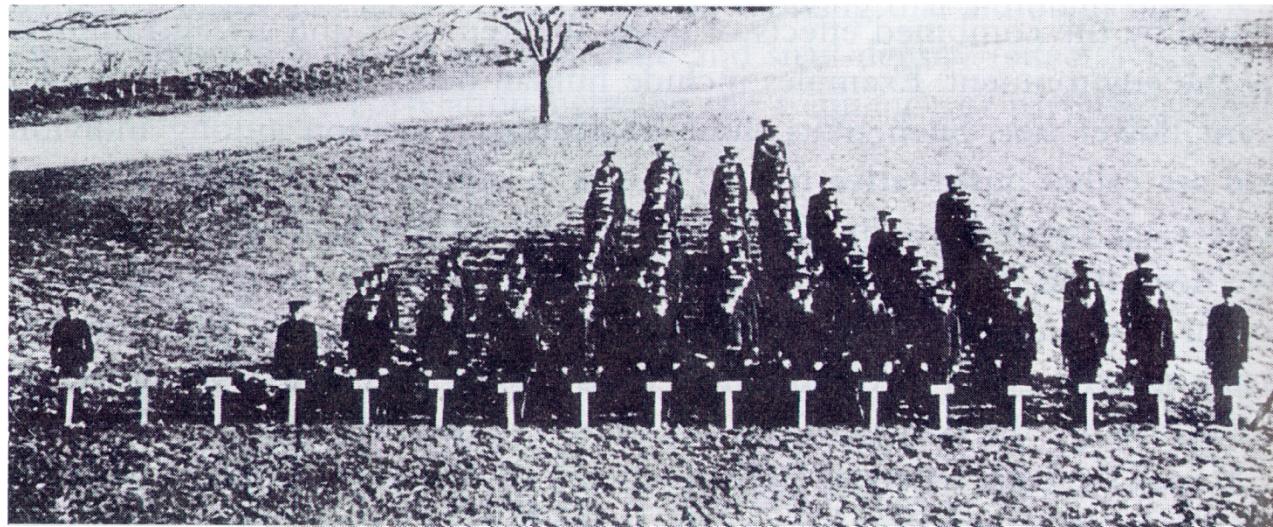


“Genética Quantitativa: Adaptação e processos evolutivos”

(a)



(b)

