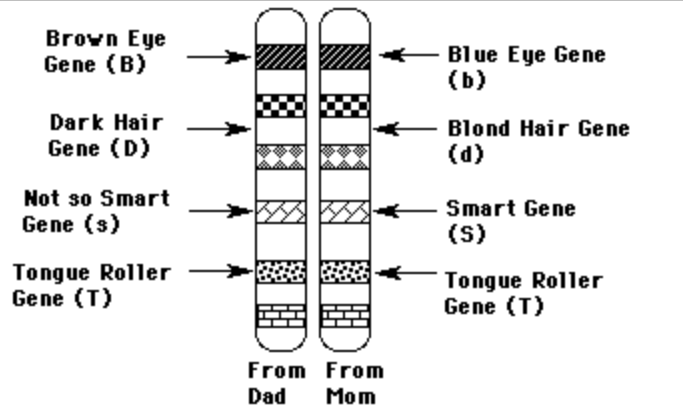


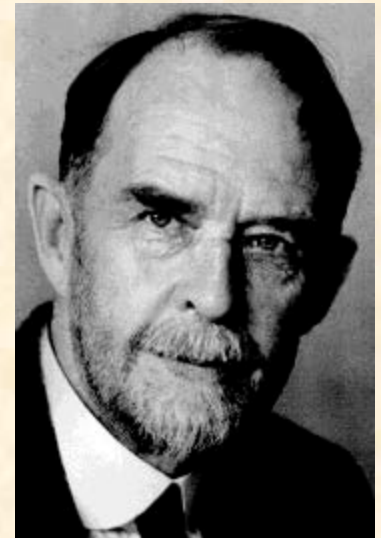
ОКО 40000 гена

**Везани гени се налазе на истом
Х Р О М О З О М У**



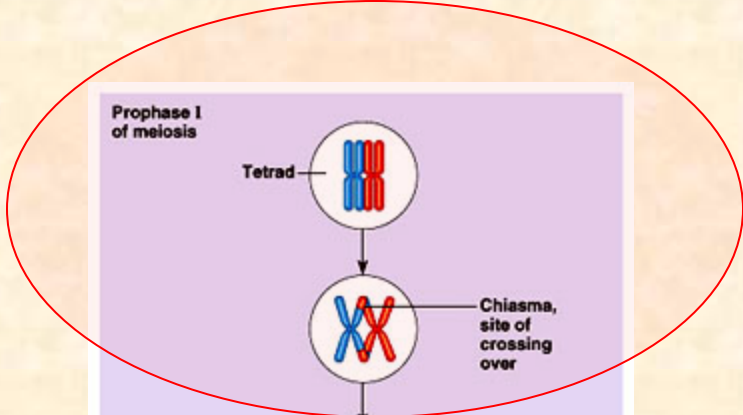
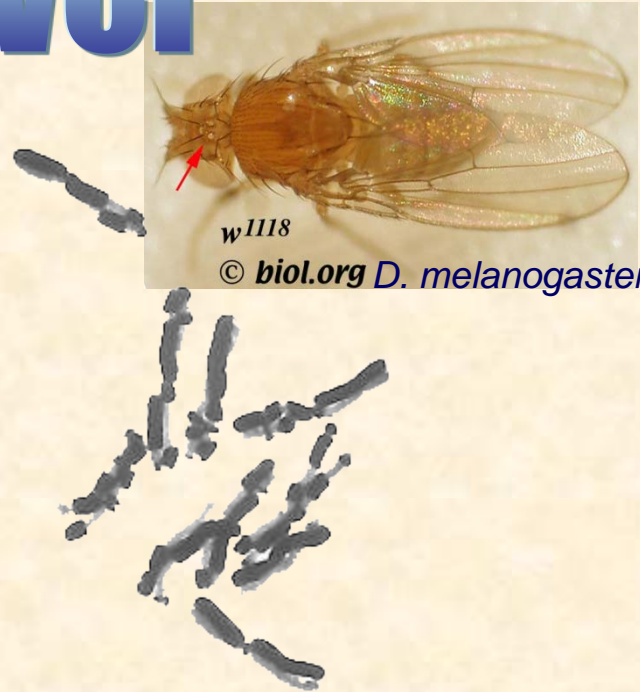
Example of a pair of chromosomes with alleles (gene pairs) from the same traits. The trait you show depends on which gene of a gene pair is strongest (those with capital letters!).

Crossing over

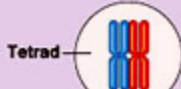


Thomas Hunt Morgan
Copyright California Institute of Technology Archives. All rights reserved.

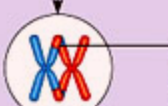
1915, 1936



Prophase I of meiosis

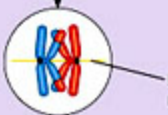


Tetrad



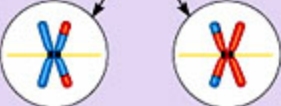
Chiasma, site of crossing over

Metaphase I



Kinetochores
microtubules

Metaphase II



Gametes



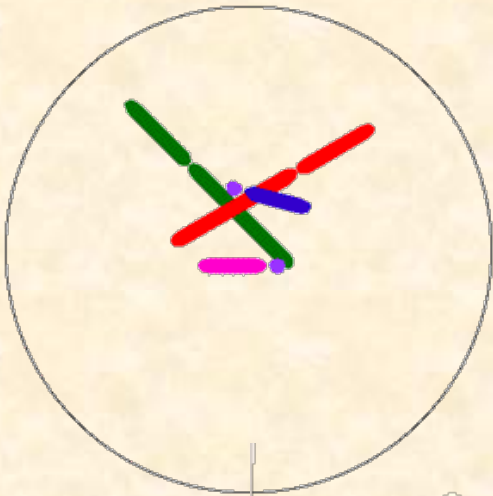
Recombinant chromosomes

Copyright © Pearson Education, Inc., publishing as Benjamin Cummings.

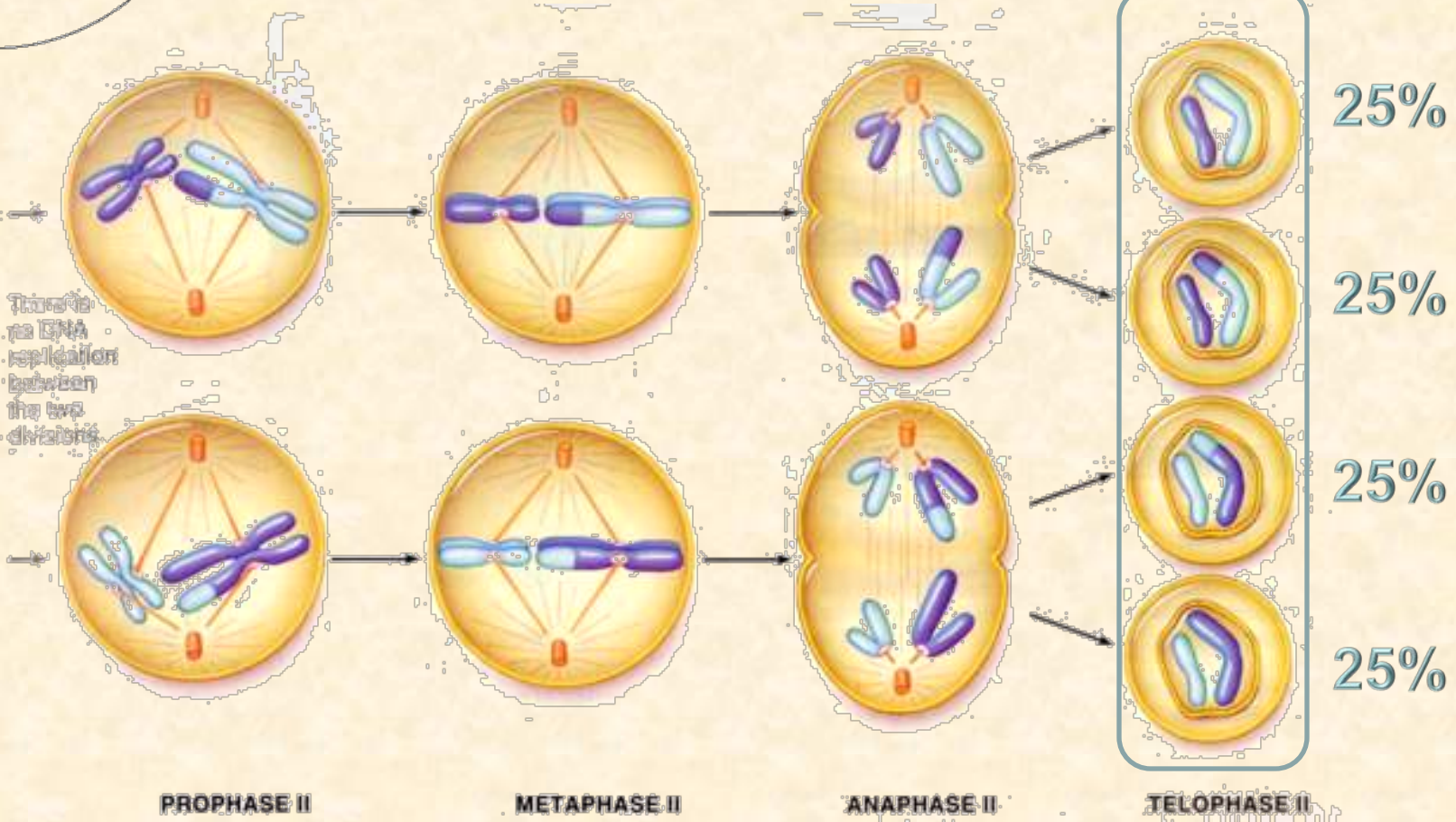
Морган установио да у профази мејозе долази до измене делова хроматида хомологних хромозома



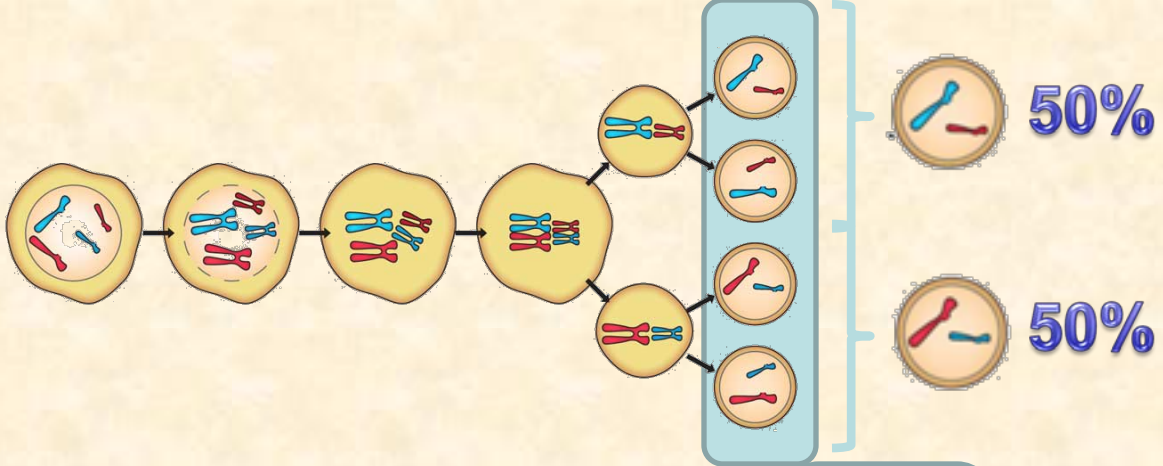
Спајање и раздвајање везаних особина



Кросинг овер



Нормално



Механизам измене:

Копирање

До прекрштања долази током удвајања ДНК.

Грешка у преписивању у само-репродукцији ДНК ланца. Крос преписивање хроматида

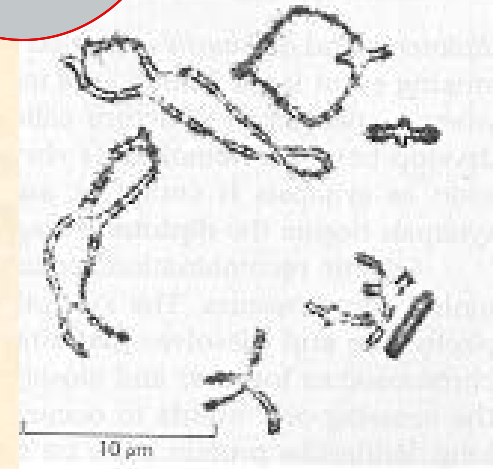
Сору choice хипотеза

Ломљење

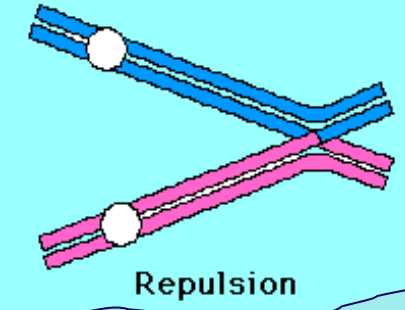
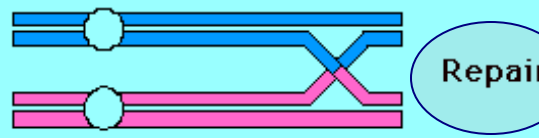
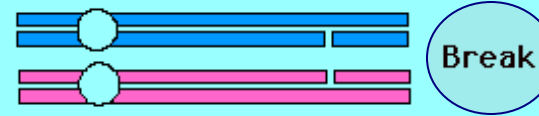
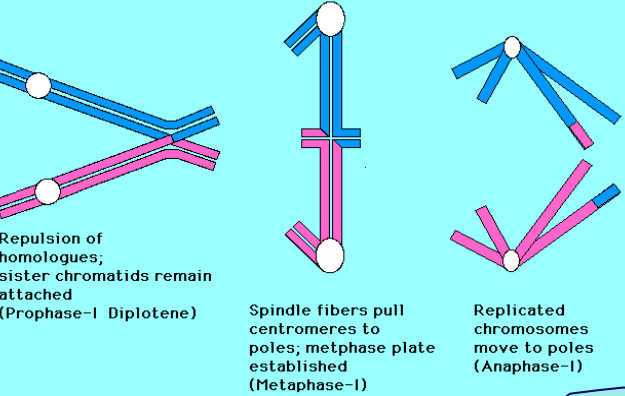
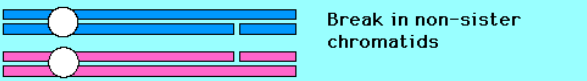
Прекрштање са изменом делова хроматида се дешава касније у пахитену, као последица кидања хромозома у ХИЈАЗМАМА.

ДНК може да се крос препише погрешно и у покушају да се поправи прекид.

Различита мишљења

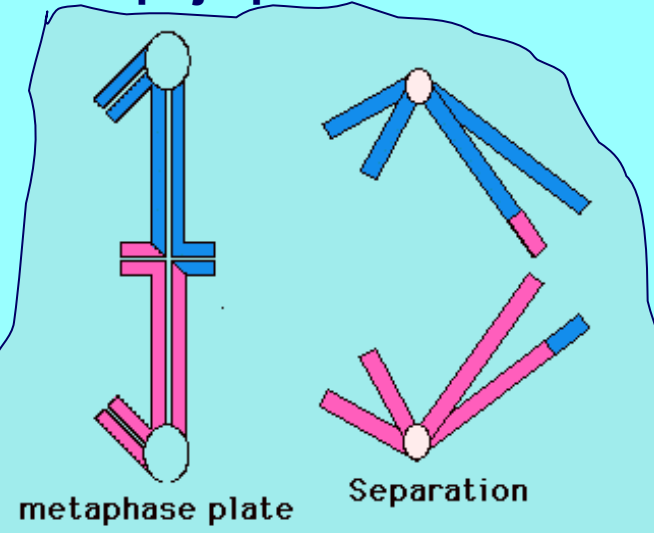


Crossing over and chiasmata

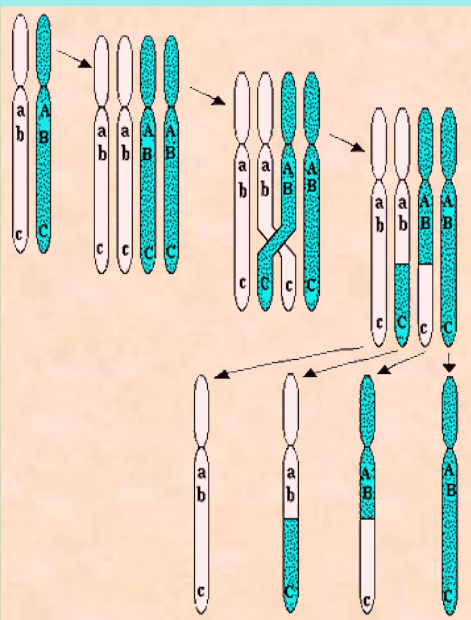
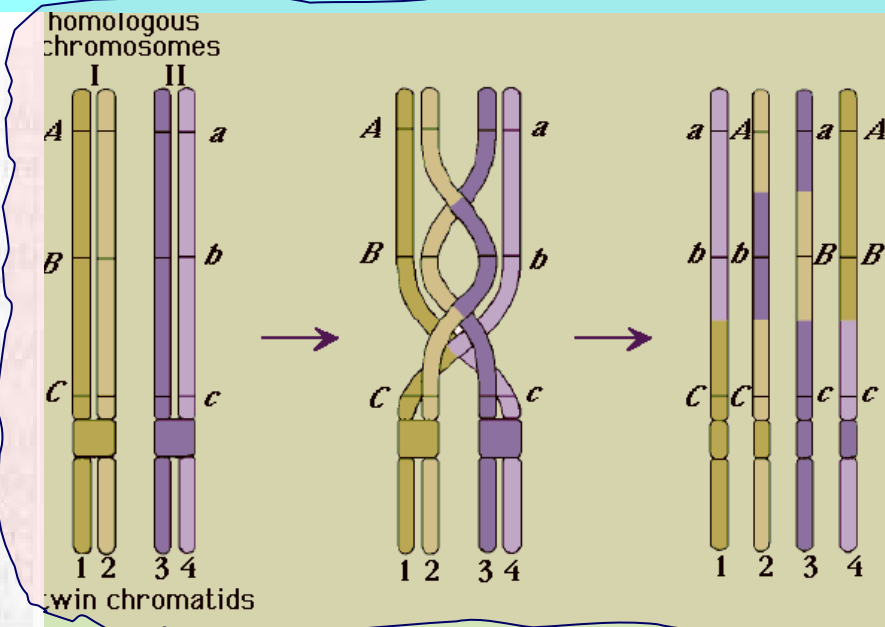
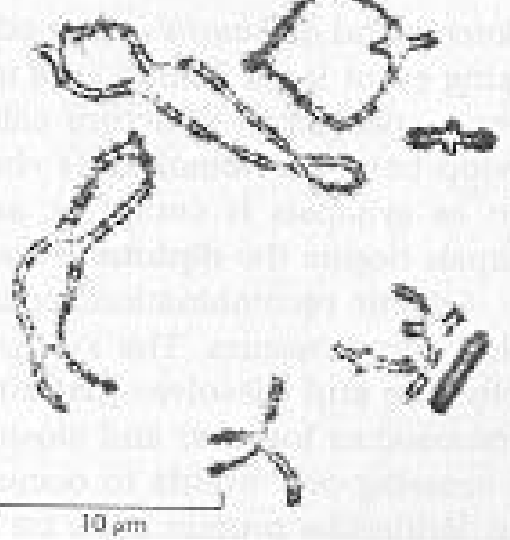


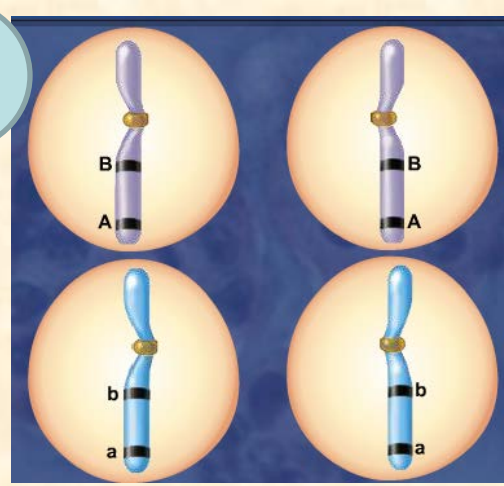
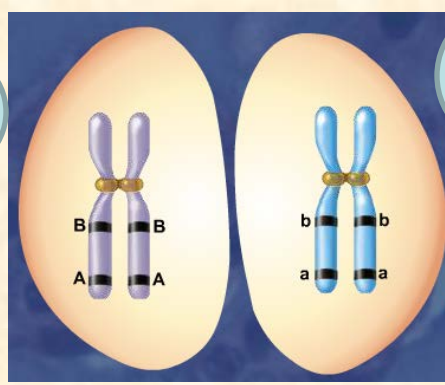
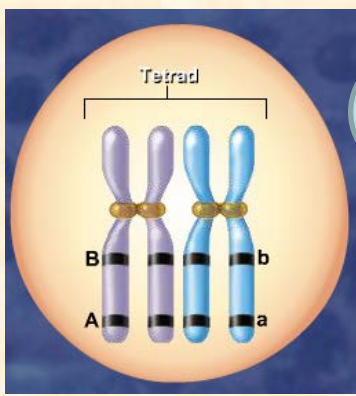
And all together, now!

