



Neue Methoden der Rebzüchtung

Von Krallenfrosch bis CRISPR

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Wieviele Rebsorten gibt es?

- Home
- About VIVC
- Database search
- Search**
- Species
- Cultivar name
- Photos
- Pedigree
- Holding institutions
- Area by countries
- Bibliography
- History of prime name changes
- Advanced search**
- Passport data
- Resistance data
- Microsatellites by profile
- Microsatellites by varieties
- Microsatellites by bibliography
- Relationships based on nine microsatellites
- Statistical information**
- Descriptors**
- Genetic resources monitoring**
- Data on breeding and genetics**
- Resistance loci/varieties**
- Markers**
- Important links
- Contact
- Disclaimer

Home / Cultivar name EXCEL Document

Cultivar name

- Cultivar name (search includes both, prime names and synonyms)
- Prime name
- Synonym

% i

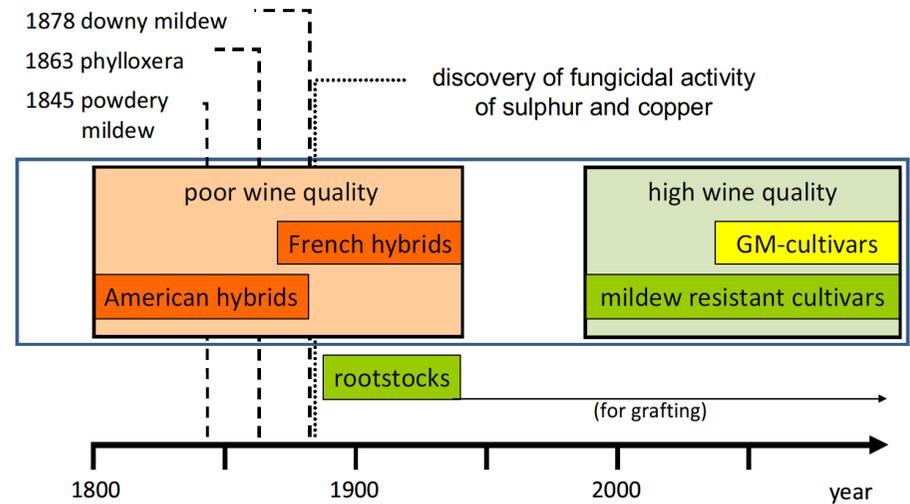
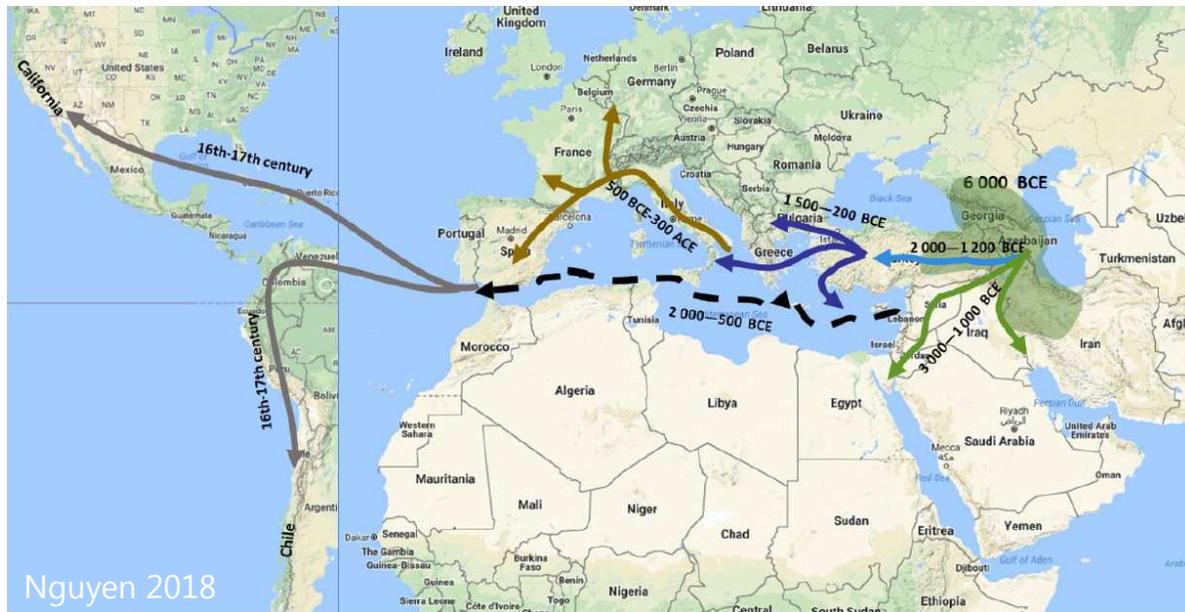
Definition of the term prime name

First « 1 **2** 3 4 5 6 7 8 9 10 » Last Go to page: 2

Showing 26-50 of **24,986** items.

Prime name ↓	Variety number VIVC	Species	Color of berry skin	Country of origin of the variety
			Select ...	
ABBOU	141	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	NOIR	MOROCCO
ABBRUZZESE BIANCA	5	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	ITALY
ABBRUZZESE CAMPOMAGGIORE	6	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	ITALY
ABBUOTO	7	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	NOIR	ITALY
ABBY CLINGOTTEN	8	VITIS LABRUSCA LINNÉ	NOIR	UNITED STATES OF AMERICA
ABDERAZAK BEN HAMAMA	24155	VITIS VINIFERA LINNÉ SUBSP. VINIFERA		ALGERIA
ABDONA	10527	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	NOIR	ITALY
ABDOULKADIRIL TZIBIL	20579	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	NOIR	DAGHESTAN
ABDULLAH	23676	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	ROUGE	TURKEY
ABECHBACH	20580	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	ALGERIA
ABEIDI	9	VITIS VINIFERA LINNÉ SUBSP. VINIFERA		SYRIAN ARAB REPUBLIC
ABEILLANE	10	VITIS VINIFERA LINNÉ SUBSP. VINIFERA		
ABEJERA	11	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	SPAIN
ABEL CHATENAY	20581	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	BLANC	FRANCE
ARFI HAI	12	VITIS VINIFERA LINNÉ SUBSP. VINIFERA	RI ANC	PORTUGAL

Geschichtliches



Töpfer et al. 2011

Wie sind die heutigen Sorten entstanden?

Zufallssämlinge



Blauburgunder
ca. 100 v. Chr.,
Mitteleuropa



Traminer
Alter unbekannt,
Osteuropa



Vernatsch
Alter unbekannt,
Südtirol?



Lagrein
Alter unbekannt,
Südtirol?



