

The introgression of a functional nuclear gene from *Poa* to *Festuca ovina*

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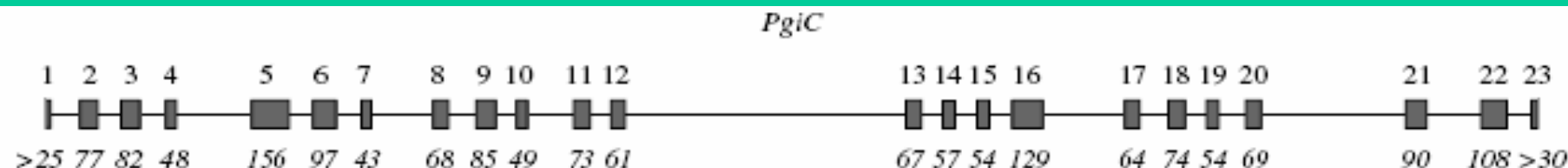


Figure 1. The *PgiC* gene as exemplified by the *d* allele of *PgiC1* in *Festuca ovina*. Exons and introns are drawn to scale. Exon sizes are the same for all genes investigated (except for the pseudogenes that lack 27 bp in exon 13), while intron sizes vary.

Table 1. Differences between *PgiC2* sequences. (Base pair positions correspond to GenBank accession no. DQ282377.)

	sequence region and position					
	exon 5 bp 876	intron 12–exon 13 bp 3258–3286	exon 15 bp 3567	intron 15 bp 3781	intron 16 bp 4140	intron 17 bp 4528
<i>PgiC2b</i>	G	present	G	G	C	G
<i>PgiC2c</i>	A	present	G	G	C	G
<i>PgiC2ψb</i>	A	deletion	T	A	C	A
<i>PgiC2ψc</i>	A	deletion	T	A	T	A

Werner Arber, Nobel Laureate 1978:

Interestingly, naturally occurring molecular evolution, i.e. the spontaneous generation of genetic variants has been seen to follow exactly the same three strategies as those used in genetic engineering¹⁴. These three strategies are:

- (a) small local changes in the nucleotide sequences,
- (b) internal reshuffling of genomic DNA segments, and
- (c) acquisition of usually rather small segments of DNA from another type of organism by horizontal gene transfer.

Arber, W. (2002)

Roots, strategies and prospects of functional genomics. *Current Science*, 83, 7, pp 826-828

<http://www.botanischergarten.ch/Mutations/Arber-Comparison-2002.pdf>

Arber, W. (2002)

Roots, strategies and prospects of functional genomics. *Current Science*, 83, 7, pp 826-828

<http://www.botanischergarten.ch/Mutations/Arber-Comparison-2002.pdf>

However, there is a principal difference between the procedures of genetic engineering and those serving in nature for biological evolution. While the genetic engineer **pre-reflects his alteration and verifies its results**, nature places its genetic variations more randomly and largely independent of an identified goal.

After an average of 10 years of safety tests the Crops are distributed to the millions in the field

Arber, W. (2002)

Roots, strategies and prospects of functional genomics. Current Science, 83, 7, pp 826-828
<http://www.botanischergarten.ch/Mutations/Arber-Comparison-2002.pdf>

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<http://www.botanischergarten.ch/Mutations/Arber-Comparison-2002.pdf>

Concepts of Intrinsic Value and Integrity of Plants in Organic Plant Breeding and Propagation

E. T. Lammerts van Bueren,* P. C. Struik, M. Tiemens-Hulscher, and E. Jacobsen

van Bueren, E.T.L., Struik, P.C., Tiemens-Hulscher, M., & Jacobsen, E. (2003)

