Transgenic Plants: From Basic Research to Agricultural Applications

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What I want to communicate

What is my bias?

What are the major "transgenic crops" today?

How do we add to, or modify plant genes?

Will new technologies "replace" GMO plants?

What do we need to do next?

NOT ALL GMOS ARE THE SAME!

I use GMO "technology" to put genes into plants for basic research and discovery.



"Mouse-eared cress" (Arabidopsis thaliana)

Mustard family (Brassicaceae)

Related to Canola, Broccoli, Cauliflower, Cabbage

Research support: the National Science Foundation, USDA, DOE, National Institutes of Health

What is my bias?

- Use knowledge-based processes to understand potential risks and rewards of new (and old) technologies
- Protect the right for farmers to farm in different sustainable ways (and make a living), and for consumers to choose foods of their preference
- > <u>Concern:</u> Over-heated rhetoric and "Fake News" obscures both the risks and rewards of GMOs.
 - GMOs will double yields and solve all agricultural problems!!!
 - GMOs will kill you, or at least make you sick, and besides...it's MONSANTO (buy organic, GMO free) !!!

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"Biotech" crops currently grown

Countries listed in order of number of acres

Country	Biotech Crops	
USA*	Maize, soybean, cotton, canola, sugar beet, alfalfa, papaya squash, apples, potatoes	
Brazil*	Soybean, maize, cotton	
Argentina*	Soybean, maize, cotton	
India*	Cotton	
Canada*	Canola, maize, soybean, sugar beet	

Table 1. Global Area of Biotech Crops in 2016: by Country (Million Hectares)**

Rank	Country	Area (Million Hectares)	Biotech Crops	
1	USA*	72.9	Maize, soybean, cotton, canola, sugar beet, alfalfa papaya, squash, potato	
2-	Brazil*	49.1	Soybean, maize, cotton	
3	Argentina*	23.8	Soybean, maize, cotton	
4	Canada*	11.6	Canola, maize, soybean, sugar beet, alfalfa	
5	India*	10.8	Cotton	
6	Paraguay*	3.6	3.6 Soybean, maize, cotton	
7	Pakistan*	2,9	2.9 Cotton	
8	China*	2.8	Cotton, papaya, poplar	
9	South Africa*	2.7	Maize, soybean, cotton	
10	Uruguay*	1.3	Soybean, maize	
17	Bolivia*	1.2	Soybean	
12	Australia*	0.9	Cotton, canola	
13	Philippines*	0.8	Malze	
14	Myanmar*	0,3	Cotton	
15	Spain*	0.1	Malze	
16	Sudan*	0,1	Cotton	
17	Mexico*	0.1	Cotton, soybean	

Table 1. Global Area of Biotech Crops in 2016; by Country (Million Hectares)**

Rank	Country	Area (Million Hectares)	Biotech Crops	
18	Colombia*	0,1	Cotton, maize	
19	Vietnam	<0.1	Maize	
20	Honduras	<0.1	Maize	
21	Chile	<0.1	Maize	
22	Portugal	<0.1	Maize	
23	Bangladesh	<0;1	Brinjal/Eggplant	
24	Costa Rica	<0.1	Cotton, soybean, pineapple	
25	Slovakia	<0.1	Maize	
26	Czech Republic	<0.1	Malze	
	Total	185.1		

^{*18} biotech mega-countries growing 50,000 hectares, or more, of biotech crops **Rounded-off to the nearest hundred thousand.

The EU has authorized GM Food crops



http://ec.europa.eu/food/dyna/gm_register/index_en.cfm/

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USA*	Maize, soybean, cotton, canola, sugar beet, alfalfa, papaya squash, apples, potatoes	
Brazil*	Soybean, maize, cotton	
Argentina*	Soybean, maize, cotton	
India*	Cotton	
Canada*	Canola, maize, soybean, sugar beet	

