350	Cell Biology Lab.
		B.S. 498	Probl. Biol. Sciences
Spring Semester	1984-85	B.S. 399H	Honors Thesis
		B.S. 498	Probl. Biol. Sciences
Spring Semester	1985-86	B.S. 498	Probl. Biol. Sciences
Fall Semester	1986-87	B.S. 350	Cell Biology
Fall Semester	1986-87	B.S. 350	Cell Biology Lab.
		B.S. 498	Probl. Biol. Sciences
Fall Semester	1987-88	B.S. 350	Cell Biology
Fall Semester	1987-88	B.S. 350	Cell Biology Lab.
		B.S. 498	Probl. Biol. Sciences
Fall Semester	1988-89	B.S. 350	Cell Biology
Fall Semester	1988-89	B.S. 350	Cell Biology Lab.
		B.S. 498	Probl. Biol. Sciences

Graduate Teaching

Fall Semester	1979-80	B.S. 898	Probl. Biol. Sciences
Spring Semester	1979-80	B.S. 998K	Membrane Biology.
Fall Semester	1980-81	B.S. 998D	Cell Biology
Spring Semester	1980-81	B.S. 998P	Flow Cytometry
		B.S. 915	Cell Biol. Seminar
Fall Semester	1981-82	B.S. 915	Cell Biol. Seminar
Spring Semester	1981-82	B.S. 909	Membrane Biology
Spring Semester	1982-83	B.S. 998P	Flow Cytometry
Fall Semester	1983-84	B.S. 915	Cell Biol. Seminar
Spring Semester	1983-84	B.S. 915	Cell Biol. Seminar
		B.S. 909	Membrane Biology
Fall Semester	1984-85	B.S. 915	Cell Biol. Seminar
Spring Semester	1984-85	B.S. 998P	Flow Cytometry
Spring Semester	1985-86	B.S. 909	Membrane Biology
		B.S. 915	Cell Biol. Seminar
Spring Semester	1986-87	B.S. 915	Cell Biol. Seminar
Fall Semester	1987-88	B.S. 915	Cell Biol. Seminar
Spring Semester	1987-88	B.S. 909	Membrane Biology
Fall Semester	1988-89	B.S. 915	Cell Biol. Seminar

The University of Arizona

Undergraduate Teaching

Spring Semester	1988-89	PLS 482	Plant Tissue Culture*
Fall Semester	1989-90	MCB 460	Plant Physiology

Spring Semester	1989-90	PLS 482	Plant Tissue Culture*
Spring Semester	1990-91	PLS 482	Plant Tissue Culture*
Spring Semester	1991-92	PLS 482	Plant Tissue Culture*
Fall Semester	1992-93	PLS 100	Intro. Plant Sciences*
Spring Semester	1992-93	MCB 410	Cell Biology*
		PLS/Ent 496d	Plant-Insect Interactions
Spring Semester	1993-94	MCB 410	Cell Biology*
Spring Semester	1994-95	MCB 410	Cell Biology*
Fall Semester	1995-96	UNIV495	Learning and the Internet Environment*
Spring Semester	1995-96	UNIV495	Learning and the Internet Environment*
Spring Semester	1995-96	MCB 410	Cell Biology*
Spring Semester	1995-96	PLS495	Senior Report
Fall Semester	1996-97	PLS439	Plant Cell Biology
Spring Semester	1996-97	PLS495	Senior Report
Fall Semester	1997-98	PLS439	Plant Cell Biology
Spring Semester	1997-98	PLS495	Senior Report
Fall Semester	1998-99	PLS439	Methods in Cell Biology
Spring Semester	1998-99	PLS495	Senior Report
Fall Semester	1999-00	PLS439	Methods in Cell Biology
Fall Semester	2000-01	PLS439	Methods in Genomics and Cell Biology
Fall Semester	2001-02	PLS439	Methods in Genomics and Cell Biology
Fall Semester	2011-12	PLS195	First Year Plant Science Colloquium*
Fall Semester	2011-12	PLS448	Plant Biochemistry and Metabolic Engineering*
Fall Semester	2011-12	PLS195	First Year Plant Science Colloquium*
Fall Semester	2012-13	PLS448	Plant Biochemistry and Metabolic Engineering*
Fall Semester	2012-13	HNRS195	First Year Honors Colloquium
Fall Semester	2013-14	HNRS195	First Year Honors Colloquium
Fall Semester	2013-14	PLS195	First Year Plant Science Colloquium*
Fall Semester	2014-15	HNRS195	First Year Honors Colloquium
Fall Semester	2014-15	PLS195	First Year Plant Science Colloquium*
Fall Semester	2015-16	HNRS195	First Year Honors Colloquium
Fall Semester	2015-16	PLS195	First Year Plant Science Colloquium*
Fall Semester	2016-17	HNRS195	First Year Honors Colloquium
Fall Semester	2016-17	PLS195	First Year Plant Science Colloquium*
Fall Semester	2017-18	PLS195	First Year Plant Science Colloquium*
Spring Semester	2017-18	HNRS195	First Year Honors Colloquium

