



Julius Kühn-Institut
Bundesforschungsinstitut für Kulturpflanzen
Federal Research Centre for Cultivated Plants

Beitrag der Züchtung zur nachhaltigen Intensivierung

Frank Ordon

www.jki.bund.de

Reaping the benefits



Science and the sustainable intensification
of global agriculture

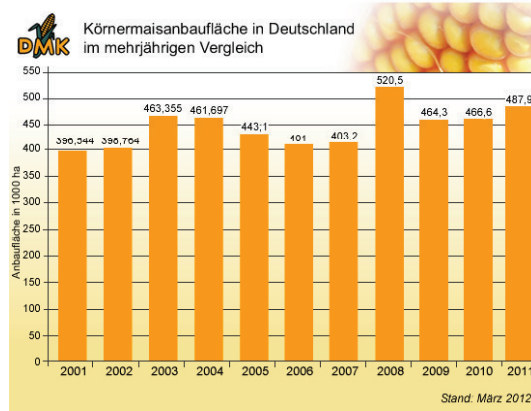
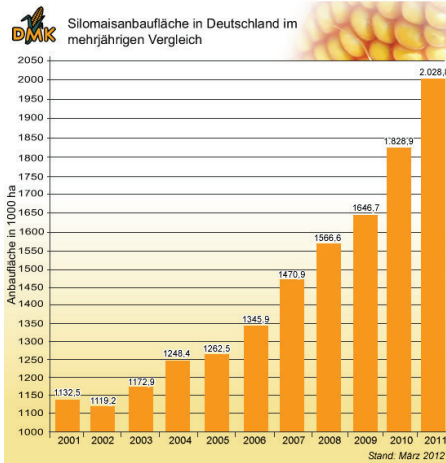
October 2009

2. UK research funders should support public sector crop breeding and genomics programmes to understand, preserve and enhance the germplasm of priority crops and train the next generation of plant breeders. International programmes in collaboration with Consultative Group on International Agricultural Research (CGIAR) centres and others in Africa and India should include millet, sorghum and rice. The top UK priority should be wheat, followed by barley, oil seed rape, potato, vegetable brassicas and other horticultural crops. Public sector support for breeding needs to emphasise longer term strategic approaches than can be expected from the private sector and develop traits from public sector research.
3. RCUK should increase support for ecosystem-based approaches, agronomy and the related sciences that underpin improved crop and soil management.
4. RCUK, and BBSRC in particular, should support long-term high-risk approaches to high-return targets in genetic improvement of crops. These targets include GM crops with improved photosynthetic efficiency or nitrogen fixation. High risk approaches might also produce GM or conventionally bred crops with reduced environmental impact because they need lower fertiliser input or could be grown as perennials. Research into conventional breeding and GM approaches to increased yield and resistance to stress and disease should also continue to be funded.

http://royalsociety.org/uploadedFiles/Royal_Society_Content/policy/publications/2009/4294967719.pdf

Institute for Resistance Research and Stress Tolerance

Entwicklung der Maisanbaufläche in Deutschland



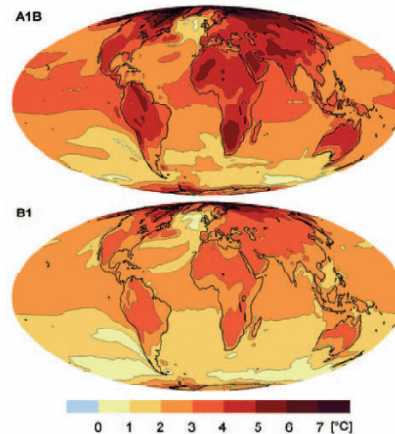
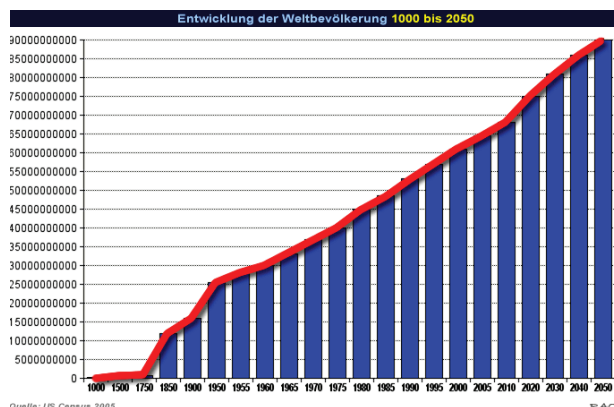
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Herausforderungen an die Pflanzenproduktion



Ernährungssicherung

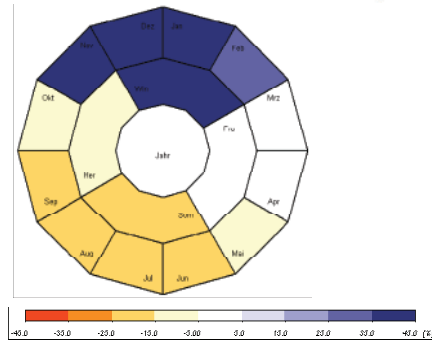
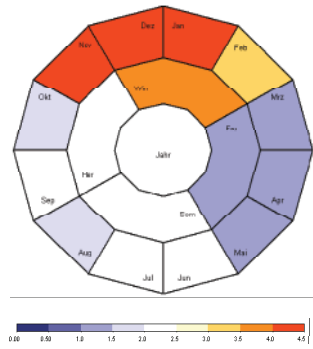
Steigende Weltbevölkerung
 Bioenergie
 Veränderte Verzehrgewohnheiten
 Klimawandel