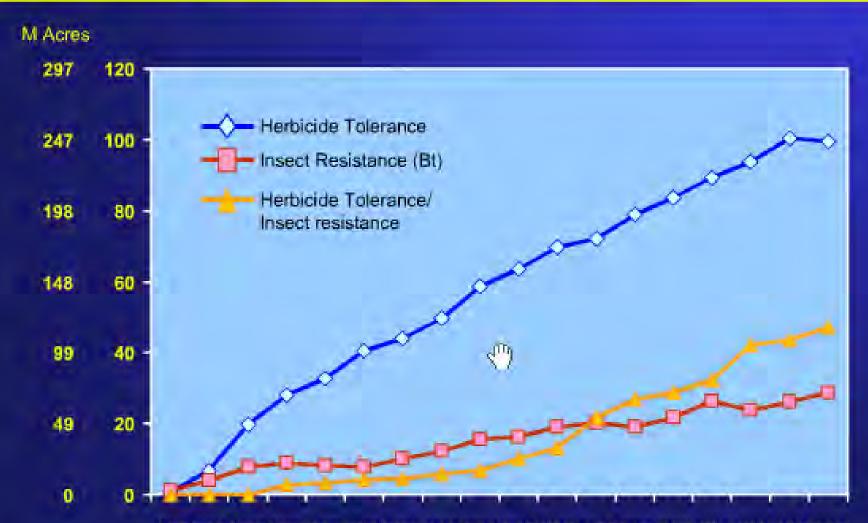
Note: There is currently NO "GMO" rice, wheat, peanut

Major genes currently in transgenic crops

- Herbicide tolerance (HT): Corn, soybean, canola, cotton, sugar beet, alfalfa, others "Roundup Ready", and others
 Gene: EPSP synthase, and others
- ➤ Insect Resistance (Bt): Corn, Cotton
 "Bacillus thuringensis toxin"
 Gene: Bt toxin (many types)

Global Area of Biotech Crops, 1996 to 2013: By Trait (Million Hectares, Million Acres)

