ŽLAHTNJENJE IN BIOTEHNOLOGIJA RASTLIN

Literatura:

Obvezna:
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Priporočena:
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Ocenjevanje:
Končna ocean je sestavljena iz
30 % kolokvij
10 % seminar
60 % izpit.

Udeležba na vajah je obvezna.

1

Učni načrt:

- Uvod: pregled nekaterih zgodovinskih mejnikov na področju žlahtnjenja rastlin, vloga sodobnega sortimenta v kmetijstvu, pomen genske raznolikosti za žlahtnjenje
- Viri genske variabilnosti, genske banke in karakterizacija akcesij.
- Osnove kvantitativnega dedovanja oz. poligensko dedovane lastnosti.
- Osnovne značilnosti žlahtnjenja samoprašnic, tujeprašnic in vegetativno razmnoženih rastlin
- Izkoriščanje spontanih in izzvanih mutacij v žlahtnjenju rastlin.
- Manipulacije ploidnosti: avto in alopoliploidnost, prednosti in omejitve.
- Pomen medvrstnih križanj in različne možnosti izvedbe vključno z biotehnološkimi postopki.
- Žlahtnjenje s pomočjo genskih markerjev.
- Moderne tehnike žlahtnjenja, tehnike genomskega preurejanja

2

Osnovi cilj žlahtnjenja rastlin je oblikovanje novih, produktivnejših, za človeka koristnejših in za okolje prijaznejših sort.

CILJI ŽLAHTNJENJA

1) PRIDELEK: količina zrna ali drugih delov rastlin za prehrano človeka, povečanje biomase pri krmnih rastlinah, količina olja v semenih, vsebnost sladkorja v sladkornem trsu, itd.

2) KAKOVOST: izboljšanje hranilne vrednosti, sestava olja (višja vsebnost oleinske maščobne kisline), itd.

3) ODPORNOST NA STRES: odpornost na bolezni, škodljivce in abiotski stres (visoke ali nizke temperature, suša, itd.)

4) ŽLAHTNJENJE ZA TRAJNOSTNO KMETIJSTVO: razvoj sort z boljšim izkoristkom hranil, zmožnost fiksacije dušika, itd.

3

Dosežki modernega žlahtnjenja rastlin

1. Povečanje količine pridelka (zaradi izboljšanja te lastnosti ali preko odpornosti na bolezni in škodljivce in z žlahtnjenjem sort z boljšim odzivom na okolje pridelave)

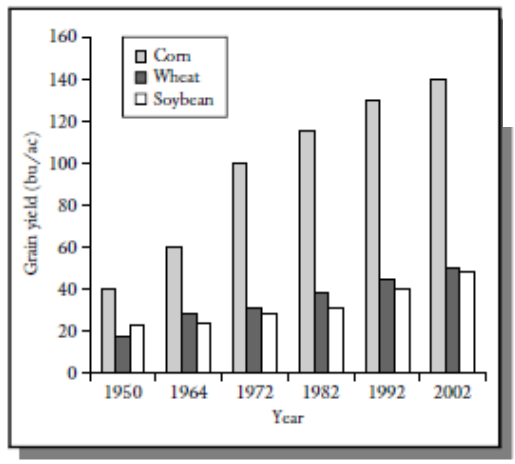
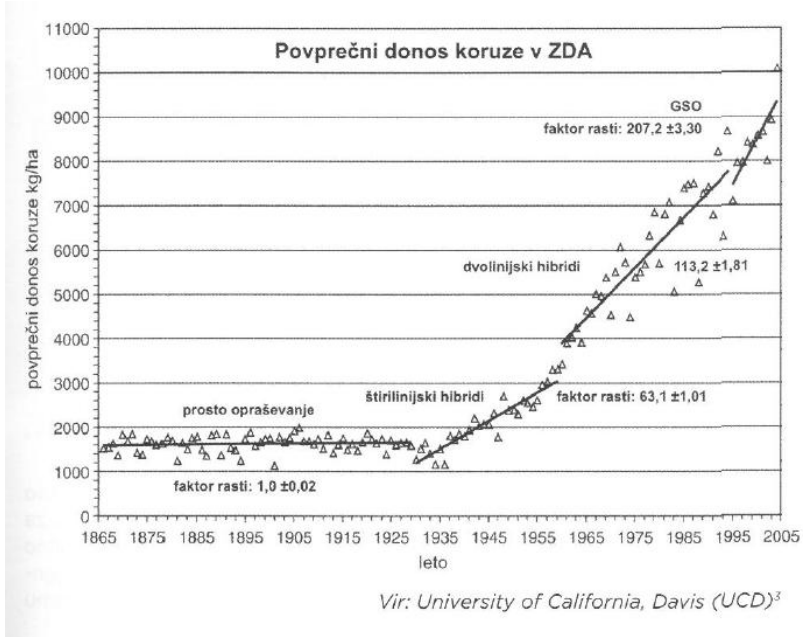


Figure 1.1 The yield of major world food crops is steadily rising, as indicated by the increasing levels of crops produced in the US agricultural system. A significant portion of this rise is attributable to the use of improved crop cultivars by crop producers. (Source: Drawn with data from the USDA.)

Acquaah, 2012, Principles of Plant Genetics and Breeding, 2nd Edition

4



Vir: Alkalaj in Bohanc. 2015. Kaj je res o GSO – Kaj ni res o GSO.

5

2. Izboljšanje hranilne vrednosti pridelkov

Povečanje deleža nekaterih esencialnih spojin, npr. provitamin A v rižu (zlati riž), lizin in treonin v žitih, cistein in metionin v stročnicah.

Lažje prebavljiva živila in varnejša za uživanje (zmanjševanje toksičnih spojin – alkaloidi (solanin pri krompirju), cianogeni glikozidi (kasava), inhibitorji tripsina pri stročnicah,…), zmanjševanje vsebnosti lignina v krmnih rastlinah.

Zlati riž
https://www.youtube.com/watch?v=9V9vcss24_Q

3. Prilagajanje rastlin biotskim in abiotskim stresnim dejavnikom (klimatske spremembe, suše, zasoljevanje tal,…)

6

Table 13.1 Essential amino acids that are low in selected major world food crops.

Crop	Deficient amino acid
Corn	Tryptophan
	Lysine
Wheat	Lysine
Rye	Tryptophan
	Lysine
Rice (polished)	Lysine
	Threonine
Millet	Lysine
Soybean	Methionine
	Cystine
	Valine
Lima bean	Methionine
	Cystine
Peanut	Lysine
	Methionine
	Cystine
	Threonine
Potato	Methionine
	Cystine

7



International Service for the Acquisition of Agri-biotech Applications (ISAAA)
https://www.isaaa.org/gmapprovaldatabase/event/default.asp?EventID=646&Event=Del/Ros1-N

8

Enrichment of tomato fruit with health-promoting anthocyanins by expression of select transcription factors

Eugenio Butelli[1], Lucilla Titta[2], Marco Giorgio[2], Hans-Peter Mock[3], Andrea Matros[3], Silke Peterek[3], Elio G W M Schijlen[4], Robert D Hall[5], Arnaud G Bovy[4], Jie Luo[1] & Cathie Martin[1]