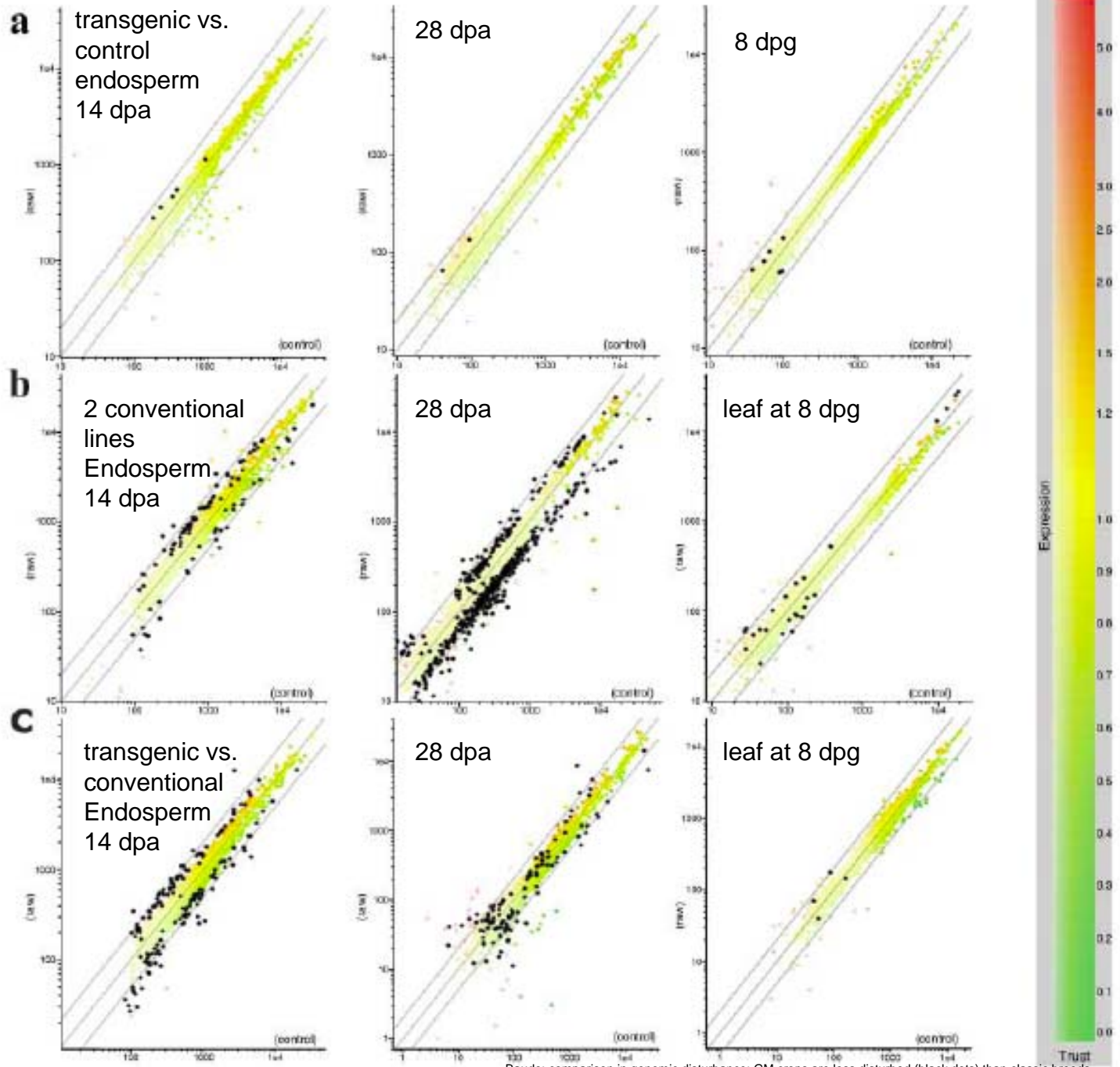
Concepts of intrinsic value and integrity of plants in organic plant breeding and propagation.

Crop Science, 43, 6, pp 1922-1929

<http://www.botanischergarten.ch/Organic/van-Bueren-Organicbreeding.pdf>

The natural approach taken by organic agriculture obviates the use of synthetic agrochemicals and emphasizes farming in accordance with agroecological principles. Also implicit in this approach is an appreciation for the *integrity* of living farm organisms, with the integrity being evaluated from a *biocentric* perspective. The ethical value assigned to integrity of organisms has challenged us to develop criteria for evaluating both integrity and breeding techniques. For cultivated plants, integrity refers to their inherent nature, their wholeness, completeness, species-specific characteristics, and their being in balance with their (organically farmed) environment. We evaluate integrity using criteria derived from four different perspectives: *integrity of life*, *plant-specific integrity*, *genotypic integrity*, and *phenotypic integrity*.

Scatter plot representation of transcriptome comparisons, Baudo et al. 2006



Baudo, M.M., Lyons, R., Powers, S., Pastori, G.M., Edwards, K.J., Holdsworth, M.J., & Shewry, P.R. (2006)

Transgenesis Has Less Impact on the Transcriptome of Wheat Grain Than Conventional Breeding. *Plant Biotechnology Journal*, 4, 4, pp 369-380