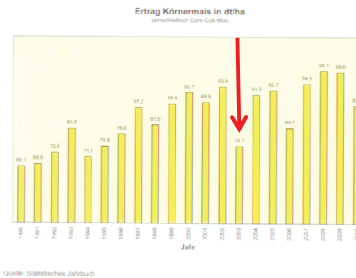
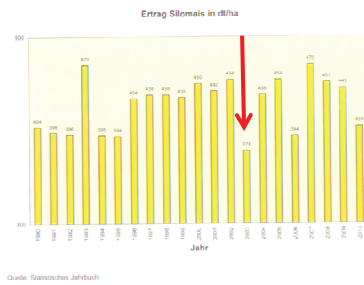
Anstieg der weltweiten Mitteltemperatur für die Zeitspanne 071 - 2100 relativ zu der Zeitspanne 1961 - 1990. © MPI Met

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Klimawandel



<http://www.umweltdaten.de/publikationen/fpdf-l/GGTSPU-styx2.bba.de-6248-7152625-DAT/3133.pdf>



aus Beschreibende Sortenliste 2011

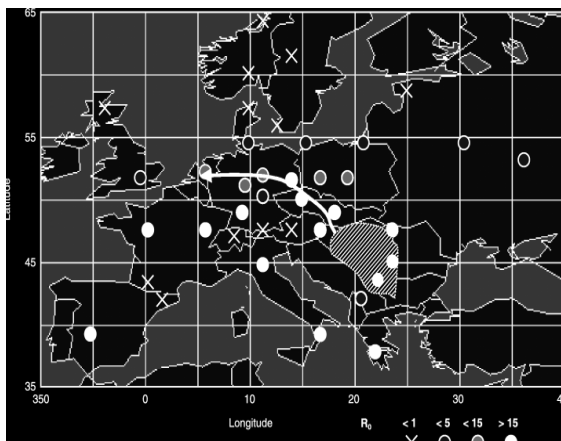
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Ausbreitung des Westlichen Maiswurzelbohrers *Diabrotica virgifera virgifera* in Europa

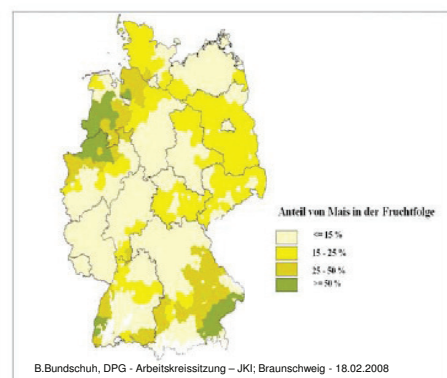


B.Bundschuh, Landwirtschaftliches Technologiezentrum Augustenberg

Reproduktionsraten von *D. virgifera* in Deutschland und potentielle Befallsgebiete

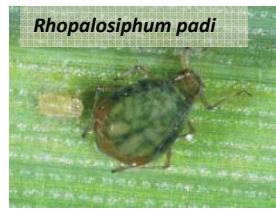


Hemerik, Bosstra, et al., 2004

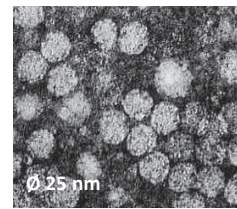


B.Bundschuh, DPG - Arbeitskreisitzung - JKI; Braunschweig - 18.02.2008

Barley yellow dwarf virus



Blattläuse als Virusüberträger



Viruspartikel
Ø 25 nm



Virusinokulation



Phänotypisierung

Genotypisierung

BMELV: Identifikation von molekularen Markern für BYDV-Resistenz in Mais

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Produktionskette



Saatgut



Produktion



Verarbeitung

Entwicklung von Sorten

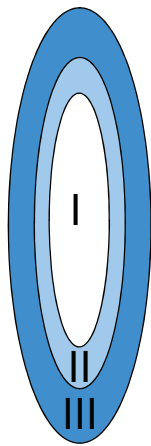
1. welche Ernteprodukte in ausreichender Menge und Qualität für die menschliche und tierische Ernährung liefern,
2. welche für die Energieversorgung sowie weitere Verwendungszwecke genügend Biomasse zur Verfügung stellen,
3. welche optimal an die sich verändernden Klimabedingungen (biotischer, abiotischer Stress) angepasst sind
4. welche, eine verbesserte Nährstoffeffizienz aufweisen