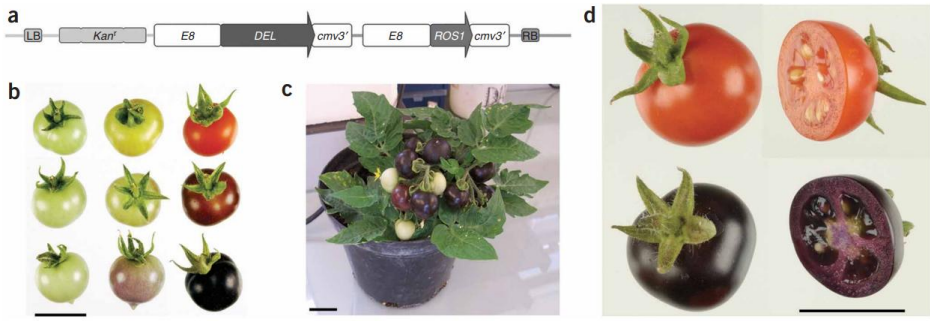
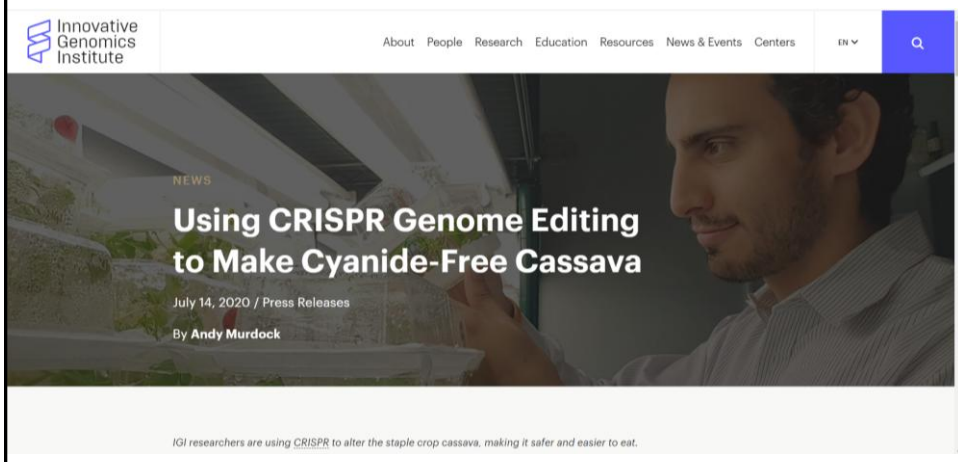


Figure 1 Fruit-specific phenotypes of T1 generation tomatoes (cv. MicroTom) expressing both *Del* and *Ros1* under the control of the *E8* promoter. (**a**) Map of T-DNA region of the binary vector used for transformation. LB, left T-DNA border region; RB, right T-DNA border region; Kan^r, *nptII* gene conferring kanamycin resistance under the control of the *nos* promoter; cmv3′, terminator region of cauliflower mosaic virus. (**b**) Phenotypic analysis of wild-type (upper row), *Del/Ros1*C (middle) and *Del/Ros1*N (lower) tomato fruit harvested at the green (left column), breaker (middle) and red (right) ripening stages. (**c**) *Del/Ros1*N tomato plant showing fruit at different stages of ripening. (**d**) Whole and cross-section of ripe wild-type and *Del/Ros1*N tomato fruit. All scale bars, 2 cm.

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4. Prilagajanje sort tehnologiji pridelave (namakano/nenamakano, mehanizirana pridelava,…)

Produktivnost sorte je odvisna od genetskega zapisa in okolja (primer: Zelena revolucija: kombinacija uporabe gnojil, sredstev za varstvo rastlin, herbicidov, mehanizacije ter razvoj novih visoko produktivnih sort je pripomogla k doseganju večjih pridelkov)

5. Razvoj novih okrasnih sort

6. Prilagajanje potreb industriji, npr.:

- različne sorte krompirja za pečenje, kuhanje, cvrtje, itd. – sorte se razlikujejo predvsem v vsebnosti sladkorja
- manjši paradižnik za v solato, večji okrogel za hamburger, paradižnik za mezgo
- daljše obdobje zorenja za vrtičkarje, istočasno zorenje za mehansko obiranje,…
- Različne sorte pšenice za kruh, testenine, pecivo.
- Podaljšan čas obstojnosti paradižnika, itd.

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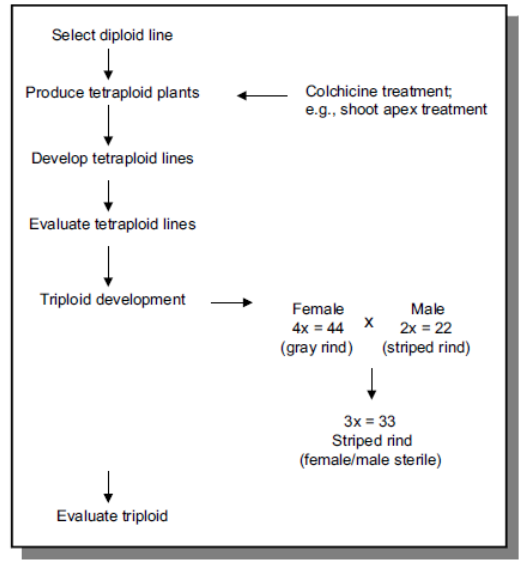


Figure 13.2 Generalized steps in the breeding of seedless melon.

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Fig. 5.14 Diversified fruit colors and shapes of modern tomato cultivars (Source: Courtesy of Yurling Bai, Wageningen UR Plant Breeding, The Netherlands)



Al-Khayri, J.M. In sod. 2016. Advances in Plant Breeding Strategies: Breeding, Biotechnology and Molecular Tools. Springer International Publishing.

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https://twitter.com/PSL_Cranfield/status/1088407008036958208/photo/1

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https://twitter.com/AgBioWorld/status/1123204741742436353/photo/1

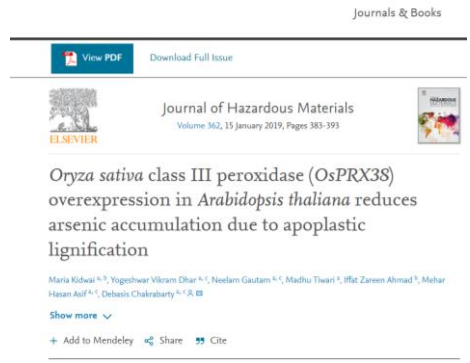
15



World banana collection at KU_Leuven

https://twitter.com/AgroBioDiverse/status/908725184428937216/photo/1

16



Arsenic is a very toxic element, found naturally in India & Bangladesh soils. Rice is the major source of this toxin. Indian scientists have developed GM Arabidopsis plants with reduced arsenic accumulation which may pave development of low-arsenic rice

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7. Prilagajanje rastlin

Fotoperioda (na fotoperiodo neobčutljivi kultivarji bodo uspevali v vseh dolžinah dneva)

Dolžina rastne dobe: zgodnje sorte je mogoče pridelovati v delih sveta s krajšo rastno dobo

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Žlahtnjenje rastlin

Konvencionalni pristop (tudi tradicionalno ali klasično žlahtnjenje)

Nekonvencionalni pristop (žlahtnjenje z uporabo najnovejših tehnologij: npr. tehnologija rekombinantne DNA, MAS.

Žlahtnjenje rastlin vključuje:

1) Določitev ciljev
2) Genski viri, ustvarjanje nove variabilnost
3) Selekcija – izbira potencialnih staršev z želenimi lastnostmi
4) Vrednotenje (pri vrednotenju gre tudi za selekcijo, kjer se primerja lastnosti superiornih genotipov).
5) Certifikacija novih sort

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Table 1.2 An operational classification of technologies of plant breeding.