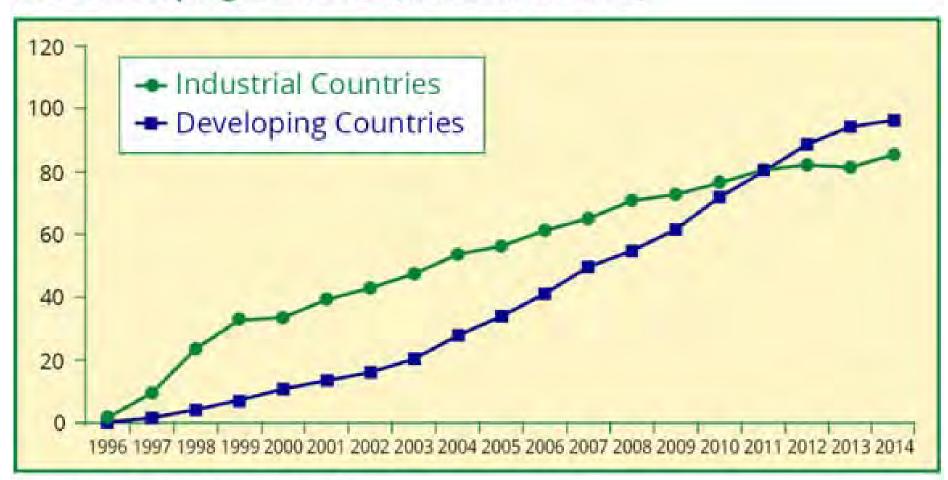




1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013

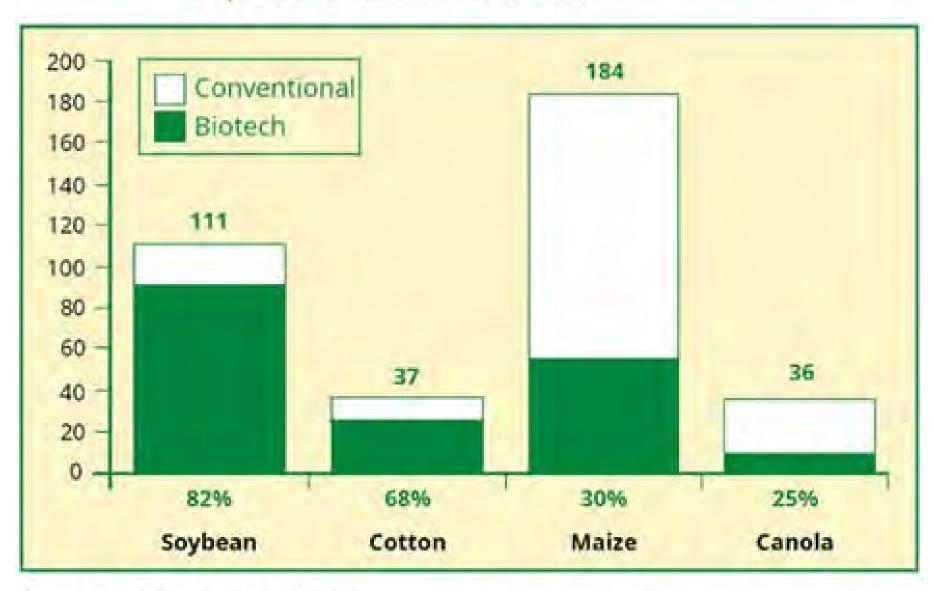
Source: Clive James, 2013

Figure 2. Global Area of Biotech Crops, 1996 to 2014: Industrial and Developing Countries (Million Hectares)



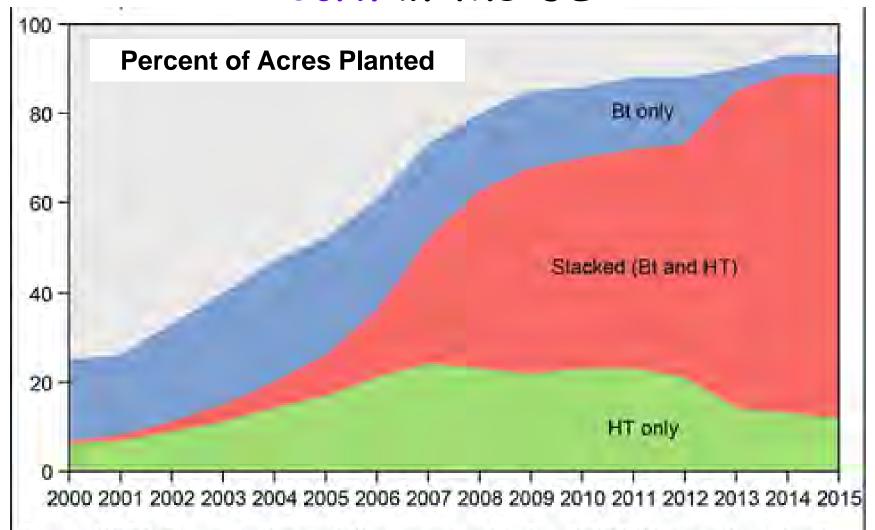
Source: Clive James, 2014.

Figure 3. Biotech Crop Area as % of Global Area of Principal Crops, 2014 (Million Hectares)



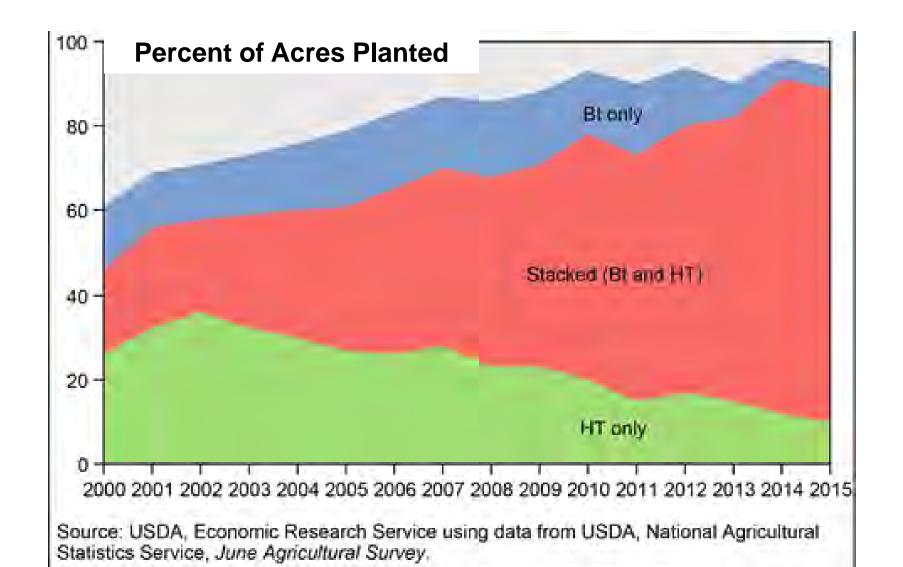
Source: Clive James, 2014.