<http://www.botanischergarten.ch/Organic/Baudo-Impact-2006.pdf>

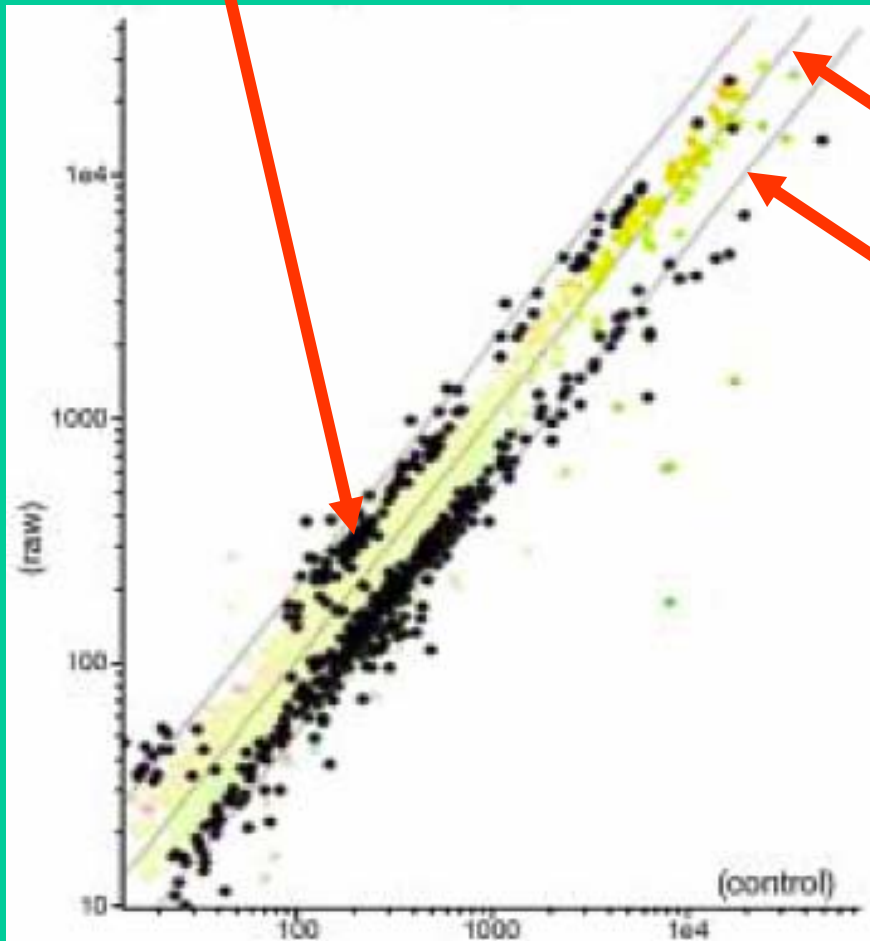
Shewry, P.R. & Jones, H.D. (2005)

Transgenic Wheat: Where Do We Stand after the First 12 Years? *Annals of Applied Biology*, 147, 1, pp 1-14

<http://www.botanischergarten.ch/Organic/Shewry-Performance-2006.pdf>

Baudo: comparison in genomic disturbance: GM crops are less disturbed (black dots) than classic breeds

Dots in black represent statistically significant, differentially expressed genes (DEG) at an arbitrary cut off > 1.5 .



The inner line on each graph represents no change in expression.

The offset dashed lines are set at a relative expression cut-off of twofold.

Coloured dots:
relative gene expression levels:
reds indicate overexpression,
yellows average expression,
greens under-expression.

**Example b) middle in slide 6:
2 conventional lines compared in
Endosperm at 28 dpa**

Scatter plot representation of transcriptome comparisons

Dots represent the normalized relative expression level of each arrayed gene for the transcriptome comparisons described

Full caption of slide 6:

Scatter plot representation of transcriptome comparisons of:

(a) transgenic B102-1-1 line vs. control L88-31 line in endosperm at 14 dpa (left), 28 dpa (middle) or leaf at 8 dpw (right);

(b) conventionally bred L88-18 vs. L88-31 line in endosperm at 14 dpa (left), 28 dpa (middle), or leaf at 8 dpw (right);

(c) transgenic B102-1-1 line vs. conventionally bred L88-18 line in endosperm at 14 dpa (left), 28 dpa (middle), or leaf at 8 dpw (right).

Dots represent the normalized relative expression level of each arrayed gene for the transcriptome comparisons described.

Dots in black represent statistically significant, differentially expressed genes (DEG) at an arbitrary cut off > 1.5 .

The inner line on each graph represents no change in expression. The offset dashed lines are set at a relative expression cut-off of twofold.

In the adjacent coloured bar (rectangle on the far right of the figure), the vertical axis represents relative gene expression levels: reds indicate overexpression, yellows average expression, and greens under-expression.