Classical/traditional tools	**Common use of the technology/tool**
Emasculation	making a completer flower female; preparation for crossing
Hybridization	crossing un-identical plants to transfer genes or achieve recombination
Wide crossing	crossing of distantly related plants
Selection	the primary tool for discriminating among variability
Chromosome counting	determination of ploidy characteristics
Chromosome doubling	manipulating ploidy for fertility
Male sterility	to eliminate need for emasculation in hybridization
Triploidy	to achieve seedlessness
Linkage analysis	for determining association between genes
Statistical tools	for evaluation of germplasm
Relatively advanced tools	
Mutagenesis	to induce mutations to create new variability
Tissue culture	for manipulating plants at the cellular or tissue level
Haploidy	used to create extremely homozygous diploid
Isozyme markers	to facilitate the selection process
In situ hybridization	detect successful interspecific crossing
More sophisticated tools	
DNA markers	
– RFLP	more effective than protein markers (isozymes)
– RAPD	PCR-based molecular marker
Advanced technology	
Molecular markers	SSR, SNPs, etc.
Marker assisted selection	facilitate the selection process
DNA sequencing	ultimate physical map of an organism
Plant genomic analysis	studying the totality of the genes of an organism
Bioinformatics	computer-based technology for prediction of biological function from DNA sequence data
Microarray analysis	to understand gene expression and for sequence identification
Primer design	for molecular analysis of plant genome
Plant transformation	for recombinant DNA work

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Primer žlahtnjenja paradižnika za odpornost na *Oidium neolycopersici*

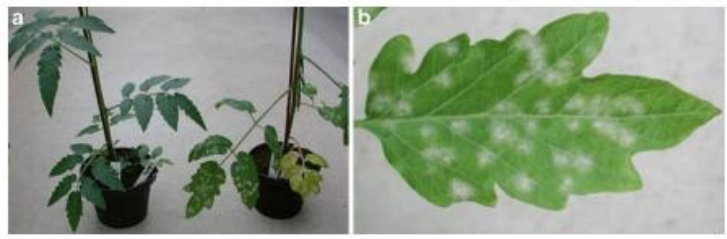


Fig. 5.2 Tomato plants inoculated with tomato powdery mildew. (**a**) The *left* plant is from tomato wild species *Solanum pervianum* LA2172, showing no powdery mildew infection; the *right* plant is from *S. lycoerpsicum* cv. Moneymaker (MM), showing fungal colonies growing on infected leaves. (**b**) A closer look at the colonization of tomato powdery mildew (*Oidium neolycopersici*) growing on the upper-side of MM leaf. Pictures were taken 15 days post inoculation (Source: Courtesy of Yurling Bai, Wageningen UR Plant Breeding, Netherlands)

Al-Khayri, Mohan Jain, Johnson. 2015. Advances in Plant Breeding Strategies: Breeding, Biotechnology and Molecular Tools. Springer International Publishing.

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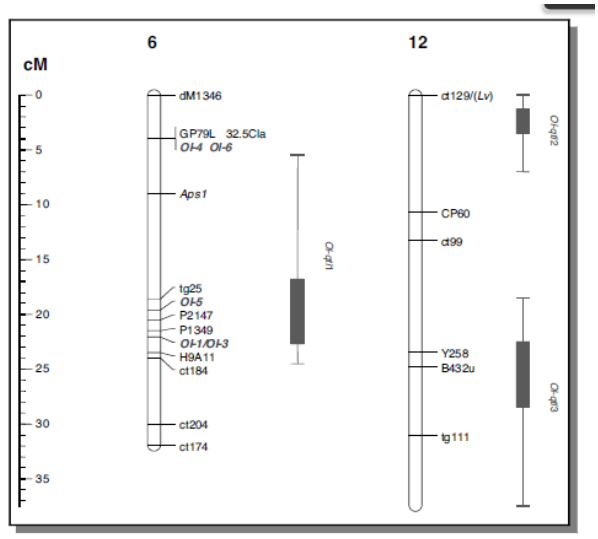


Figure B3.2 The chromosome locations of tomato loci for resistance to tomato powdery mildew caused by *Oidium neolycopersici*. On the left, genetic distance in cM is shown. On the right, map positions of markers and resistance loci are shown on tomato chromosome 6 and 12, respectively. The donors for *Ol-1, Ol-3, Ol-5* are *Solanum habrochaites* G1. 1560, G1. 1290, PI247087, respectively; for *Ol-4* is *S. peruvianum* LA2172 and for *Ol-qtls* are *S. neorickii* G1.1601. *Ol-6* is identified from an advanced breeding line with unknown source. As to *Ol-qtls*, bars indicate the QTL interval for which the inner bar shows a one-LOD support and the outer one shows a two-LOD support interval. Figure courtesy of Yuling Bai.

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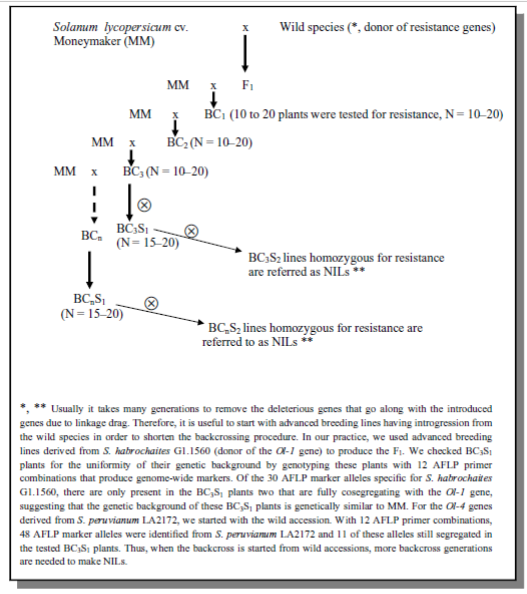


Figure B3.4 Cross-pollinating scheme on the generation of near-isogenic lines (NIL) harbouring dominant resistance genes to tomato powdery mildew. Via backcrosses, new traits are introduced from wild tomato relatives. During the backcrosses, selection of resistant plants can be performed via (i) disease test and/or (ii) marker assisted selection (MAS, Figure B3.4). In addition, selected plants should have a similar morphology to the recurrent parent. Figure courtesy of Yuling Bai.

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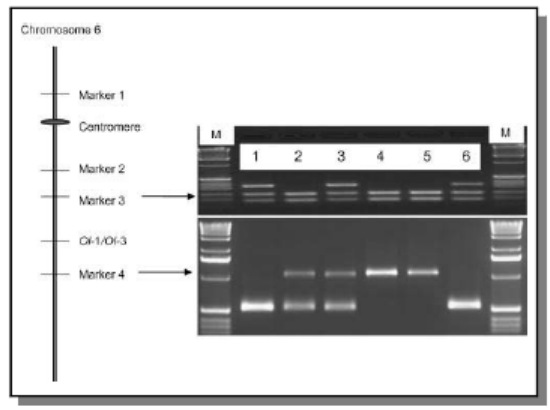


Figure B3.3 Illustration of marker assisted selection (MAS). On the left, a genetic linkage map of tomato chromosome 6 showing that the *Ol-1* and *Ol-3* genes, conferring resistance to tomato powdery mildew, are located at the same locus and are flanked by Markers 3 and 4. On the right, electrophoretic patterns of PCR markers showing marker genotypes of six plants; the upper panel for Marker 3 and the lower panel for Marker 4. Plants 1–4 are either BC_3 plants (for Marker 3) and BC_3S_1 plants (for Marker 4). Plants 5 and 6 are parental plants that are susceptible and resistant to tomato powdery mildew, respectively. M indicates DNA size marker of 1kb ladder. For MAS, marker flanking the target gene is often used. For Marker 3, BC_3 plants 1 and 3 are selected and expected to be resistant to powdery mildew since they have the marker allele of the resistant parent (plant 6). For Marker 4, plants 1–3 are selected and expected to be resistant since they have the resistant marker allele as the resistant parental plant 6 (plant 1 is homozygous and plants 2 and 3 are heterozygous). Figure courtesy of Yuling Bai.