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Klassische Pflanzenzüchtung

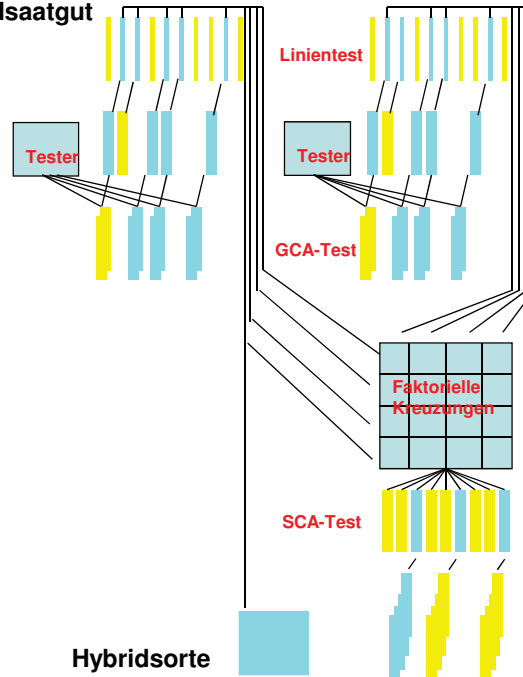


Erfassung genetischer Variation



Nutzung genetischer Variation

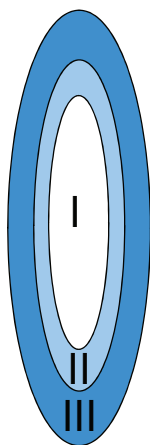
- I. Erstellung von Inzuchtlinien mit möglichst guter Eigenleistung
- II. Identifizierung von Linien mit maximaler Kombinationseignung
- III. Gelenkte Kreuzung durch gezielte Bestäubung zur Erzeugung von Hybridsaatgut