Последице:
рекомбинација везаних особина
већи број врста гамета



Хијазме у дијакинези



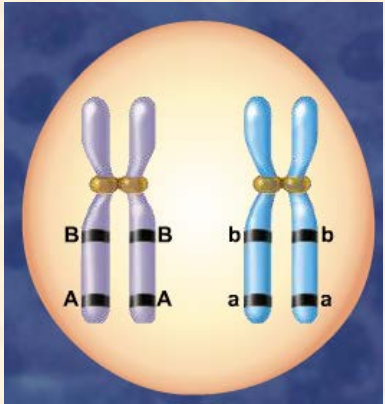


Без кросинг овера

Профаза I
Пахитен

Дијаде

Тетраде



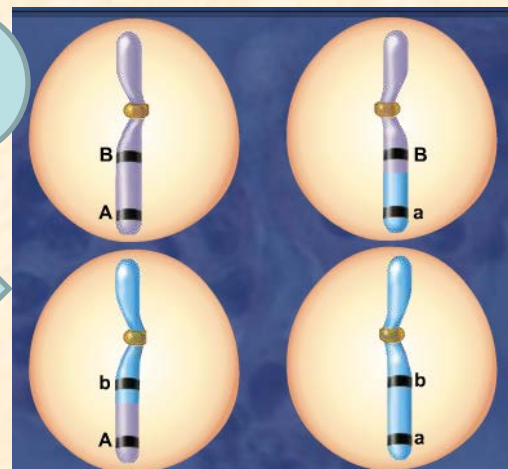
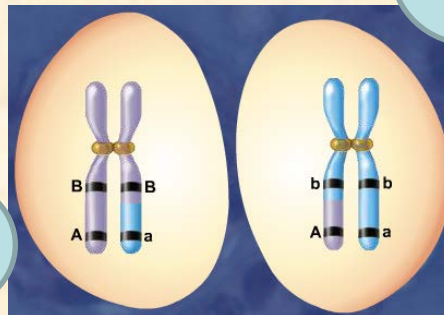
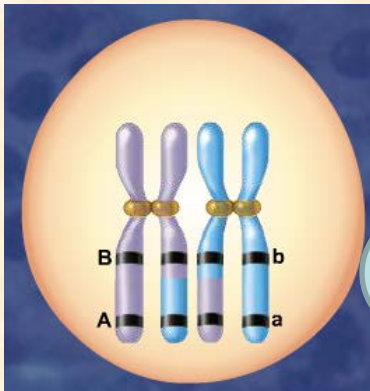
Профаза I

Профаза I
Пахитен

Дијаде

Тетраде

Са кросинг овером



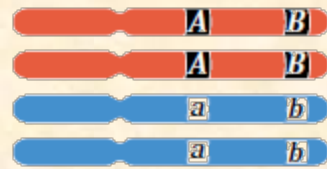
(a) Без кросинг овера

1 Homologous chromosomes pair in prophase I.

2 If no crossing over occurs...



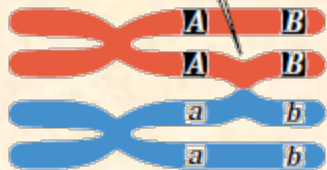
Meiosis II



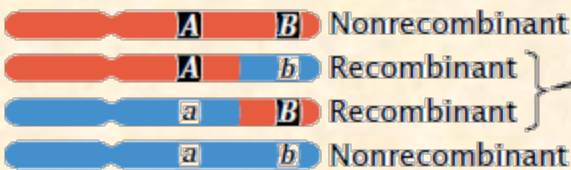
3 ...all resulting chromosomes in gametes have original allele combinations and are nonrecombinants.

(b) Са кросинг овером

1 A crossover may occur in prophase I.



Meiosis II

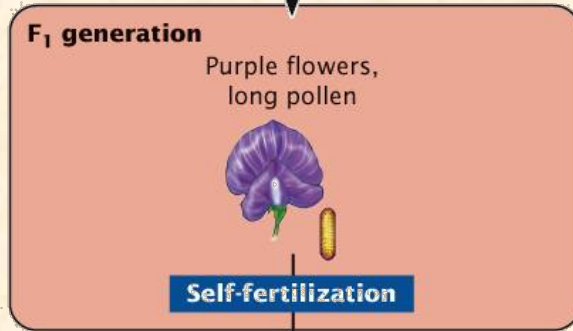
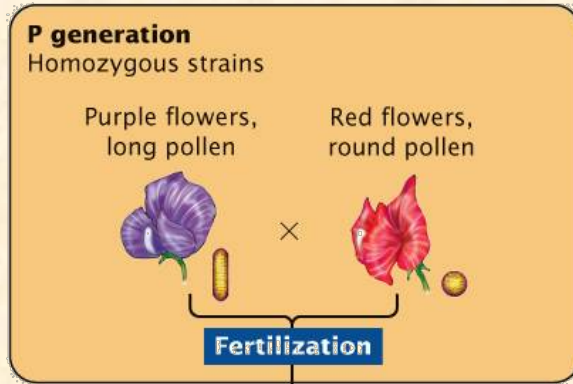


2 In this case, half of the resulting gametes will have unchanged chromosomes (nonrecombinants)...

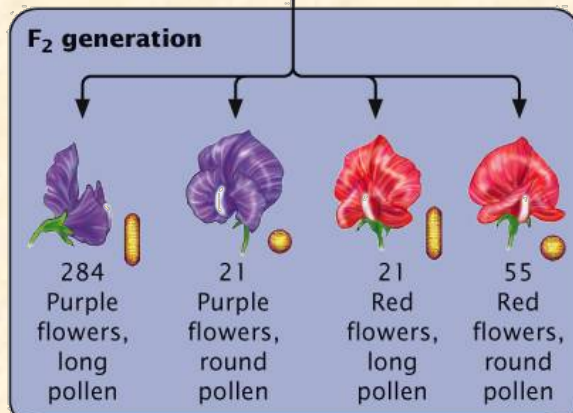
3 ...and half will have recombinant chromosomes.

СЛАТКИ ГРАШАК (*Lathyrus odoratus*)

Methods Cross two strains homozygous for two different traits.



Results



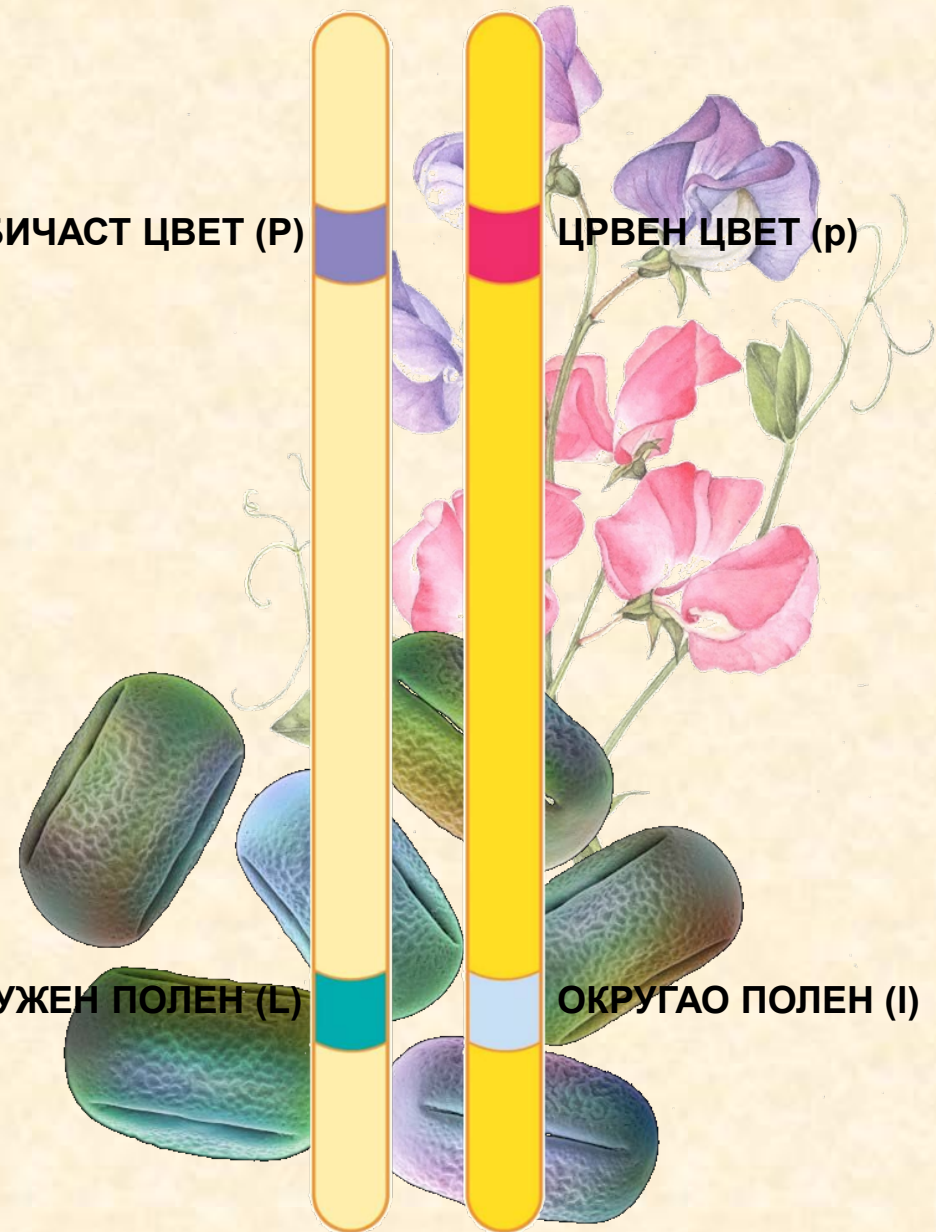
Conclusion: F₂ progeny do not appear in the 9:3:3:1 ratio expected with independent assortment.

ЉУБИЧАСТ ЦВЕТ (P)

ЦРВЕН ЦВЕТ (p)

ИЗДУЖЕН ПОЛЕН (L)

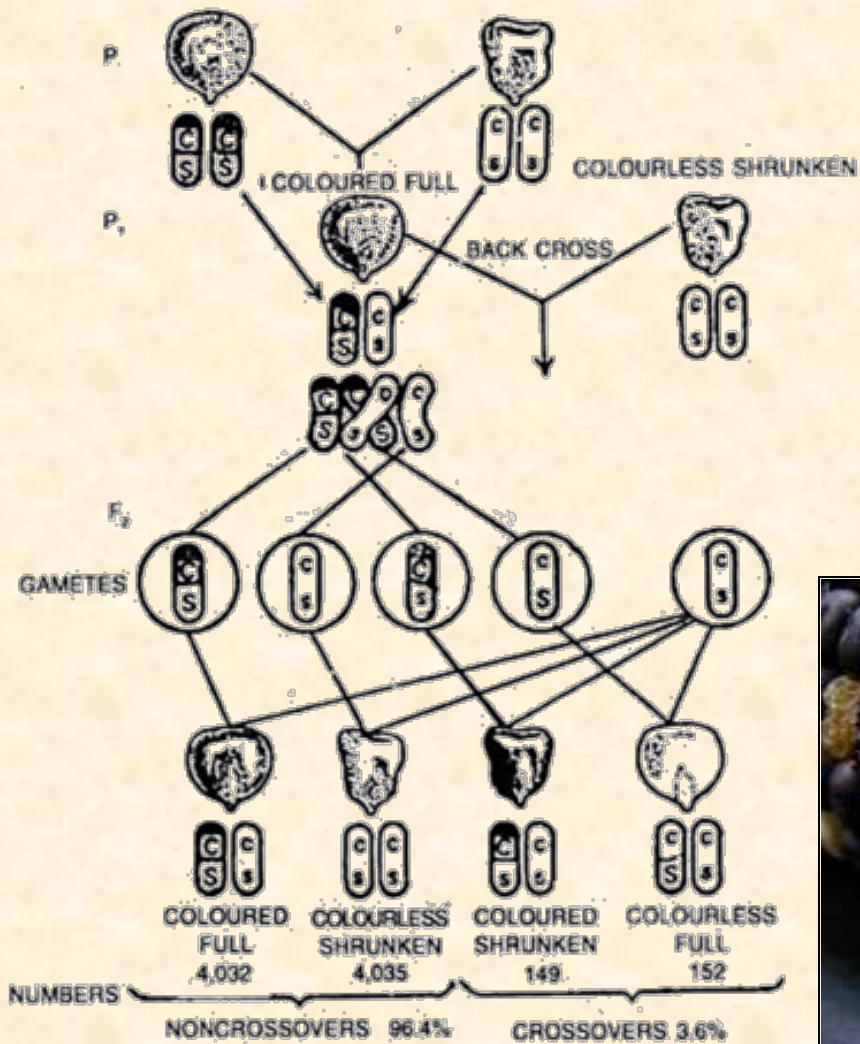
ОКРУГАО ПОЛЕН (l)



COLOURED FULL

COLOURLESS SHRUNKEN

КУКУРУЗ (Zea mays)



ОБОЈЕНО ЗРНО (C)



БЕЗБОЈНО ЗРНО (c)



ПУНО ЗРНО (S)



СМЕЖУРАНО ЗРНО (s)

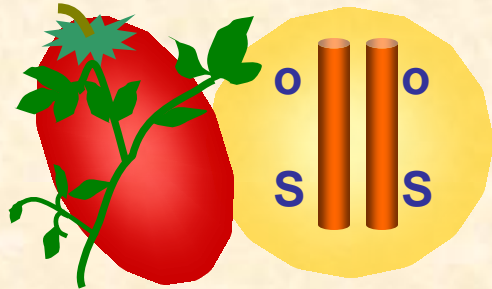


Особине везане

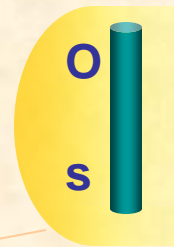
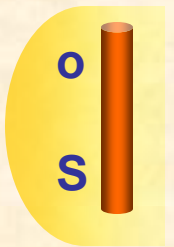
Гени за облик плода и грађу цвасти

на истом хромозому

Издужен плод
Једноставна цваст



Округли плод
Сложена цваст



F1

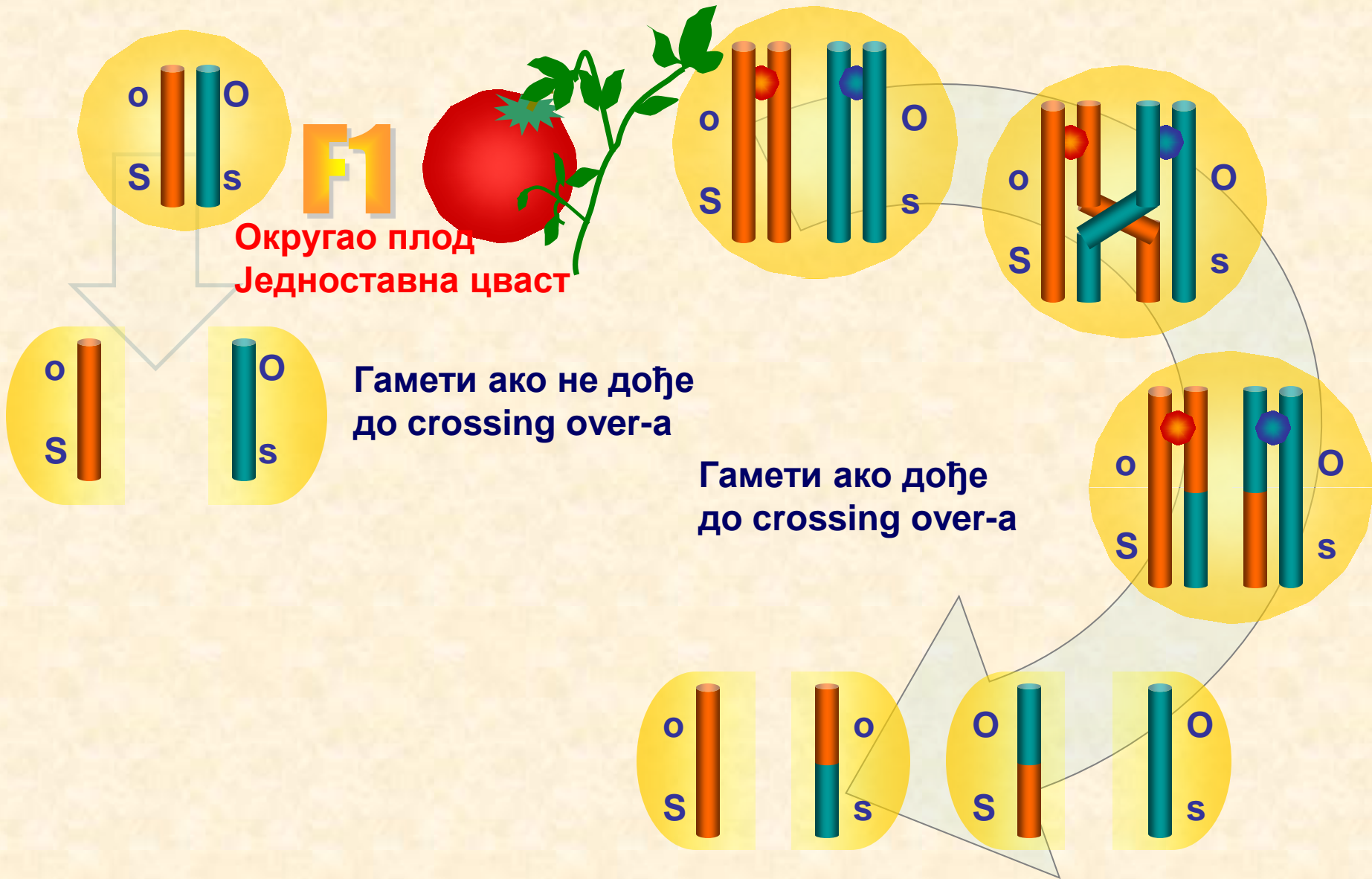


F1



Округао плод
Једноставна цваст





o O
S s

F1



o O
S s

o O
S s

o O
S s

Гамети ако не дође до crossing over-a

Гамети ако дође до crossing over-a

o O
S s

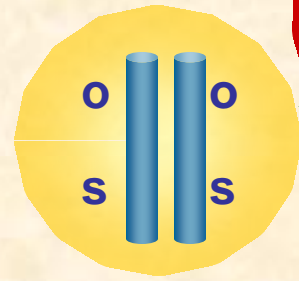
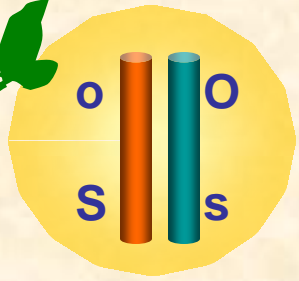
o O
S s

O O
S s

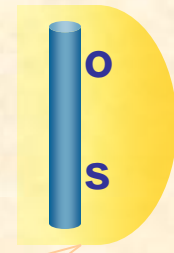
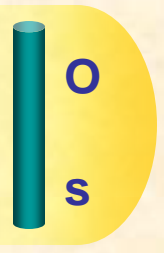
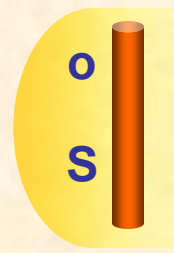
Тест укрштање без с.о.:

Округао плод
Једноставна цваст

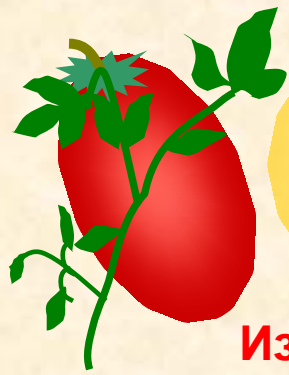
F1



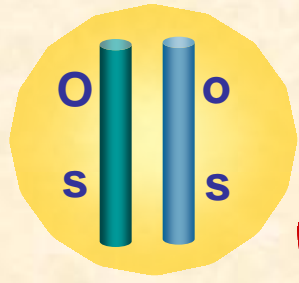
Издужен плод
Сложена цваст



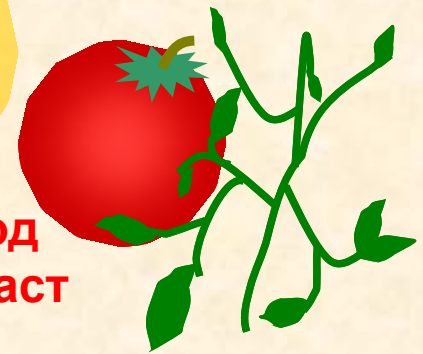
Fb1



Издужен плод
Једноставна цваст



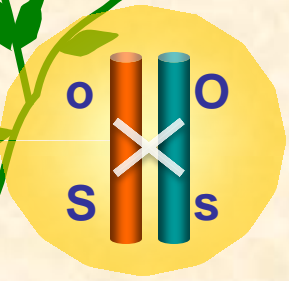
Округли плод
Сложена цваст



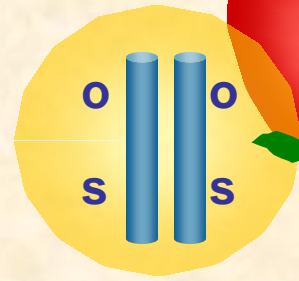
Тест укрштање са с.о.:

Округао плод
Једноставна цваст

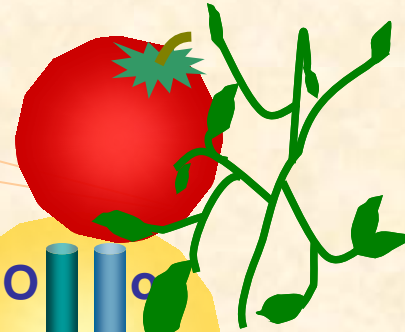
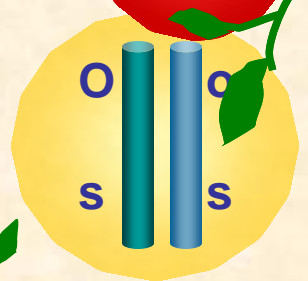
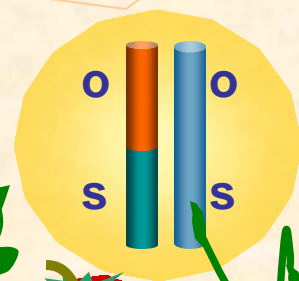
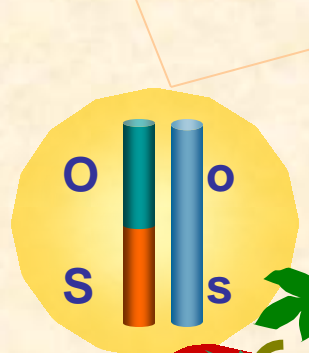
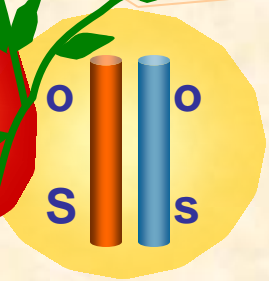
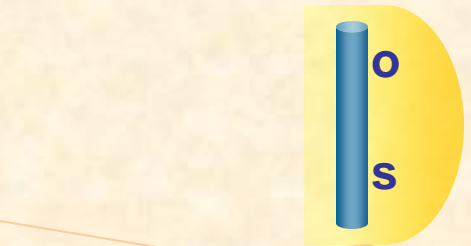
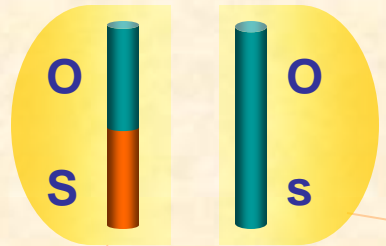
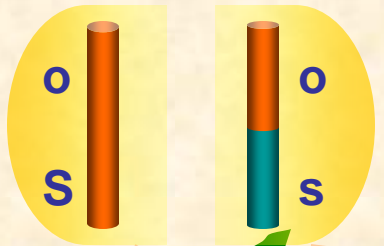
F1



×



Издужен плод
Сложена цваст



F2

83 Издужен плод
Једноставна цваст

X

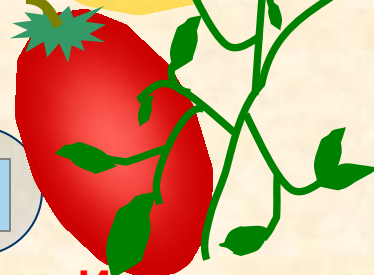
1

23 Округао плод
Једноставна цваст



1

19 Издужен плод
Сложена цваст

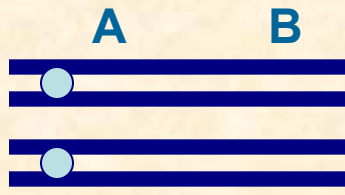


Округли плод
Сложена цваст

X

85

Серија спајања



A B

ABAB

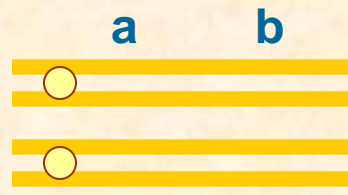


A B

AB

g.

X



a b

a b

abab

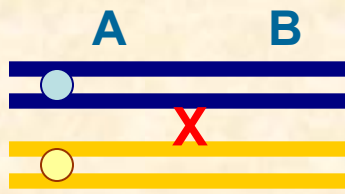


a b

ab

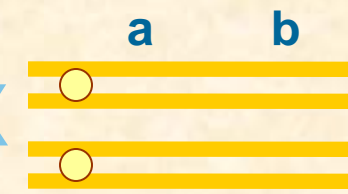
X

F1



A B

ABab

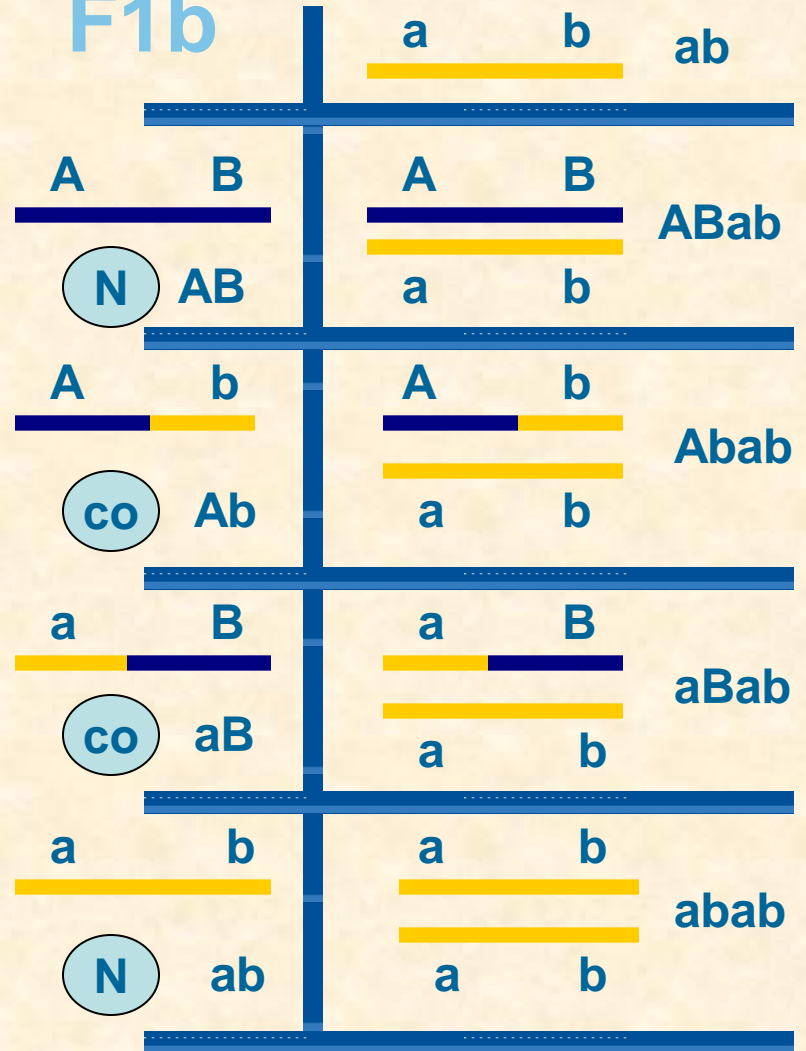


a b

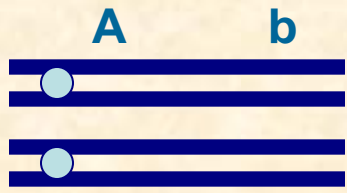
a b

abab

F1b



Серија раздвајања



A b

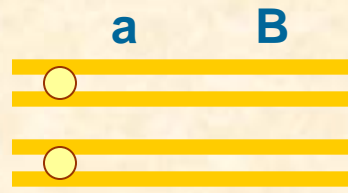
AbAb



A b

Ab

X



a B

a B

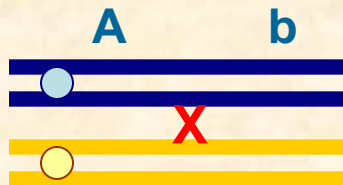
aBaB



a B

aB

X



A b

AbaB

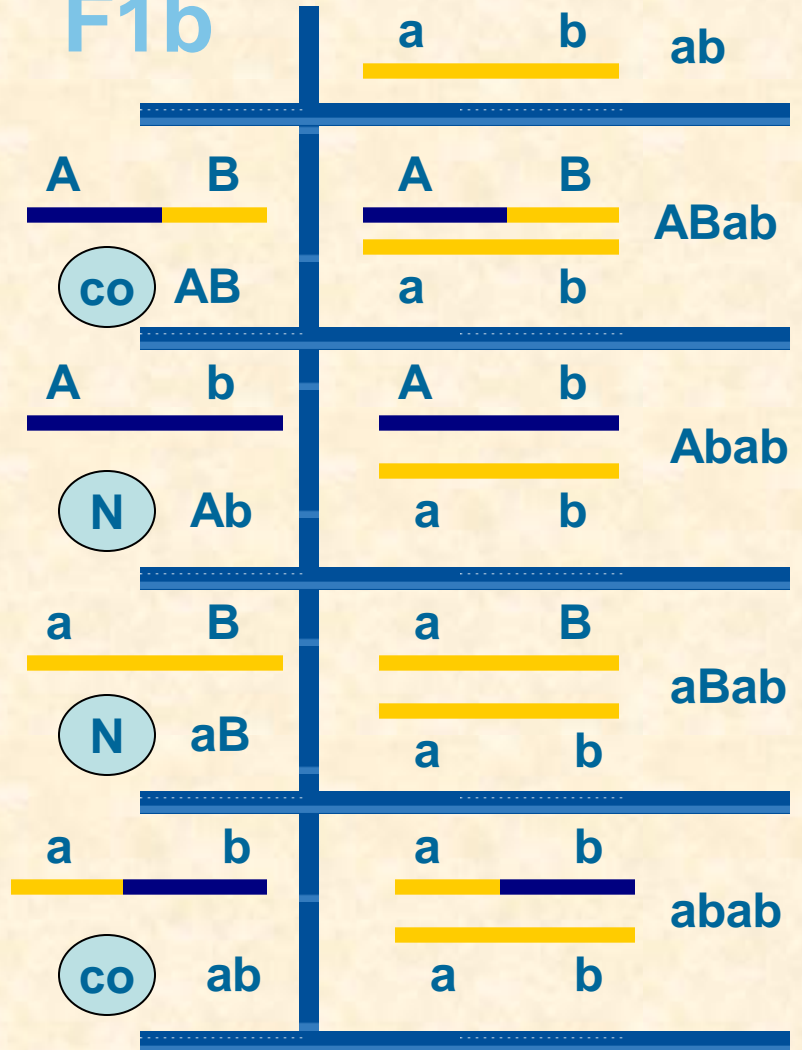


a b

a b

abab

F1b



g.

F1

Хромозомске мапе

ГЕНЕТИЧКЕ МАПЕ [cM] – дају релативне позиције генских локуса одређене на основу степена рекомбинације (учестаност кросинг овера). Резултат су генетичких (цитогенетичких) анализа.

ФИЗИЧКЕ МАПЕ [Kbp] – показују права (физичка) растојања између генских локуса (у броју нуклеотида). Резултат су поступака молекуларне генетике.

1B хромозом пшенице

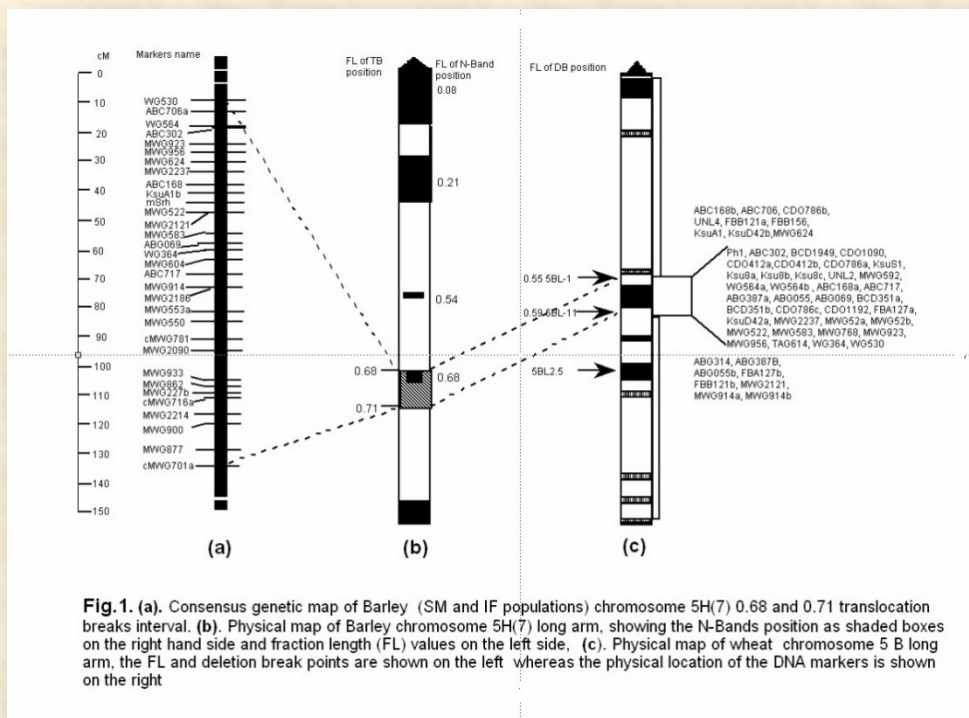
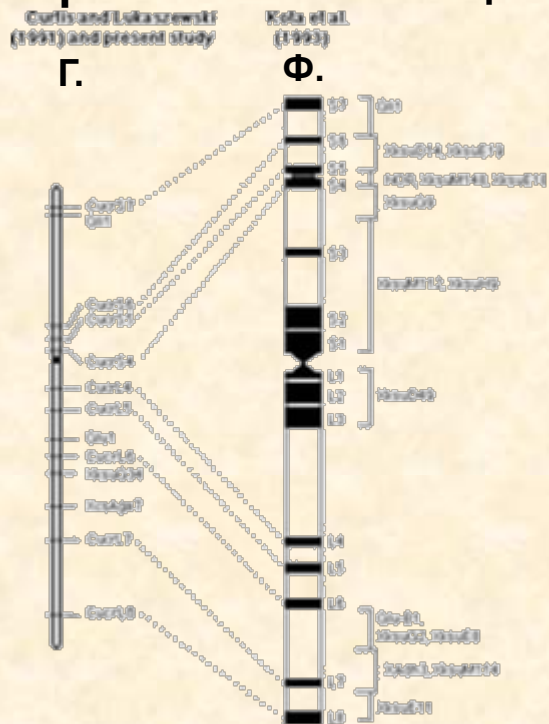


Fig. 1. (a). Consensus genetic map of Barley (SM and IF populations) chromosome 5H(7) 0.68 and 0.71 translocation breaks interval. (b). Physical map of Barley chromosome 5H(7) long arm, showing the N-Bands position as shaded boxes on the right hand side and fraction length (FL) values on the left side. (c). Physical map of wheat chromosome 5 B long arm, the FL and deletion break points are shown on the left whereas the physical location of the DNA markers is shown on the right

Genetic and physical maps of chromosome 1B of wheat. Short arms are at the top. The map by Kota et al. (1993) was constructed on a physical chromosome length (%) basis and the Curtis and Lukaszewski (1991) map is based on linkage of C-bands, protein and DNA markers. Markers preceded by an X are DNA markers and C are C-bands. Dotted lines show orthologous loci. The darkened region on the linkage map and the constriction on the physical map represent the centromeres.

Процент crossing over - a

Утврђује се најлакше и најтачније из резултата тест укрштања, јер се јасно разликују фенотипови који су резултат crossing over – а, од нормалних фенотипова

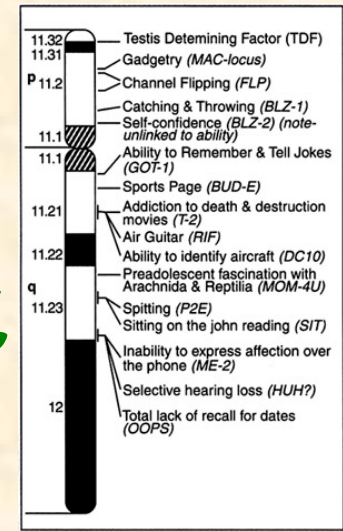
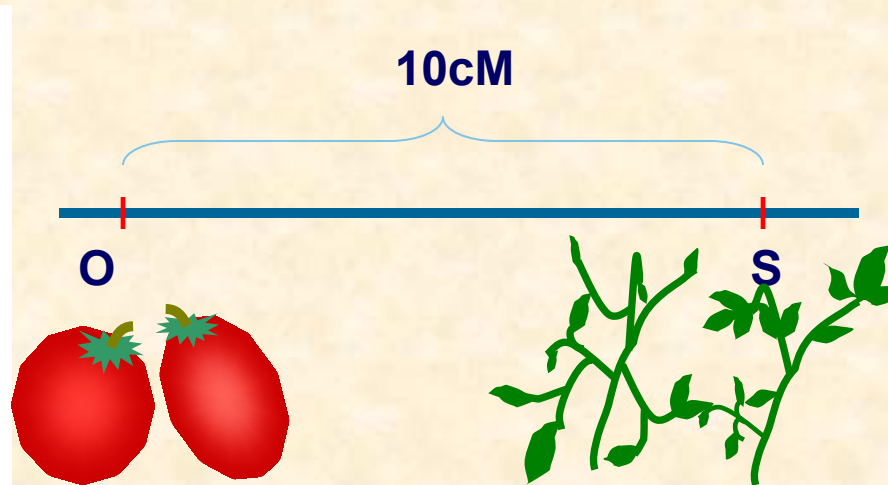
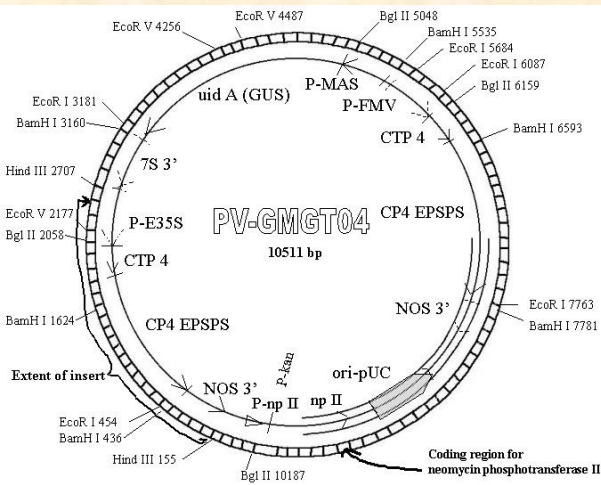
$$\%CO = \frac{\sum CO}{\sum \text{СВИХ}}$$

X	83		Издужен плод Једноставна цваст
1	23		Округао плод Једноставна цваст
1	19		Издужен плод Сложена цваст
X	85		Округли плод Сложена цваст