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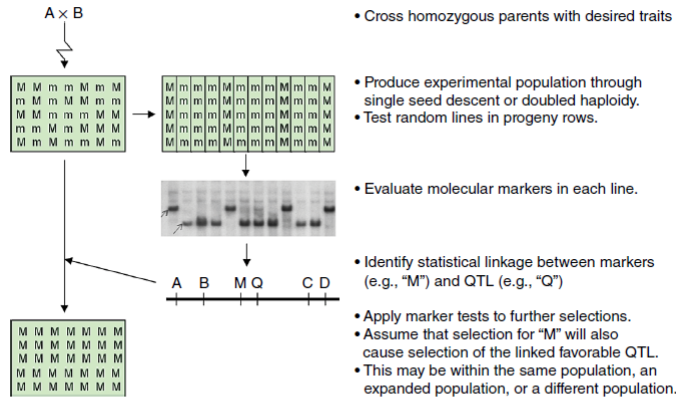


Figure 3.16. A simplified strategy for marker-assisted selection (MAS). Here, a significant association between a QTL (Q) and a molecular marker allele (M) is identified in an experimental population. This information is applied in future populations in order to select Q indirectly through its linkage to M.

Stewart. 2016. Plant biotechnology and genetics. Principles, Techniques and Applications. 2nd ed. John Wiley & Sons.

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PREGLED ZGODOVINE ŽLAHTNJENJA RASTLIN

700 BCE Asirci in Babilonci ročno opraševali dateljeve palme

Motiv opraševanja dateljeve palme na asirskem reliefu



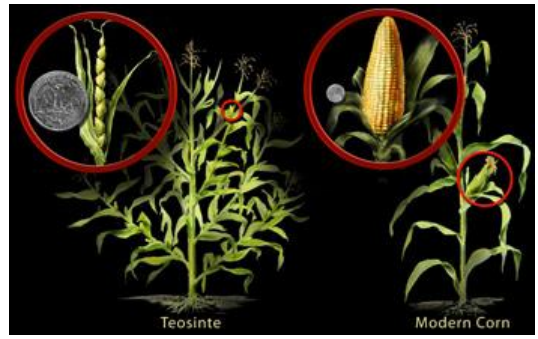
Fig. 1 Winged creature pollinating a date palm by hand on an Assyrian relief. Picture from the Bowdoin College Museum of Art, Brunswick, Maine

…and also Theophrastos [370–285 bce] wrote that if the dust of one flower was shaken over other flowers fertilisation took place

Klerk. 2018. The roots of pollen analysis: the road to Lennart von Post

26

Koruza je bila domesticirana iz teosinta



https://www.nsf.gov/news/news_summ.jsp?cntn_id=104207

Maize was domesticated from teosinte, a wild grass growing in the lower reaches of the Balsas River Valley of Central Mexico, around 9,000 years ago. There is evidence maize was first cultivated in the Maya lowlands around 6,500 years ago, at about the same time that it appears along the Pacific coast of Mexico.

https://www.sciencedaily.com/releases/2020/06/200603151158.htm

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PREGLED ZGODOVINE ŽLAHTNJENJA RASTLIN

Rudolf Camerarius (1665-1721) – profesor filozofije na Univerzi Tubingen v Nemčiji. Objavil študijo leta 1694, kjer je opisal vlogo posameznih organov moških in ženskih cvetov pri oploditvi in dokazal, da je za oploditev potreben pelod.

Fairchild (1719) prvi umetni hybrid (nagelj x brkati nageljček *(Dianthus barbatus)*)

Joseph Gottlieb Koelreuter (1733-1806). Prvi sistematični poskus s križanjem tobaka – prvi umetni hibridi s tobakom.

Thomas Knight (1759-1838) – izvedel več križanj med leti 1811 in 1833 pri več kulturnih rastlinah. Osredotočil se je le na kombinacije, kjer je bila uporabna variabilnost F1 generacije. Zanimive rastline se je lahko ohranilo le z vegetativnim razmnoževanjem.

28

Louis de Vilmorin (1816-1860). Iz družine, ki je ustanovila prvo semenarsko in žlahtniteljsko podjetje. Vpeljal metodo žlahtnjenja z rodovnikom (pedigree method). Z objavo Note on the Creation of a New Race of Beetroot and Considerations on Heredity in Plants" leta 1856 postavil temelje modernega semenarstva.

Gregor Johann Mendel – zakoni dedovanja (1865)

Wilhelm Johannsen 1903 – avtor teorije čistih linij (večkratno samoopraševanje vodi v homozigotnost. Variabilnost znotraj čistih linij zaradi vpliva okolja in tako ugotovil, da je fenotip rezultat genotipa in okolja.

George Shull (1908, 1909) – koncept heteroze (proučeval vpliv inbridinga in navzkrižnega križanja (cross breeding) pri koruzi). Shull conducted extensive research to develop inbreeds to produce hybrids.

Iskanje novih genov za vključitev v domesticirane rastline je narekovalo proučevanje domestikacije in širitve kulturnih rastlin, z namenom, da bi našli prednike in divje sorodnike za uporabo v žlahtnjenju.

N.I. Vavilov, 1925 – opis osmih centrov izvora gojenih rastlin.

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Primer žlahtnjenja v času pred Mendlom:

- Duchesne (17. stol.) je v botaničnem vrtu v Parizu križal *Fragaria x ananasa*

- 1747 Margraaf določil v korenu sladkorne pese 6 % saharoze. V začetku 19. stol. je Achard z masovno selekcijo povečal vsebnost saharoze na 11 %. Kasneje so s z uporabo Vilmorinove pedigree metode uspeli povečati vsebnost na 16 %.

30

Hardy in Weinberg (1908) – njuna teorija postavila temelje žlahtniteljskim metodam za žlahtnjenje tujeprašnic

Fisher (1918) – z Mendlovimi zakoni dedovanja obrazložil kontinuirano variabilnost.

Sir Otto Frankel – uveljavil izraz genski viri (1967) – opozoril na pomen genskih virov za žlahtnjenje in izrazil skrb nad izgubo genskega materiala zaradi množične pridelave novejših sort, ki so izpodrivale pokrajinske populacije gojenih rastlin.

1974 – ustanovitev mednarodnega urada za rastlinske genske vire (**IBPGR**), kasneje (1992) preimenovan v Mednarodni inštitut za rastlinske genske vire (**IPGRI**) zadolžen za zbiranje, vrednotenje in ohranjanje genskega materiala. Od 2006 **Bioversity International**, sedaj pa združenje Bioversity International in CIAT (od 2019)

Herb Boyer, Stanley Cohen in Paul Berg – začetek genskega inženiringa – s tehnologijo rekombinantne DNA v bakterijo vstavili tujo DNA (1973).

31

Norman East Borlaug – *oče zelene revolucije*

Razvoj visoko produktivnih sort pšenice in tehnologij pridelave (gnojenje, namakanje, obdelava tal, varstvo)

Križanje pritlikavega genotipa pšenice (Norin 10) z mehiško - odporna na poleganje, nižje rasti, pri čemer se je pridelek iz 750 kg/ha povečal na 3200 kg/ha.