Pflanzenzüchterisches Instrumentarium

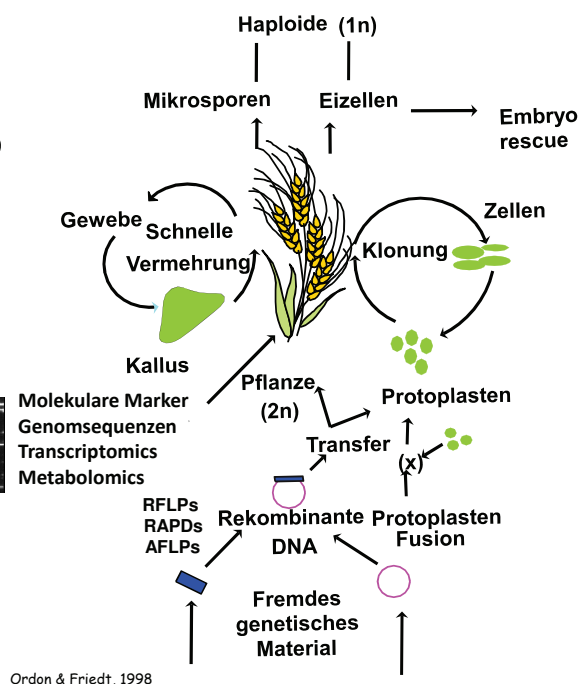


Genpool



Biotechnologie

Gen-



Ordon & Friedt, 1998

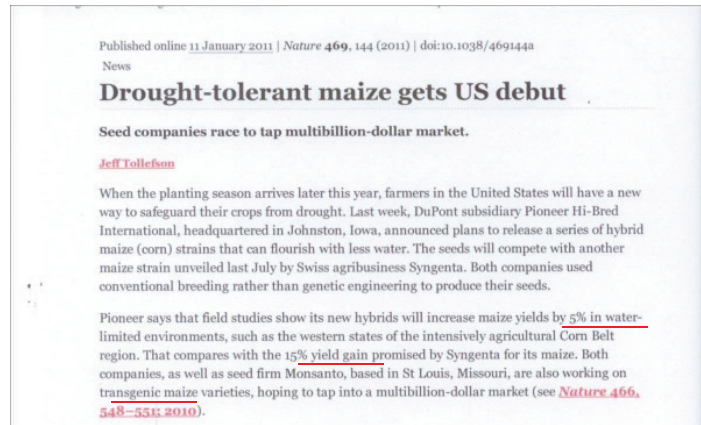
Gentechnik - Trockentoleranz



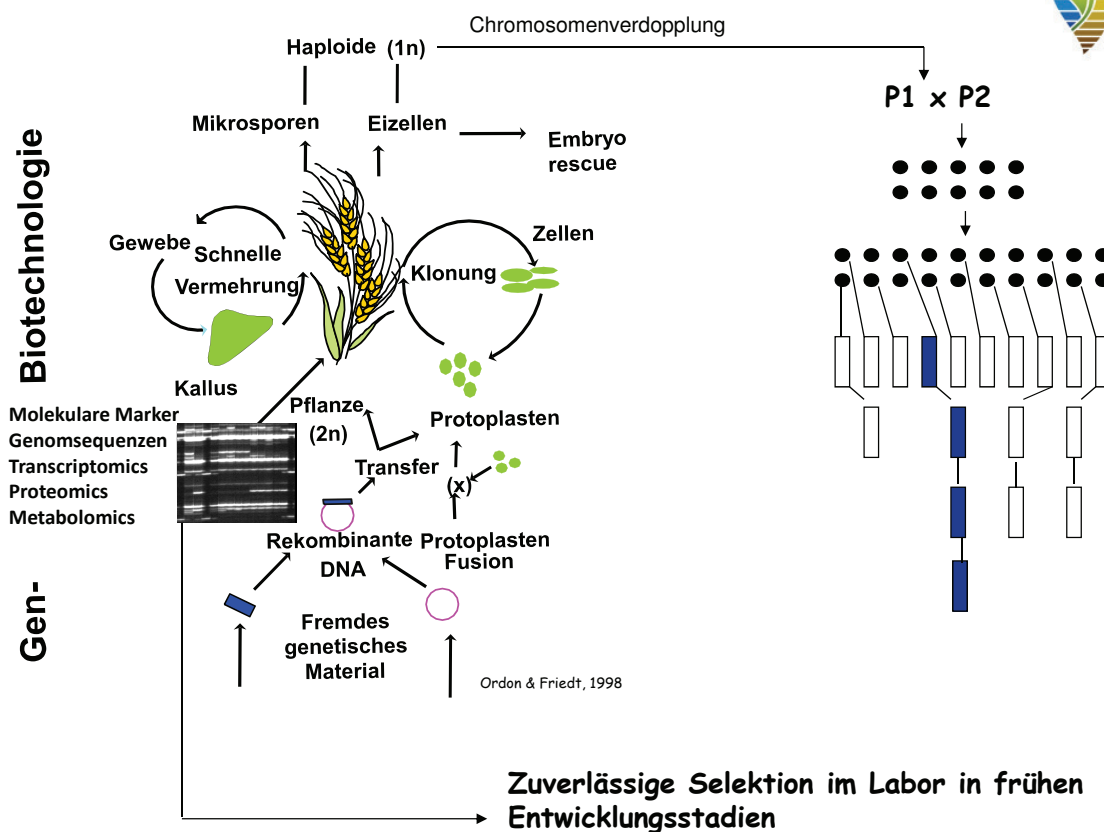
More crop per drop. Tests of genetically modified rice (top right), canola (middle right), and corn (bottom right) show that they withstand dry spells better than unmodified controls (left).

Pennisi 2008. Science 320: 171-173

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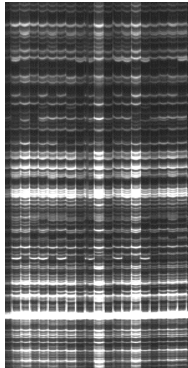


Pflanzenzüchterisches Instrumentarium

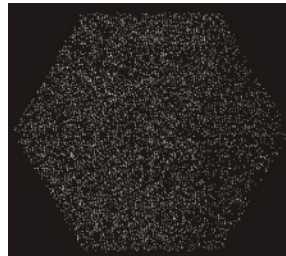


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AFLPs

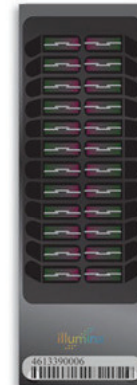


The GoldenGate Assay



http://barleygenetics.net/luke/site/html/agouebi/guide_to_illumina_genotyping.htm atlas-biolabs.de