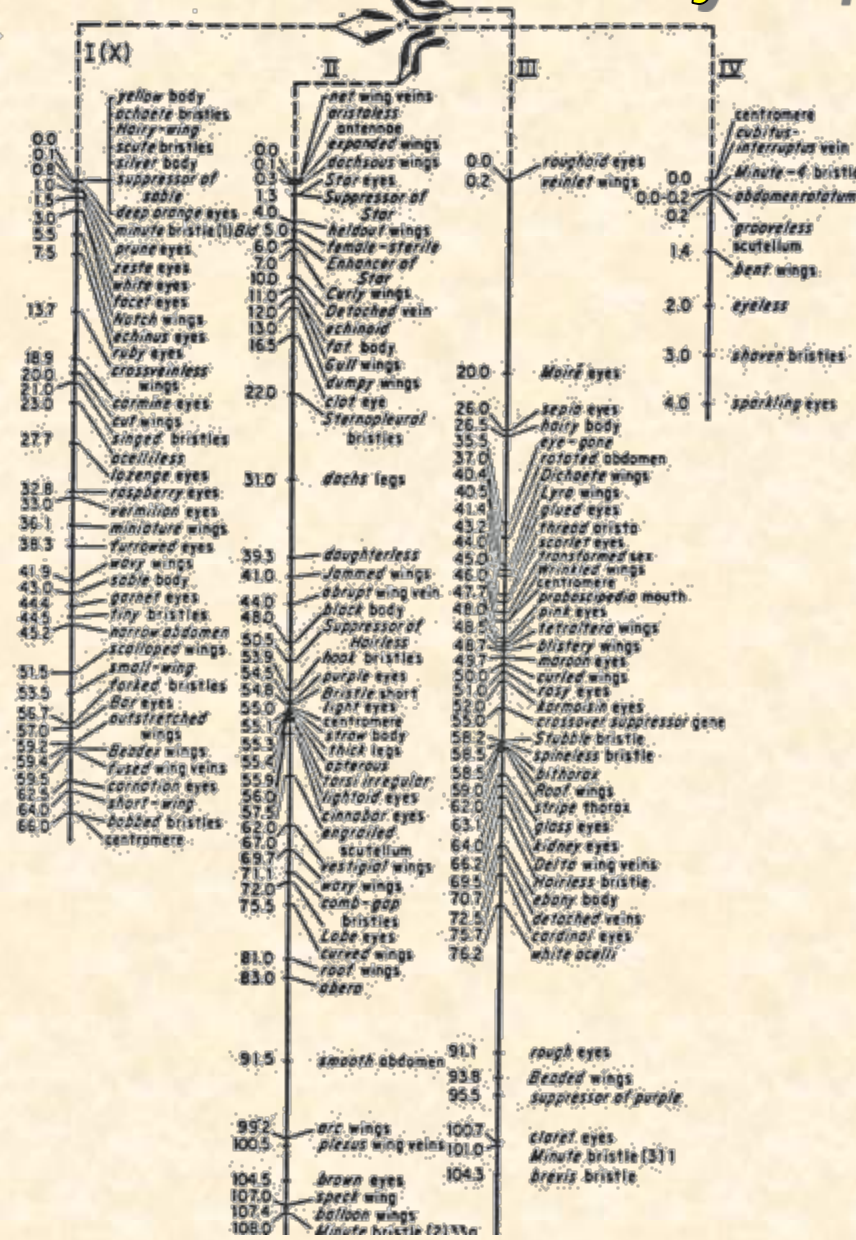
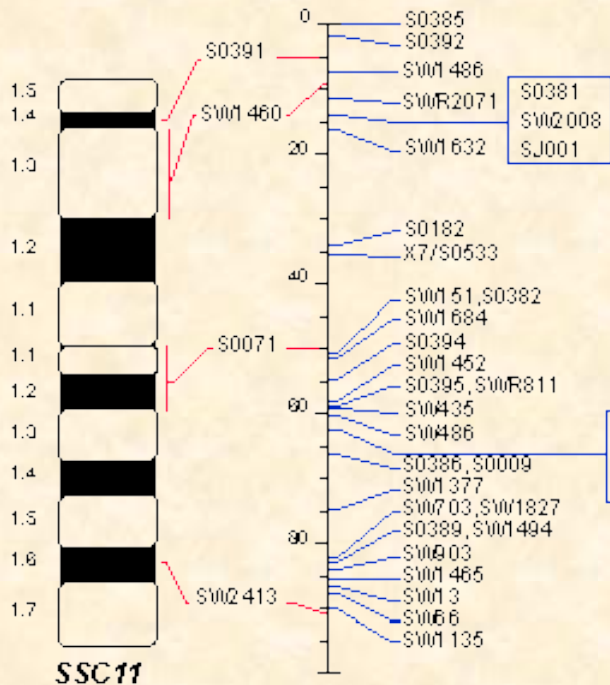
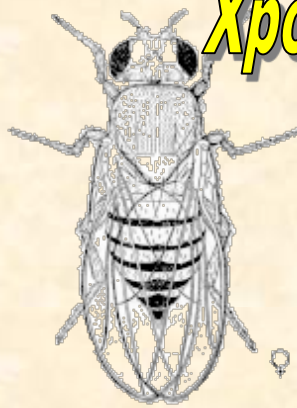
$$\%CO = (23+19)/(83+23+19+85)$$

$$\%CO = 42/210 = 0.20 * 100 = 20$$

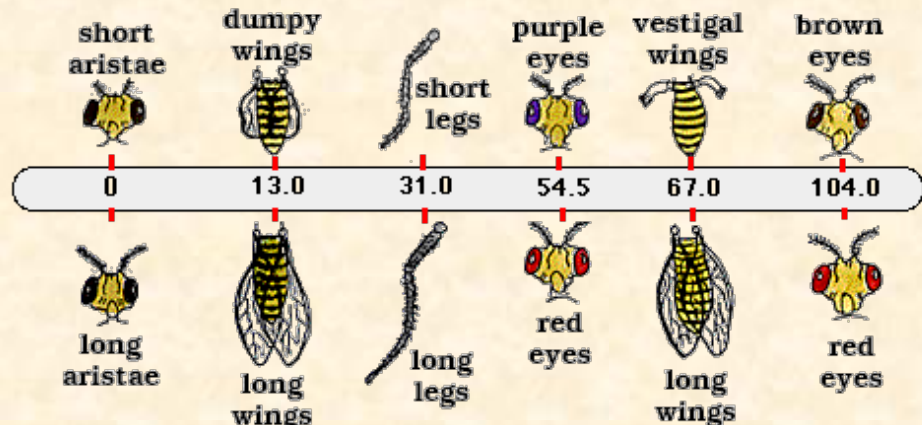
- Особине се сврставају у групе и има онолико група колико има хромозома.
- Процент **crossing over**-а указује на релативне међусобне позиције гена
- Фреквенција **crossing over**-а може да буде поремећена (да се не заснива само на међусобној удаљености гена.
- **Crossing over** се ретко дешава у близини центромере.
- Код мужјака винске мушице не долази до **crossing over**-а (разлог непознат).
- **Екстремне температуре повећавају** проценат **crossing over**-а.
- Старост организма повећава проценат **crossing over**-а.
- **Хромозомске аберације смањују, или онемогућавају** **crossing over** у једној регији хромозома.
- Молекуларно-генетички приступи (где је то могуће) прецизнији за стварање хромозомских мапа.
- **Дихаплоиди и транслокациони преломи, молекуларни маркери омогућавају** мапирање и минор гена.



Хромозомска мапа винске мушице



MUTANT



а) Утврђено на хромозому 6:
mul 2, вишецветни класић
ea 7, ранозрелост
uc 2, unicum
o, наранџаста лема
gs 4, стакласти рукавац
x_n, Nepal xantha (мембрана –
пластиди)
msg 6, генетичка мушка стерилност
msg,,bk, генетичка мушка стерилност

б) Вероватно на хромозому 6:
g, бледо-зелена боја
alb,,f, albino
se6, штур ендосперм
f6, хлоротични клијанци

Јечам



revised linkage map for chromosome 6.

Sat. mul2 ms,, bk ea7 uc2 o gs 4 se 6 x_n Amy 1 L.
centromere

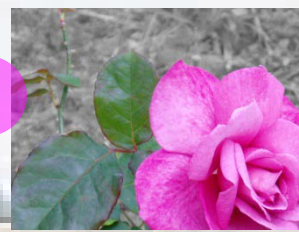
Orange lemma (o) is very close to the centromere and likely in the long arm.

Основни број хромозома генома руже је $n=7$, или $2n=14$ хромозома. Неке се појављују као триплоиди $3n=21$ (три сета од 7), или тетраплоиди $4n=28$ (четири сета од 7).

РУЖА



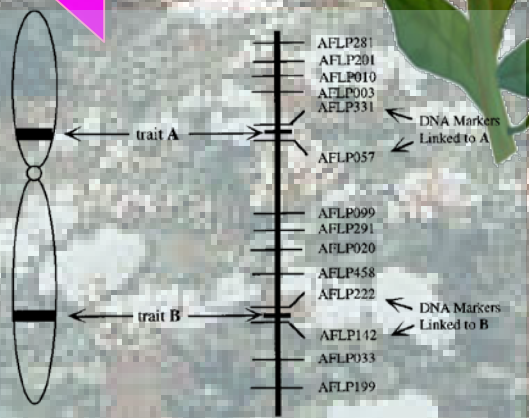
“black spot” отпорност



5 или 10 и више латица



бодље и без бодљи



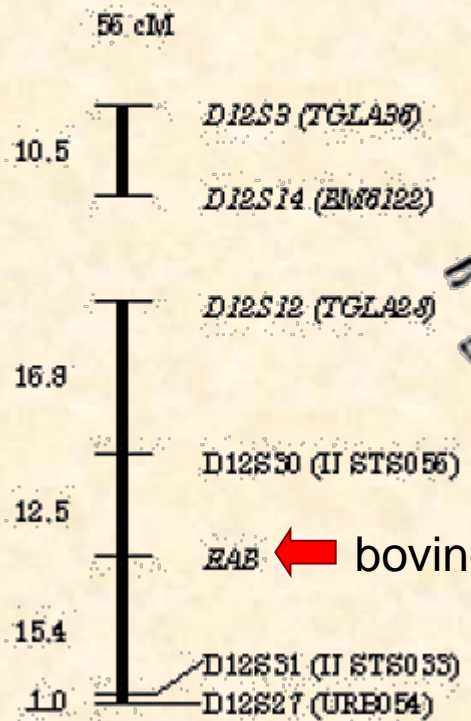
време цветања



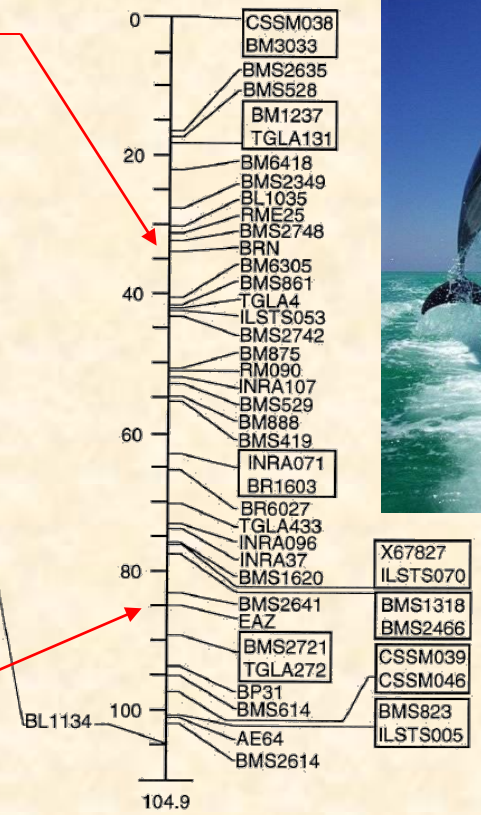
Говедо (*Bos taurus*) $2n=60$



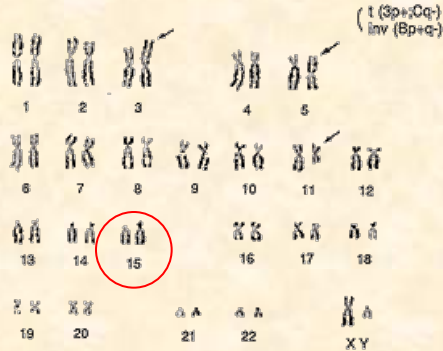
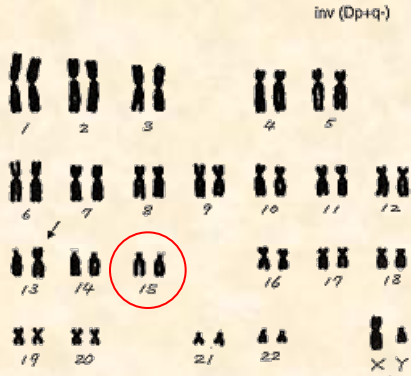
BTA 12
U27



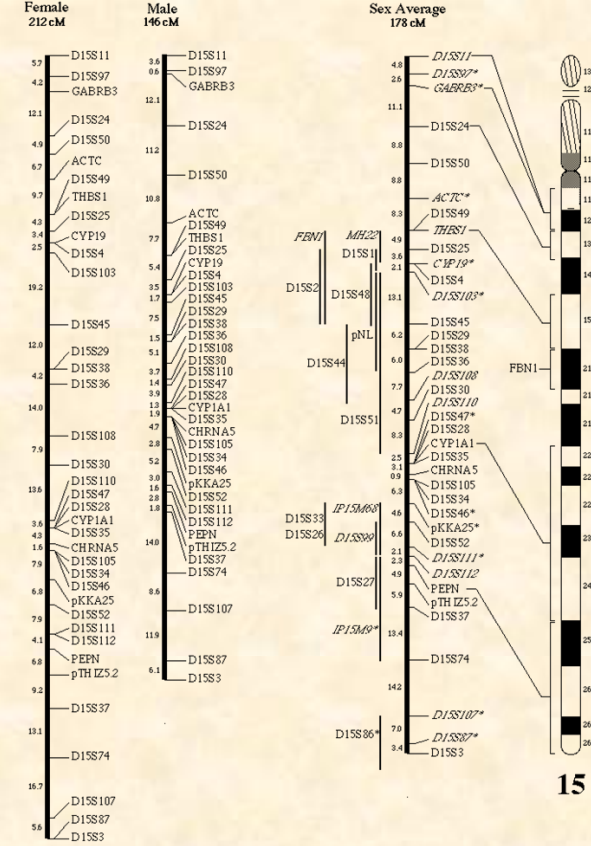
brain ribonuclease [angiogenin]



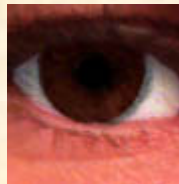
erythrocyte antigen Z [Z blood group] [erythrocytic antigen Z]



15q



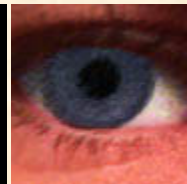
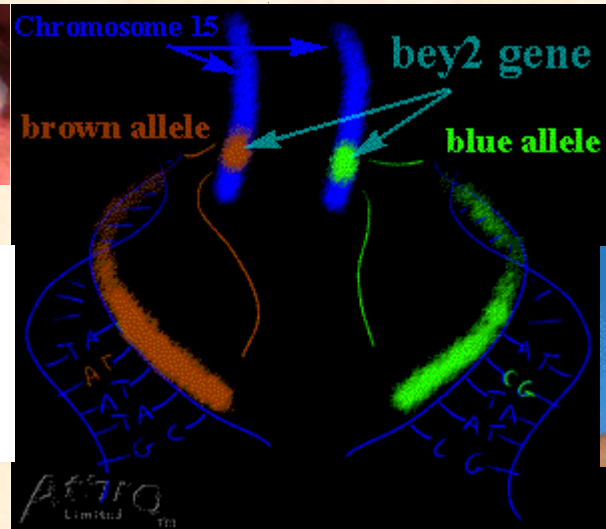
Crossing over



BEY2

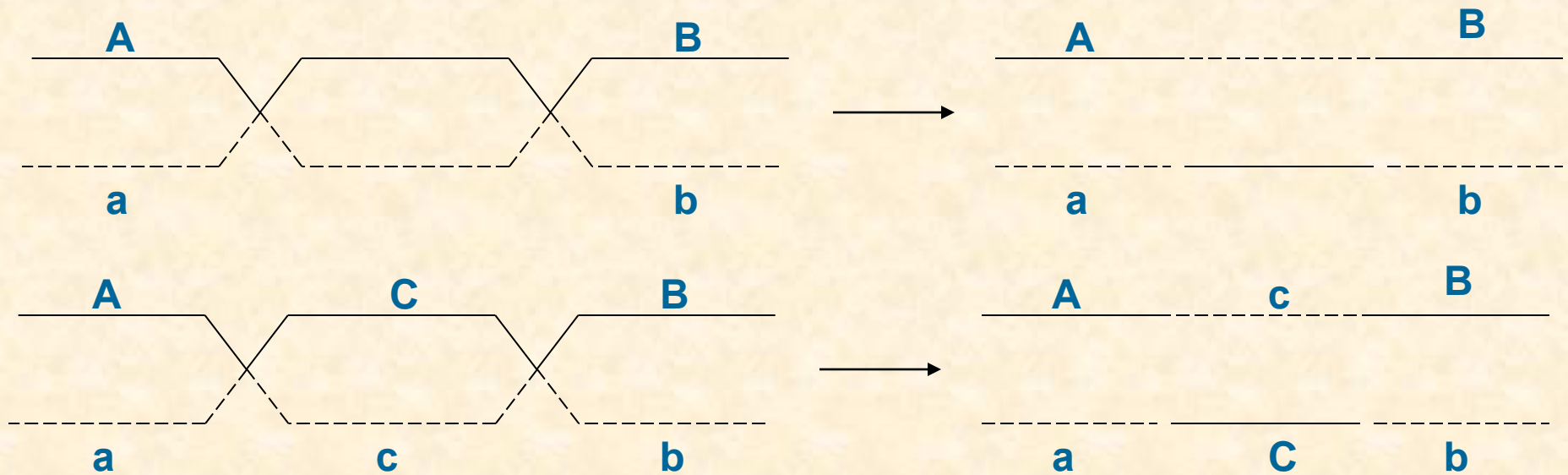


HCL3



Двоструки crossing over

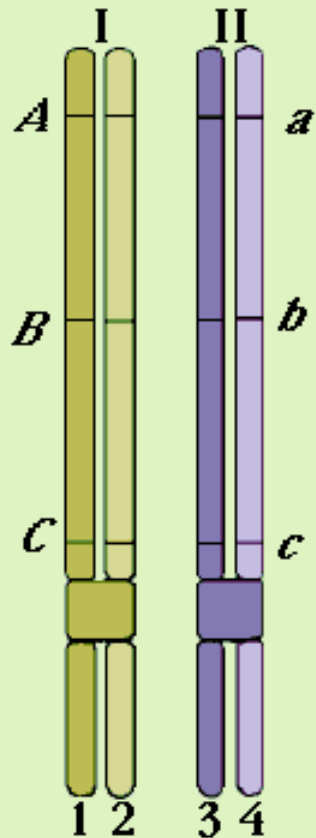
За тачније утврђивање удаљености између два гена погоднији су резултати тест укрштања три везана гена, него два везана гена, јер може да дође до двоструког crossing over-а па се добијају фенотипови као да није било crossing over-а.



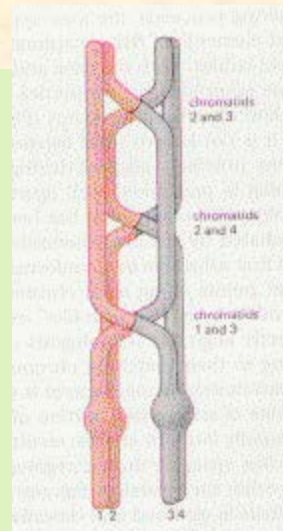
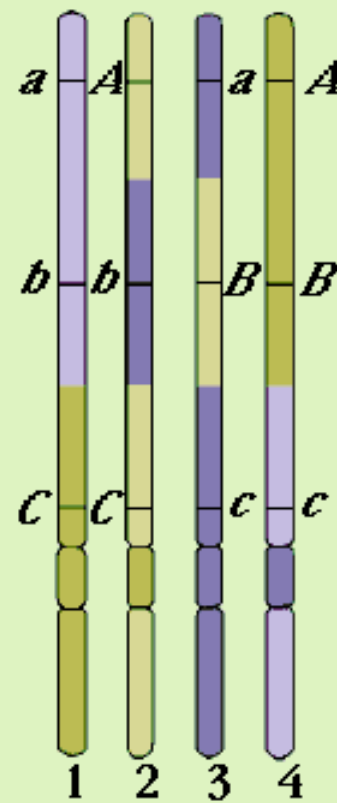
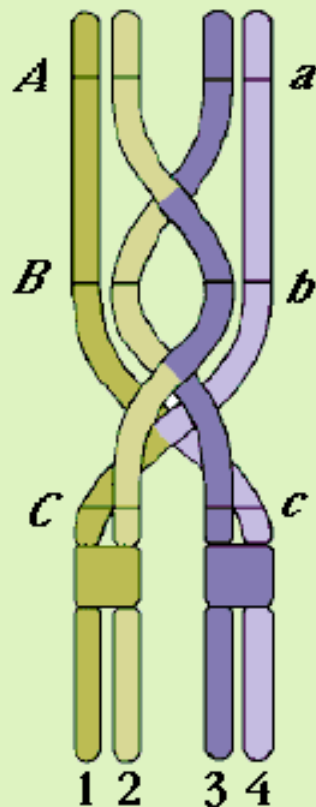
По тест укрштању највише организама са родитељским особинама, нешто мање са једноструким crossing over-ом (A-C) и (C-B), а најмање са двоструким crossing over-ом (A-C-B).