Graduate Teaching

Fall Semester	1989-90	MCB 560	Plant Physiology
Spring Semester	1989-90	PLS 582	Plant Tissue Culture*
		PLS 920	Graduate Dissertation
Spring Semester	1990-91	PLS 582	Plant Tissue Culture*
		PLS 920	Graduate Dissertation
Spring Semester	1991-92	PLS 582	Plant Tissue Culture*
Spring Semester	1992-93	PLS 920	Graduate Dissertation
Fall Semester	1993-94	PLS 920	Graduate Dissertation
Spring Semester	1993-94	PLS 920	Graduate Dissertation
Fall Semester	1994-95	PLS 920	Graduate Dissertation
Fall Semester	1995-96	UNIV699	Learning and the Internet Environment*

Fall Semester	1996-97	PLS539	Plant Cell Biology
Fall Semester	1997-98	PLS539	Plant Cell Biology
Fall Semester	1998-99	PLS539	Methods in Cell Biology
Fall Semester	1999-00	PLS539	Methods in Cell Biology
Fall Semester	2000-01	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2001-02	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2002-03	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2002-03	PLS660	Introduction to the Plant Sciences
Fall Semester	2003-04	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2003-04	PLS660	Introduction to the Plant Sciences
Fall Semester	2004-05	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2004-05	PLS660	Introduction to the Plant Sciences
Fall Semester	2005-06	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2006-07	PLS560	Introduction to the Plant Sciences
Fall Semester	2007-08	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2008-09	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2009-10	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2010-11	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2011-12	LS548	Plant Biochemistry and Metabolic Engineering*
Fall Semester	2012-13	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2013-14	PLS548	Plant Biochemistry and Metabolic Engineering*
Fall Semester	2014-15	PLS539	Methods in Genomics and Cell Biology
Fall Semester	2016-17	PLS539	Methods in Genomics and Cell Biology

Summary of University Service

At the University of Nebraska, I served on a variety of campus-wide committees including: the Biotechnology Advisory Committee, Graduate Council, and the University Academic Planning Committee. I also served on Search Committees for the position of Vice-Chancellor for Research and Dean of Graduate Studies, and for the Director of Biotechnology. Within the School of Biological Sciences, I served on the Graduate Recruitment Committee, the Seminar Committee, the Goals and Priorities Committee, the General Education Committee, the Library Committee, and the Greenhouse Committee, and I served as Fulbright Advisor.

At the University of Arizona, I have served on campus-wide committees including: Honors Faculty, the University Promotion and Tenure Committee, Advisory to the Provost (two three-year terms), the Vice-President's Committee on Indirect Costs, the Biotechnology Division Advisory Committee, the Biotechnology Flow Cytometry Users' Committee, the Plant-Insect Interactions Research Training Group Steering Committee, the Committee on Academic Freedom and Tenure, the University-wide Task Force on Undergraduate Education, a CCIT committee to establish campus-wide WWW guidelines, Orchestra Nova (Univ. Arizona Music Department), and the Executive Committee of the Center for Insect Sciences. My College-wide activities include: the Promotion and Tenure Committee (two one-year terms), the Cultural Diversity Action Committee, the Committee on Undergraduate Curriculum Innovation, a Regents' Professor Nominating Committee, a Review Team for Cooperative Extension Programs, and the AgInfo Team. My Departmental/School activities include: Chair, Internet Technology Committee (produced the current School Website), Chair, Academic Peer Review Committee (developed the Self-study document for our 2013 School external review (80 pages plus 15 appendices)), the Steering Committee advisory to the Plant Sciences Head, the Annual Peer Evaluation Committee, the Academic Personnel Policies Committee, the Interdisciplinary Plant Biology Seminar Program (I initiated the very successful external seminar program operated by the School over the last 25 years), Faculty Search Committees (twelve), the

Curriculum Committee, the Graduate Committee, the Grants and Awards Committee, the Social Committee, and the Safety Committee.

Service to the Profession and Community

Reviewing Assignments

I receive regular grant reviewing assignments for N.S.F., N.I.H., U.S.D.A., and D.O.E. I have also reviewed grant proposals for S.E.R.C. (Great Britain), N.R.C. (Canada), and the Marsden Fund of the Royal Society of New Zealand. I served on the external advisory committee for the Czech Academy of Sciences in 2012, evaluating all programs in that country. I am on the editorial board of *Cytometry*, and *Plant Methods*, and have been on the editorial boards of *Plant Physiology* and *Plant Molecular Biology*. I am Editor-in-Chief for a specialty section of *Frontiers in Genetics*. I also have served as a reviewer for manuscripts for a wide variety of journals, including *Science*, *Nature*, *Plant Cell*, *Plant Journal*, *Journal of Cell Biology*, *Plant Physiology*, *Protoplasma*, *Physiologia Plantarum*, *Plant Cell Reports*, *Journal of Plant Physiology*, *Proc. Natl. Acad. Sci. U.S.A.*, *Plant Cell Tissue & Organ Culture*, *Annals of Botany*, *Biology of the Cell*, *Biotechniques*, *Plant Science*, *Plant Physiology*, *Crop Science*, *Critical Reviews in Plant Sciences*, *Cancer Research*, *Trends in Plant Science*, *Sexual Plant Reproduction*, *Plant Systematics and Evolution*, *Genome*, *Planta*, *Genetics*, *Stain Technology*, *Nucleic Acids Research*, and *Theoretical and Applied Genetics*.