MaizeSNP50 DNA Analysis Kits



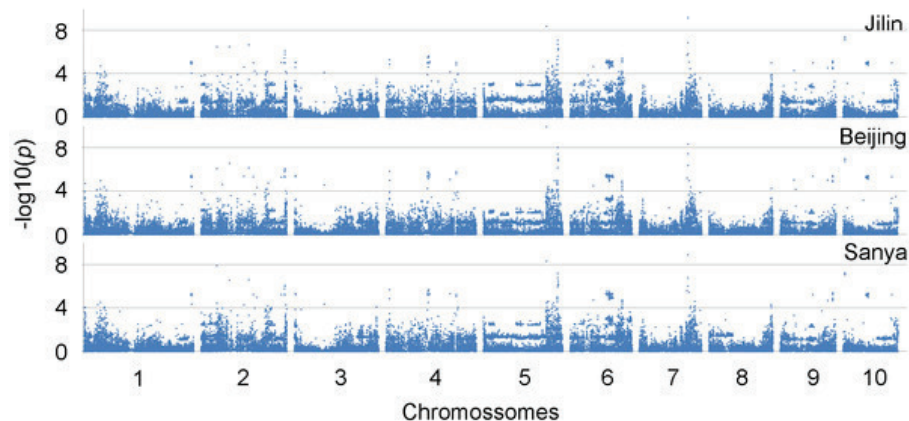
atlas-biolabs.de

OPEN ACCESS Freely available online

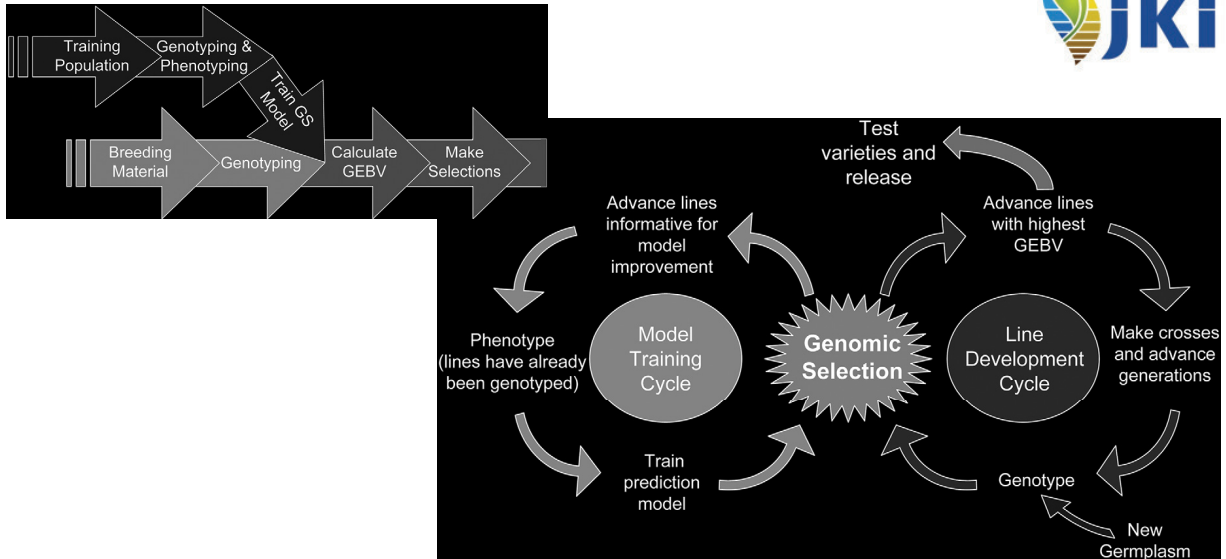
PLoS one

Genome-Wide Association Study Identifies Candidate Genes That Affect Plant Height in Chinese Elite Maize (*Zea mays* L.) Inbred Lines

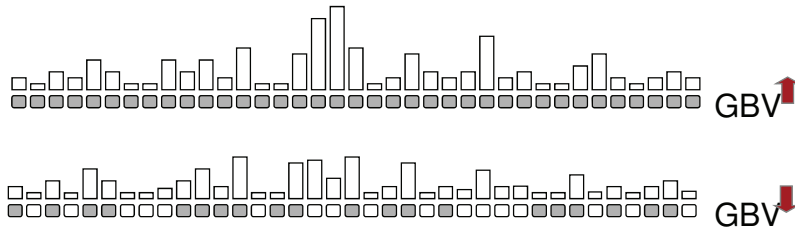
Jianfeng Weng¹, Chuanxiao Xie², Zhuanfang Hao³, Jianjun Wang, Changlin Liu, Mingshun Li, Degui Zhang, Li Bai, Shihuang Zhang*, Xinhai Li*



Pflanzenzüchterisches Instrumentarium : Genomic Selection



Heffner, E.L., M.E. Sorrells, J.L. Jannink, 2009: Genomic selection for Crop Improvement. *Crop Science* 49, 1-12.



$$GBV = \sum_{i=1}^{49990} \mathbf{x}_i \hat{\mathbf{g}}_i$$

Chris Schoen

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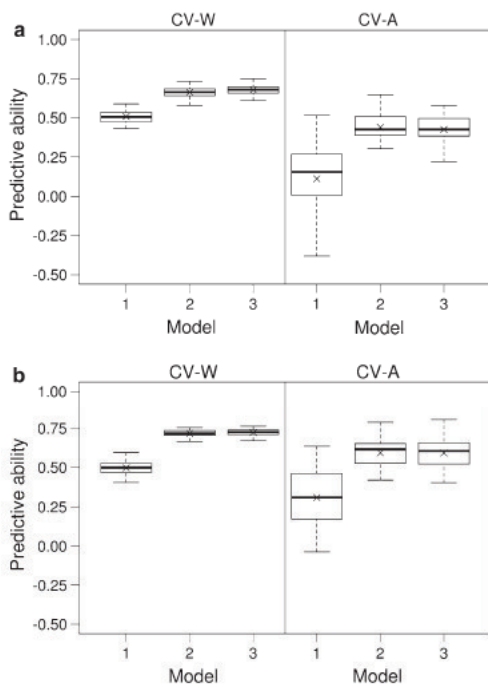


Fig. 2 Predictive abilities obtained with cross-validation with within family sampling (CV-W) and across family sampling (CV-A) for Models 1, 2 and 3 for traits grain dry matter yield (a) and grain dry matter content (b). The symbol × indicates the mean