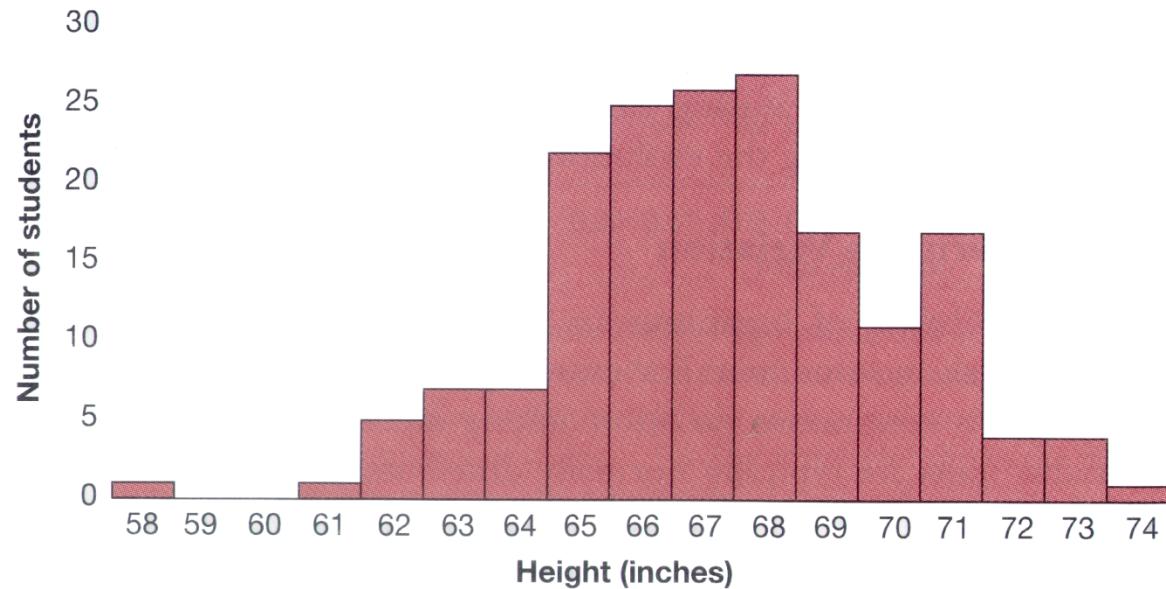
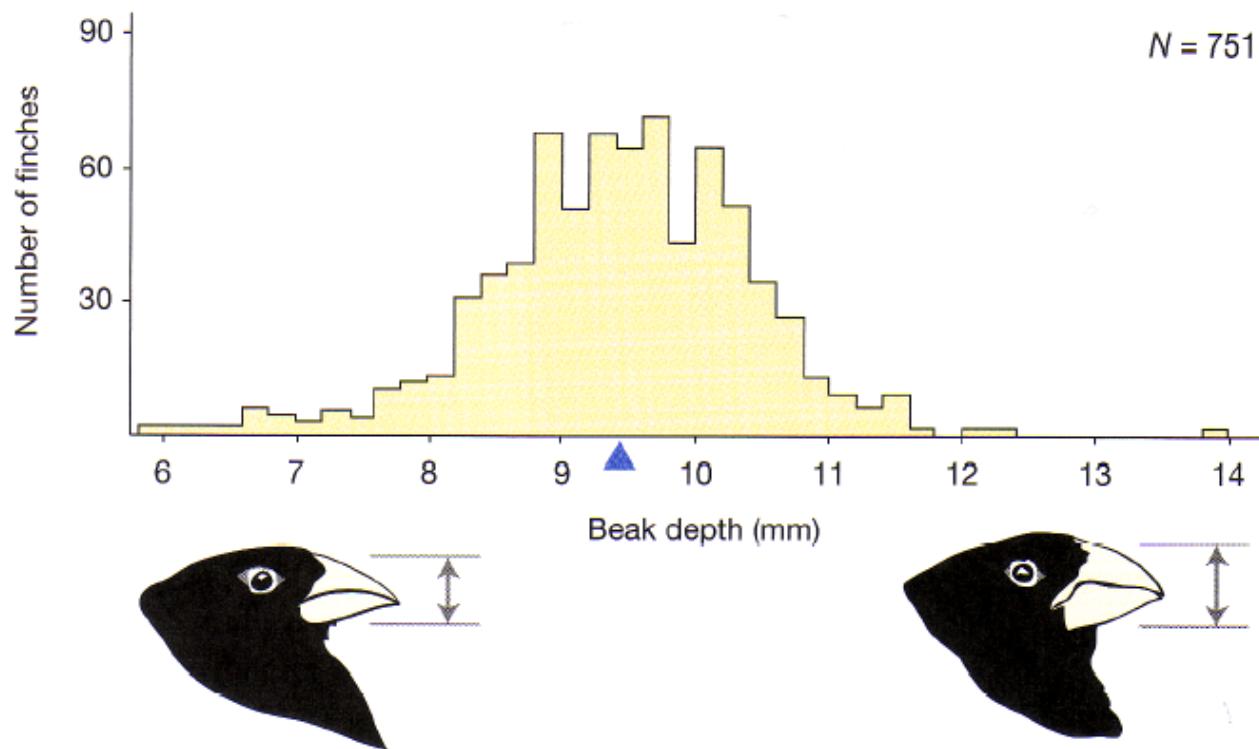


Figure 6.11 Normally distributed variation in a trait

(a) A photograph, published in the *Journal of Heredity* in 1914 by Albert Blakeslee, of a group of students at Connecticut Agricultural College sorted by height. The arrangement of the students forms a living histogram. (b) A graphical histogram representing the distribution of heights among the students shown in (a).