Other Service Work

Member, U.S.D.A.-N.R.I. grant review panel (Genetic Mechanisms for Crop Improvement), 1983-85.
Invited participant at the Governor's Conference on Economic Development and Employment, 1984.
Invited speaker to the Lancaster County Medical Association, 1984.
Invited to meet with the Governor to discuss the fiscal year 1985-86 Budget: 1985.
Consultant to the Mayor of Lincoln and representatives of Lancaster County studying the impact of Biotechnology on local economic development, 1985.
Member, D.O.E. grant review panel, 1989.
Invited speaker, Nebraska Criminal Defense Lawyers Annual Meeting, 1988.
Review Team Member: N.S.F. survey of Plant Molecular Biology Research in Mexico, July 1990.
Member, Organizational Committee for the Third International Plant Molecular Biology Congress, held in Tucson in October 1991.
Volunteer, Science Teaching, Manzanita Elementary School, Tucson, 1990.
Volunteer, Science Teaching, Flowing Wells High School, Tucson, 1991.
Volunteer, Manzanita School Fourth Grade Science Camp, 1991.
Instructor, Manzanita School Fifth Grade Science Camp, 1991.
Member, Congressional Liaison, Public Policy, and Public Information Committee, American Society for Cell Biology, 1992-2000.
Member, Catalina Foothills High School Science Curriculum Committee, 1993-97.
Member, Catalina Foothills School District Systems Dynamics Advisory Committee and Middle School Math Advisory Committee, 1994-96.
Member, Steering Committee, Community Infrastructure and Telecommunication Alliance, 1993-94.
Member, Organizing Committee for an International Biodiversity Conference held in Tucson in 1994.
Consultant, Monsanto Corporation, 1995-97.
Consultant, High Throughput Genomics, Inc., 2000-2004.
Consultant, Ventana Medical Systems, Inc., 2000-2004, 2012-2013.
Member, Scientific Advisory Board, Accuri Cytometers, Inc., Ann Arbor MI, 2008-2011.
Senior Editor, *Methods in Plant Cell Biology Parts A and B* (*Methods in Cell Biology Series*, volumes 49 and 50, Academic Press), 1994-95.
College of Agriculture Representative, N.A.B.C. Ethics Committee, 1995-96.
External examiner, University of Auckland, New Zealand, 1998, 2010, 2011.

External examiner, University of Adelaide, Australia, 2012.
External examiner, University of Johannesburg, South Africa, 2013.
Member, review panel for N.A.S.A.-A.I.B.S. grant proposals in Washington, D.C., 1994.
Member, N.I.H. Special Emphasis Study Section (S10 Shared Instrumentation), 1998, 2001.
Member, N.I.H. Study Section (N.C.I.-I.M.A.T.), 2004-2006.
Member, N.I.H. Study Section (I.S.D.), 2007.
Member, N.I.H. Study Section (Innovative Technologies for Cancer Biospecimen Science), 2013-2015.
Member, N.S.F. Review Panel (Major Research Instrumentation), 2002-2004.
Member, N.S.F. Review Panel (Biochemical Engineering & Biotechnology), 2012-2014.
Member, U.S.D.A.-B.A.R.D. Review Panel, 2013-2015.
Member, N.S.F. Review Panel (Integrated Graduate Education and Research Training), 1998, 2000.
Member External Advisory Committees: N.S.F. Plant Genome Polyploidy project (Tom Osborn, Univ. Wisconsin, PI); N.S.F. Plant Genome Rice Blast project (Ralph Dean, North Carolina State University, PI); N.S.F. Plant Genome Sorghum Project (Lee Pratt, University of Georgia, PI), 2001-2005.
External reviewer, promotion and tenure cases: Rutgers University, 2000; University of Tennessee, 2001; Colorado State University, 2001; University of Nebraska-Omaha, 2005, 2006.
Counselor, International Society for Analytical Cytology (I.S.A.C.), 2000-2004.
Organizational committee, 2nd International Symposium on Rice Functional Genomics, Tucson, 2004.
Founding Member, Board of Directors, Tucson Chamber Artists, Inc., 2005-2014.
Secretary, Board of Directors, Tucson Chamber Artists, Inc., (Professional Choral Ensemble), 2006-2008
Vice-Chair, Board of Directors, Tucson Chamber Artists, Inc., 2008-2010.
Member, Tucson Symphony Orchestra Chorus, 2005-present.
Consultant, Chromocell Corporation, North Brunswick NJ, 2015-2016.