Heunisch
Alter unbekannt,
Osteuropa

Spontane Mutationen



Ruländer
Farbmutationen von Blauburgunder



Weißburgunder

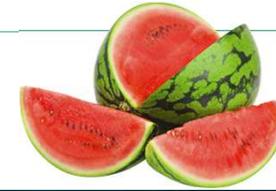


Gewürztraminer
Mutation des Traminer

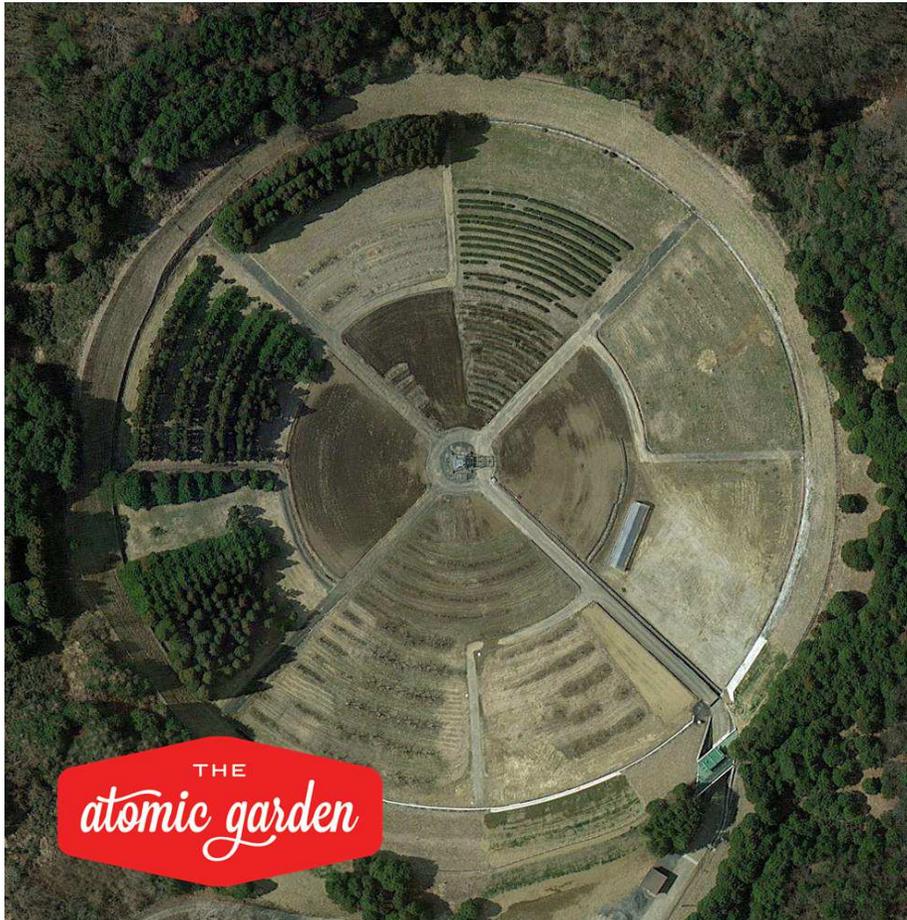


Lagrein-Klone

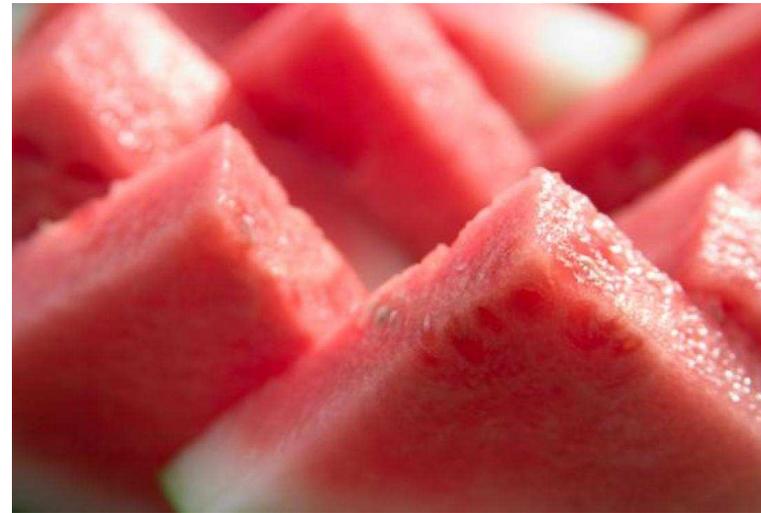
Auslesezüchtung



Mutagenese in den 60ern

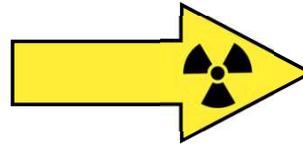


Induzierte Mutationen



Induzierte Mutationen bei der Rebe

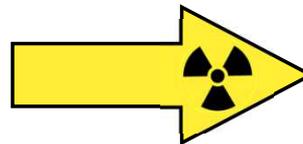
Fernão Pires



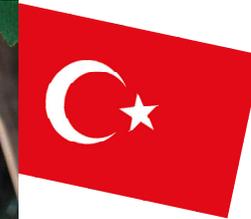
10 Gy Gamma-Strahlen
[POR, 1975]



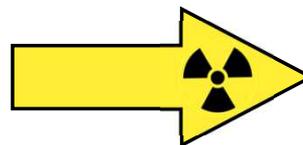
Pembe Çekirdeksiz



45 Gy Gamma-Strahlen
[TÜR, 2017]



Golden Delicious



50 Gy Gamma-Strahlen
[A, 1984]



Golden Haidegg



Klassische Züchtung



Müller-Thurgau
D, 1882



Kerner
D, 1929



Manzoni bianco
I, 1930-1935



Zweigelt
A, 1922



Cabernet Cortis
D, 1982



Solaris
D, 1975

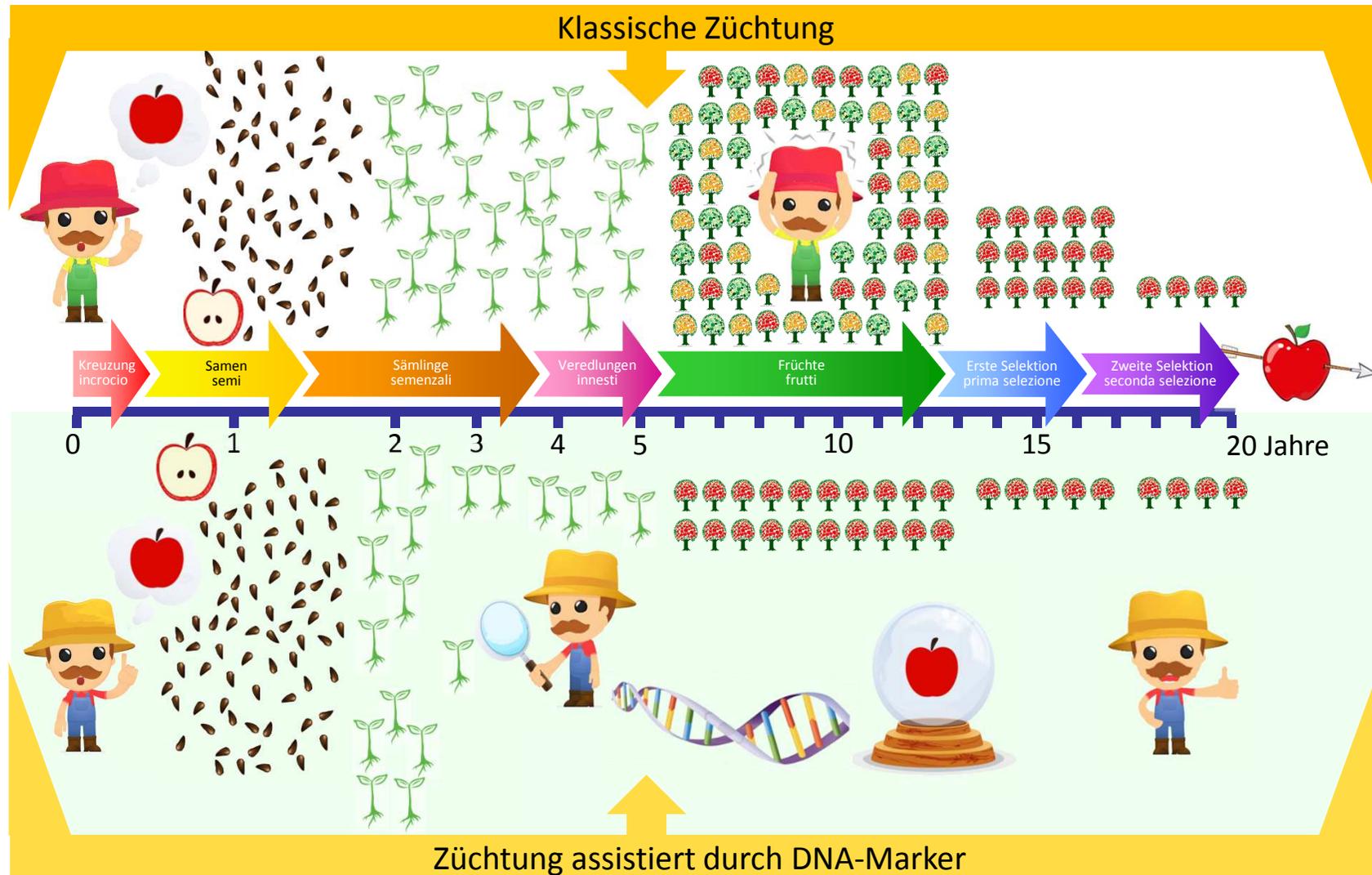


Muscaris
D, 1987



Sauvignon gris
D, 1983

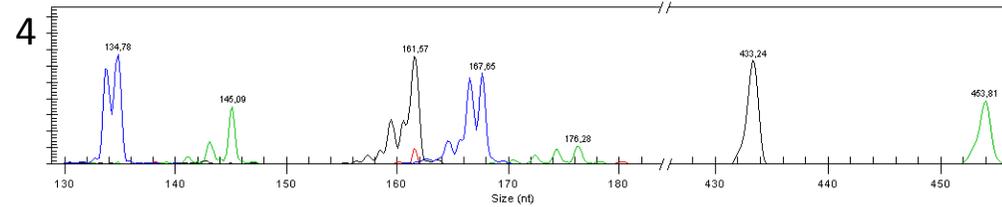
Klassische Züchtung



Klassische Züchtung mit Marker-gestützter Selektion



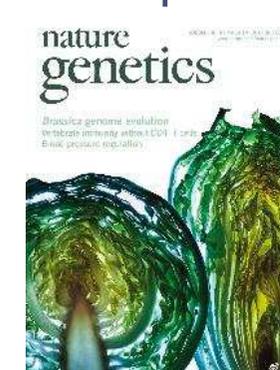
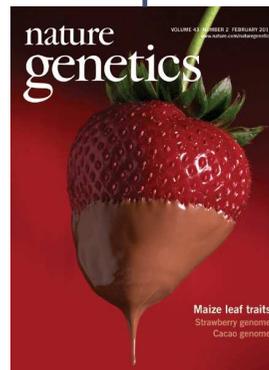
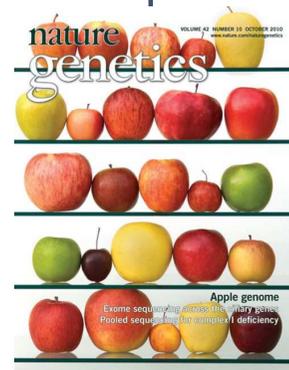
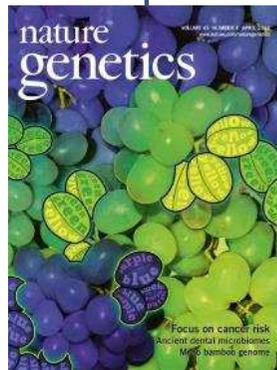
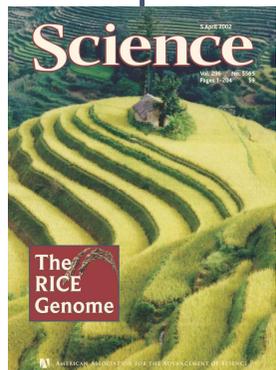
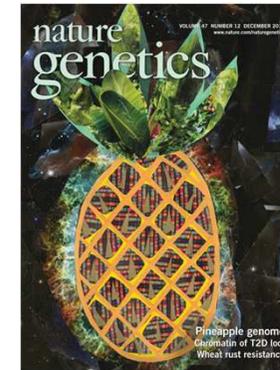
MAS (Marker-assisted selection)



nachher...