Zaradi uspeha križanja pšenice, je bilo enako narejeno pri rižu, na Filipinih 1960.

Dr. Norman Borlaug je leta 1970 prejel Nobelovo nagrado za mir.



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CENTRI IZVORA KMETIJSKIH RASTLIN

Ruski genetik in agronom, Nikolai Ivanovich Vavilov je v okviru odprav v dvajsetih in tridesetih letih 20. stol. zbral semena in rastlinski material številnih kultiviranih rastlin in divjih sorodnikov. Semena je gojil in proučeval botanične in ekonomske lastnosti, predvsem za žlahtniteljske namene.

Njegovi zaključki:
Območje z največjo genetsko raznolikostjo določene kulture predstavlja *center izvora*. Na osnovi geografske porazdelitve variabilnosti za posamezne vrste je določil osem *centrov izvora*.

center diverzitete / center izvora!

33



Fig. 3.1. The twelve megacentres of cultivated plants (Zeven and Zhukovsky, 1975).

34

Table 3.2. Cultivated plants and their regions of diversity. Based on Zeven and Zhukovsky (1975) and Zeven and de Wet (1982)

1 Chinese–Japanese Region
- Prosomillet, Fox tail millet, Naked oat
- Soybean, Adzuki bean
- Leafy mustard
- Orange/*Citrus*, Peach, Apricot, Litchi
- Bamboo, Ramie, Tung oil tree, Tea

2 Indochinese–Indonesian Region
- Rice
- Rice bean, Winged bean
- Cucurbits/Ash gourd
- Mango, Banana, Rambutan, Durian, Bread fruit, *Citrus*/Lime, Grapefruit
- Bamboos, Nutmeg, Clove, Sago-palm, Ginger, Taros and Yams, Betel nut, Coconut

3 Australian Region
- *Eucalyptus*, *Acacia*, *Macadamia* nut

4 Hindustani Region
- Rice, Little millet
- Black gram, Green gram, Moth bean, Rice bean, *Dolichos* bean, Pigeonpea, Cowpea, Chickpea, Horse gram, Jute
- Eggplant, Okra, Cucumber, Leafy mustard, Rat's tail radish, Taros and Yams
- *Citrus*, Banana, Mango, Sunnhemp, Tree cotton
- Sesame, Ginger, Turmeric, Cardamom, Arecanut, Sugarcane, Black pepper, Indigo

5 Central Asian Region
- Wheat (Bread/Club/Shot), Rye
- *Allium*/Onion, Garlic, Spinach, Peas, Beetroot, Faba bean
- Lentil, Chickpea
- Apricot, Plum, Pear, Apple, Walnut, Almond, Pistachio, Melon, Grape, Carrot, Radish
- Hemp/*Cannabis*, Sesame, Flax, Safflower

6 Near Eastern Region
- Wheat (Einkorn, Durum, Poulard, Bread), Barley, Rye/*Secale*
- Faba bean, Chickpea, French bean, Lentil, Pea
- *Brassica oleracea*, *Allium*, Melon, Grape, Plum, Pear, Apple, Apricot, Pistachio, Fig, Pomegranate, Almond
- Safflower, Sesame, Flax
- Lupins, Medics

Table 3.2 continued

7 Mediterranean Region
- Wheat (Durum, Turgidum), Oats
- *Brassica oleracea*, Lettuce, Beetroot, Colza
- Faba bean, Radish
- Olive, *Trifolium*/Berseem, Lupins, *Crocus*, Grape, Fennel, Cumin, Celery, Linseed

8 African Region
- Wheat, (Durum, Emmer, Poulard, Bread)
- African rice, Sorghum, Pearl millet, Finger millet, Teff
- Cowpea, Bottle gourd, Okra, Yams, Cucumber
- Castor bean, Sesame, Niger, Oil palm, Safflower, Flax
- Cotton, Kenaf, Coffee
- Kola, Bambara groundnut, Date palm, Ensete, Melons

9 European–Siberian Region
- Peach, Pear, Plum, Apricot, Apple, Almond, Walnut, Pistachio, Cherry
- Cannabis, Mustard (black), Chicory, Hops, Lettuce

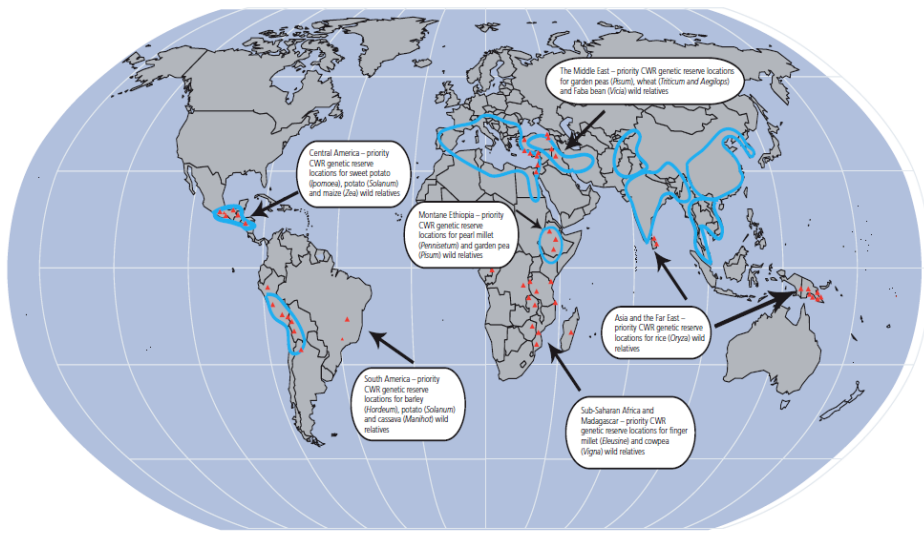
10 South American Region
- Potato, Sweet potato, *Xanthosoma*
- Lima bean, Amaranth, *Chenopodium*, *Cucurbita*, Tomato, Tobacco, Lupin
- Papaya, Pineapple
- Groundnut, Sea island cotton
- Cassava, Cacao, Rubber tree, Passion fruit

11 Central American and Mexican Region
- Maize, French bean, Potato, *Cucurbita*, Pepper/Chilli, Amaranth, *Chenopodium*, Tobacco, Sisal hemp, Upland cotton

12 North American Region
- Jerusalem artichoke, Sunflower, Plum, Raspberry, Strawberry

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FIGURE 1.1
Global priority genetic reserve locations for wild relatives of 12 food crops



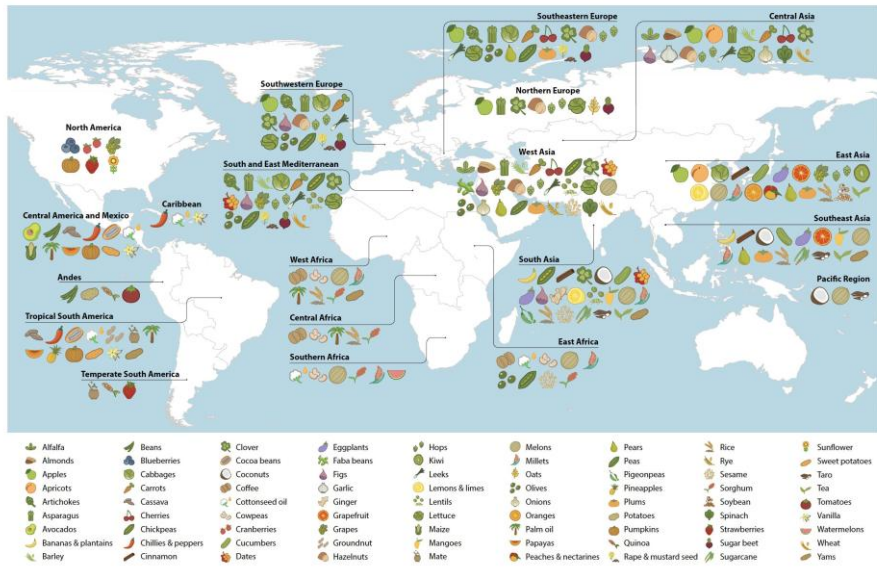
Source: Maxted, N. & Kell, S.P. 2009. The eight Vavilov centres of origin/diversity of cultivated plants, indicated by the enclosed lines, are likely to contain further priority sites for other crop genepools.