Adoption of Genetically Engineered Corn in the US



Source: USDA, Economic Research Service using data from USDA, National Agricultural Statistics Service, June Agricultural Survey.

Adoption of Genetically Engineered Cotton in the US



What I want to communicate

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What is a GENE?

Let's start with DNA and putting it in context.

The four major <u>Macromolecules</u> of life: (i.e. big stuff, e.g. relative to an atom)

Nucleic acids: DNA-Deoxyribonucleic acid RNA-Ribonucleic acid Store and transmit information

Proteins: Made of Amino acids (20 kinds) - Workhorses of our cells/bodies

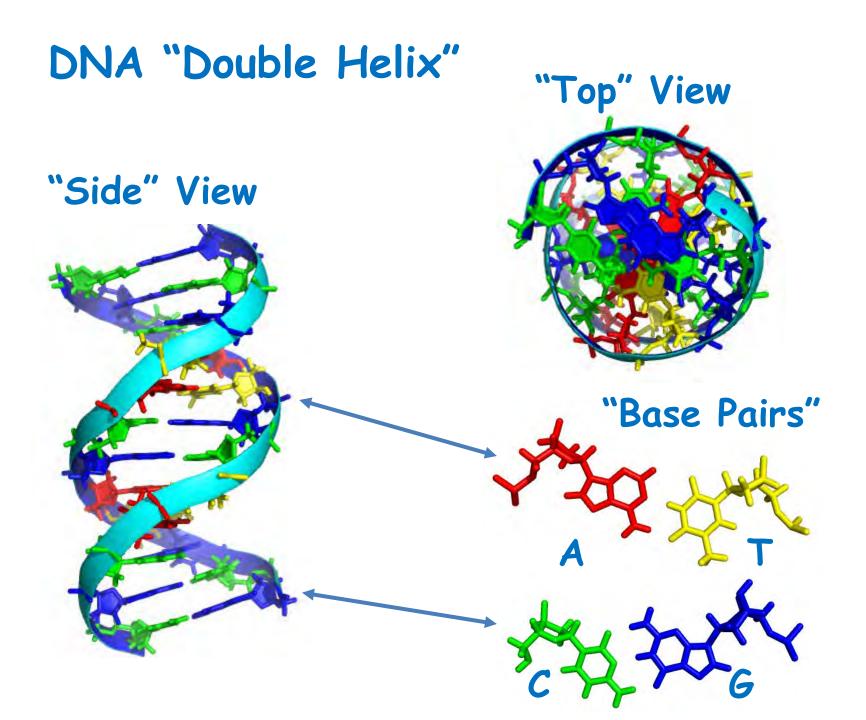
Lipids: Store energy (fat), lots of other functions

Carbohydrates: Store energy, other stuff too

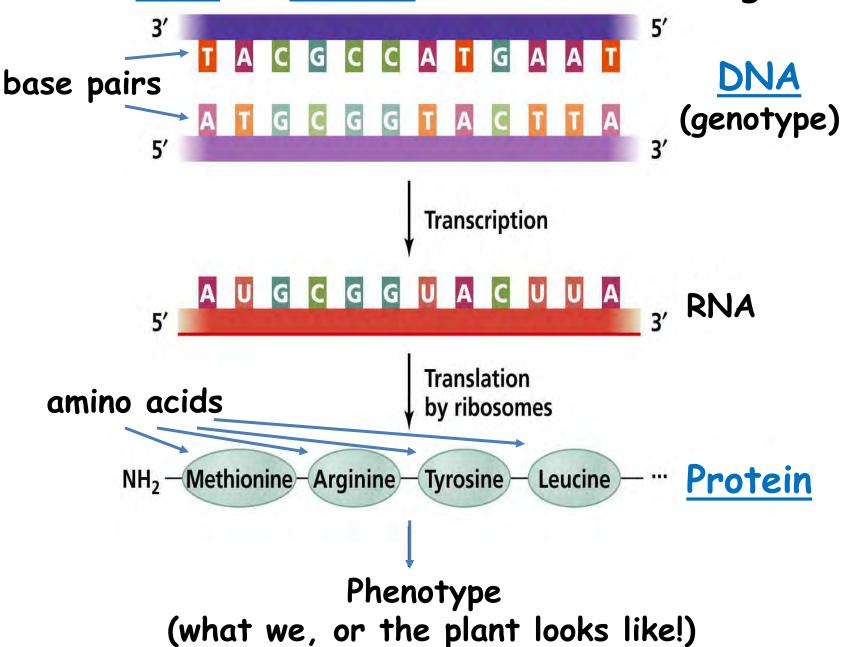
1953 - Defining the structure of DNA James Watson and Francis Crick