Das Genom als offenes Buch



Wettlauf um das Rebengenom



The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla

The French–Italian Public Consortium for Grapevine Genome Characterization*

The analysis of the first plant genomes provided unexpected evidence for genome duplication events in species that had previously been considered as true diploids on the basis of their genetics^{1–3}. These polyploidization events may have had important consequences in plant evolution, in particular for species radiation and adaptation and for the modulation of functional capacities^{4–10}. Here we report a high-quality draft of the genome sequence of grapevine (*Vitis vinifera*) obtained from a highly homozygous genotype. The draft sequence of the grapevine genome is the fourth one produced so far for flowering plants, the second for a woody species and the first for a fruit crop (cultivated for both fruit and beverage). Grapevine was selected because of its important place in the cultural heritage of humanity beginning during the Neolithic period¹¹. Several large expansions of gene families with roles in aromatic features are observed. The grapevine genome has not undergone recent genome duplication, thus enabling the discovery of ancestral traits and features of the genetic organization of flowering plants. This analysis reveals the contribution of three ancestral genomes to the grapevine haploid content. This ancestral arrangement is common to many dicotyledonous plants but is absent from the genome of rice, which is a monocotyledon. Furthermore, we explain the chronology of previously described whole-genome duplication events in the evolution of flowering plants.

All grapevine varieties are highly heterozygous; preliminary data showed that there was as much as 13% sequence divergence between alleles, which would hinder reliable contig assembly when a whole-genome shotgun strategy was used for sequencing. Our consortium therefore selected the grapevine PN40024 genotype for sequencing. This line, originally derived from Pinot Noir, has been bred close to full homozygosity (estimated at about 93%) by successive selfings, permitting a high-quality whole-genome shotgun assembly.

A total of 6.2 million end-reads were produced by our consortium, representing an 8.4-fold coverage of the genome. Within the assembly, performed with Arachne¹², 316 supercontigs represent putative allelic haplotypes that constitute 11.6 million bases (Mb). These values are in good fit with the 7% residual heterozygosity of PN40024 assessed by using genetic markers. When considering only one of the haplotypes in each heterozygous region, the assembly (Table 1a) consists of 19,577 contigs (N_{50} = 65.9 kilobases (kb)), where N_{50} corresponds to the size of the shorter supercontig or contig in a subset representing half of the assembly size) and 3,514 supercontigs (N_{50} = 2.07 Mb) totalling 487 Mb. This value is close to the 475 Mb previously reported for the grapevine genome size¹³.

Using a set of 409 molecular markers from the reference grapevine map¹⁴, 69% of the assembled 487 Mb, arranged into 45 ultracontigs

Received 5 April; accepted 7 August 2007.
Published online 26 August 2007.



A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety

Riccardo Velasco^{1,2*}, Andrey Zharkikh^{2,3*}, Michela Troggio^{1,3*}, Dustin A. Cartwright^{1,2}, Alessandro Cestaro¹, Dmitry Pruss², Massimo Pindo¹, Lisa M. FitzGerald², Silvia Vezzulli¹, Julia Reid², Giulia Malacarne¹, Diana Iliev², Giuseppina Coppola¹, Bryan Wardell², Diego Micheletti¹, Teresita Macalma², Marco Facci¹, Jeff T. Mitchell², Michele Perazzoli¹, Glenn Eldredge², Pamela Gatto¹, Rozan Oyzerski², Marco Moretto¹, Natalia Gutin², Marco Stefanini¹, Yang Chen², Cinzia Segala¹, Christine Davenport², Lorenzo Demattè¹, Amy Mraz², Juri Battilana¹, Keith Stormo⁵, Fabrizio Costa¹, Quanzhou Tao⁵, Azeddine Si-Ammour¹, Tim Harkins⁴, Angie Lackey⁴, Clotilde Perbost³, Bruce Taillon³, Alessandra Stella⁶, Victor Solovyev⁹, Jeffrey A. Fawcett⁷, Lieven Sterck⁸, Klaas Vandepoele⁷, Stella M. Grando¹, Stefano Toppo⁸, Claudio Moser¹, Jerry Lanchbury², Robert Bogden², Mark Skolnick², Vittorio Sgarabella⁶, Satish K. Bhatnagar², Paolo Fontana¹, Alexander Gutin², Yves Van de Peer⁷, Francesco Salamini⁶, Roberto Viola¹

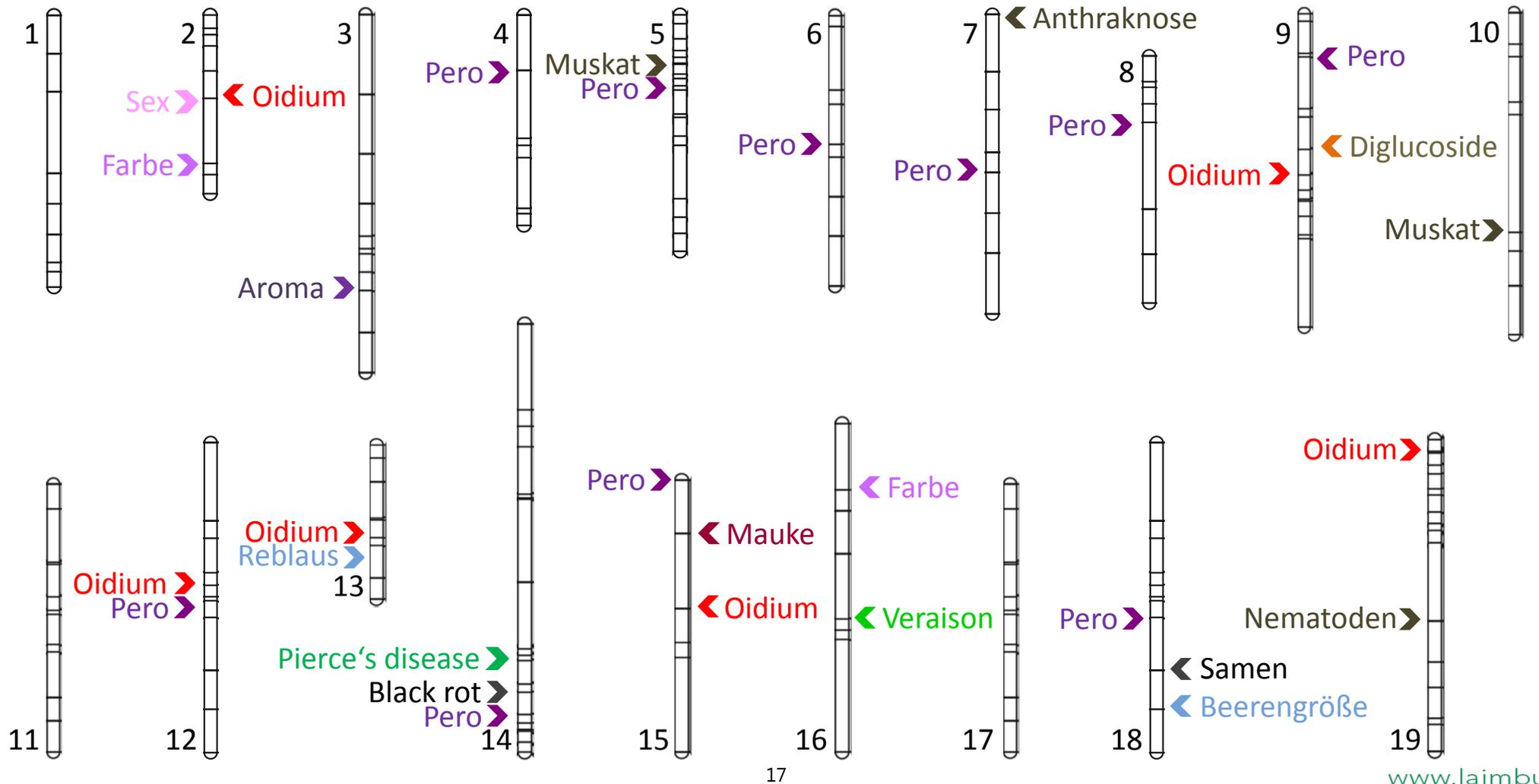
¹IASMA Research Center, San Michele all'Adige, Trento, Italy, ²Myriad Genetics Inc, Salt Lake City, Utah, United States of America, ³3454 Life Sciences Corporation, Branford, Connecticut, United States of America, ⁴Roche Diagnostics Corporation, Roche Applied Science, Indianapolis, Indiana, United States of America, ⁵Amplicon Express Inc., Pullman, Washington, United States of America, ⁶Technology Park Lodi, Lodi, Italy, ⁷Department of Plant Systems Biology, VIB, Gent University, Gent, Belgium, ⁸Department of Biological Chemistry, Padova University, Padova, Italy, ⁹Department of Computer Science, Royal Holloway, University of London, Egham, Surrey, United Kingdom