Values are expressed as n -fold changes. The horizontal axis of this bar represents the degree to which data can be trusted: dark or unsaturated colour represents low trust and bright or saturated colour represents high trust.

Transgenesis has less impact on the transcriptome of wheat grain than conventional breeding

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Differences observed in gene expression in the endosperm between conventionally bred material were much larger in comparison to differences between transgenic and untransformed lines exhibiting the same complements of gluten subunits. These results suggest that the presence of the transgenes did not significantly alter gene expression and that, at this level of investigation, transgenic plants could be considered substantially equivalent to untransformed parental lines.

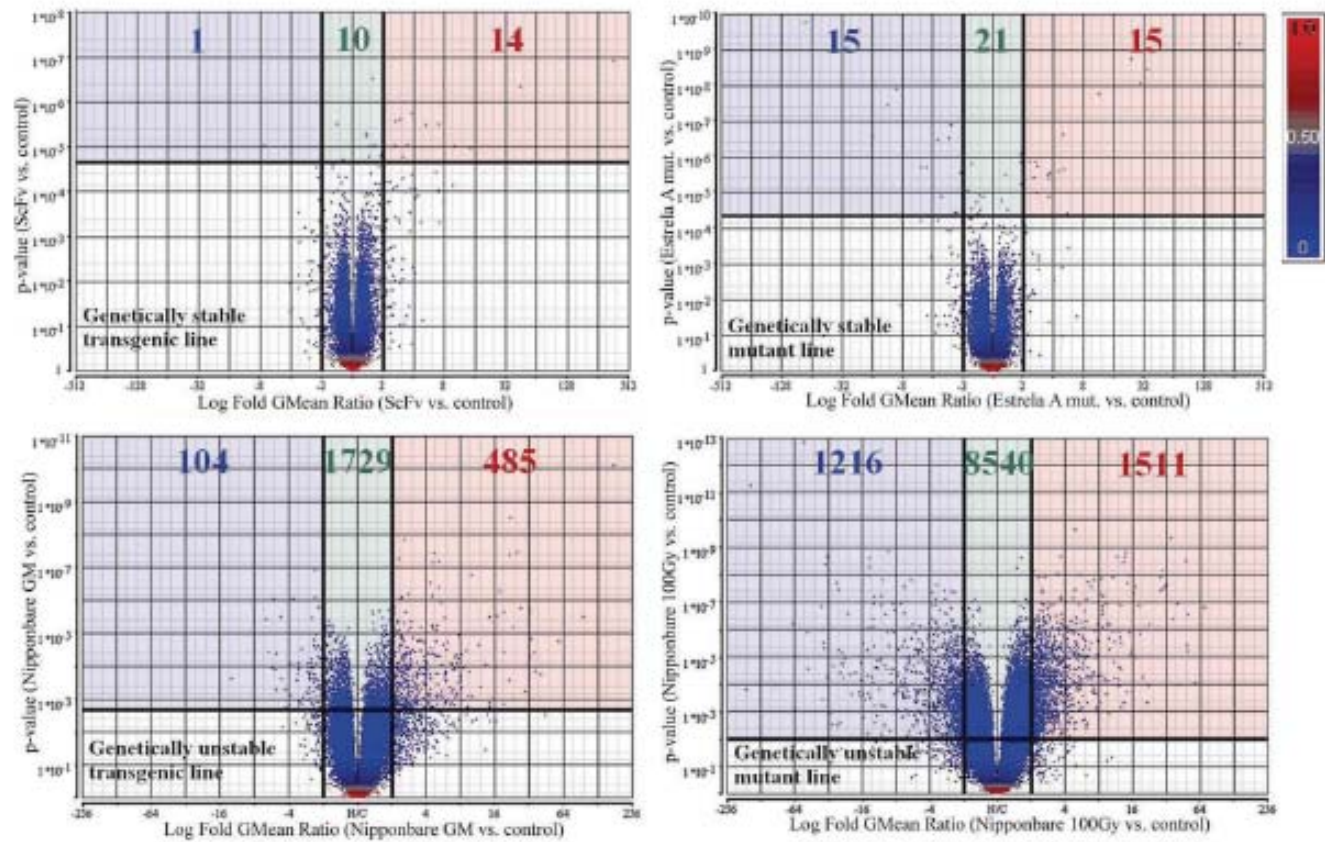


Fig. 2. Volcano plots for differentially expressed genes. Differentially expressed genes appear above the thick horizontal lines. Genes induced >2 -fold are on the right of the right vertical lines, and the ones repressed >2 -fold are on the left of the left vertical line. The numbers corresponding to the differentially expressed genes induced >2 -fold for each experiment (red-shadowed area) are red, and those corresponding to the genes repressed >2 -fold (blue-shadowed area) are blue. The green-shadowed area corresponds to differentially expressed genes that were up- or down-regulated <2 -fold (green-colored numbers). Blue-colored genes are those with P between 0 and 0.5, and red-colored genes are those with P between 0.5 and 1.