Figure 3.3 Beak depth in medium ground finches This histogram shows the distribution of beak depth in medium ground finches on Daphne Major in 1976, at the start of the Grant study. A few birds have shallow beaks, less than 8 mm deep. Most birds have medium beaks, 8 to 11 mm deep. A few birds have deep beaks, more than 11 mm deep. (N stands for sample size; the blue arrow along the x axis indicates the mean, or average.)

When variation in the characteristics of organisms is plotted, it is common to observe a bell-shaped curve like the one formed by this histogram. The extent, cause, and nature of variation in traits is a focus of Chapter 4 and Chapter 7.



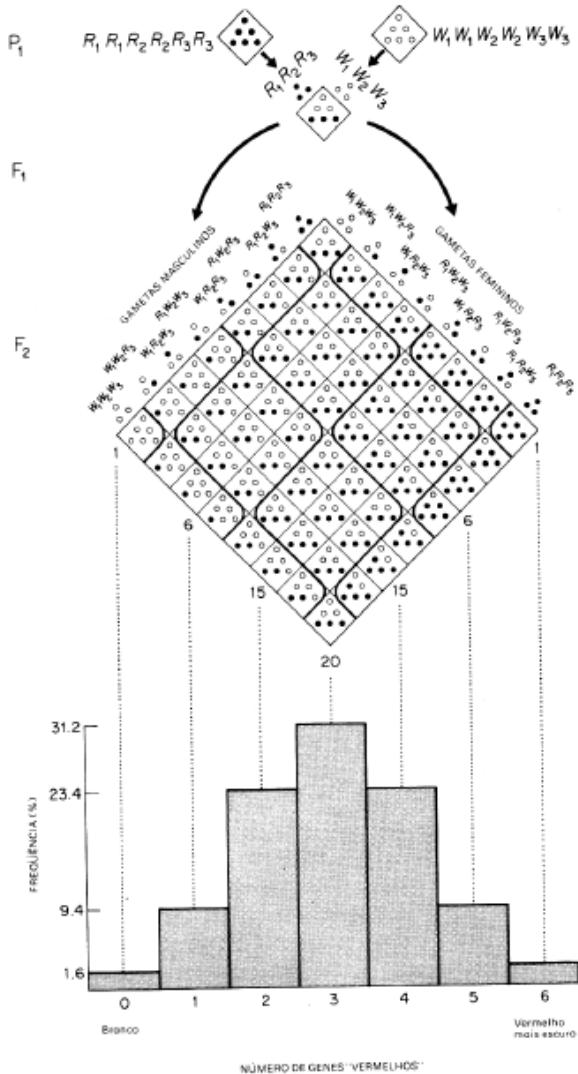
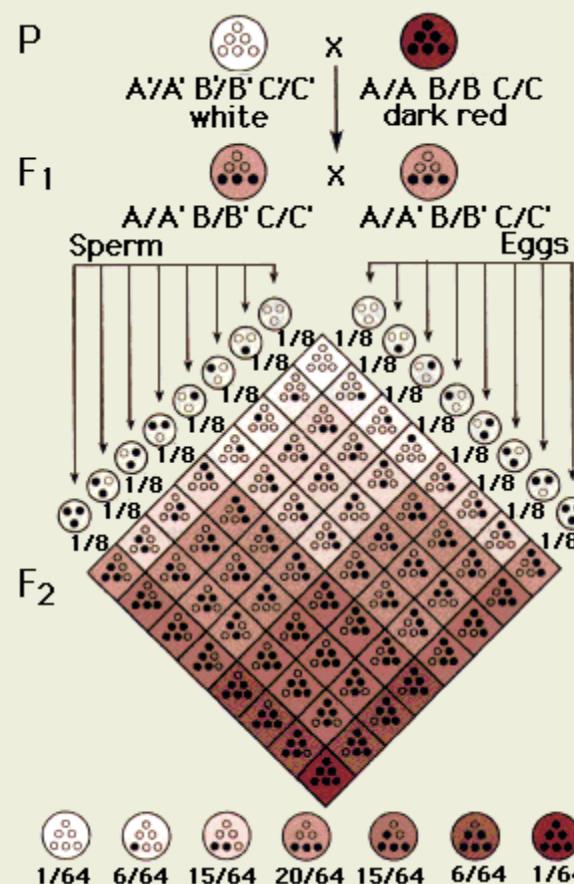