Background. Worldwide, grapes and their derived products have a large market. The cultivated grape species *Vitis vinifera* has potential to become a model for fruit trees genetics. Like many plant species, it is highly heterozygous, which is an additional challenge to modern whole genome shotgun sequencing. In this paper a high quality draft genome sequence of a cultivated clone of *V. vinifera* Pinot Noir is presented. **Principal Findings.** We estimate the genome size of *V. vinifera* to be 504.6 Mb. Genomic sequences corresponding to 477.1 Mb were assembled in 2,093 metacontigs and 435.1 Mb were anchored to the 19 linkage groups (LGs). The number of predicted genes is 29,585, of which 96.1% were assigned to LGs. This assembly of the grape genome provides candidate genes implicated in traits relevant to grapevine cultivation, such as those influencing wine quality, via secondary metabolites, and those connected with the extreme susceptibility of grape to pathogens. Single nucleotide polymorphism (SNP) distribution was consistent with a diffuse haplotype structure across the genome. Of around 2,000,000 SNPs, 1,751,176 were mapped to chromosomes and one or more of them were identified in 86.7% of anchored genes. The relative age of grape duplicated genes was estimated and this made possible to reveal a relatively recent *Vitis*-specific large scale duplication event concerning at least 10 chromosomes (duplication not reported before). **Conclusions.** Sanger shotgun sequencing and highly efficient sequencing by synthesis (SBS), together with dedicated assembly programs, resolved a complex heterozygous genome. A consensus sequence of the genome and a set of mapped marker loci were generated. Homologous chromosomes of Pinot Noir differ by 11.2% of their DNA (hemizygous DNA plus chromosomal gaps). SNP markers are offered as a tool with the potential of introducing a new era in the molecular breeding of grape.

Citation: Velasco R, Zharkikh A, Troggio M, Cartwright DA, Cestaro A, et al (2007) A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. PLoS ONE 2(12): e1326. doi:10.1371/journal.pone.0001326

Received October 5, 2007; Accepted November 21, 2007; Published December 19, 2007

Züchtungsgrundlagen: Genom, Erbinformation



Klassische Züchtung: Beispiel Resistente Sorten



'Blauburgunder'

×



Muscadinia rotundifolia



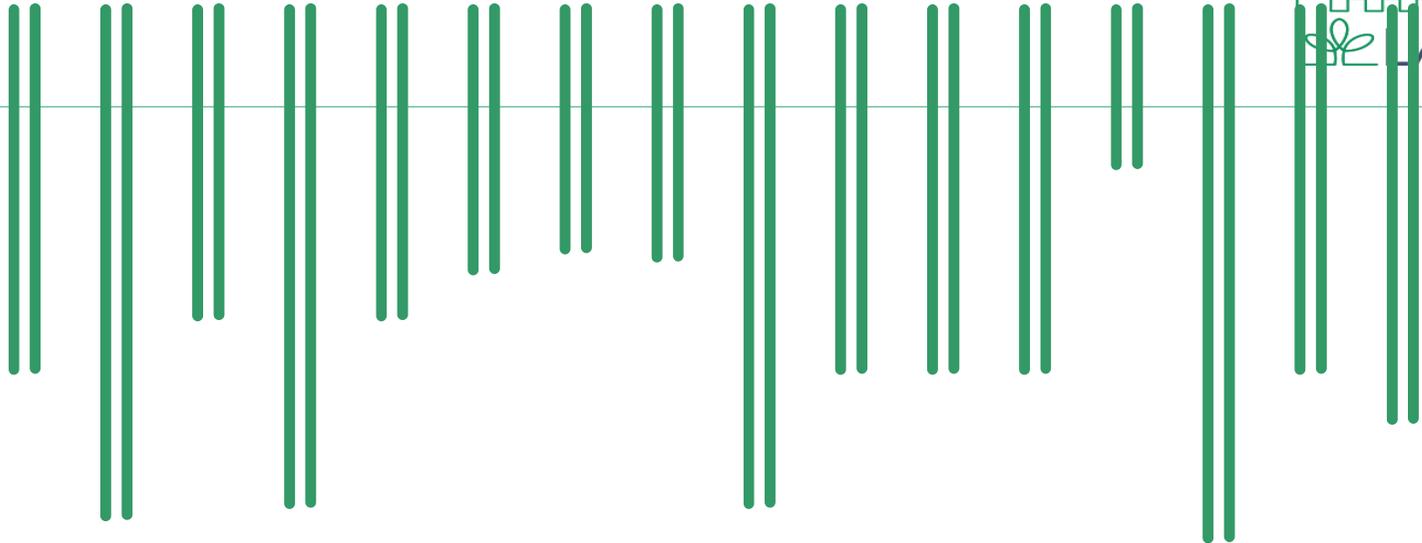
neue mehltresistente Sorte



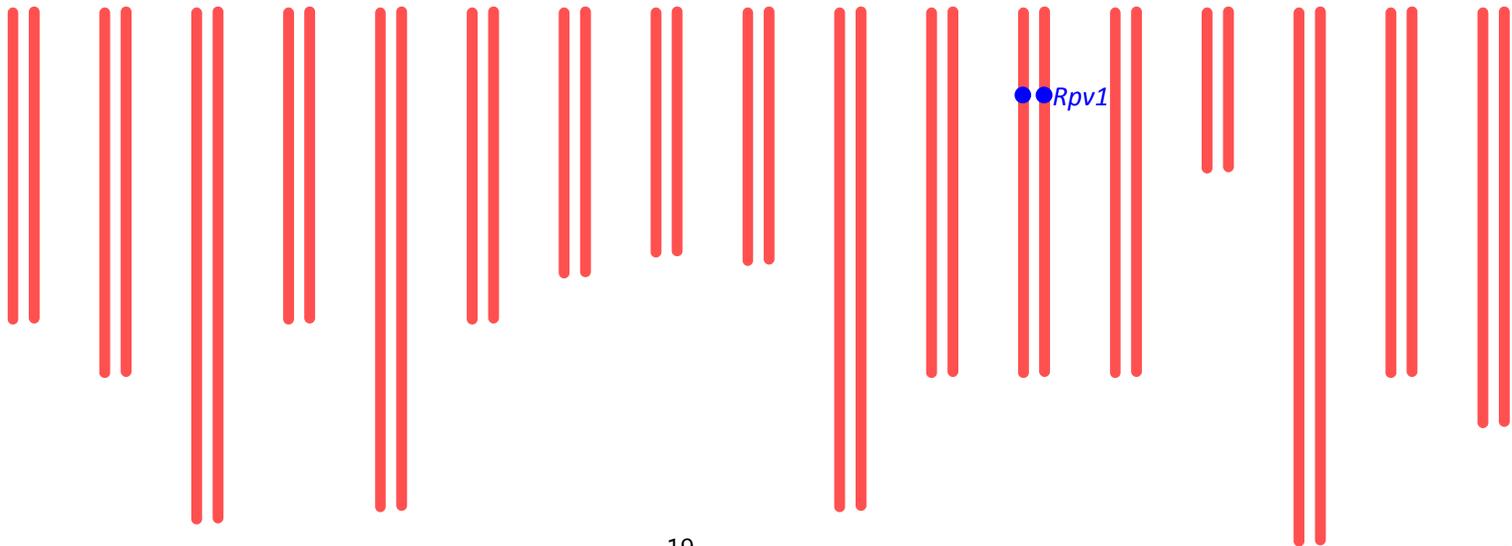
'Blauburgunder'