Theor Appl Genet (2011) 123:339–350
DOI 10.1007/s00122-011-1587-7

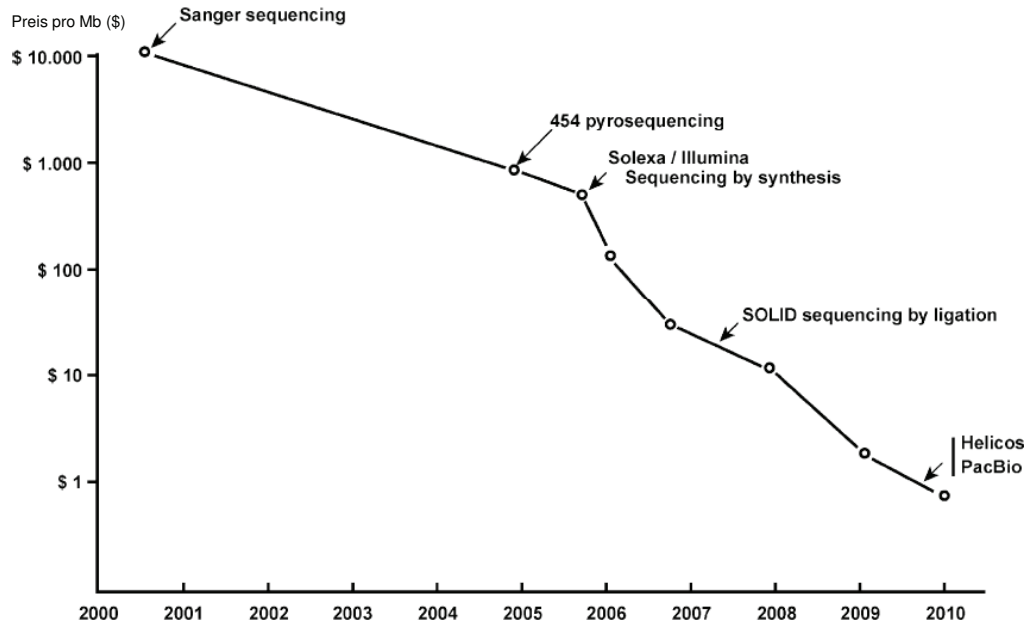
ORIGINAL PAPER

Genome-based prediction of testcross values in maize

Theresa Albrecht · Valentin Wimmer · Hans-Jürgen Auinger · Malena Erbe · Carsten Knaak · Milena Ouzunova · Henner Simianer · Chris-Carolin Schön

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Sequenzierungskosten



M. Delseny et al. (2010) *Plant Sci.* 179: 407-422

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Genome-wide patterns of genetic variation among elite maize inbred lines

Jinsheng Lai^{1,2,7}, Ruiqiang Li^{3,7}, Xun Xu^{3,7}, Weiwei Jin^{2,7}, Mingliang Xu^{2,7}, Hainan Zhao^{1,2}, Zhongkai Xiang^{1,2}, Weibin Song^{1,2}, Kai Ying⁴, Mei Zhang^{1,2}, Yiping Jiao^{1,2}, Peixiang Ni³, Jianguo Zhang³, Dong Li³, Xiaosen Guo³, Kaixiong Ye³, Min Jian³, Bo Wang³, Huisong Zheng³, Huiqing Liang³, Xiuqing Zhang³, Shoucai Wang², Shaojiang Chen², Jiansheng Li², Yan Fu⁴, Nathan M Springer⁵, Huanming Yang³, Jian Wang³, Jingrui Dai², Patrick S Schnable⁴ & Jun Wang^{3,6}

NATURE GENETICS VOLUME 42 | NUMBER 11 | NOVEMBER 2010

Marianne Bänziger (CIMMYT): „In our ‘seeds of discovery’ program we plan to invest 50 Mio. \$ to sequence our entire maize and wheat diversity panels: 25.000 maize accessions x 30 individuals each = 750.000 genomes“

53rd Ann. Maize Genetics Conf., March 2010

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Genomic and metabolic prediction of complex heterotic traits in hybrid maize

Christian Riedelsheimer¹, Angelika Czedik-Eysenberg², Christoph Grieder¹, Jan Lisec², Frank Technow¹, Ronan Sulpice², Thomas Altmann³, Mark Stitt², Lothar Willmitzer^{2,4} & Albrecht E. Melchinger¹

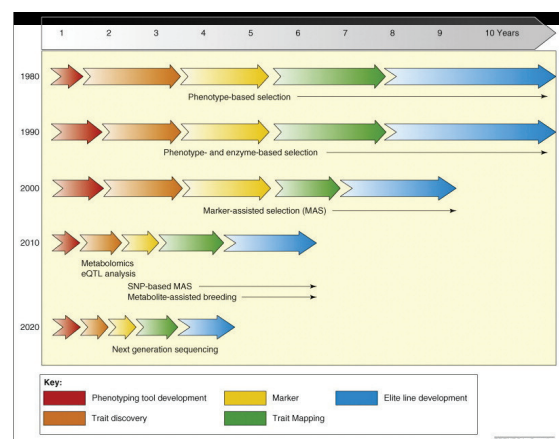
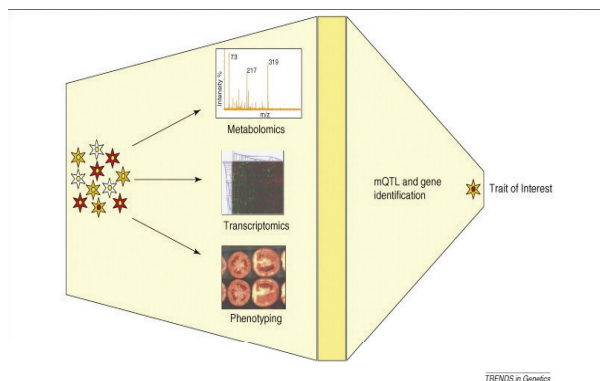
Table 1 Summary of whole-genome and metabolic prediction

GCA	h_{GCA}^2	w_M^2	SNPs			Metabolites		
			$r_{(y,y)}$	$r_{(g,g)}$	s.d.	$r_{(y,y)}$	$r_{(g,g)}$	s.d.
Dry matter yield	0.89	0.73	0.74	0.78	0.07	0.48	0.60	0.11
Plant height	0.95	0.72	0.70	0.72	0.06	0.52	0.63	0.10
Dry matter concentration	0.96	0.72	0.78	0.80	0.07	0.66	0.79	0.06
Female flowering	0.98	0.71	0.80	0.81	0.06	0.67	0.80	0.07
Starch content	0.93	0.73	0.70	0.73	0.07	0.59	0.71	0.07
Sugar content	0.94	0.74	0.69	0.72	0.06	0.55	0.67	0.09
Lignin content	0.82	0.73	0.72	0.80	0.05	0.50	0.64	0.10

Predictive abilities $r_{(y,y)}$ and prediction accuracies $r_{(g,g)}$ averaged over all cross-validation runs and their s.d. are shown for models using either SNPs or metabolites. Heritabilities of the predicted traits (h_{GCA}^2) are given as well as the repeatabilities of the used metabolic profile (w_M^2) calculated as the weighted sum of the repeatabilities of the individual metabolites (see Online Methods).