FIGURA 11.1 Herança da cor do grão no trigo. Cada ponto preto representa um gene "vermelho". (Redesenhado com pequena modificação e com permissão da Macmillan Publishing Co., Inc., de *Genetics*, por Monroe W. Strickberger.)



Nilsson-Ehle (1909)



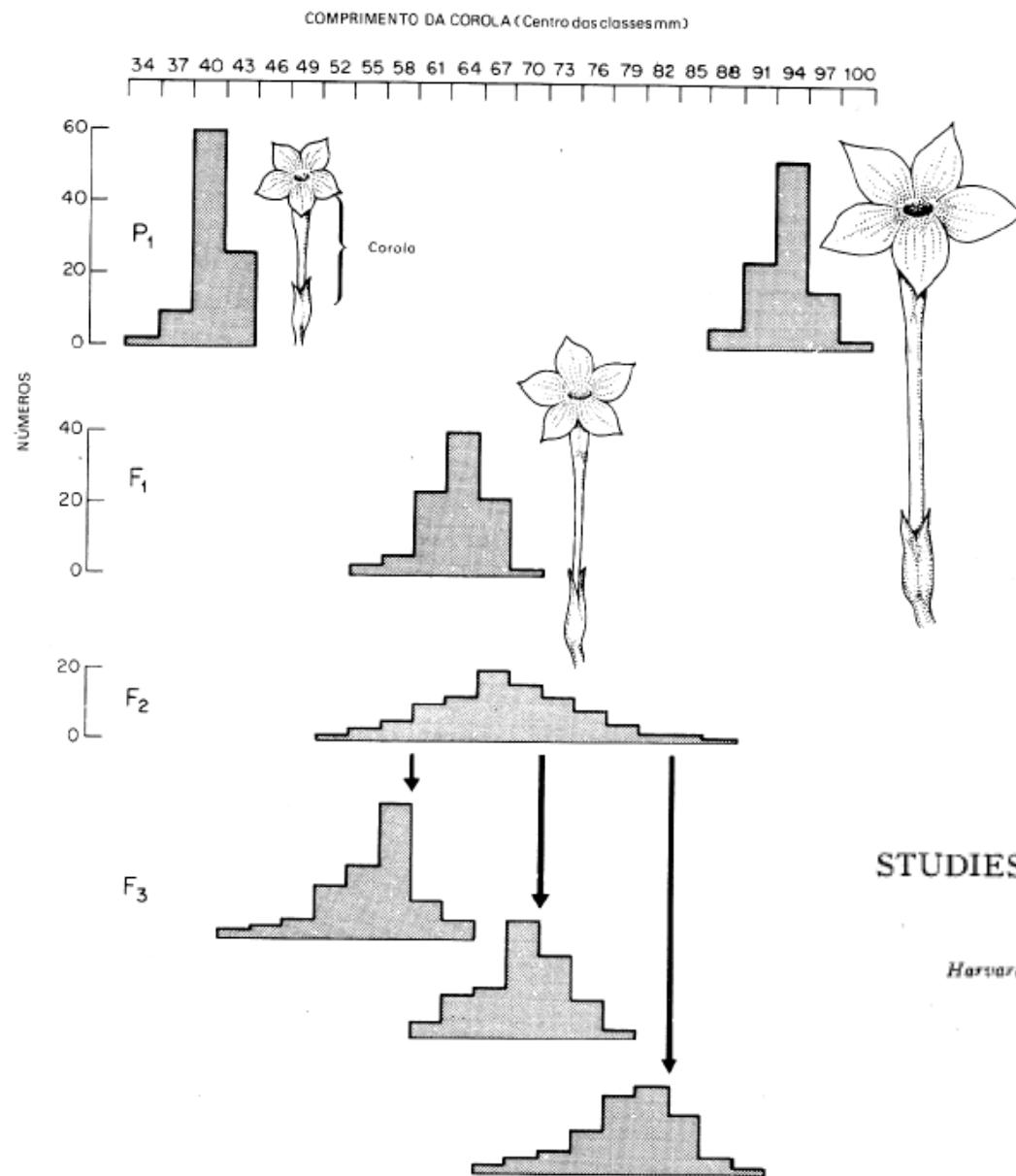
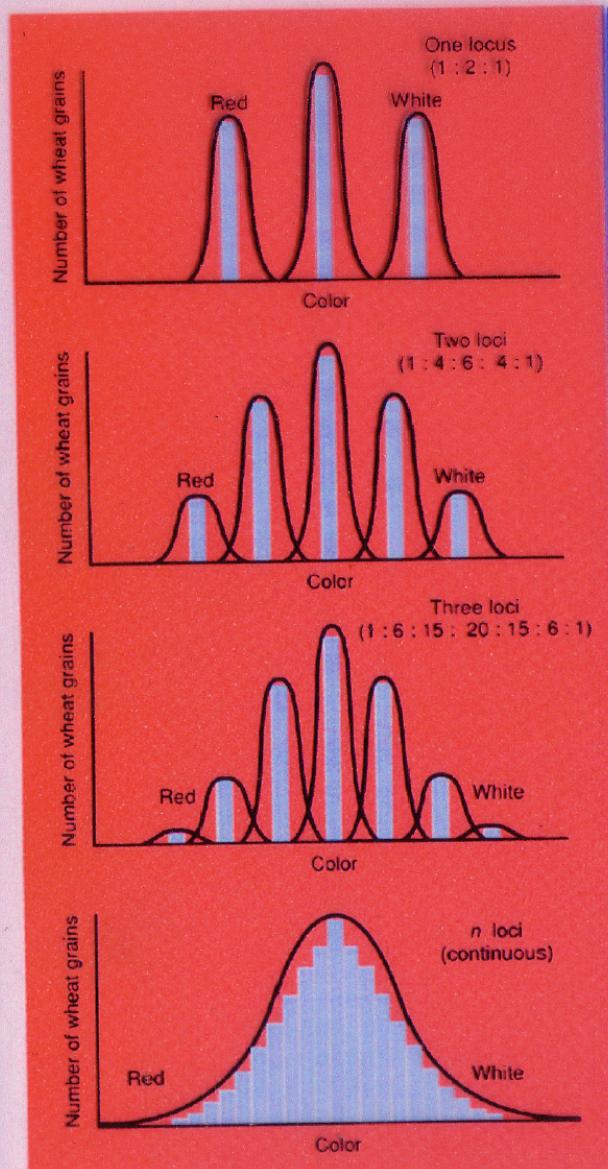