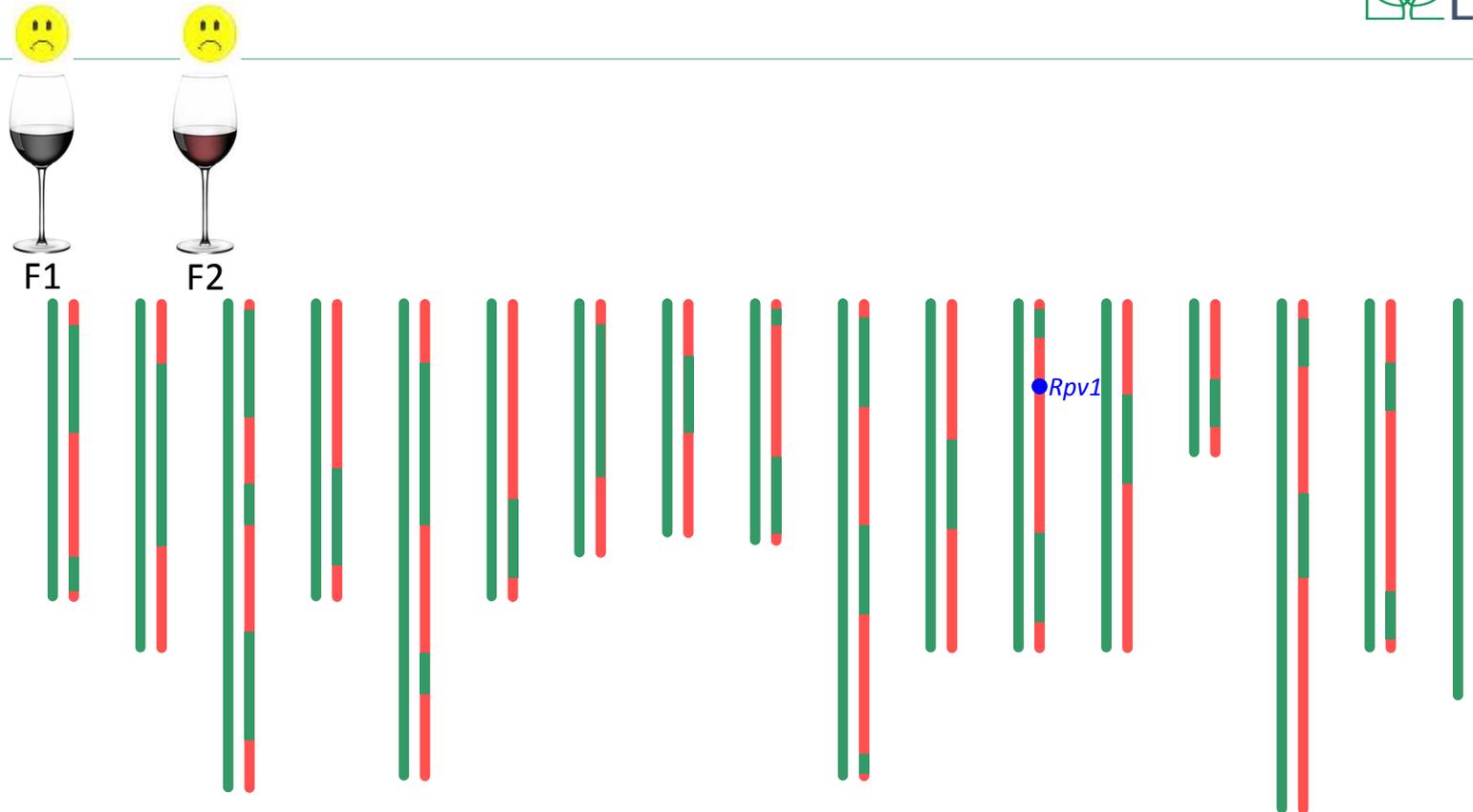


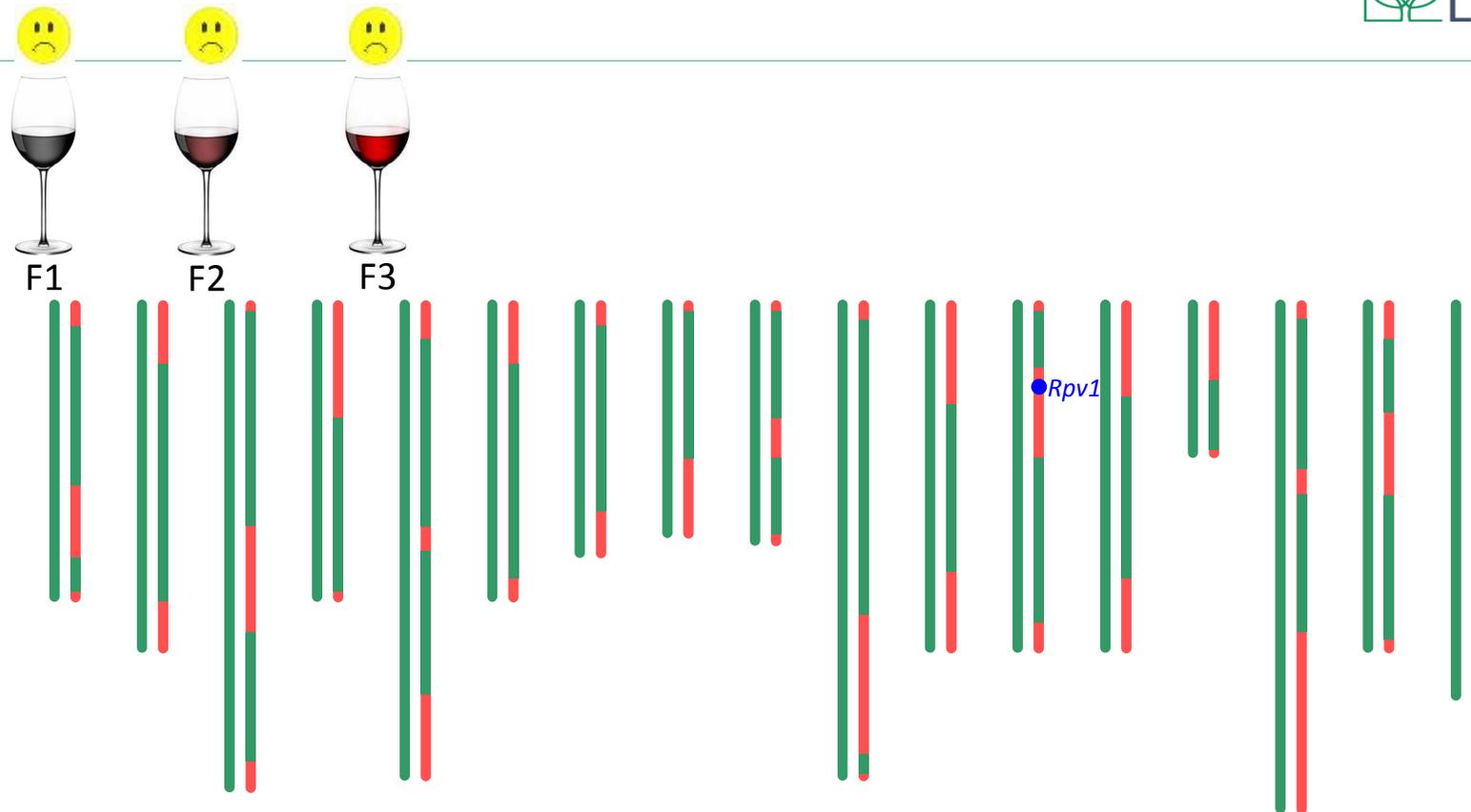
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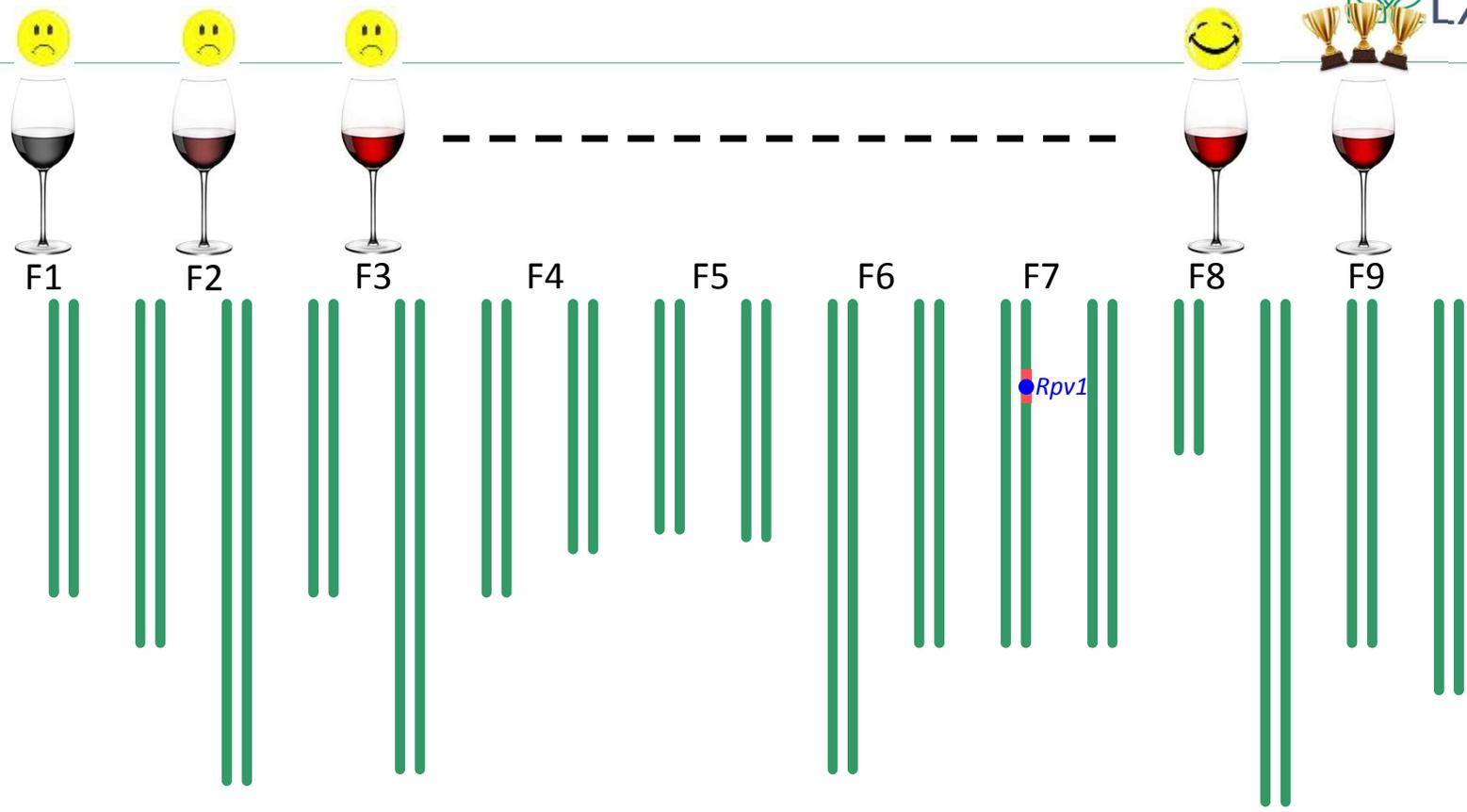