Batista, R., Saibo, N., Lourenco, T., & Oliveira, M.M. (2008)

Microarray analyses reveal that plant mutagenesis may induce more transcriptomic changes than transgene insertion. Proceedings of the National Academy of Sciences of the United States of America, 105, 9, pp 3640-3645
<http://www.botanischergarten.ch/Genomics/Batista-Microarray-Analysis-2008.pdf>

Marit R. Myhre · Kristin A. Fenton · Julia Eggert ·
Kaare M. Nielsen · Terje Traavik

The 35S CaMV plant virus promoter is active in human enterocyte-like cells

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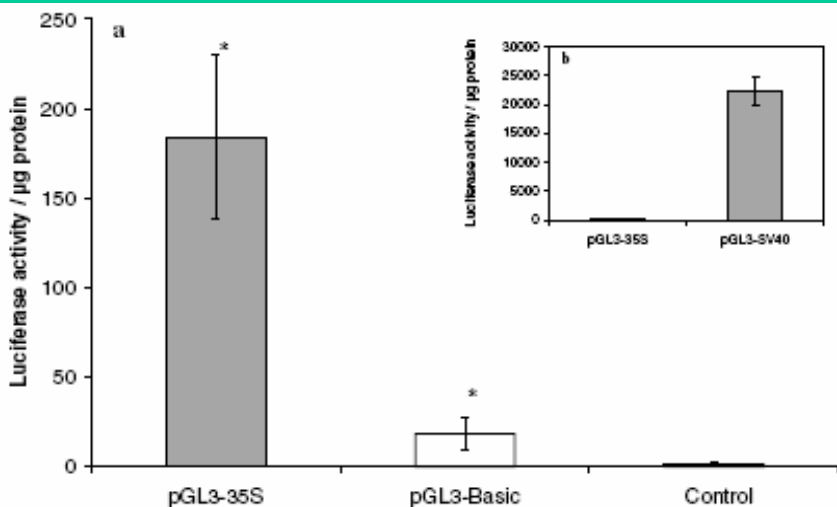


Fig. 5 Spectrophotometric quantification of Luciferase activity in Caco-2 cells. **(a)** Untransfected or transfected with pGL3–35S or the pGL3-basic (promoterless) plasmids. The results represent the mean plus standard deviation of four experiments with minimum three parallels of each reporter plasmids. The measured Luciferase activities were normalized for total protein. The typical protein content was 0.7–2.3 µg µl⁻¹. *Statistically significant difference ($p=0.0004$). **(b)** Comparison of Luciferase activity in Caco-2 cells transfected with pGL3-SV40 and pGL3–35S

Semi-holistic approach
A paper on the
35S promoters activities
on animal cell cultures
and not mentioning that
we eat this promoter
daily with our normal
Food without ANY harm

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The 35s Camv Plant Virus Promoter Is Active in Human Enterocyte-Like Cells. European Food Research and Technology, 222, 1-2, pp 185-193
<http://www.botanischergarten.ch/35S/Myhre-Cauliflower-Active-2006.pdf>

INDUCTION OF INSTABILITY AT SELECTED LOCI IN MAIZE

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Received April 14, 1953

IN previous reports (McCLINTOCK 1950, 1951), studies of the origin and expression of genic instability at a number of known loci in the maize chromosomes were summarized. It was concluded that changes in genic expression result from chromosome alterations at the locus of a gene and these are initiated by units other than those composing the gene itself. The mutations are considered, therefore, not as changes in the potentials of genic action, but rather chromosomal modifications at the locus effecting the kind and the degree of genic expression. The extragenic chromatin units have specificity in that

McClintock, B. (1950)

The Origin and Behavior of Mutable Loci in Maize. Proc Natl Acad Sci U S A, 36, 6, pp 344-55

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Citation&list_uids=15430309

McClintock, B. (1953)

Induction of Instability at Selected Loci in Maize. Genetics, 38, 6, pp 579-99

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Citation&list_uids=17247459 AND

<http://www.botanischergarten.ch/Genomics/McClintock-Instability-Maize-1953.pdf>

Historic paper of McClintock about transposons



Sectorial splitting
'Oberländer Mais from Thusis'
Grisons, Switzerland