Crossing over између различитих хроматида

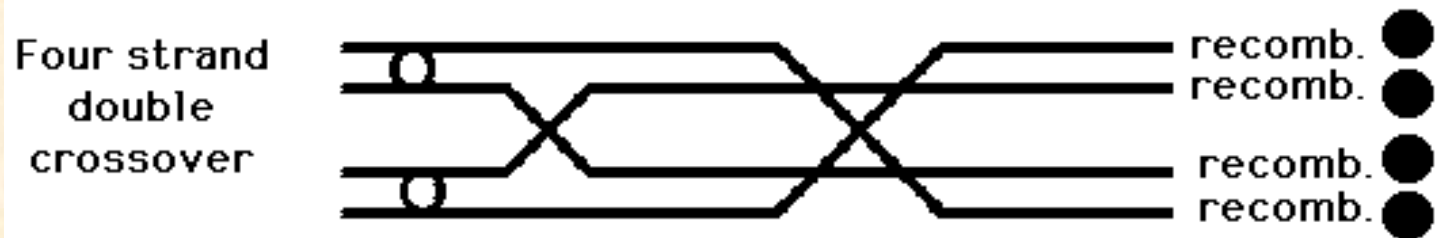
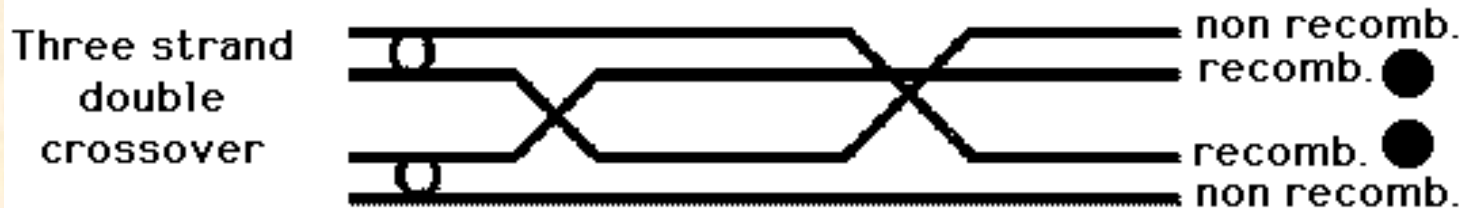
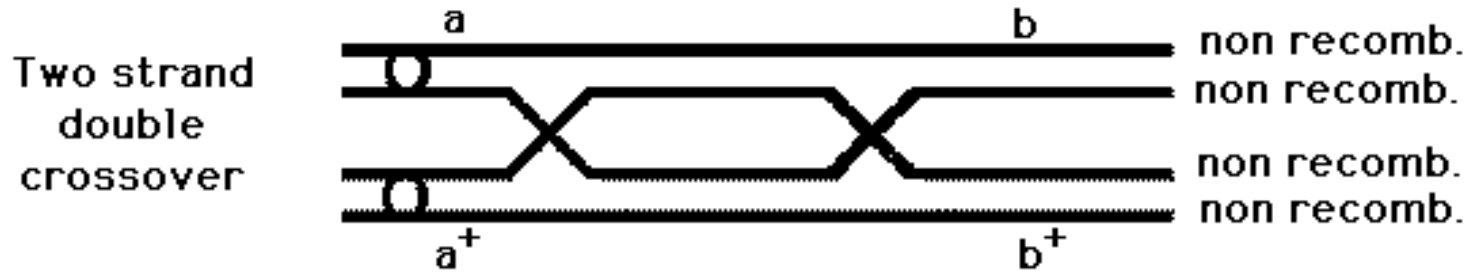
homologous chromosomes



twin chromatids



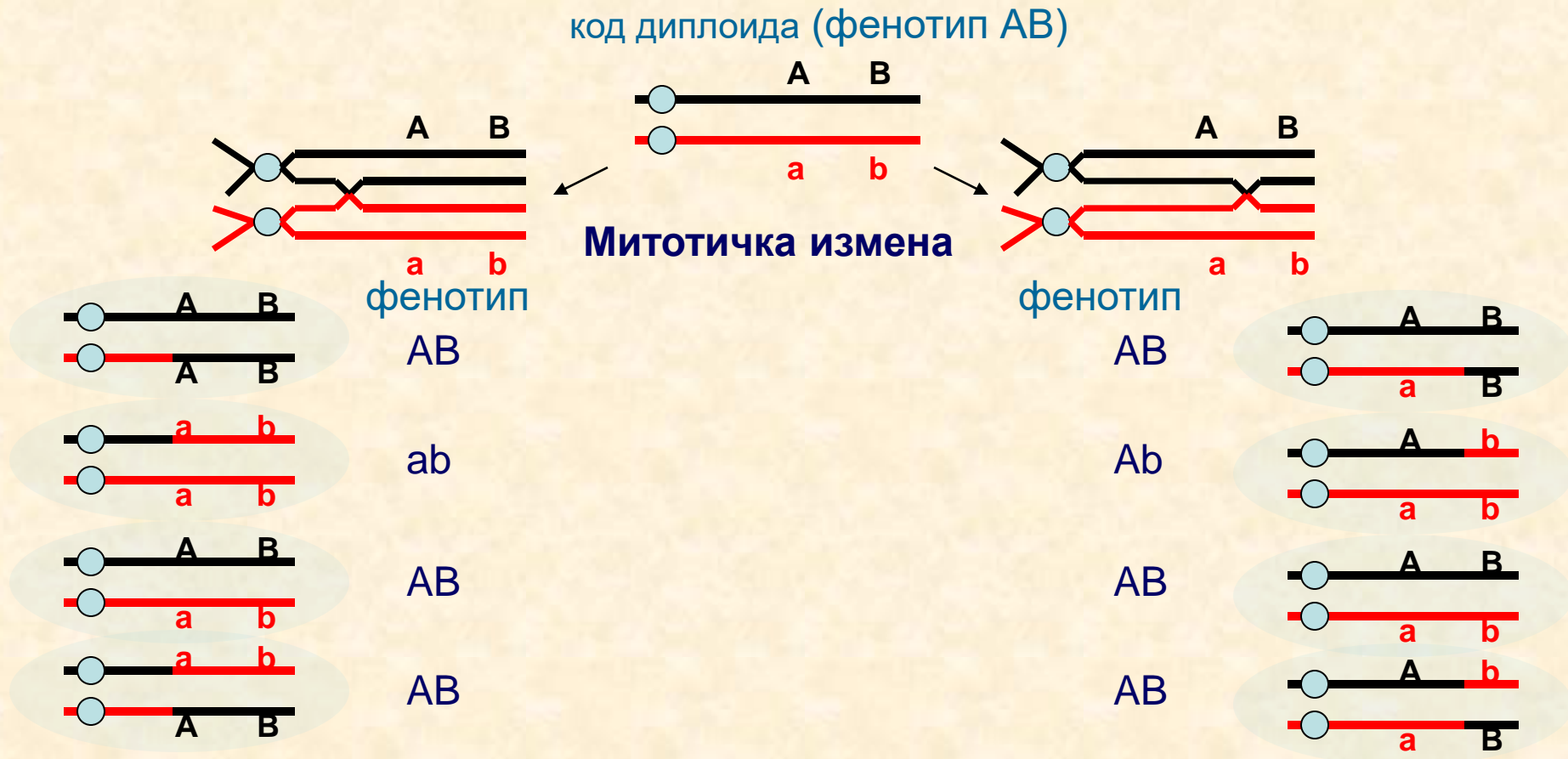
Компликоване могућности:



Crossing over у митозии

Када су хомологни хромозоми близу, у стадијуму хроматида, може да дође до crossing over-а.

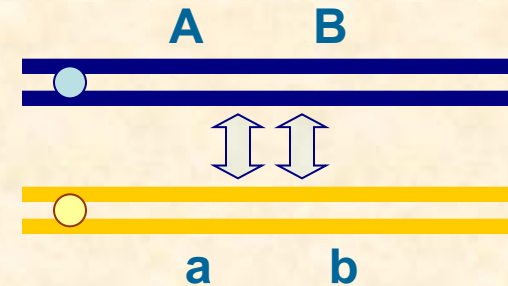
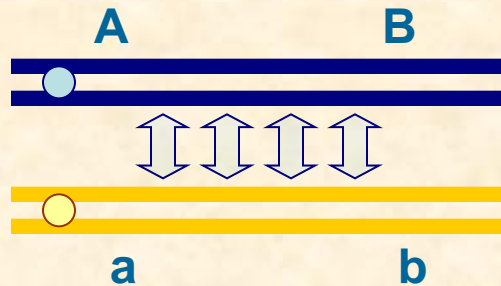
Ако је организам хетерозиготан ствара се различито соматско ткиво, код микроорганизама се добија фенотипски различито потомство, као да се радило о укрштању.



Неки искази везани са crossing over:

GO

Crossing over се чешће дешава између гена који су међусобно удаљенији на хромозому



GO

Crossing over је генски регулисан процес

GO

Учестаност crossing over-а зависи од позиције гена на појединим деловима хромозома, као где су генске позиције у односу на центромеру, или крајеве хромозома

GO

Crossing over индивидуа има мање од не-crossing over

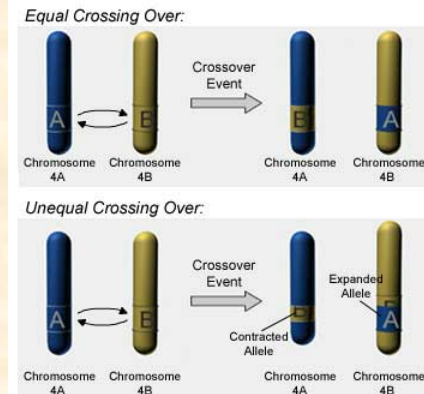
GO

Crossing over гамети се означавају са 1, а нормални гамети са X

GO

Постоји crossing over са неједнаком изменом

Figure Q-3: The Unequal Crossing Over Model



In equal crossing over, the entire segment of allele A switches places with the entire segment of allele B. But in unequal crossing over, only part of B switches places, leaving the rest behind to add to the length of B. The result is a shorter (contracted) segment B on chromosome 4A and a larger (expanded) segment comprised of all of A and part of B on chromosome 4B.

Значај

GO

Crossing over омогућава рекомбиновање гена везаних на једном хромозому

GO

Стварају се нове рекомбинације родитељских гена – НОВА ГЕНЕТИЧКА ВАРИЈАБИЛНОСТ

$$2^{23} \times 8 \times 10^6 + 2^{23} = ?$$
The diagram illustrates the calculation of genetic variability. It features a cell on the left with a nucleus containing a chromosome, labeled with 8×10^6 . To its right is the expression 2^{23} . Further right is a plus sign, followed by another 2^{23} , an equals sign, and a question mark. A chromosome is depicted between the second 2^{23} and the equals sign.

GO

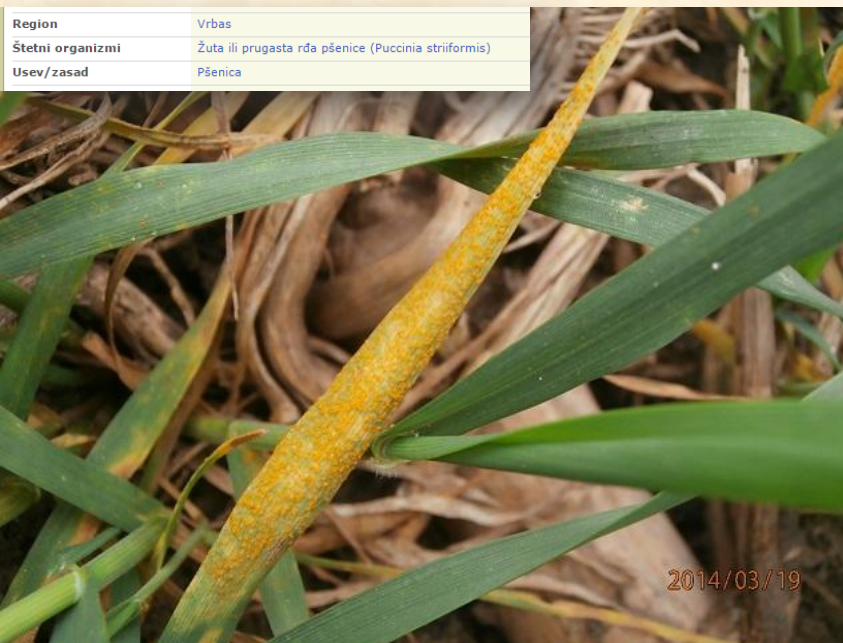
У оплемењивању даје шансу разбијања негативних везаности

ПРИМЕР:

ДА ЛИ СУ НОВЕ РАСЕ СТИГЛЕ У СРБИЈУ?

С обзиром на то да се нове расе патогена могу веома брзо развијати, важно је да се усеви контролишу у смислу обилазака парцела и активности које се односе на третирање усева фунгицидима где је то потребно у производној 2013/2014. години, на више локалитета у Војводини и Србији дошло је до јаче појаве рђе на пшеници. На основу симптоматолошких карактеристика, боје, облика и величине уредо и телеутоспора доминира патоген *Puccinia striiformis* f.sp. *tritici* – проузроковач жуте рђе. На појединим парцелама у производњи интензитети заразе се крећу од 40 до 60 одсто, а у генетској колекцији на Римским Шанчевима и до 90 одсто. Овај патоген до сада није представљао већи проблем у производњи пшенице у Србији, па се није ни радило на проучавању вирулентности његове популације.

Жута рђа се у Србији јављала спорадично, а током 1997. др Радивоје Јевтић и сарадници забележили су њену јачу појаву на неким генотиповима у генетској колекцији на локалитету Римски Шанчеви. Све до 2013. године била је безначајна и минорна болест на пшеници. Топла јесен, блага и влажна зима током производне 2013/2014. године погодовале су опстанку проузроковача жуте рђе и проузроковале проблем у пролеће 2014. Патоген је био активан у усевима током јесени и зиме, креирајући потенцијал за епидемијски развој овог пролећа.





Review

Genes for resistance to stripe rust on chromosome 2B and their application in wheat breeding

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^b School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu 610054, China

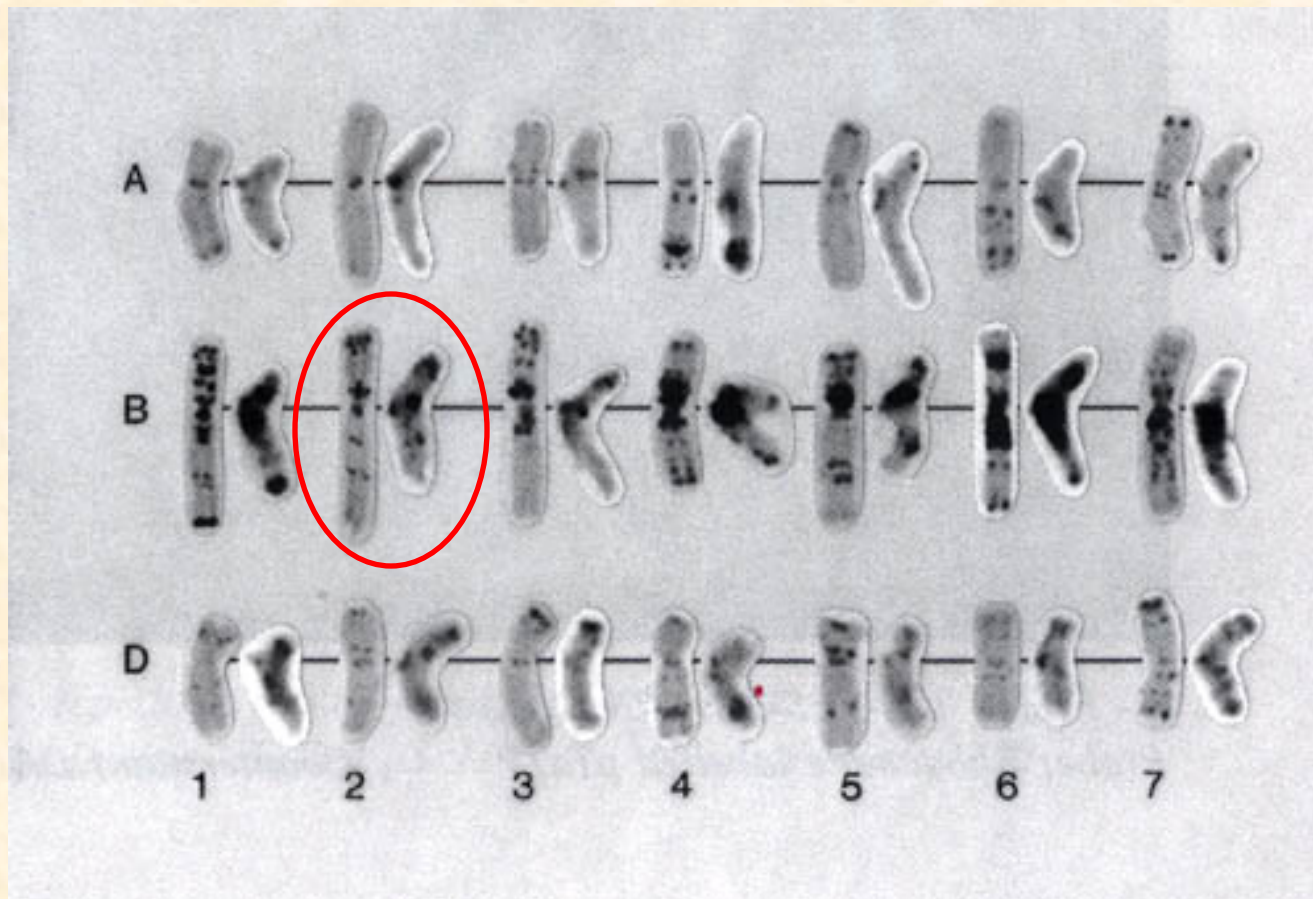
Received 2 January 2008; received in revised form 25 February 2008; accepted 25 February 2008

Abstract

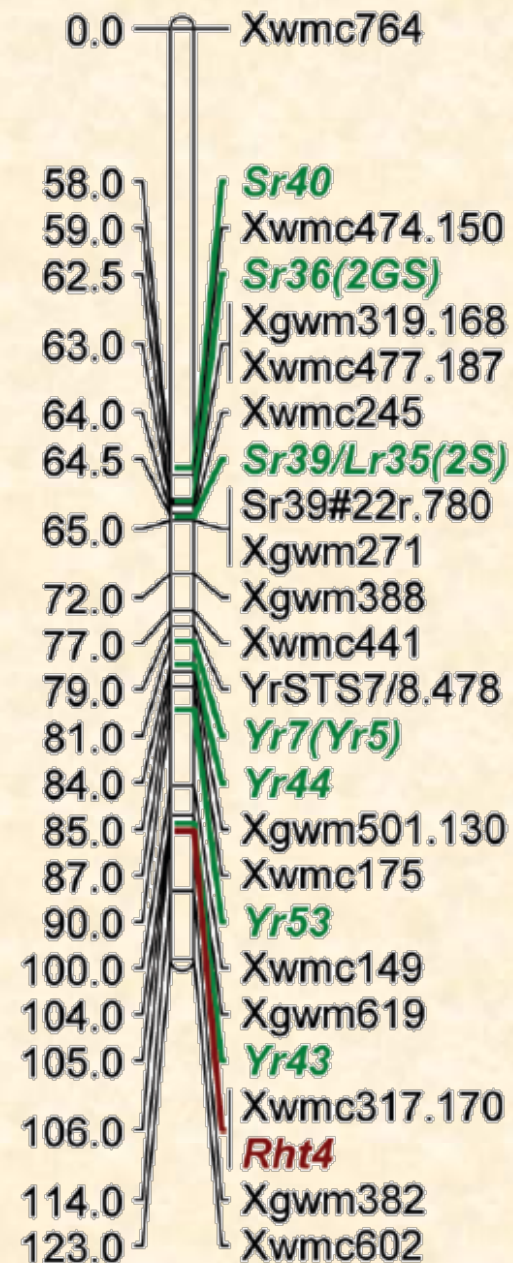
Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is one of the most damaging diseases of wheat worldwide. Growing resistant cultivars is the most economic and environmental friendly way to control the disease. There are many resistance genes to stripe rust located on wheat chromosome 2B. Here, we propose a strategy to construct the recombinant wheat chromosome 2B with multiple resistances to stripe rust by making crosses between wheat lines or cultivars carrying *Yr* genes and using marker-assisted selection, based on the reported information about resistance spectrum, chromosomal location, and linked markers of the genes. Pyramiding the resistance genes on 2B would afford a valuable strategy to control the disease by cultivating varieties with durable resistance. The possibility, efficiency, and prospect of the suggested strategy are reviewed in the paper.

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Keywords: *Puccinia striiformis*; *Yr* gene; 2B chromosome; Stripe rust; Marker-assisted selection



2B

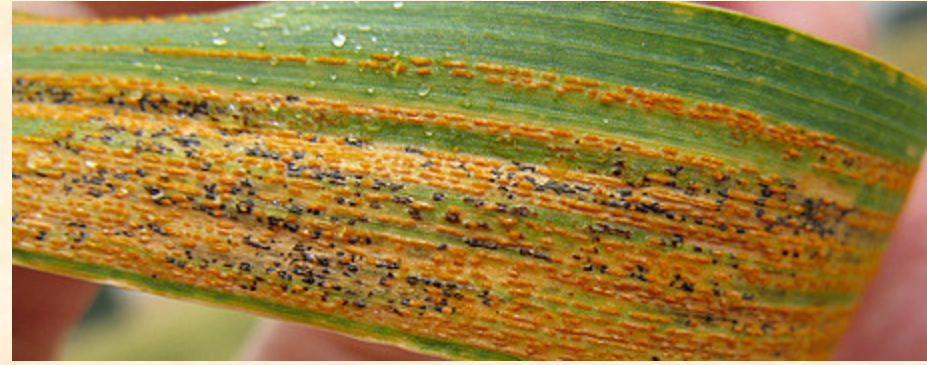


Yr5 – отпорност на расу PSTv-37

yr5 – неотпорност на расу PSTv-37

Yr43 – отпорност на расу PSTv-34

yr43 – неотпорност на расу PSTv-34



Отпорност на жуту рђу раса: **PSTv-37**

Нетпорност на жуту рђу раса: **PSTv-34**

Отпорност на жуту рђу раса: **PSTv-34**

Нетпорност на жуту рђу раса: **PSTv-37**



Yr5yr43/Yr5yr43



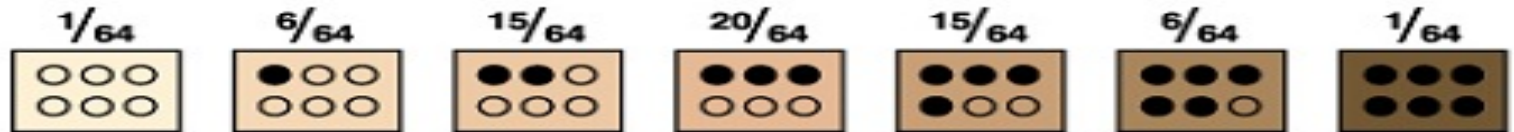
yr5Yr43/yr5Yr43



Како може да се добије сорта пшенице отпорна на обе расе жуте рђе?