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ORIGINS AND PRIMARY REGIONS OF DIVERSITY OF AGRICULTURAL CROPS

CIAT
International Center for Tropical Agriculture
Since 1967 Science to cultivate change

Khoury CK, Achicanoy HA, Bjorkman AD, Navarro-Racines C, Guarino L, Flores-Palacios X, Engels JMM, Wiersema JH, Dempewolf H, Sotelo S, Ramírez-Villegas J, Castañeda-Álvarez NP, Fowler C, Jarvis A, Rieseberg LH, and Struik PC (2016). Origins of food crops connect countries worldwide. Proc. R. Soc. B 283: 20160792. DOI: 10.1098/rspb.2016.0792.



https://blog.ciat.cgiar.org/origin-of-crops/

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SPREMEMBE MED DOMESTIKACIJO

Table 10.2 Characteristics of domestication syndrome traits.

General effect	Specific traits altered
1 Increased seedling vigor (more plants germinating)	- loss of seed or tuber dormancy - large seeds
2 Modified reproductive system	- increased selfing - vegetatively reproducing plants - altered photoperiod sensitivity
3 Increased number of seeds harvested	- non-shattering - reduced number of branches (more fruits per branch)
4 Increased appeal to consumers	- attractive fruit/seed colors and patterns - enhanced flavor, texture, and taste of seeds/fruits/tubers (food parts) - reduced toxic principles (safer food) - larger fruits - reduced spikiness
5 Altered plant architecture and growth habit	- compact growth habit (determinacy, reduced plant size, dwarfism) - reduced branching

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POMEN GENSKE RAZNOLIKOSTI ZA ŽLAHTNJENJE

Primeri izbruhov bolezni zaradi pomanjkanja genetske variabilnosti:
- Krompirjeva plesen, 1845, Irska
- Žitna progasta rja, 1917, ZDA, (*Wheatless days*)
- Bengalska lakota, 1943

VIRI GENSKE VARIABILNOST

Shranjevanje pridelka iz zdravih rastlin, ali glede na velikost semena, plodov, barvo,.. in uporaba semena naslednje leto > žlahtnjenje za odpornost in druge lastnosti > čez čas se tako ustvari populacija rastlin, prilagojena na lokalne razmere – nastanejo t.i. s strani pridelovalca selekcionirane sorte oz. krajevne ali lokalne populacije (ang. *landraces*)

- Sodobne sorte
- Starejše sorte, ki niso več v uporabi
- Sorodne vrste (divje) kmetijske rastline

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Genska erozija

Sodobne sorte so v razvitih državah že skoraj povsem izpodrinile stare krajevne populacije in tudi stare sorte. Zmanjšanju števila gojenih primitivnih kultivarjev, kot tudi zmanjšanje zastopanost divjih sorodnikov zaradi degradacije okolja imenujemo genska erozija.

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GENSKE BANKE

Smernice za zbiranje genskih virov
http://cropgenebank.sgrp.cgiar.org/index.php/procedures-mainmenu-242/collecting

Ostalo gradivo na temo upravljanja z genskimi bankami je dostopno na:

https://www.genebanks.org/
http://cropgenebank.sgrp.cgiar.org/
https://www.fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/gbs/en/

Slovenska rastlinska genska banka (SRGB)
https://www.gov.si/teme/genski-viri-v-rastlinski-pridelavi/

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Deskriptorji

FAO/Bioversity Multi-Crop Passport Descriptors V.2.1 [MCPD V.2.1]
https://www.fao.org/plant-treaty/tools/toolbox-for-sustainable-use/details/en/c/1367915/

The MCPD, developed jointly by Bioversity International (formerly IPGRI) and FAO, is a widely used international standard to facilitate germplasm passport information exchange. These descriptors are compatible with Bioversity's crop descriptor lists, with the descriptors used by the FAO World Information and Early Warning System (WIEWS) on plant genetic resources (PGR), and with the GENESYS global portal.

Deskriptorji so razdeljeni v 4 kategorije:
1) Potni list (Passport Information)
Osnovni podatki, zapisani ob zbiranju rastlinskega materiala (čas, kraj, ime,…)

2) Karakterizacija
Opis opaženih lastnosti s katerimi je mogoče ločevati med drugim podobnim materialom.

3) Preliminarno vrednotenje in

4) Temeljito vrednotenje.

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Ex situ hranjenje rastlinskega materiala

TABLE 1.2
Comparison between the collections maintained by selected national genebanks in 1995 and 2008[a]

Country	Genebank	1995 (no.)			2008 (no.)			Change (%)		
		Genera[b]	Species	Accessions	Genera	Species	Accessions	Genera	Species	Accessions
Brazil	CENARGEN	136	312	40 514	212	670	107 246	56	115	165
Canada	PGRC	237	1 028	100 522	257	1 166	106 280	8	13	6
China	ICGR-CAAS	-	-	358 963	-	-	391 919	-	-	9
Czech Republic	RICP	34	96	14 495	30	175	15 421	-12	82	6
Ecuador	INIAP/DENAREF	207	499	10 835	272	662	17 830	31	33	65
Ethiopia	IBC	71	74	46 322	151	324	67 554	113	338	46
Germany	IPK Gatersleben[c]	633	2 513	147 436	801	3 049	148 128	27	21	0
Hungary	ABI	238	742	37 969	294	915	45 321	24	23	19
India	NBPGR	73	177	154 533	723	1 495	366 333	890	745	137
Japan	NIAS	-	-	202 581	341	1 409	243 463	-	-	20
Kenya	KARI-NGBK	140	291	35 017	855	2 350	48 777	511	708	39
Nordic Countries	NGB[d]	88	188	24 241	129	319	28 007	47	70	16
Russian Federation	VIR	262	1 840	328 727	256	2 025	322 238	-2	10	-2
Netherlands	CGN	30	147	17 349	36	311	24 076	20	112	39
Turkey	AARI	317	1 941	32 122	545	2 692	54 523	72	39	70
United States of America	NPGS[e]	1 582	8 474	411 246	2 128	11 815	508 994	35	39	24
Average		**289**	**1 309**	**140 205**	**502**	**2 098**	**178 294**	**74**	**60**	**27**

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Comparison between the collections maintained by AVRDC and the CGIAR centres in 1995 and 2008

Centre [a]	1995 (no.)			2008 (no.)			Change (%)		
	Genera	Species	Accessions	Genera	Species	Accessions	Genera	Species	Accessions
AVRDC	63	209	43 205	160	403	56 522	154	93	31
CIAT	161	906	58 667	129	872	64 446	-20	-4	10
CIMMYT	12	47	136 259	12	48	173 571	0	2	27
CIP	9	175	13 418	11	250	15 046	22	43	12
ICARDA	34	444	109 223	86	570	132 793	153	28	22
ICRAF	3	4	1 005	3	6	1 785	0	50	78
ICRISAT	16	164	113 143	16	180	118 882	0	10	5
IITA	72	155	36 947	72	158	27 596	0	2	-25
ILRI	358	1 359	13 470	388	6	18 763	0	28	39
INIBAP/Bioversity	2	21	1 050	2	1 746	1 207	0	10	15
IRRI	11	37	83 485	11	23	109 161	0	5	31
WARDA	1	5	17 440	1	39	21 527	0	20	23
Total	**494**	**2 813**	**627 312**	**612**	**3 446**	**741 319**	**24**	**23**	**18**

Sources: Individual genebanks; System-wide Information Network for Genetic Resources (SINGER) Web site 2008; WIEWS 1996, 1995 data for IITA and ICRAF are from SINGER CD 1997. Undetermined genera were not counted.