A GENE is a section of DNA with a specific sequence of "base pairs" that encodes the information required to make a protein



From DNA to Protein - The Central Dogma



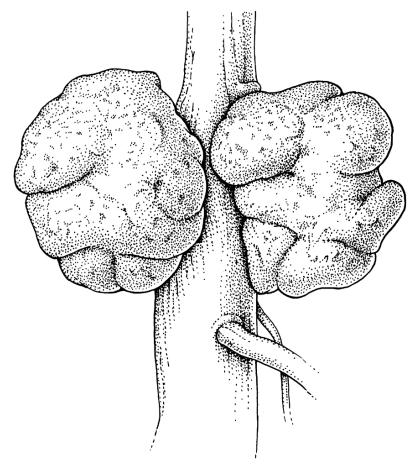
How much DNA is in each plant cell?

		DNA amount	
Common name	Latin name Mill	ion "base pairs	
Wheat	Triticum aestivum	15,966	
Onion	Allium cepa	15,290	
Garden pea	Pisum sativum	3,947	
Com	Zea mays	2,292	
Asparragus	Asparagus officinalis	1,308	
Tomato	Lycopersicum esculentu	m 907	
Sugarbeet	Beta vulgaris	758	
Apple	Malus X domestica	743	
Common bean	Phaseolus vulgaris	637	
Cantaloupe	Cucumis melo	454	
Grape	Vitis vinifera	483	

Plants and mammals, including humans, have on average about 25,000 to 35,000 GENES, i.e. Segments of DNA base pairs that specify unique PROTEINS.



Caused by infection with a bacterium named "Agrobacterium"





Caused by infection with a bacterium named "Agrobacterium"



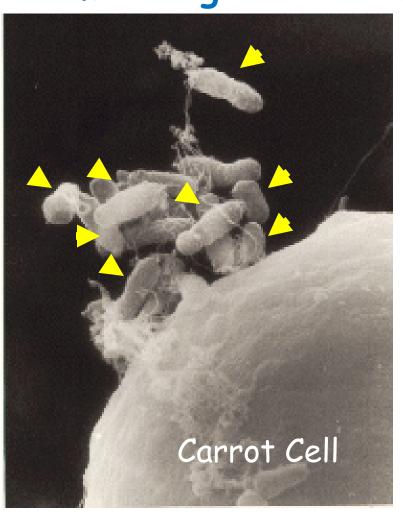


Caused by infection with a bacterium named "Agrobacterium"





Caused by infection with a bacterium named "Agrobacterium"



Cell, Vol. 11, 263~271, June 1977, Copyright © 1977 by MIT

Stable Incorporation of Plasmid DNA into Higher Plant Cells: the Molecular Basis of Crown Gall Tumorigenesis