Одговор може да буде у виду решења помоћу хромозома, словним ознакама гена или описно дат!





ПОЛИГЕНО НАСЛЕЂИВАЊЕ

НАСЛЕЂИВАЊЕ КВАНТИТАТИВНИХ СВОЈСТАВА

Fraction of population



Шта су?

Неке од квантитативних особина

Неке врсте отпорности на болести



This April Genet (2013) 136:2425-2449
DOI 10.1007/s00122-013-2159-9

REVIEW

Quantitative trait loci of stripe rust resistance in wheat

G. M. Rosewarne · S. A. Herrera-Foessel · R. P. Singh · J. Huerta-Espino · C. X. Lan · Z. H. He

Received: 12 March 2013 / Accepted: 12 July 2013 / Published online: 17 August 2013
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Abstract
Key message Over 140 QTLs for resistance to stripe rust in wheat have been published and through mapping flanking markers on consensus maps, 49 chromosomal regions are identified.
Abstract Over thirty publications during the last 10 years have identified more than 140 QTLs for stripe rust resistance in wheat. It is likely that many of these QTLs are identical genes that have been spread through plant breeding into diverse backgrounds through phenotypic selection under stripe rust epidemics. Allelism testing can be used to differentiate genes in similar locations but in different genetic backgrounds; however, this is problematic for QTL studies where multiple loci segregate from any one parent. This review utilizes consensus maps to illustrate important genomic regions that have had effects against stripe rust in wheat, and although this methodology cannot distinguish alleles from closely linked

genes, it does highlight the extent of genetic diversity for this trait and identifies the most valuable loci and the parents possessing them for utilization in breeding programs. With the advent of cheaper, high throughput genotyping technologies, it is envisioned that there will be many more publications in the near future describing ever more QTLs. This review sets the scene for the coming influx of data and will quickly enable researchers to identify new loci in their given populations.

Abbreviations
AFLP Amplified fragment length polymorphism
AUDPC Area under disease progress curve
CAPS Cleaved amplified polymorphic sequences
cM Centimorgan
DART Diversity array technology
EST Expressed sequence tag
HTAP High temperature adult plant

Evolution 184: 23–36, 2009.
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25

Quantitative trait loci analysis in *Theobroma cacao* using molecular markers. Inheritance of polygenic resistance to *Phytophthora palmivora* in two related cacao populations

Polygenic resistance to *Phytophthora palmivora* in cacao

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Received: 4 April 1999; accepted: 21 January 2000

Key words: Cacao, disease resistance, genetic mapping, *Phytophthora palmivora*, QTL

Summary

Two related segregating populations of *Theobroma cacao* L. were analysed for their resistance to *Phytophthora palmivora*. The first F₂ population was obtained by crossing two susceptible cacao clones of Catoño (a highly heterozygous genotype) and Pound 12 (a highly heterozygous genotype) and the second population was obtained by backcrossing a single F₁ tree with Catoño. The genetic maps obtained for each population were compared. The F₂ map includes 162 loci and the backcross has 140 loci. The two maps, F₂ and BC₁, exhibit high co-linear loci segregation covering respectively, 772 and 914 cM. *Phytophthora* resistance was assessed by measuring the size increase of a lesion at five (DK5) and ten days (DK10) after pod inoculation. Six different QTLs were detected in the F₂ and BC₁ populations. One QTL was found in both populations, and appeared to be a major component of disease resistance, and explaining nearly 48% of the phenotypic variance in the F₂ population. The absence of some QTL detection in the BC₁ in comparison with the F₂ population is due to the lack of transmission of the favourable alleles for these QTLs from the single F₁ tree used for the backcross. The phenotypic variance explained by the action of the quantitative trait alleles indicated that genetic factors of both major and minor effects were involved in the control of the character studied. QTLs conferring increased resistance to *Phytophthora* were identified in both susceptible parents, suggesting the presence of transgressive traits and the possibility of selection in cacao. Phenotypic and epistatic effects for the QTLs were also detected. Finally, the use of marker assisted selection (MAS) in cacao breeding programs is discussed.

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Quantitative Trait Loci Analysis of Powdery Mildew Disease Resistance in the *Arabidopsis thaliana* Accession Kashmir-1

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Manuscript received June 26, 2000
Accepted for publication April 24, 2001

ABSTRACT

Powdery mildew diseases are economically important diseases, caused by obligate biotrophic fungi of the Erysiphales. To understand the complex inheritance of resistance to the powdery mildew disease in the model plant *Arabidopsis thaliana*, quantitative trait loci analysis was performed using a set of recombinant inbred lines derived from a cross between the resistant accession Kashmir-1 and the susceptible accession Columbia *glabrous*1. We identified and mapped three independent powdery mildew quantitative disease resistance loci, which act additively to confer disease resistance. The locus with the strongest effect on resistance was mapped to a 500-kbp interval on chromosome III.

RESEARCH

Published October 8, 2013

Mapping Quantitative Trait Loci for Powdery Mildew Resistance in Flax (*Linum usitatissimum* L.)

Parvaneh Asgariya, Sylvie Cloutier,* Scott Duguid, Khalid Rashid, AghaFakhr Mirakhi, Mitali Banik, Ghodrattollah Saedi, P. Asgariya, A.F. Mishda, G. Saedi, Dep. of Agronomy and Plant Breeding, Indian Univ. of Technology, Indian, Pant. S. Cloutier,* M. Rashid, Mendon Research Station, Agriculture and Agri-Food Canada, 101 Route 100, Sherbrooke, MB, Canada, R1T 2A9, S. Duguid, K. Asgariya, Mendon Research Station, Agriculture and Agri-Food Canada, Food Canada Research and Technology (RUT), Indian Ministry of Science, Research and Technology and an Agriculture and Agri-Food Canada (A-Base gram. Received 7 May 2013. *Corresponding author (Sylvie.Cloutier@itrc.gc.ca).

ABSTRACT
Powdery mildew (*Oidium lini* Skovitz, [PM]), an obligate biotrophic ascomycete, is a common and widespread foliar disease of flax in most growing areas of the world. In this study, we constructed a linkage map using 143 simple sequence repeat (SSR) markers and an F₂ population of 300 individuals generated from a cross between the susceptible cultivar Norman and the resistant cultivar Linus. The F₂-derived F₂ families were phenotyped in the field and in a controlled environment grown chamber. The F₂-derived linkage map covered 1241 cM and was largely colinear with the previously published consensus map. Quantitative trait loci (QTL) analysis was performed and three QTLs for PM resistance were identified. The first QTL, located on LG1, 7, and 9 were consistently using phenotypic data from both field and grown chamber studies. These QTL explains 6% of the phenotypic variation exhibiting a mainly dominant gene action. This work represents a first step toward understanding the genetics of PM resistance in flax and map-based cloning of candidate genes underlying the QTL.

Abbreviations: ANOVA, analysis of variance; AFLP, amplified fragment length polymorphism; BAM, binary algorithm map; CIM, composite interval mapping; EST, expressed sequence tag; LAI, leaf area index; LG, linkage group; LOD, logarithmic odds; PM, powdery mildew; QTL, quantitative trait loci; SNP, single nucleotide polymorphism; SSR, simple sequence repeat; WGS, whole genome shotgun.

FLAX (*Linum usitatissimum* L., 2n = 2x = 36), a historically important and versatile diploid species, is widely grown in Egypt, Belgium, France, and across China, it is a high-quality cellulose-rich cash crop. This research was supported by the Canadian Institutes of Health Research (CIHR) and the Government of Ontario.

Journal of the American Society for Horticultural Science

J. AMER. SOC. HORT. SCI. 133(6):844–851, 2008.

Detection of Quantitative Trait Loci and Inheritance of Root-knot Nematode Resistance in Sweetpotato

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ADDITIONAL INDEX WORDS. *Ipomoea batatas*, *Meloidogyne incognita*, RKN, quantitative trait loci

ABSTRACT. Resistance to root-knot nematodes [*Meloidogyne incognita* (Kofoid & White) Chitwood] in sweetpotato [*Ipomoea batatas* (L.) Lam.] was studied in a mapping population consisting of 240 progeny derived from a cross between 'Beauregard', the predominant cultivar in the United States, and 'Tanzania', an African landrace. Quantitative trait loci (QTL) analyses to locate markers associated with resistance to root-knot nematodes (RKN) were performed using genetic maps based on parental segregation in 'Beauregard' and 'Tanzania' consisting of 726 and 947 single-dose amplified fragment length polymorphism (AFLP) markers, respectively. RKN resistance in the progeny was highly skewed with most of the progeny exhibiting medium to high levels of resistance. Single-point analysis of variance and interval mapping revealed seven consistently significant QTL in 'Tanzania' and two significant QTL in 'Beauregard'. In 'Tanzania', three QTL were associated with reduction in resistance as measured by the number of RKN egg masses and explained ~20% of the variation. Another four QTL had positive effects on resistance and explained ~21% of the variation. Other minor QTL explained ~2% or less of the variation but were not always consistent across geographical locations. In 'Beauregard', two QTL had positive effects on RKN resistance and explained ~6% of the observed variation. Based on molecular and phenotypic data, RKN resistance in sweetpotato is hypothesized to be conferred by several genes, but at least nine AFLP markers (seven from 'Tanzania' and two from 'Beauregard') are associated with genomic regions that have the biggest effect in the number of egg masses of RKN produced in the root system.



Број зрна

STUDY OF INHERITANCE FOR GRAIN YIELD AND RELATED TRAITS IN BREEDING POPULATIONS OF WHEAT (*Triticum aestivum* L.)

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SUMMARY

The study was conducted to investigate the inheritance pattern of grain yield and component traits related to grain yield in wheat (*Triticum aestivum* L.) using five varieties/lines –Pasban-90, Sehar-06, NR 356, DN-62 and ZAS-70 –, and their six derived F₂ hybrids at the University of Agriculture, Faisalabad, Pakistan. Heritability and genetic advance were determined for number of tillers per plant, flag leaf area, spike density, number of grains per spike, 1000-grain weight and grain yield per plant. The results revealed moderate to high heritability estimates coupled with high genetic advance for tillers per plant, grains per spike, 1000-grain weight and grain yield per plant. These estimates for flag leaf area were relatively low, whereas spike density exhibited moderate heritability along with low genetic advance in all cross combinations. Prospects of quick genetic improvement through selection are evident for most of the traits studied due to presence of higher heritability and genetic advance values. The most promising cross combinations were Pasban-90×DN-62 and Sehar-06×NR-356, suggesting that these crosses should be given attention in further breeding programs to develop high-yielding wheat varieties. Furthermore, the study also revealed that flag leaf area, grains per spike and 1000-grain weight had significant contribution in determining grain yield. Thus, these traits can be used as their utility as direct selection criteria for the wheat breeding populations.



Принос усева



HIGH YIELD

Bulgarian Journal of Agricultural Science, 17 (No 6) 2011, 783-788
Agricultural Academy

QUANTITATIVE INHERITANCE OF SOME WHEAT AGRONOMIC TRAITS

F. AYKUT TONK*, E. ILKER and M. TOSUN
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Abstract

AYKUT TONK.F., E. ILKER and M. TOSUN, 2011. Quantitative inheritance of some wheat agronomic traits. *Bulg. J. Agric. Sci.*, 17: 783-788

The objective of this study was to estimate gene effects for some agronomical traits (plant height, number, spike length, spikelet number per spike, peduncle length, flag leaf sheath length and flag leaf area) of Basribey x Atilla-12 cross in order to improve six generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) of Basribey x Atilla-12 cross in the Aegean Region. Genetic analyses were conducted by the joint scaling test based on three and six parameter models. In addition to additive effects, epistatic effects were significant for all measured traits due to different origins of the study. It was suggested that selection for all agronomical traits should be effective in the six generations due to epistatic gene effects.

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Full Length Research Paper
Inheritance of grain yield and its correlation with yield components in bread wheat (*Triticum aestivum* L.)
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Provincial Key Laboratory of Agrobiolgy, Jiangsu Academy of Agricultural Sciences, Nanjing, China
Received 15 June 2012; Accepted 16 November 2012

The genetic effect of grain yield plant⁻¹ and its correlation with yield component traits were studied in a diallel cross of seven wheat parents during the crop season 2009-2010. The results showed that the additive effect played an important role in the inheritance of grain yield plant⁻¹, indicating that additive effect played an important role in the inheritance of grain yield plant⁻¹. The additive effect was highly significant (P<0.01) for grain yield plant⁻¹, suggesting that the trait was also controlled by non-additive effect. The estimates of the best combiner for grain yield plant⁻¹ was Ningmai 9. The additive-dominance model was adequate for grain yield plant⁻¹ and it was controlled by the over-dominance model. Grain yield plant⁻¹ might be controlled by two groups of genes and exhibited moderate sense heritability (h²=49.51%). The statistical analysis revealed that grain yield plant⁻¹ was significantly correlated with tillers plant⁻¹ (r₁=0.524, r₂=0.595) and number of grains spike⁻¹ (r₁=0.528, r₂=0.507) phenotypically and genotypically levels. The information obtained from this study will be helpful for wheat breeders trying to develop new varieties with high-yielding potential.

Key words: Combining ability, diallel cross, grain yield, inheritance, *Triticum aestivum* L.

Indonesian Journal of Agricultural Science 8(2), 2007: 53-59

THE INHERITANCE OF YIELD AND YIELD COMPONENTS OF FIVE WHEAT HYBRID POPULATIONS UNDER DROUGHT CONDITIONS

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Број цветова

Mapping Quantitative Trait Loci for Green Bean Traits of Horticultural Importance

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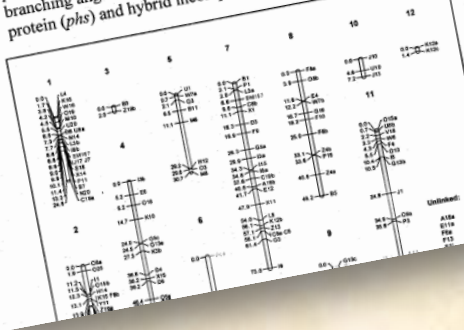
Oregon Bush Blue Lake (BBL) green beans are uniquely different from other snap beans. They possess dark blue-green pods with very low fiber that process well but retain their quality even after long duration in a commercial kitchen. The plants are high yielding and have good cold tolerance during germination and emergence. However BBL beans have poor growth habit and potentially higher off-type frequency than snap beans of Midwest origin. Oregon BBL beans are difficult to recombine with other snap beans. For example, it took Frazier about 20 years to convert Blue Lake beans from pole to bush growth habit (Myers and Baggett, 1999). We initiated this research to determine why BBL beans were difficult to recombine with other snap beans, and how the process might be facilitated.

We determined from a phylogenetic molecular marker study that Oregon BBL cultivars are of Mesoamerican center of domestication (Davis & Myers, 2002). Not only do they possess S phaseolin, but also cluster with the Andean center of domestication. The objectives of the current work was to develop a molecular marker map for the BBL background and to identify molecular markers linked to important quantitative traits in green bean. We would use markers to facilitate introgression of desirable traits into the BBL background.

The recombinant inbred (RI) mapping population was developed from the cross 'Mini OSU 5630 where 80 lines in the F₂:F₇ and subsequent generations were used. The Harri cultivar Minnette typifies Andean snap bean types. The population segregated for characters important to processing (pod length, color, shape, size, fiber, and shine [*ace*]), plant traits (branching angle and length, leaf size, and lodging resistance) as well as phaseolin seed protein (*phs*) and hybrid incompatibility between the two centers of origin (conditione

The population was in a trial (replicate with pods from a vest being graded and analyzed at Plant.

Of the three scored traits, a hibited normal regation, but / known segre discovered / are loosely We also



Genetic Mapping of Quantitative Trait Loci Underlying Flowering Time in Chrysanthemum (*Chrysanthemum morifolium*)

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Abstract

Flowering time is an important trait in chrysanthemum, but its genetic basis remains poorly understood. An intra-specific mapping population bred from the cross between the autumn-flowering cultivar 'Yuhualuoying' and the summer-flowering 'Aoyunhanxiao' was used to determine the number and relative effect of QTL segregating for five measures of flowering time. From flowering time data recorded over two consecutive seasons, 35 additive QTL were detected, each explaining between 5.8% and 22.7% of the overall phenotypic variance. Of these, 13 were detected in both years. Nine genomic regions harboring QTL for at least two of the five traits were identified. Ten pairs of loci epistatically determined the flowering time, but their contribution to the overall phenotypic variance was less than for the additive QTL. The results suggest that flowering time in chrysanthemum is principally governed by main effect QTL but that epistasis also contributes to the genetic architecture of the trait, and the major QTL identified herein are useful in our ongoing efforts to streamline the improvement of chrysanthemum via the use of molecular methodology.

Citation: Zhang F, Chen S, Jiang J, Guan Z, Fang W, et al. (2013) Genetic Mapping of Quantitative Trait Loci Underlying Flowering Time in Chrysanthemum (*Chrysanthemum morifolium*). PLoS ONE 8(12): e83023. doi:10.1371/journal.pone.0083023

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Competing interests: The authors have declared that no competing interests exist.

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Мајмун цвет или Мошус цвет, припада роду Scrophulariaceae и породици Phrymaseae

Evolution. 2002 Nov;56(11):2138-55.

Minor quantitative trait loci underlie floral traits associated with mating system divergence in *Mimulus*.

Fishman L¹, Kelly AJ, Willis JH.

Author information

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Abstract

The genetic basis of species differences provides insight into the mode and tempo of phenotypic divergence. We investigate the genetic basis of floral differences between two closely related plant taxa with highly divergent mating systems, *Mimulus guttatus* (large-flowered outcrosser) and *M. nasutus* (small-flowered selfer). We had previously constructed a framework genetic linkage map of the hybrid genome containing 174 markers spanning approximately 1800 cM on 14 linkage groups. In this study, we analyze the genetics of 16 floral, reproductive, and vegetative characters measured in a large segregating *M. nasutus* x *M. guttatus* F₂ population (N = 526) and in replicates of the parental lines and F₁ hybrids. Phenotypic analyses reveal strong genetic correlations among floral traits and epistatic breakdown of male and female fertility traits in the F₂ hybrids. We use multitrait composite interval mapping to jointly locate and characterize quantitative trait loci (QTLs) underlying interspecific differences in seven floral traits. We identified 24 floral QTLs, most of which affected multiple traits. The large number of QTLs affecting each trait (mean = 13, range = 11-15) indicates a strikingly polygenic basis for floral divergence in this system. In general, QTL effects are small relative to both interspecific differences and environmental variation within genotypes, ruling out QTLs of major effect as contributors to floral divergence between *M. guttatus* and *M. nasutus*. QTLs show no pattern of directional dominance. Floral characters associated with pollinator attraction (corolla width) and self-pollen deposition (stigma-anther distance) share several pleiotropic or linked QTLs, but unshared QTLs may have allowed selfing to evolve independently from flower size. We discuss the polygenic nature of divergence between *M. nasutus* and *M. guttatus* in light of theoretical work on the evolution of selfing, genetics of adaptation, and maintenance of variation within populations.

Heritability and correlation studies of certain quantitative traits in table grapes, *Vitis* spp.¹⁾

by

E. FIROOZABADY and H. P. OLMO

Untersuchungen zu Heritabilität und Korrelation quantitativer Merkmale bei Tafeltrauben (*Vitis* spp.)

Zusammenfassung: Bei den Abkömmlingen von *Vitis vinifera* × *V. rotundifolia*-Kreuzungen wurden die Heritabilität von 10 Merkmalen und ihre phänotypischen Korrelationen berechnet; es wurden 46 Familien mit über 1000 Nachkommen bearbeitet, die aus Kreuzungen zwischen 26 Eltern hervorgegangen waren. Messungen der Trauben- und Beerenmerkmale wurden über 4 Jahre (1976—1979) durchgeführt; 1976 wurde auch die allgemeine Wüchsigkeit gemessen. Die Heritabilität wurde aus der Regression zwischen den jahrgangsbereinigten Leistungsmittelwerten der einzelnen Sämlinge und den Mittelwerten ihrer Eltern errechnet. Sie betrug für: Gewicht der Einzeltraube 0,12, Beerendichte der Trauben 0,55, Einzelbeerengewicht 0,49, Festigkeit der Beerenhaut 0,75, Konsistenz des Beerenfleisches 1,04, Mostgewicht 0,34, Mostsäure 0,15, allgemeine Wüchsigkeit 0,10. Die Heritabilität des Traubenertrages je Rebe war praktisch 0 (−0,08). Da — abgesehen von der allgemeinen Wüchsigkeit — die Genauigkeit dieser Berechnungen sehr hoch ist, dürften sie eine verlässliche Prognose der genetisch bedingten Leistungssteigerung erlauben, wenn Sämlinge aufgrund ihrer eigenen Leistungsfähigkeit als Kreuzungseltern selektiert werden. Die zu erwartende Leistung der Nachkommenschaft zufällig gekreuzter hochleistungsfähiger Eltern wurde errechnet. Die Bedeutung der geschilderten genetischen Beziehungen für Züchtungsprogramme und Selektionsverfahren wird diskutiert.