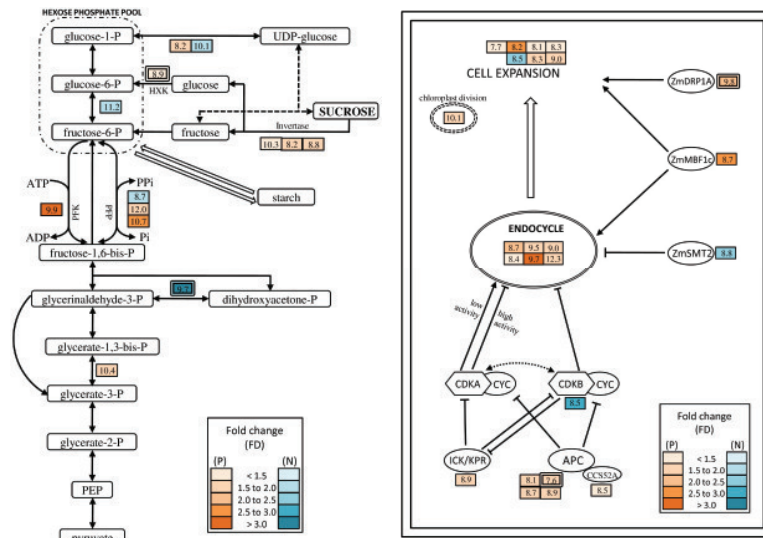
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Pflanzenzüchterisches Instrumentarium



Fernie, A.R., N. Schauer, 2008: Trends in Genetics 25, 39-48

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Fu et al, 2010. BMC Plant Biology 10:63

Nährstoffeffizienz

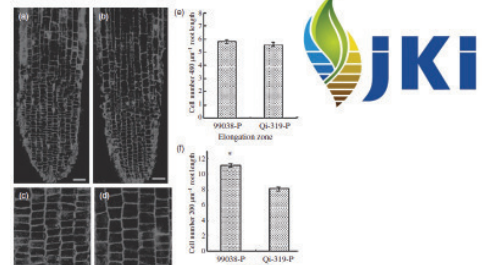
The Plant Journal (2008) 55, 927–939

doi: 10.1111/j.1365-3113X.2008.03561.x

Comparative proteome analyses of phosphorus responses in maize (*Zea mays* L.) roots of wild-type and a low-P-tolerant mutant reveal root characteristics associated with phosphorus efficiency

Kunpeng Li, Changzheng Xu, Zhaoxia Li, Kewei Zhang, Aifang Yang and Juren Zhang*
School of Life Science, Shandong University, 27 Shanda South Road, Jinan, Shandong 250100, China

167 differentiell exprimierte Gene unter P+ und P- zwischen sensitivem und tolerantem Genotyp

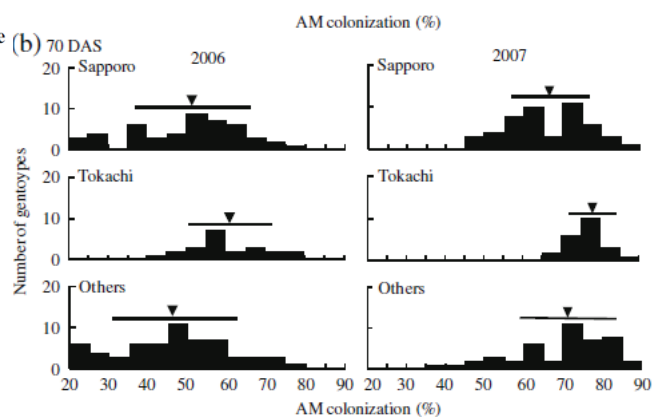


Plant Soil (2010) 327:441–453
DOI 10.1007/s1104-009-0073-3

REGULAR ARTICLE

How does arbuscular mycorrhizal colonization vary with host plant genotype? An example based on maize (*Zea mays*) germplasms

G.-H. An · S. Kobayashi · H. Enoki · K. Sonobe · M. Muraki · T. Karasawa · T. Ezawa



Resistenzen

Kolben- und Stängelfäule

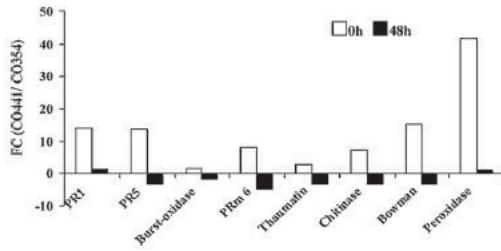


Fig. 1. Fold change (FC) of differentially expressed genes before (0 h) and after (48 h) infection in kernels of the CO441 resistant line compared to the CO354 susceptible line.