Muscadinia rotundifolia



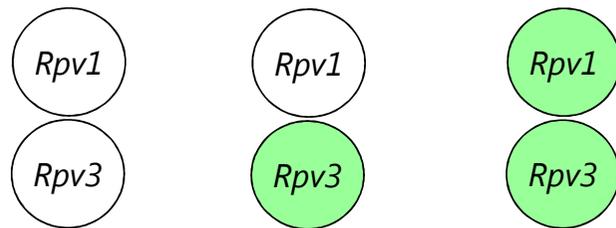




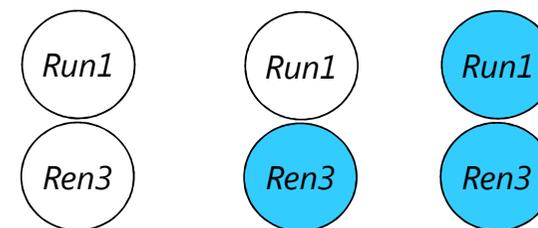


Je mehr Resistenzgene desto höher und nachhaltiger die Resistenz

Peronospora



Oidium



PIWI-Sorten im Test



Ergebnisse

0 Resistenzgene: 12 Sorten Leon Millot...

1 Resistenzgen: 60 Sorten Palatina, Vinera, Muscat Bleu...

2 Resistenzgene: 78 Sorten

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Helios, Aromera, Bianca, Regent,
Donauriesling, Johanniter, Prior...

Cabernet Carbon...

Cabernet Jura...

3 Resistenzgene: 13 Sorten

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

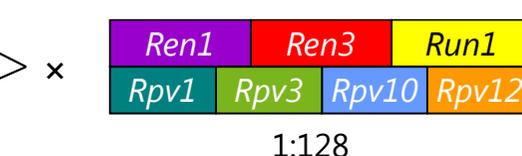
Cabernet Blanc, Pinotin...

Bronner, Solaris, Cabernet Cortis...

4 Resistenzgene: 3 Sorten

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12

Ren1	Ren3	Run1	
Rpv1	Rpv3	Rpv10	Rpv12



Abkürzung: Transgenetik



Acker-Schmalwand



Erbse



Afrikanischer Krallenfrosch



Tausendschön
(Gartenfuchsschwanz)



Birne



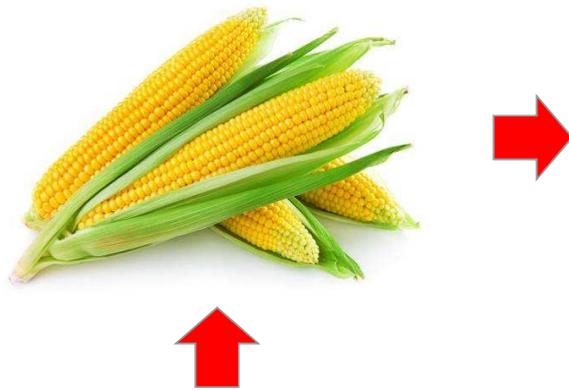
Weizen



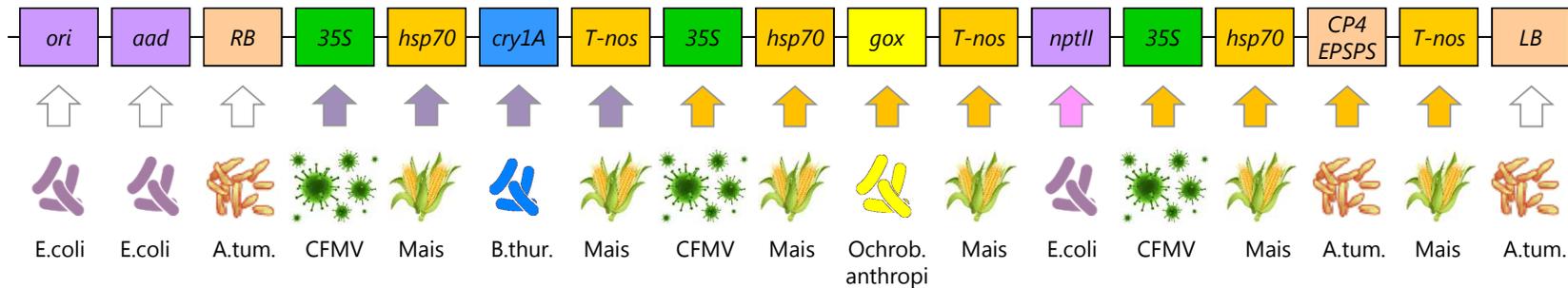
Löwenmaul

Transgenetik

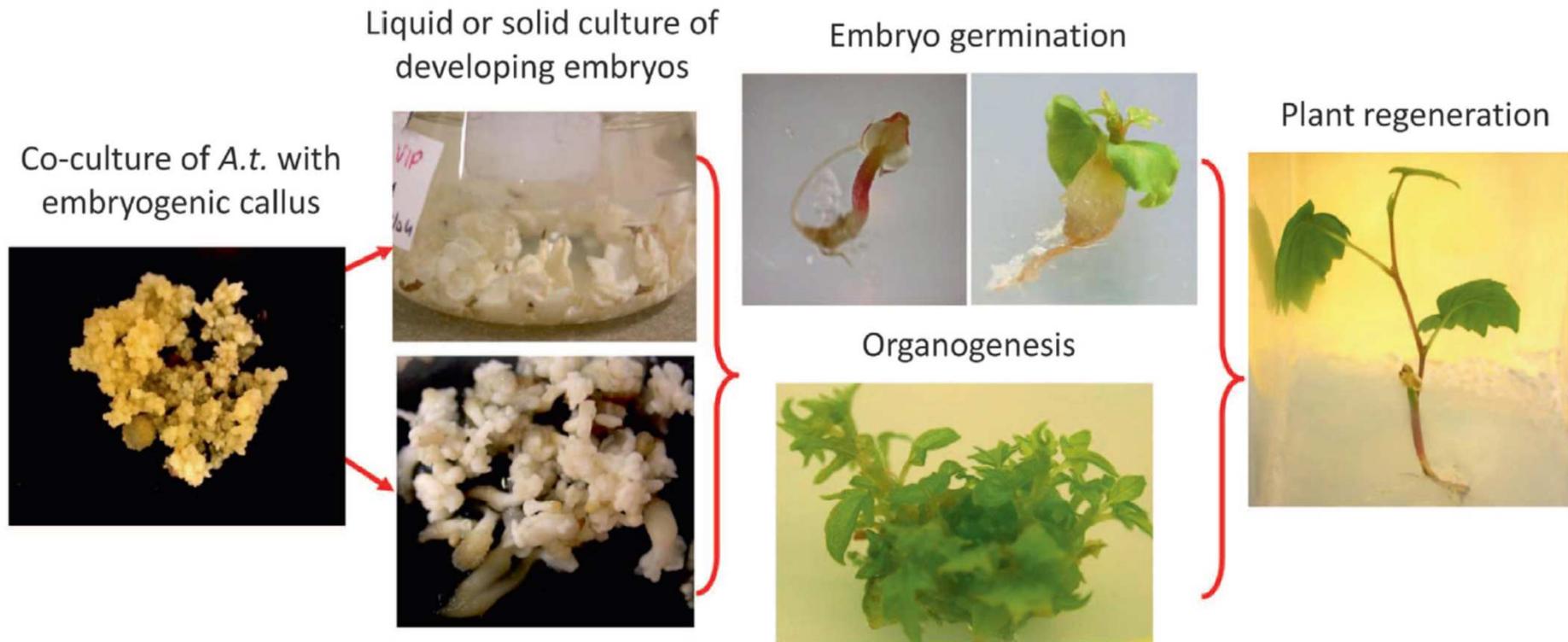
Der Klassiker:
Herbizidresistenter Bt-Mais von Monsanto



Transgene DNA in MON810-Mais (Monsanto)



Methode Transgenetik



SELECTION PHASE (about 6-9 months)

REGENERATION PHASE (about 3-4 months)