Key words: genetic selection, statistics, table grape, yield, must quality, growth.



Emir. J. Food Agric. 2010, 22(1): 89-94
<http://ffa.ueu.ac.ae/ejfa.shtml>

Short Communication

Chamomile biodiversity and essential oil qualitative-quantitative characteristics in Egyptian production and Iranian landraces

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Abstract: This study presents the genetic and environmental variations of essential oil and its sesquiterpene composition (*l*- α -bisabololoxide A, *l*- α -bisabololoxide B, *l*- α -bisabololoxide A, *l*- α -bisabololoxide B) in natural growing chamomile population in Iran in comparison with the cultivars, which are cultivated in Egypt. The highest contents of *l*- α -bisabololoxide A, *l*- α -bisabololoxide A and *l*- α -bisabololoxide B were typical for chamomile plants, which flower anthodia were collected in various places in Egypt. These results showed that there is a Bisabololoxide chemo type B of chamomile plants only. Contribution presents the results of the chamomile essential oil qualitative-quantitative characteristics of chemo types that are originated from different geographical parts of the Iranian country. The Zagros Mountains, as a nature barrier, divided the Chamomile populations: one to the Persian Gulf with the very high *l*- α -bisabolol content and one to the Alborz Mountains/Caspian Sea/ with the very high *l*- α -bisabololoxide A content. This Chamomile biodiversity on a relative small area was created during long time process (evolution) in regard to influence of eco-physiological conditions (biotic and abiotic factors) on the concrete place of chamomile population growth.

Keywords: Biodiversity, composition, essential oil, *Matricaria recutita*.



Садржај шећера



Садржај масти у месу
Дебљина леђне сланине



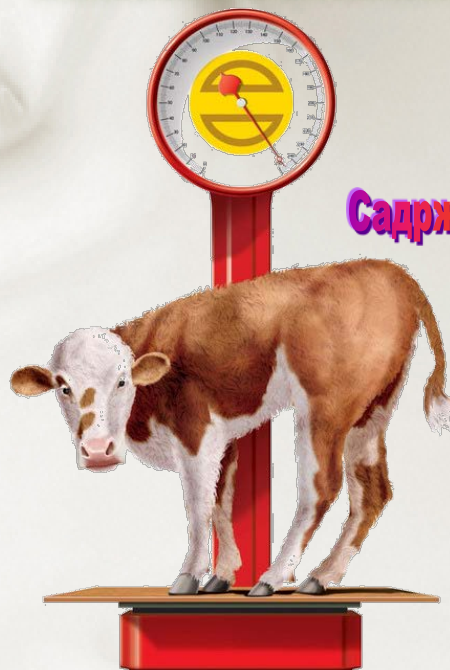
Носивост



Млечност



Садржај протеина у месу



Телесна маса животиња



Tobin/Dusheck, Asking About Life, 2/e Figure 16.6

Number of individuals



Height in inches

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© 1999 Oxford University Press. Human Biology, 2/e, Figure 16.6

Крвни притисак

Mapping of a blood pressure quantitative trait locus to chromosome 15q in a Chinese population

Xin Xu¹, Jianhua Yang³, John Rogus¹, Changzhong Chen^{1,3}, Nicholas Schork^{1,4} and Xiping Xu^{1,2,3*}

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Received August 12, 1999; Revised and Accepted September 27, 1999

Blood pressure is a complex trait of pivotal biological importance, in which 20–50% of interindividual variation is genetically determined. Whereas genes have been identified in several rare Mendelian forms of hypertension, little progress has been made in understanding the genetics of blood pressure variation in the general population. Recently, we screened the human genome using rural Chinese sibling pairs with extreme blood pressure and identified suggestive linkage for two chromosomal regions. By refining the trait definition and genotyping additional markers, we detected significant linkage (maximum lod score = 3.77) near D15S203 in lower extreme diastolic blood pressure sibling pairs. Using a second independent data set from the same geographical area, we marginally replicated ($P = 0.05$) this result, suggesting that this locus is very likely to be involved in the regulation of diastolic blood pressure.

identified in several rare (6–11), little progress has genetics of blood pressure. Previous genetic studies concentrated on hypertens pathways that are importa sure, most notably the ren Among all candidate ge otensinogen (AGT) gene I pathogenesis of essential h Instead of focusing only genes from physiological whole genome scan on ex tensive) sibling pairs ascer of >200 000 people in / Screening Set v.9, which elite markers with an aver two new candidate bloc (QTL) regions with maxim

Heart Rate and Blood Pressure Quantitative Trait Loci for the Airpuff Startle Reaction

Rebecca L. Jaworski, Martin Jirout, Shamara Closson, Laura Breen, Pamela L. Flodman, M. Anne Spence, Vladimir Kren, Drahomira Krenova, Michal Pravenec, Morton P. Prinz

Abstract—The airpuff startle reaction is a probe of sensori-autonomic processing and is useful for studies of genetic control of stress-induced cardiovascular activity. Using a Wistar-Kyoto-Spontaneously Hypertensive Rat F2 cross, we reported an airpuff-elicited strain-dependent and trial-dependent bradycardia, the absence of which cosegregated with hypertension. Here, we use the mapping power of the HXB-BXH recombinant inbred rat strains ($n=23$) to locate quantitative trait loci (QTL) for this and associated cardiovascular phenotypes. Rats (12 weeks old), with indwelling femoral arterial catheters, were subjected to repeated airpuff stimuli (100 ms, 12.5 psi, 28 trials). Basal mean arterial pressure (MAP), delta MAP, and delta heart rate response to airpuff stimuli were analyzed as the average over 28 trials. There was a significant strain effect on the cardiovascular phenotypes measured. One QTL for the bradycardia elicited by the first airpuff stimulus was identified on chromosome 2 (D2rat 62/63; logarithm of odds [LOD] 2.9) mapping near a reported blood pressure locus. Further QTL were identified for basal MAP (RN08), stimulus-elicited tachycardia on trials 2 to 5 (RN01 and RN010), and delta MAP (RN06). Our results indicate that chromosomes 1, 2, and 10 are involved in heart rate responses to airpuff startle stimulus, and chromosomes 6 and 8 are involved in pressor responses. This study is the first to identify stress-related heart rate loci and provides additional support for our prior cosegregation results. Furthermore, we have established the utility of this experimental paradigm to identify loci responsible for cardiovascular regulation during stress in genetic hypertensive models. (*Hypertension*. 2002;39[part 2]:348–352.)

Key Words: behavior ■ blood pressure ■ bradycardia ■ tachycardia ■ heart rate ■ genomics

Physiol Genomics, 2004 Mar 12;17(1):60–8.

Quantitative trait loci that determine lipoprotein cholesterol levels in an intercross of 129S1/SvImJ and CAST/Ei inbred mice.

Lyons MA¹, Wittenburg H, Li R, Walsh KA, Korstanje R, Churchill GA, Carey MC, Palonen B.

Author information

Abstract

To identify genetic determinants of lipoprotein levels, we are performing quantitative trait locus (QTL) analysis on a series of mouse intercrosses in a "daisy chain" experimental design, to increase the power of detecting QTL and to identify common variants that should segregate in multiple intercrosses. In this study, we intercrossed strains CAST/Ei and 129S1/SvImJ, determined HDL total, and non-HDL cholesterol levels, and performed QTL mapping using Pseudomarker software. For HDL cholesterol, we identified two significant QTL on chromosome (Chr) 1 (Hdlq5, 82 cM, 60–100 cM) and Chr 4 (Hdlq10, 20 cM, 10–30 cM). For total cholesterol, we identified three significant QTL on Chr 1 (Chol7, 74 cM, 65–80 cM), Chr 4 (Chol8, 12 cM, 0–30 cM), and Chr 17 (Chol9, 54 cM, 20–60 cM). For non-HDL cholesterol, we identified significant QTL on Chr 8 (Nhdq1, 34 cM, 20–60 cM) and Chr X (Nhdq2, 6 cM, 0–18 cM). Hdlq10 was the only QTL detected in two intercrosses involving strain CAST/Ei: Hdlq5, Hdlq10, Nhdq1, and two suggestive QTL at D7Mit246 and D15Mit115 coincided with orthologous human lipoprotein QTL. Our analysis furthers the knowledge of the genetic control of lipoprotein levels and points to the importance of Hdlq10, which was detected repeatedly in multiple studies.

Abstract

J Am Acad Child Adolesc Psychiatry. 2010 Aug;49(8):783–93. doi: 10.1016/j.jaac.2010.01.026. Epub 2010 May 5.

Quantitative genetics in the era of molecular genetics: learning abilities and disabilities as an example.

Harworth CM¹, Plomin R.

Author information

Abstract

OBJECTIVE: To consider recent findings from quantitative genetic research in the context of molecular genetic research, especially genome-wide association studies. We focus on findings that go beyond merely estimating heritability. We use learning abilities and disabilities as examples.

METHOD: Recent twin research in the area of learning abilities and disabilities was reviewed.

RESULTS: Three findings from quantitative genetic research stand out for their far-reaching implications for child and adolescent psychiatry. First, common disorders such as learning disabilities and attention deficit hyperactivity disorder (ADHD) are highly heritable. Second, the normal distribution (the Comminfluence across diverse learning abilities and disabilities is genetically as are behaviors and g (the Nature of Nurture Hypothesis).

CONCLUSIONS: Quantitative genetic research provides important findings in the area of learning abilities and disabilities. © 2010 American Academy of Child and Adolescent Psychiatry.

Behavior Genetics, Vol. 24, No. 2, 1994

DNA Markers Associated with High Versus Low IQ: The IQ Quantitative Trait Loci (QTL) Project

Robert Plomin,¹ Gerald E. McClearn,¹ Deborah L. Smith,¹ Sylvia Vignetti,¹ Michael J. Chorney,² Karen Chorney,³ Charles P. Venditti,³ Steven Kasarda,² Lee A. Thompson,² Douglas K. Detterman,³ Johanna Daniels,^{4,5} Michael Owen,^{4,5} and Peter McGuffin¹

Received 30 Sept. 1993—Final 20 Oct. 1993

General cognitive ability (intelligence, often indexed by IQ scores) is one of the most highly heritable behavioral dimensions. In an attempt to identify some of the many genes (quantitative trait loci; QTL) responsible for the substantial heritability of this quantitative trait, the IQ QTL Project uses an allelic association strategy. Allelic frequencies are compared for the high and low extremes of the IQ dimension using DNA markers in or near genes that are likely to be relevant to neural functioning. Permanent cell lines have been established for low IQ ($N = 82$; $N = 183$), middle IQ (mean IQ = 105; $N = 100$), and high IQ ($N = 100$) groups. Two markers were identified for the low IQ group: a two-allele marker and for 26 comparisons for 14 multiple-allele markers. Two markers yielded significant ($p < .01$) allelic frequency differences between the high- and the low-IQ groups in the combined sample—a new HLA marker for a gene unique to the human species and a new brain-expressed triplet repeat marker (CTG83). The prospects for harnessing the power of molecular genetic techniques to identify QTL for quantitative dimensions of human behavior are discussed.

KEY WORDS: Cognitive ability; intelligence; quantitative trait loci (QTL); allelic association; DNA markers.

Способност учења

IQ



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Телесна маса Ниво холестерола

Генетичка анализа:

Број гена
Однос гена



Начин наслеђивања



Оплемењивање

КВАЛИТАТИВНЕ ОСОБИНЕ



GG

x

gg

F1



Gg

F2

GG, Gg, Gg, gg



3

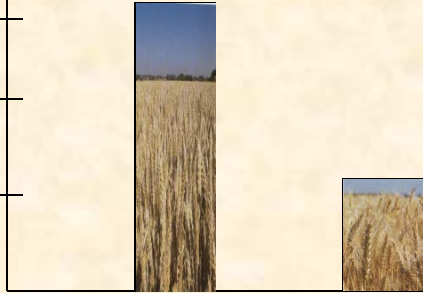
=

1



f (%)