[a] World Vegetable Centre (former Asian Vegetable Research and Development Centre, AVRDC); Centro Internacional de Agricultura Tropical (CIAT); Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT); Centro Internacional de la Papa (CIP); International Centre for Agricultural Research in the Dry Areas (ICARDA); International Centre for Research in Agroforestry [now the World Agroforestry Centre] (ICRAF); International Crops Research Institute for the Semi-Arid Tropics (ICRISAT); International Institute of Tropical Agriculture (IITA); International Livestock Research Institute (ILRI); International Network for the Improvement of Banana and Plantain, (INIBAP); International Rice Research Institute (IRRI); West African Rice Development Association [now the Africa Rice Centre - AfricaRice] (WARDA).

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TABLE 3.3
Global germplasm holdings in terms of type of accession (mean percentage) for groups of crops included in Appendix 2

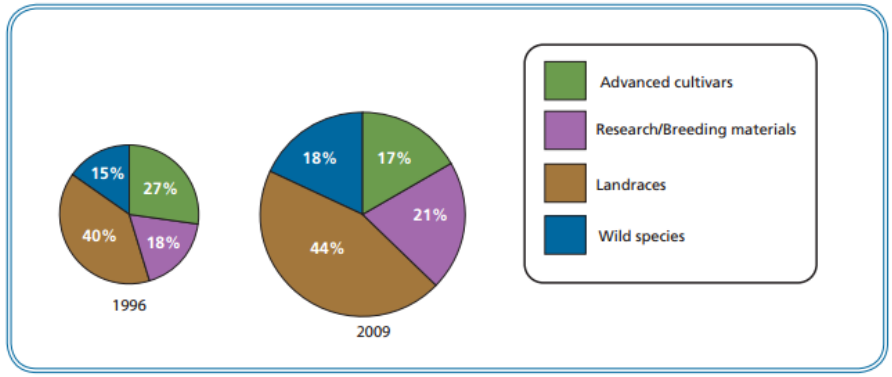
Commodity group	No. of accessions	% Wild species	% Landraces	% Breeding materials	% Advanced cultivars	% Others
Cereals	3 157 578	5	29	15	8	43
Food legumes	1 069 897	4	32	7	9	49
Roots and tubers	204 408	10	30	13	10	37
Vegetables	502 889	5	22	8	14	51
Nuts, fruits and berries	423 401	7	13	14	21	45
Oil crops	181 752	7	22	14	11	47
Forages	651 024	35	13	3	4	45
Sugar crops	63 474	7	7	11	25	50
Fibre crops	169 969	4	18	10	10	57
Medicinal, aromatic, spice and stimulant crops	160 050	13	24	7	9	47
Industrial and ornamental plants	152 325	46	1	2	4	47
Other	262 993	29	4	2	2	64
Total/overall mean	**6 998 760**	**10**	**24**	**11**	**9**	**46**

Source: WIEWS 2009

Vir: http://www.fao.org/docrep/013/i1500e/i1500e.pdf

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FIGURE 3.6
Types of accessions in *ex situ* germplasm collections in 1996 and 2009 (the size difference in the charts represents the growth in total numbers of accessions held *ex situ* between 1996 and 2009)



Source: WIEWS 1996 and 2009

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Sources of information at the accession/sample/species level

At the genebank level

The following genebanks have information on their holdings online:

- Centre for Genetic Resources, Plant Genetic Resources (CGN-PGR), the Netherlands (www.cgn.wur.nl/UK/CGN+Plant+Genetic+Resources)
- Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany (www.ipk-gatersleben.de/Internet)
- Centro de Recursos Fitogenéticos (C.R.F.), Spain (wwwx.inia.es/webcrf/CRFing/PaginaPrincipal.asp)
- N. I. Vavilov All-Russian Scientific Research Institute of Plant Industry (VIR), Russian Federation (www.vir.nw.ru/data/dbf.htm)
- Recursos Genéticos e Biotecnologia (EMBRAPA), Brazil (www.cenargen.embrapa.br)
- ISOPlexis, Centro de Estudos da Macaronésia, Centro de Competência das Ciências da Vida, Universidade da Madeira, Portugal (www3.uma.pt/cem/isoplexis/coleccao.html)
- Kew's Millennium Seed Bank, Wakehurst Place, UK (http://data.kew.org/sid/about.html)

The information systems of these genebanks allow the user to browse, search and view information on their germplasm holdings. Many offer the possibility to download the search results, and some include a function for requesting germplasm samples.

https://cropgenebank.sgrp.cgiar.org/images/file/procedures/collecting2011/Chapter8-2011.pdf

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At the national level

Many countries have established national inventories on plant genetic resources that are freely and widely available online. This enables participating countries to contribute to their biodiversity and conservation obligations at the national level and to meet the requirements of international agreements such as the Convention on Biological Diversity (CBD), the Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (GPA), the International Treaty on Plant Genetic Resources for Food and Agriculture ("the Treaty") and the Global Biodiversity Information Facility (GBIF).

- Australian Plant Genetic Resource Information Service (AusPGRIS) (www2.dpi.qld.gov.au/extra/asp/auspgris)
- National Inventory of Plant Genetic Resources for Food and Agriculture, Austria (www.genbank.at)
- Genetic Resources Institute of the National Academy of Sciences, Azerbaijan (www.cac-biodiversity.org/aze/aze_instgen.htm)
- Canadian Plant Germplasm System (PGRC) (http://pgrc3.agr.gc.ca/about-propos_e.html)
- Plant Genetic Resources Documentation (EVIGEZ), Czech Republic (http://genbank.vurv.cz/genetic/resources)
- Estonia (www.sordiaretus.ee)
- Bureau des Ressources Génétiques (BRG), France (www.brg.prd.fr/index.php)
- Informationssystem Genetische Ressourcen (GENRES), Germany (www.genres.de/pgrdeu)
- Japan National Institute of Agrobiological Sciences (NIAS) Genebank (www.gene.affrc.go.jp/databases_en.php)
- Lithuanian Institute of Agriculture (www.lzi.lt)
- Centre for Genetic Resources, Plant Genetic Resources (CGN-PGR), the Netherlands (www.cgn.wur.nl/UK/CGN+Plant+Genetic+Resources)
- Nordic Countries (Denmark, Finland, Iceland, Norway, Sweden) (www.nordgen.org/ngb)
- Plant Breeding and Acclimatization Institute (IHAR), Poland (www.ihar.edu.pl/gene_bank)
- N. I. Vavilov All-Russian Scientific Research Institute of Plant Industry (VIR) (www.vir.nw.ru/data/dbf.htm)
- Agricultural Institute of Slovenia (www.kis.si/pls/kis/!kis.web)
- Centro de Recursos Fitogenéticos (CRF), Spain (wwwx.inia.es/webcrf/CRFing/PaginaPrincipal.asp)
- USDA Agricultural Research Service, National Genetic Resources Program (NGRP), USA (www.ars-grin.gov)

These national inventories collate information from different data sources (germplasm collections) and constitute a network of centres and people dedicated to conserving the genetic diversity of crop plants and their wild relatives.