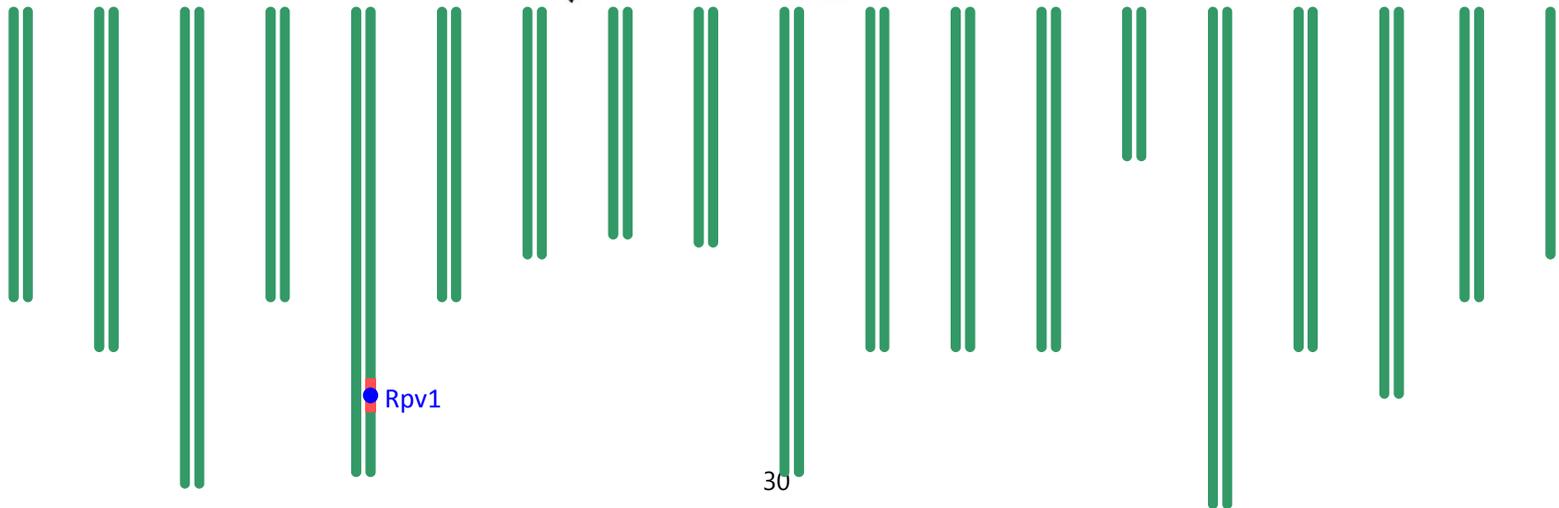
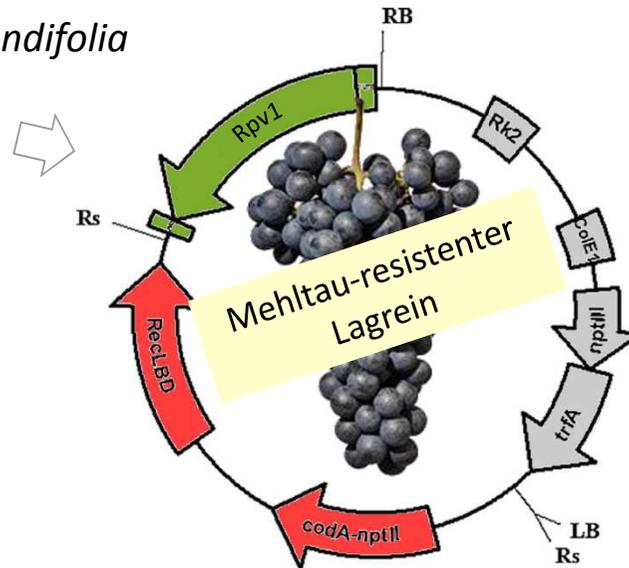
Feldversuche mit transgenen Reben

Paese	data	Varietà	Gene	Origine	Fenotipo
Italy	05/1999 09/2006	Thompson seedless; Silcora	Auxin synthesis	<i>P. savastanoi</i> (batterio)	Parthenocarpic
Australia	06/2003 06/2008	Shiraz; Sultana; Cabernet; Sauvignon; Chardonnay.	ppo Ufgt dfr inv	<i>V. vinifera</i> <i>V. vinifera</i> <i>V. vinifera</i> <i>V. vinifera</i>	Altered browning Altered berry skin Altered anthocyanin/tannin synthesis Altered sucrose content of fruit Altered flowers and fruit
Canada		Cabernet Franc	Superoxid dismutase	<i>Arabidopsis thaliana</i>	Cold tolerance
France	06/2005 10/2009	Roostok 41 B	CP genes from GFLV	GFLV	Virus resistant
Romania	01/2003 30/2006	Russalka; Roostok 41B.	CP genes from: GFLV, GVA and GVB	GFLV; GVA; GVB.	Virus resistant
Germany	07/1999 10/2009 (Interrupted)	Dornfelder; Riesling; Seyval Blanc.	chi26; bgl32; rip-30	<i>Hordeum vulgare</i>	Fungal resistant
United State	03/2006 12/2011				Bacteria resistant
	04/2000 04/2010	Chardonnay; Merlot.	chi	<i>Trichoderma harzianum</i> (fungo)	Fungal resistant
	05/1998 11/2008		chi	<i>T. harzianum</i>	Fungal resistant
	04/2007 04/2008		En42; MSI-99; MagII; PGL; Synthetic antimicrobial peptide.	<i>T. harzianum</i> ; <i>Xenopus laevis</i> (rana africana); <i>Amaranthus caudatus</i> .	Fungal resistant; Bacteria resistant
	04/2006 04/2007	Chardonnay; Merlot.	PGL; MagII	<i>A. caudatus</i> ; <i>X. laevis</i> .	Bacteria resistant
	07/2007 07/2008	NR Rootstock	CP gene	GLRaV-2; GLRaV-3; GFLV	Virus resistance
	05/2005 05/2009	Niagara; Concord	Drr206	<i>Pisum sativum</i>	Fungal resistant
	06/2004 06/2014	Chardonnay Thompson Seedless; Rootstock Saint George.	Polygalacturonase inhibitor protein	<i>P. communis</i>	Fungal resistant
	11/2007 09/2008			<i>V. vinifera</i>	Fungal resistant Bacteria resistant



Cisgenetik

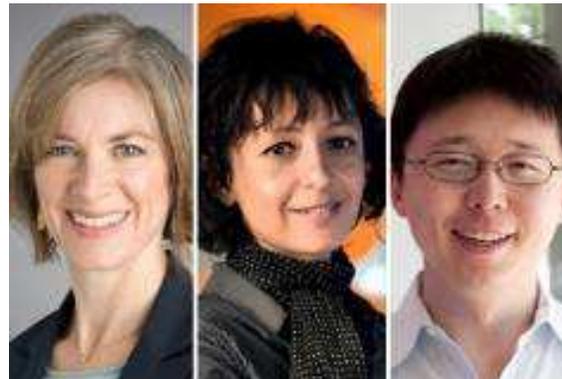
Muscadina rotundifolia



Transgenetik: Gezielter Transfer über Artgrenzen hinweg

CRISPR

clustered regularly interspaced short palindromic repeats

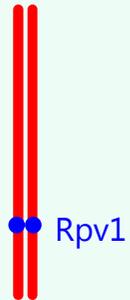


<p>RESEARCH ARTICLE</p> <p>17 AUGUST 2012 VOL 337 SCIENCE</p> <p>A Programmable Dual-RNA–Guided DNA Endonuclease in Adaptive Bacterial Immunity</p> <p>Martin Jinek,^{1,2*} Krzysztof Chylinski,^{3,4*} Ines Fonfara,⁴ Michael Hauer,^{2,†} Jennifer A. Doudna,^{1,2,5,6,‡} Emmanuelle Charpentier^{4,‡}</p>	<p>nature protocols</p> <p>Protocol Published: 24 October 2013</p> <p>Genome engineering using the CRISPR-Cas9 system</p> <p>F Ann Ran, Patrick D Hsu, Jason Wright, Vineeta Agarwala, David A Scott & Feng Zhang </p> <p>Nature Protocols 8, 2281–2308 (2013) Download Citation </p>
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Genome Editing