Differential activation of defense genes and enzymes in maize genotypes with contrasting levels of resistance to *Fusarium verticillioides*
 Alexandra Lamballe^{a,c}, Jamila Bernardi^a, Adriano Marocco^a, Antonio Logrieco^b, Costantino Piccolini^a

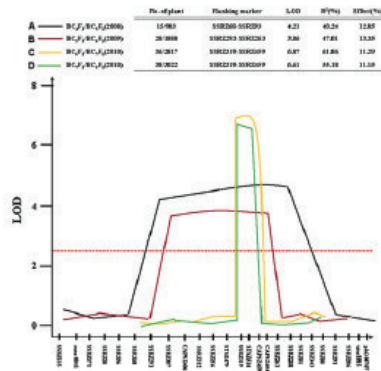


Fig. 4 Diagram of QTL plots for *qRfg2* in four advanced backcross generations. The logarithm of odds (LOD) profile, relative position of *qRfg2* and relevant markers are displayed by using QTL cartographer version 2.5. a QTL plot of 15 BC_{2.5} families consisting of 983 BC₂F₁ plants. b QTL plot of 28 BC_{2.6} families consisting of 1888 BC₂F₁ plants. c QTL plot of 36 BC_{2.7} families consisting of 2817 BC₂F₁ plants. d QTL plot of 38 BC_{2.8} families consisting of 3022 BC₂F₁ plants

Theor Appl Genet (2012) 124:585–596
 DOI 10.1007/s00122-011-1731-4

ORIGINAL PAPER

Fine-mapping of *qRfg2*, a QTL for resistance to *Gibberella* stalk rot in maize

Dongfeng Zhang · Yongjie Lin · Yanling Guo · Qin Yang · Jianrong Ye · Shaojiang Chen · Mingliang Xu

Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a *GST* gene



Randall J. Wisser^{a,1}, Judith M. Kolkman^b, Megan E. Patzoldt^a, James B. Holland^c, Jianming Yu^d, Matthew Krakowsky^e, Rebecca J. Nelson^b, and Peter J. Balint-Kurti^e

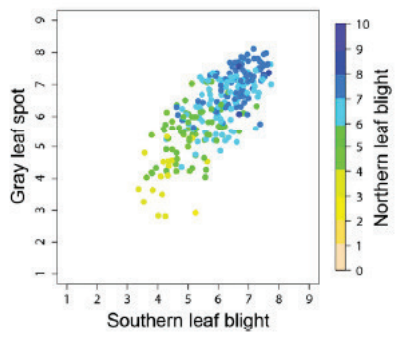


Fig. 1. Scatterplot of breeding values for resistance to SLB, GLS, and NLB. Each point corresponds to a different inbred line; breeding value-based inbred line ranks are available in Table S4. Axes span the full range of the measurement scales (for NLB, the transformed scale) for which resistance increases with increasing values. A color scale is used to indicate breeding values for NLB resistance.

PNAS 2011: 108, 7339-7344

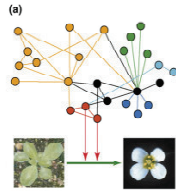
Verschiedene Allele der Glutathion-S-Transferase beeinflussen Resistenzniveau gegen die genannten Pathogene

Zusammenfassung und Ausblick



-Sequenzinformation
-omics Technologien

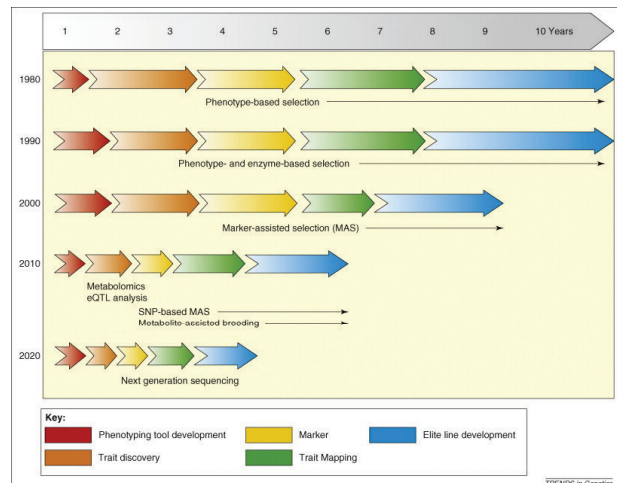
Identifikation von Genen
bzw. Netzwerken



G. Hammer et al. 2006: Trends in Plant Science 11, 587-593

Erfassung der allelischen
Diversität und deren Wirkung

Nutzbarmachung durch geeignete
Markertechnologien und gentechnische Verfahren



Fernie, A.R., N. Schauer, 2008: Trends in Genetics 25, 39-48

Zusammenfassung und Ausblick



Die Maiszüchtung kann durch ein sich stetig weiterentwickelndes Instrumentarium gezielter und schneller auf zukünftige Herausforderungen reagieren und damit einen entscheidenden Beitrag zur nachhaltigen Intensivierung der Maisproduktion und zur Bewältigung der zukünftigen Herausforderungen leisten.

Entsprechende Sorten bilden die Grundlage für pflanzenbauliche Optimierungen im Rahmen der nachhaltigen Intensivierung.