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At the regional/subregional level

At the regional and subregional level, there are initiatives to collate and make available data on national holdings. These initiatives are normally undertaken to assist countries in meeting their national, regional and global commitments regarding documentation and information on their plant genetic resources.

An example of such a regional initiative is EURISCO (http://eurisco.ecpgr.org/home_page/home.php), a web-based catalogue that provides information about *ex situ* plant germplasm collections maintained in Europe. The EURISCO catalogue contains passport data on more than 1 million accessions of crop diversity from 41 countries, representing 5,396 genera and 35,235 species (genus-species combinations including synonyms and spelling variants). EURISCO is hosted at and maintained by Bioversity International on behalf of the Secretariat of the European Cooperative Programme for Plant Genetic Resources (ECPGR).

ECPGR also maintains a series of European central crop databases established through the initiative of individual institutes and of ECPGR working groups. The ECPGR Central Crops Databases (ECCDBs) (www.ecpgr.cgiar.org/germplasm_databases/list_of_germplasm_databases/crop_databases.html#c5509) include the following:

- Cereals: *Avena*, Barley, Maize, *Secale*, Triticale, Wheat
- Forages: *Dactylis, Festuca, Lolium, Phleum, Poa, Medicago* (annual and perennial), Minor Forage Grasses (*Agropyron, Agrostis, Alopecurus, Arrhenatherum, Bromus, Phalaris, Trisetum*), Minor Forage Legumes (*Astragalus, Anthyllis, Coronilla, Desmodium, Hedysarum, Lotus, Melilotus, Onobrychis, Ornithopus, Physanthyllis, Tetragonolobus, Vicia*), *Trifolium* spp., *Trifolium subterraneum, Vigna*
- Oil and Protein Crops: *Arachis, Cicer, Glycine, Lathyrus, Lens, Lupinus, Phaseolus, Pisum, Vicia faba, Vigna*

- Sugar, Starch and Fibre Crops: Hemp, *Beta*, Flax, Potato (cultivated), Potato (wild bearing tubers)
- Temperate Fruits: *Malus, Prunus, Pyrus, Ribes/Rubus, Vitis*, Minor Fruit Trees
- Vegetables: *Allium, Brassica*, Chicory, Cucurbits, *Cyphomandra, Physalis*, Eggplant, *Lactuca, Beta*, Lettuce, Minor Leafy Vegetables, Pepino, Pepper, Potato (cultivated and wild), Spinach, Tomato, Umbellifer

The databases hold passport data and, to varying degrees, characterization and primary evaluation data of the major collections of the respective crops in Europe.

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At the global level

As its germplasm information-exchange network, the Consultative Group on International Agricultural Research (CGIAR) and its partners implemented the System-wide Information Network for Genetic Resources (SINGER) (http://singer.cgiar.org), which provides easy access to information about the diversity maintained by SINGER members, covering more than half a million accessions of crops and wild relatives.

As a result of the collaboration between Bioversity International on behalf of the CGIAR, the Global Crop Diversity Trust and the Secretariat of the Treaty, a global portal to information about plant genetic resources has been established, bringing together data from SINGER, EURISCO and the US Germplasm Resources Information Network (GRIN). The portal, GENESYS (www.genesys-pgr.org), is a gateway through which germplasm accessions from genebanks around the world can be found and ordered directly through the web interface. In addition to passport data, the system provides access to characterization and evaluation data as well as to environmental information associated with the accessions' collecting sites.

From 1974 to 2003, Bioversity International (under its previous names of IBPGR and IPGRI) supported germplasm collecting missions around the world. The IBPGR/IPGRI Supported Missions Database (http://singer.cgiar.org/index.jsp?page=coll-sample-data) gives access, at a sample level, to passport data for about 130,000 samples, as well as access to 27,000 original reports, collecting forms and other documents in PDF format.

The Global Biodiversity Information Facility (GBIF) (http://data.gbif.org/welcome.htm;jsessionid=37820DBEE26CAA62FAB10ADD1EE5B67D) is focused on making biodiversity data available online for scientific research, conservation and sustainable development. Enabling access to 293,485,946 data records, the GBIF information infrastructure is an internet-based index of a globally distributed network of interoperable databases that contain primary biodiversity data: information on museum specimens, field observations of plants and animals in nature, and results from experiments. The search interface also supports searches about the occurrence of species at particular times and places.

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Number of seeds to be stored

Number of seeds to be stored The number of seeds to be stored will depend on the species being conserved. FAO/IPGRI Genebank Standards (1994) recommends that for material which shows little morphological variation (genetically homogeneous) 3000 seeds are acceptable, but 4000 seeds are preferable to represent each accession.

For materials showing large amount of morphological variation (heterogeneous) an accession should consist of at least 4000 seeds, but 12000 seeds are preferred. It is easier in a genebank to work in weights. However, seeds numbers can easily be converted from weights. An inter-conversion of numbers and weights is possible, if we know the 100-seed or 1000-seed weight.

Equation 1.

$$\text{Number of seeds in the sample} = \frac{\text{Sample weight (g)} \times 100}{\text{Weight of 100 seeds (g)}}$$

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Table 4.3. Recording and calculation of seed moisture content.

Accession no.	Replicate/ container no.	Wt of empty container with lid (g)	Wt of container with lid + seed before drying (g)	Wt of container with lid + seed after drying (g)	Moisture content % (wb)	
		W1	W2	W3	(W2-W3)/ (W2-W1) × 100	Average (R I + R II)/2
	R I					
	R II					
	R I					
	R II					
	R I					
	R II					
	R I					
	R II					

Example:

Accession no.	Replicate/ container no.	Wt of empty container with lid (g) (W1)	Wt of container with lid + seed before drying (g) (W2)	Wt of container with lid + seed after drying (g) (W3)
	R 1	10.3245	14.8668	14.4356
	R 2	10.1442	14.9948	14.5365

Calculation:

Rep 1:

$$\% \text{ Moisture content} = \frac{14.8668-14.4356}{14.8668-10.3245} \times 100 = 9.47$$

Rep 2:

$$\% \text{ Moisture content} = \frac{14.9948-14.5365}{14.9948-10.1442} \times 100 = 9.45$$

$$\text{Moisture content (fresh-weight basis)} = \frac{9.47+9.45}{2} = 9.46\%$$

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Glede na dolžino shranjevanja ločimo:
Bazna kolekcija – vzorci shranjeni za dalj časa (več kot 20 let) z nizko vsebnostjo vode (3-6 %) in temperature med -18 in -20 °C. Ni namenjena za distribucijo. Namenjena obnovi aktivnih kolekcij ter kot varnostna kopija za prihodnje generacije.

Aktivna kolekcija - vzorci shranjeni za srednje dolgo obdobje (10 do 15 let) pri 0 °C in vsebnostjo vode 8 %. Te kolekcije so namenjene za razmnoževanje oz. obnavljanje, ocenjevanje in razdeljevanje.

Delovne kolekcije – kolekcije, s katerimi upravljajo žlahtnitelji in so namenjene za temeljito vrednotenje, selekcijo in križanje. Dolžina shranjevanja od 3 do 5 let pri 5 do 10 °C in 8 do 10 % vlage.

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