Muscadina rotundifolia



Resistenzgen dazu



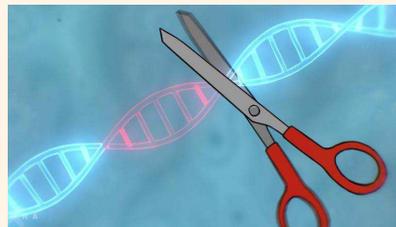
Lagrein



anfällig

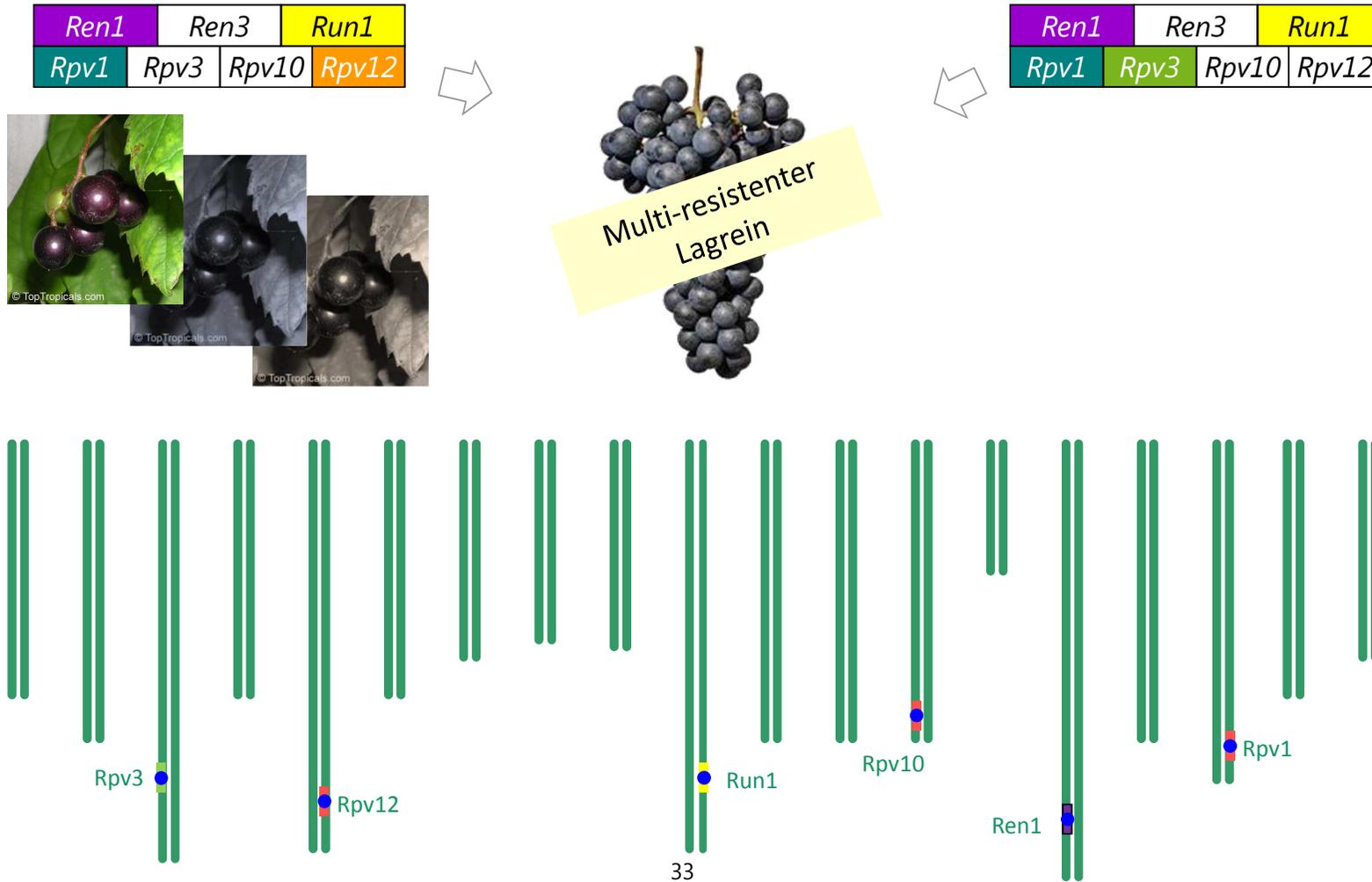


Anfälligkeitstgen raus



tolerant

Genome Editing



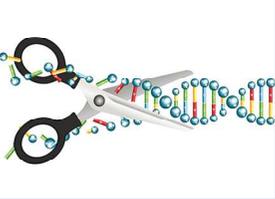
Genetisches Portfolio der Rebe

Peronospora	Gen heute nutzbar	Quelle
<i>Rpv1</i>	Ja für Cisgenetik. Bisher nur für Forschungszwecke transgen genutzt (Australien).	Feechan et al. 2013. Plant J. 76(4):661-74
<i>Rpv3</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>Rpv10</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>Rpv12</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>DMR6</i>	Ja für CRISPR/Cas9. Derzeit in Testung (FEM).	Giacomelli et al. 2017. 20th GiESCO International Meeting.
Oidium		
<i>Run1</i>	Ja für Cisgenetik. Bisher nur für Forschungszwecke transgen genutzt (Australien).	Feechan et al. 2013. Plant J. 76(4):661-74
<i>Ren1</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>Ren3</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>Ren4</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>Ren9</i>	Nein. Gen noch nicht ausreichend erforscht.	
<i>MLO6/7/13</i>	Ja für CRISPR/Cas9. Derzeit in Testung (FEM).	Giacomelli et al. 2017. 20th GiESCO International Meeting.
An weiteren Resistenzgenen wird geforscht (Reblaus, Black rot, ...) und stehen zukünftig zur Verfügung.		

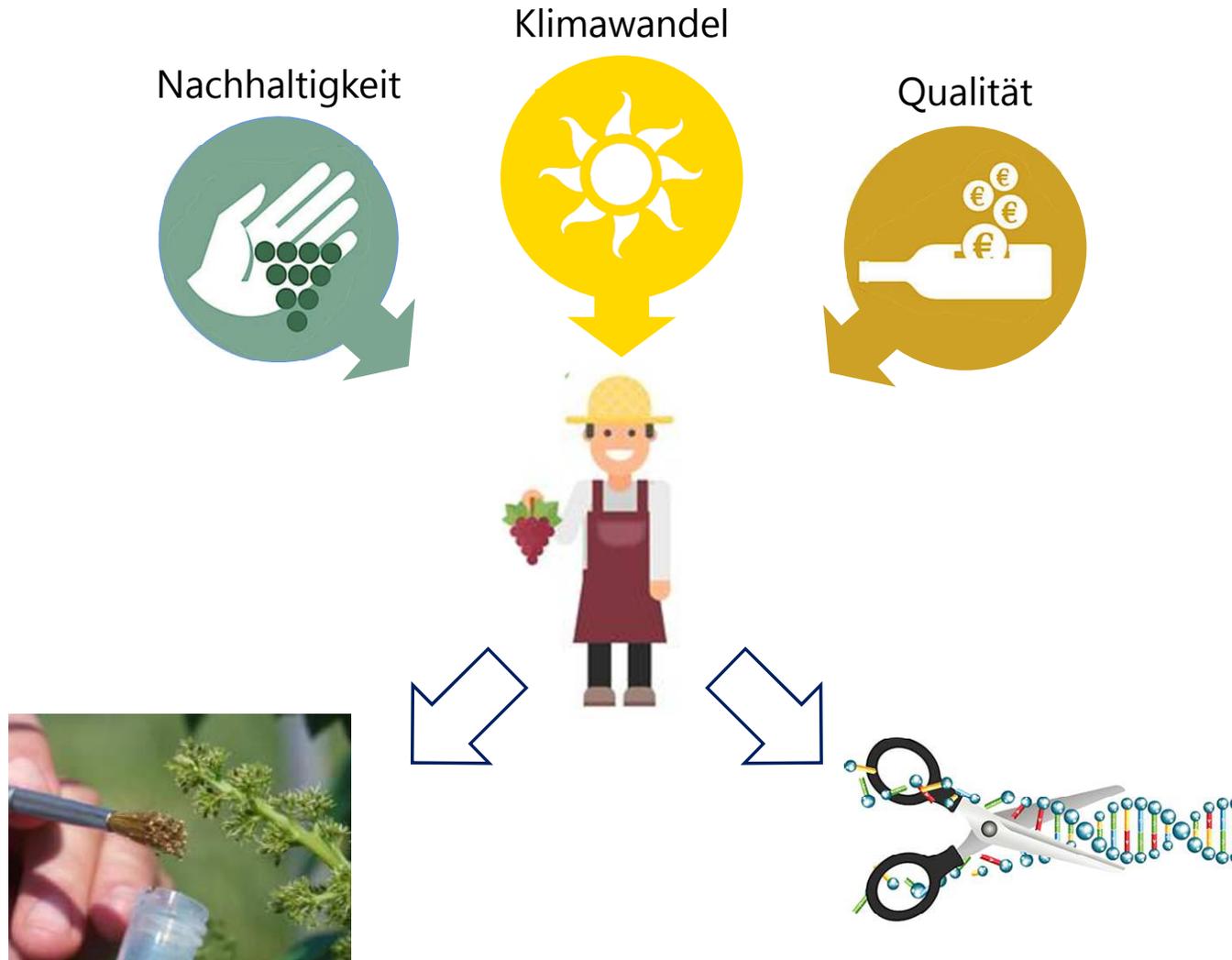


1:128



	Chancen	Herausforderungen
<p>Klassische Züchtung mit Marker-gestützter Selektion</p> 	<ul style="list-style-type: none">• Anpassung an Klimawandel• Kombination von mehreren Resistenzgenen möglich• Echte Sorteninnovation	<ul style="list-style-type: none">• Zeitintensiv• Erreichen der Zuchtziele dem Zufall überlassen• Akzeptanz beim Konsumenten?
<p>Genome Editing</p> 	<ul style="list-style-type: none">• Bestehende Qualitätssorten können beibehalten und verbessert werden• Von spontaner Mutation nicht zu unterscheiden• Großes Potenzial in naher Zukunft	<ul style="list-style-type: none">• Genetisches Portfolio noch klein• Gesetzliche Lage• Akzeptanz beim Konsumenten?• Restrisiko noch zu klären• Nicht nachweisbar

Take home message



Danke für Ihre Aufmerksamkeit.
Grazie per la Sua attenzione.
Thank you for your attention.



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