75
50
25

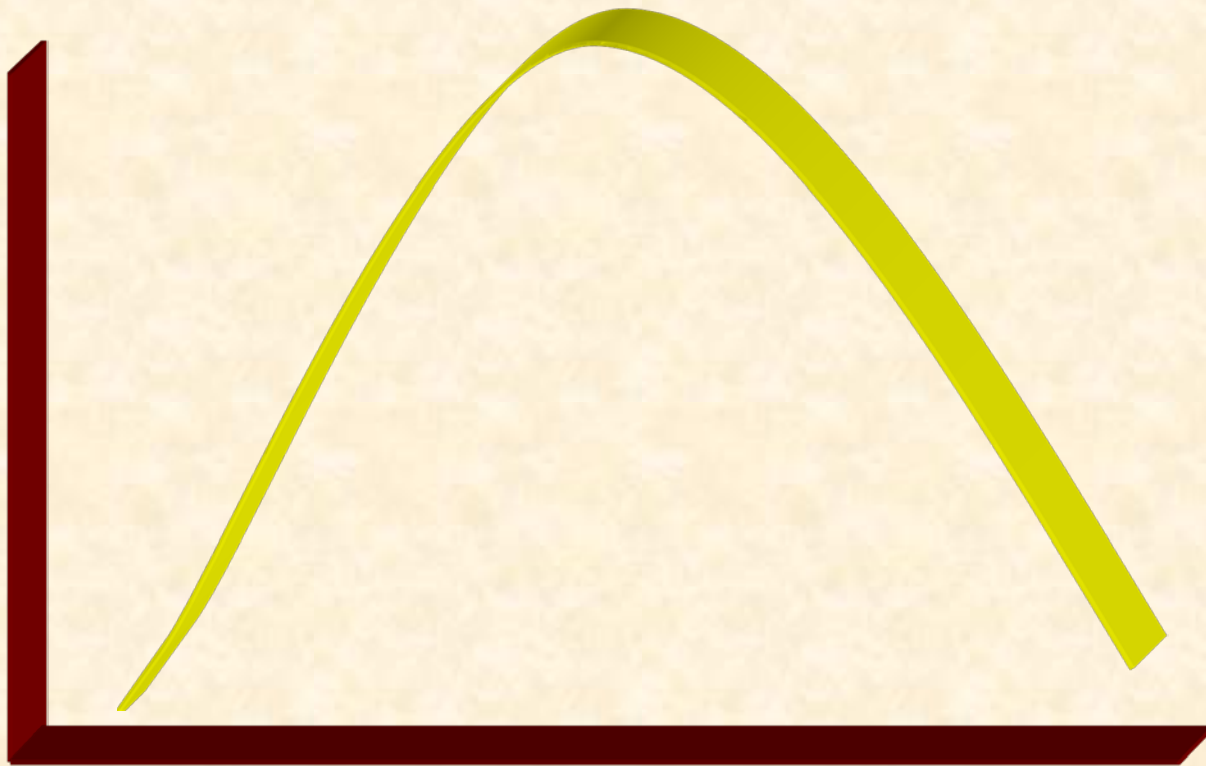


МАЈОР ГЕНИ
ДИСКОНТИНУИРАНА ВАРИЈАБИЛНОСТ

КВАНТИТАТИВНЕ ОСОБИНЕ

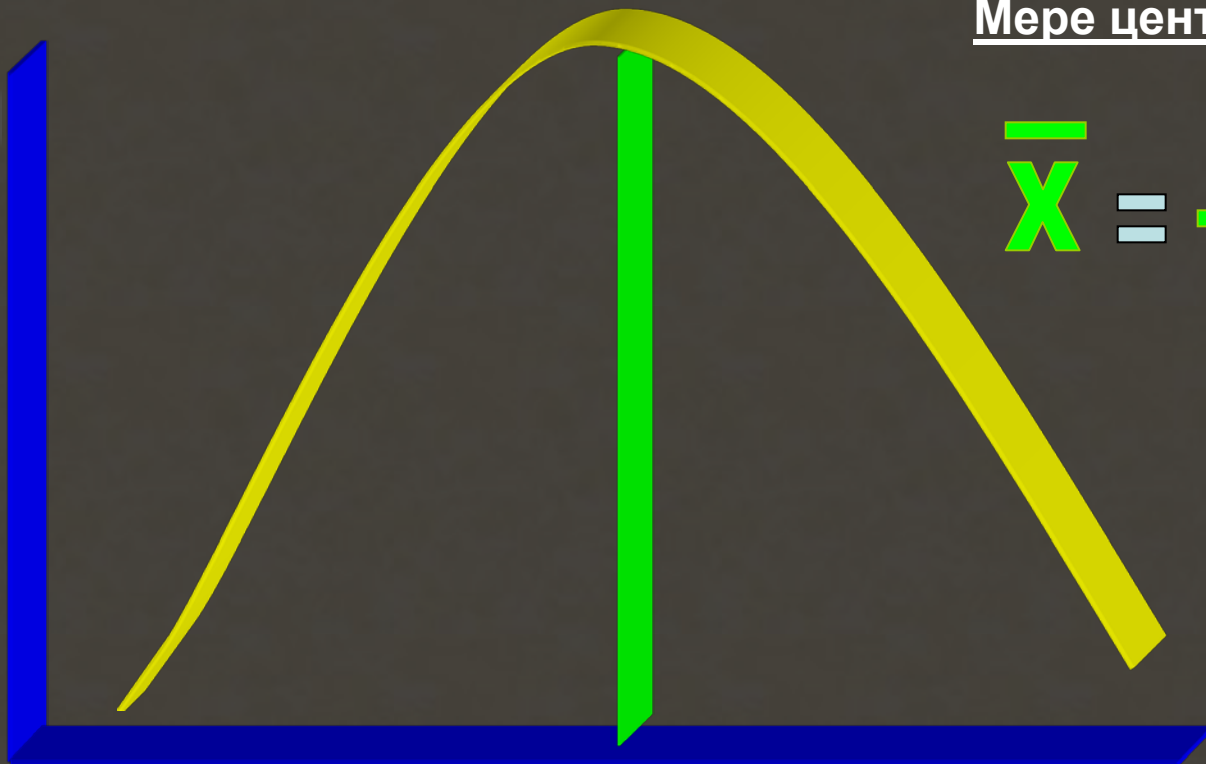
МИНОР ГЕНИ

КОНТИНУЕЛНА ВАРИЈАБИЛНОСТ



Мере централне тенденције

$f(\%)$



$$\bar{x} = \frac{\sum x}{N}$$

\bar{x}

x

Мере варијације

$$\sigma = \sqrt{\frac{\sum (x - \bar{x})^2}{N - 1}}$$

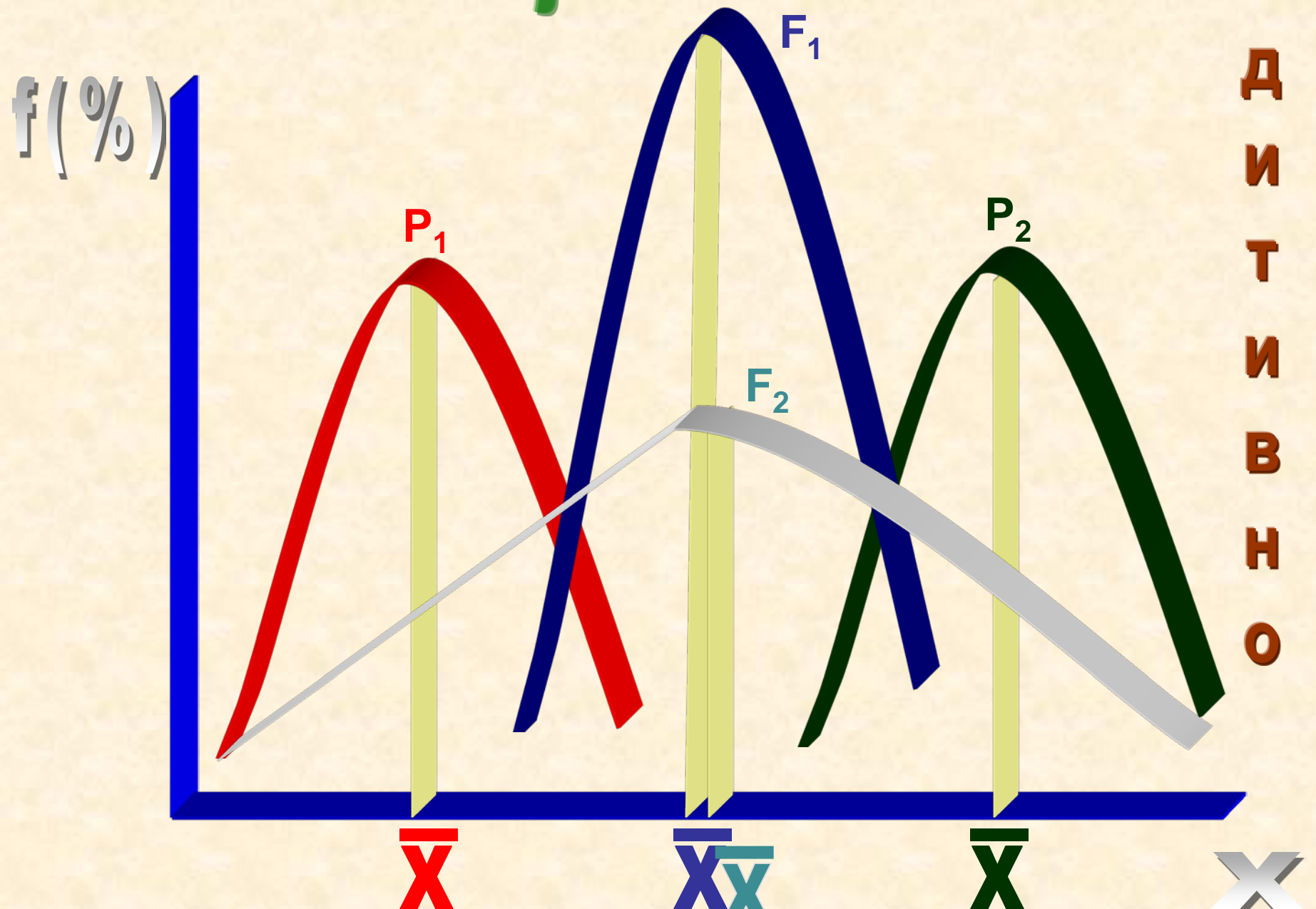
σ^2

$$V = \frac{\sigma \times 100}{\bar{x}} (\%)$$

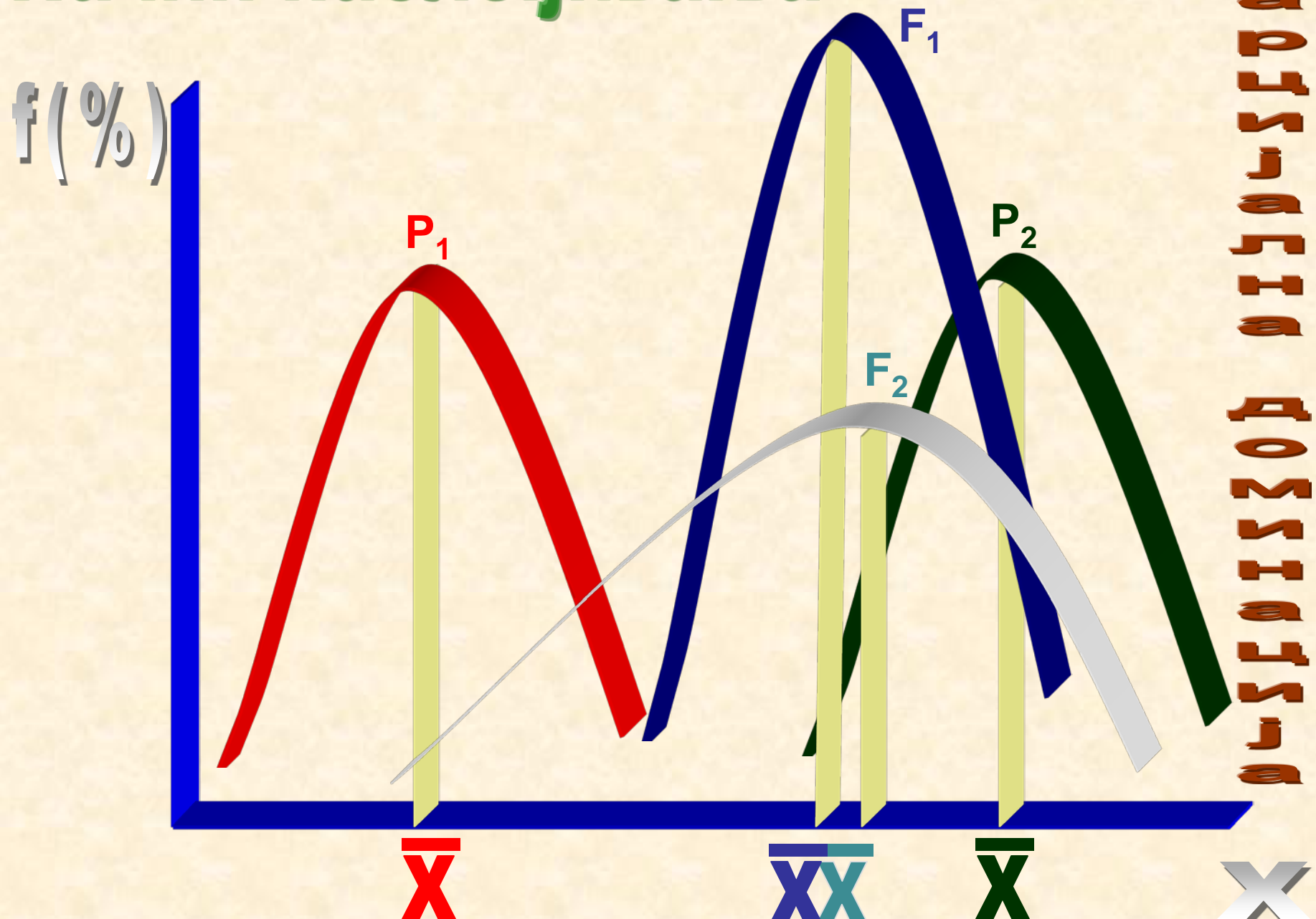
$$s_{\bar{x}} = \frac{\sigma}{\sqrt{N}}$$

Начин наслеђивања

А
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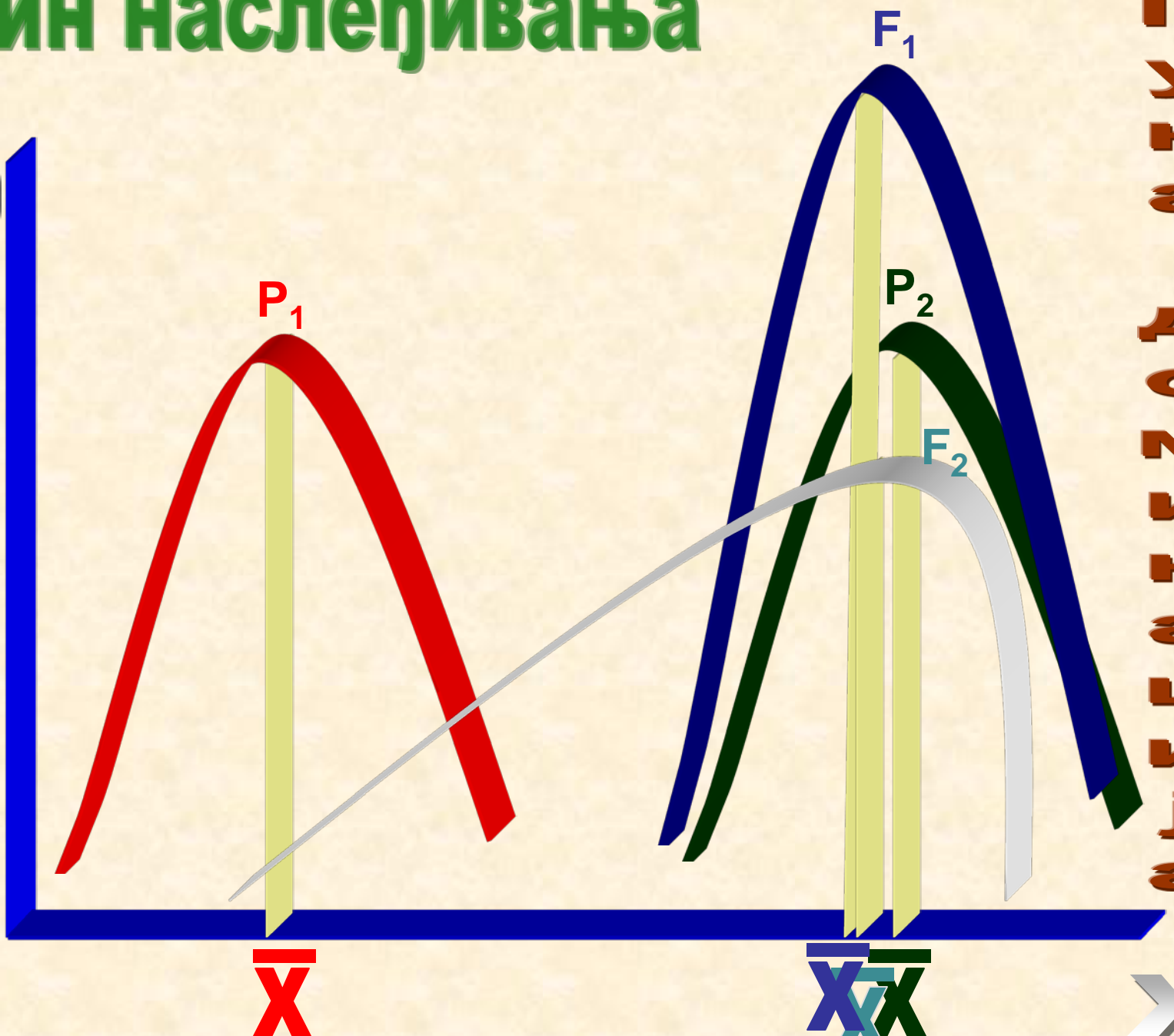
Начин наслеђивања



СВОЈУ-ОБИЊ ДОЗУЈУ-О

Начин наслеђивања

$f(\%)$

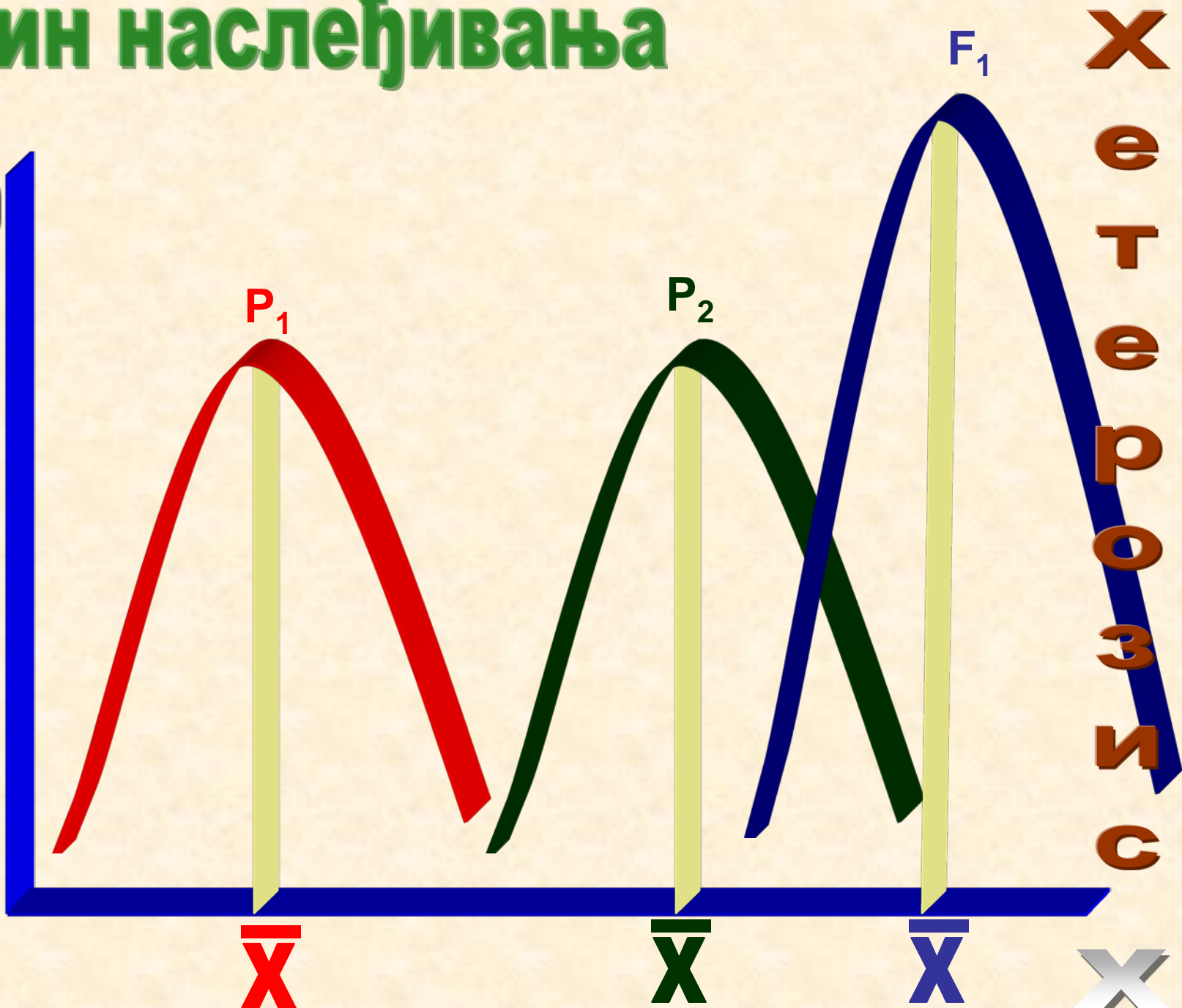


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X

Начин наслеђивања

$f(\%)$



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\bar{X}

\bar{X}

X

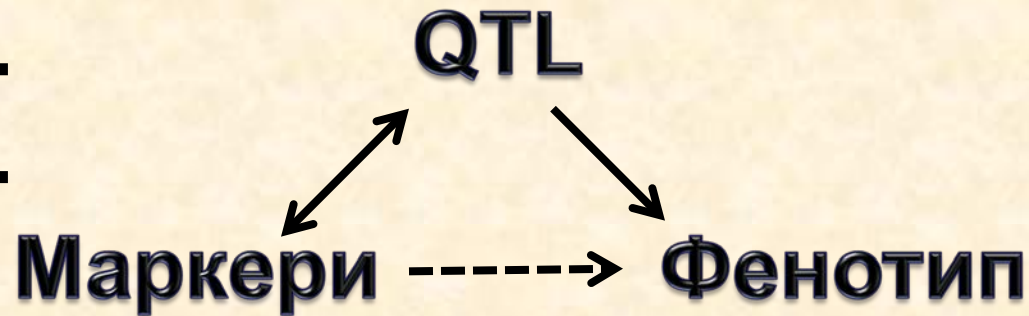
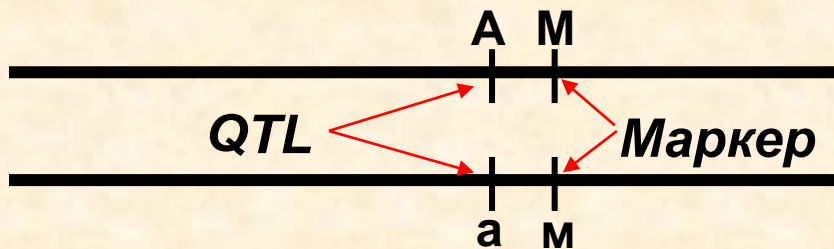
QTL Mapping

МАПИРАЊЕ ПОЛИГЕНА

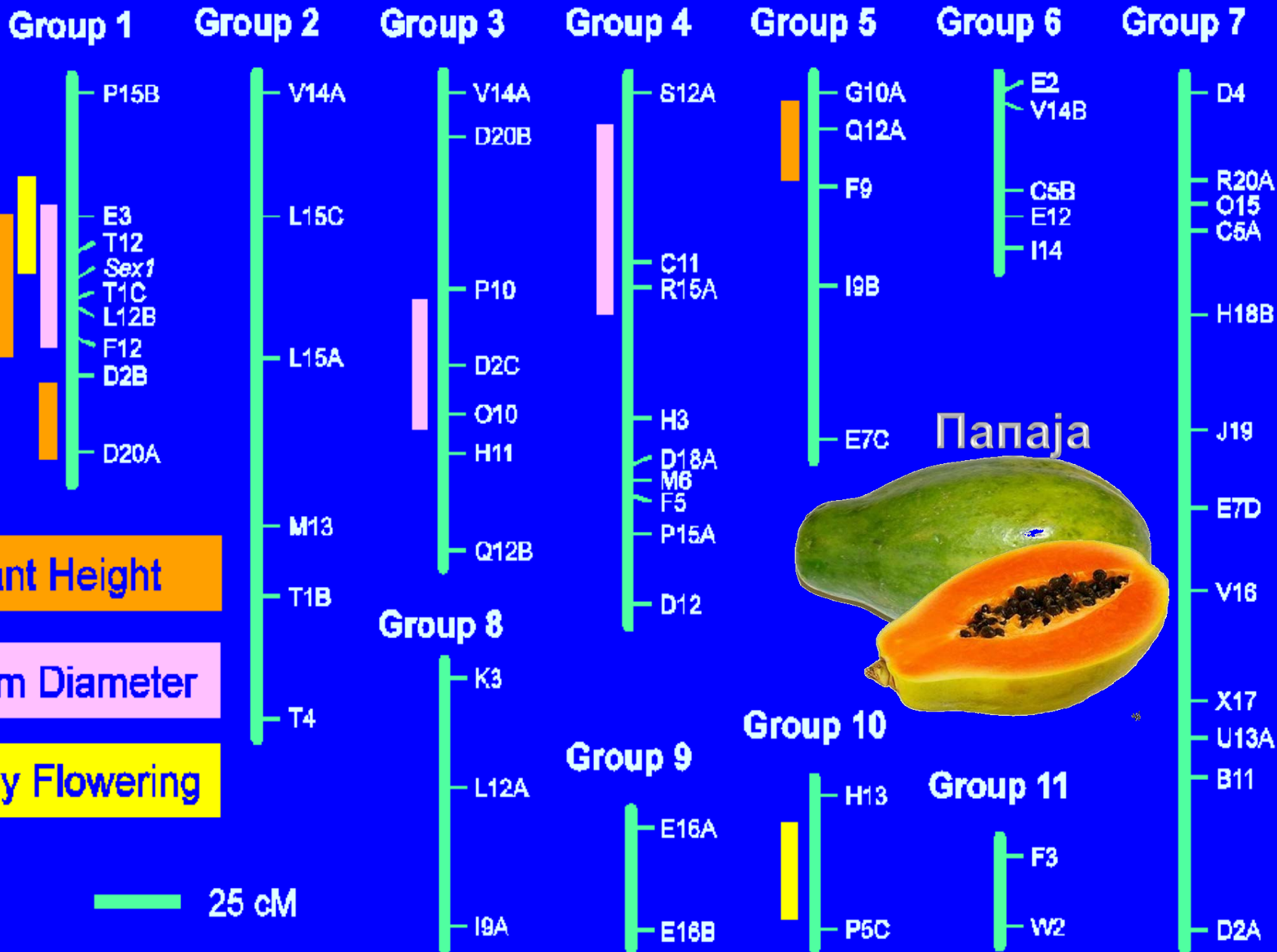
Циљеви:

- Идентификација геномских региона (QTL) који доприносе варијацији особине.
- Добијање процене позиције полигена - QTL.
- Процена утицаја полигена - QTL.

Статистичка структура:



QTLs for Growth and Flowering



КОМПОНЕНТЕ ФЕНОТИПСКЕ ВАРИЈАБИЛНОСТИ



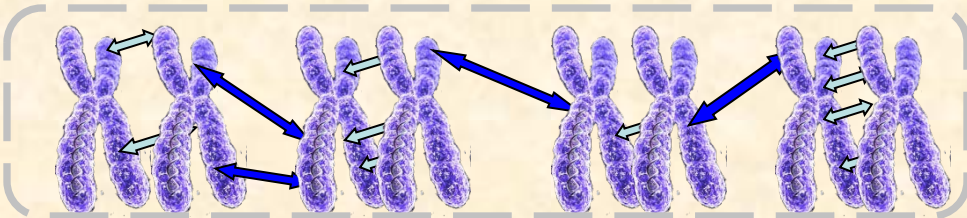
$$F = G + E$$

$$\sigma_F^2 = \sigma_G^2 + \sigma_E^2$$

$$\sigma_F^2 = \sigma_G^2 + \sigma_E^2 + \sigma_{GE}^2$$

$$\sigma_F^2 = \sigma_G^2 + \sigma_E^2 + \sigma_{GE}^2 + \sigma_{\text{Greska}}^2$$

$$\sigma_F^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2 + \sigma_E^2 + \sigma_{GE}^2 + \sigma_{\text{Greska}}^2$$



$$0 < h^2 < 1 \text{ (100\%)}$$

$$h^2 \nearrow \rightarrow G \nearrow$$

$$h^2 \searrow \rightarrow E \nearrow$$

Херитабилност

h^2 или H

$$h^2 = \frac{\sigma^2_G}{\sigma^2_F} \quad \text{херитабилност у ширем смислу}$$

$$h^2 = \frac{\sigma^2_A}{\sigma^2_F} \quad \text{херитабилност у ужем смислу}$$

$$h^2 = \frac{\sigma^2_{F2} - \sigma^2_{F1}}{\sigma^2_{F2}} * 100 \text{ [\%]}$$

Burton, 1952.

$$h^2 = \frac{\sigma^2_{F2} - \sqrt{\sigma^2_{P1} * \sigma^2_{P2}}}{\sigma^2_{F2}} * 100$$

Mahmud & Kramer, 1951.

$$h^2 = \frac{\sigma^2_{F2} - \frac{\sigma^2_{P1} + \sigma^2_{P2} + \sigma^2_{F1}}{3}}{\sigma^2_{F2}} * 100$$

Mather, 1949.