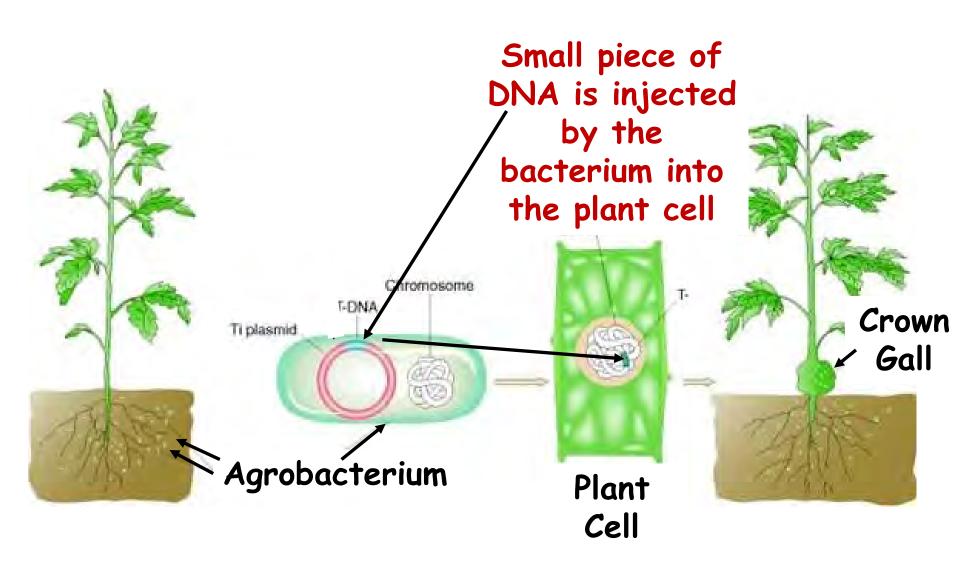
Mary-Dell Chilton,* Martin H. Drummond,*
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Summary

Evidence is presented that crown gall turcaused by the incorporation of part of a value plasmid carried by the inciting bacterium bacterium tumefaciens. The rate of reass of labeled plasmid DNA was slightly according to the presence of tobacco crown gall tumbut not normal tobacco DNA. Treatment DNA with DNA ase abolished the accelerate determine whether all plasmid sequent represented in tumor DNA, the labeled DNA was separated into specific fragme digestion with restriction endonuclease.



How does Agrobacterium make "tumors"?



Agrobacterium can move genes into plants that the bacteria use to grow, so....

We can use Agrobacterium to put any gene into plants.

Putting a GENE of choice into plants using Agrobacterium was first achieved in 1983

NATURE VOL. 303 19 MAY 1983

NATURE VOL. 303 19 MAY 1983

ARTICLES

20

Expression of chimaeric genes transferred into plant cells using a Ti-plasmid-derived vector

Luis Herrera-Estrella', Ann Depicker', Marc Van Montagu' & Jeff Schell'

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Foreign genes introduced into plant cells with Ti-plasmid vectors are not expressed. We have constructed an expression vector derived from the promoter sequence of nopaline synthase, and have inserted the coding sequences of the octopine synthase gene and a chloramphenical acetyltransferase gene into this vector. These chimaeric genes are functionally expressed in plant cells after their transfer via a Ti-plasmid of Agrobacterium tumefaciens.

CROWN gall formation on dicotyledonous plants by Agrobacterium tumefaciens is the result of the transfer and covalent integration of a segment (called T-region) of the Ti-plasmid into the chromosomal DNA of plant cells (for reviews see refs 1-4). Insertion of foreign DNA sequences within the T-region of Ti-plasmids leads to their co-transfer and integration into the plant genome. To date inserts of up to 50 kilobases (kb) from pTiT37 (refs 15, 16). Although both genes are encoded by plasmids of bacterial origin, they share more characteristics with eukaryotic genes than with prokaryotic genes. Both octopine and nopaline synthase genes, designated ocs and nos respectively, have a sequence similar to the so-called 'TATA' or 'Goldberg-Hogness' box¹⁷ in the 5' region upstream of the start of transcription, and a sequence 'AATAA' similar to the

Proc. Natl. Acad. Sci. USA Vol. 80, pp. 4803-4807, August 1983 Genetics

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Expression of bacterial genes in plant cells

(plant protoplasts/transformation/foreign DNA/antibiotic resistance/selectable markers)

ROBERT T. FRALEY, STEPHEN G. ROGERS, ROBERT B. HORSCH, PATRICIA R. SANDERS, JEFFERY S. FLICK, STEVEN P. ADAMS, MICHAEL L. BITTNER, LESLIE A. BRAND, CYNTHIA L. FINK, JOYCE S. FRY, GERALD R. GALLUPPI, SARAH B. GOLDBERG, NANCY L. HOFFMANN, AND SHERRY C. WOO

Monsanto Company, 800 North Lindbergh Boulevard, St. Louis, Missouri 63167

Communicated by Howard A. Schneiderman, April 25, 1983

Monsanto Company, 800 North Lindbergh Boulevard, St. Louis, Missouri 63167