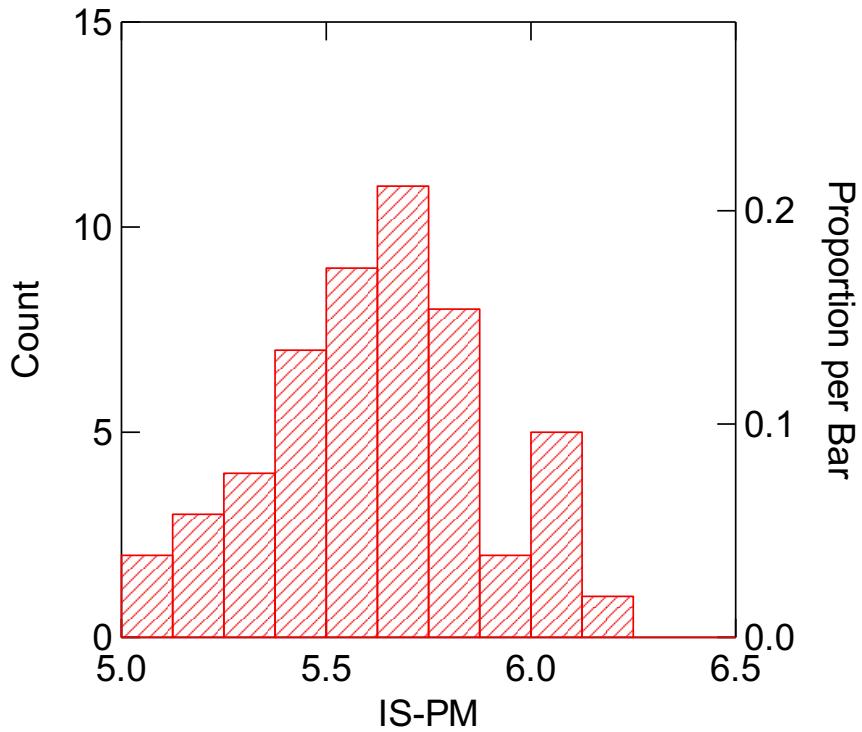
FIGURA 11.2 Experimentos de cruzamento referentes ao tamanho da flor em *Nicotiana longiflora*. (Dados de East, 1915. Redesenhado e ligeiramente modificado com permissão da Macmillan Publishing Co., Inc., de *Genetics*, por Monroe W. Strickberger.)

E. M. East (1916)

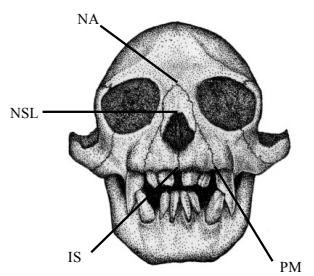
Figure 18.5 The change in shape of the distribution as increasing numbers of loci control grain color in wheat. If each locus is segregating two alleles with each affecting the same trait, eventually a continuous distribution will be generated in the F_2 generation.



Média fenotípica e variância de um caráter fenotípico



	IS-PM
N of cases	52
Mean	5.626
Variance	0.072



$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$$

$$s^2 = \frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2,$$

Valor fenotípico = valor genotípico + desvio ambiental

$$P = G + E$$

Organismos de reprodução sexuada passam adiante seus genes e não seus genótipos!

Logo, para deduzir as propriedades de uma população em conjunto com a sua estrutura familiar nós temos que lidar com a transmissão do “valor” dos pais para os filhos e isto não pode ser feito por meio dos valores genotípicos apenas, porque os pais passam adiante apenas seus genes e não seus genótipos intactos para a próxima geração, genótipos sendo criados novamente em cada geração pela fusão de gametas.

Precisamos de uma medida de “valor” que se refere aos genes e não aos genótipos

Efeito médio de um alelo em particular é o desvio médio em relação a média da população daqueles indivíduos que recebem este alelo de um dos pais com o outro alelo vindo ao acaso da população.

Colocando isto de outra forma:

Pegue um número de gametas todos carregando o alelo A_1 , una estes gametas com outros gametas vindo ao acaso da população; a média dos genótipos assim produzidos desvia da média populacional por uma quantidade que é o *efeito médio* do gene A_1 .

Qual a importância disto?

É um conceito que permite fazer a ligação entre a genética Mendeliana Clássica (na qual a segregação de genes individuais pode ser seguida através das gerações) com a genética quantitativa (aonde isto não é possível), permitindo atribuir ao indivíduo uma medida de valor que pode ser mensurada... Este “valor” é chamado de **valor de acasalamento**

NOTE-SE: Efeito médio de uma alelo é um conceito dual: individual e populacional (“tomado ao acaso”)

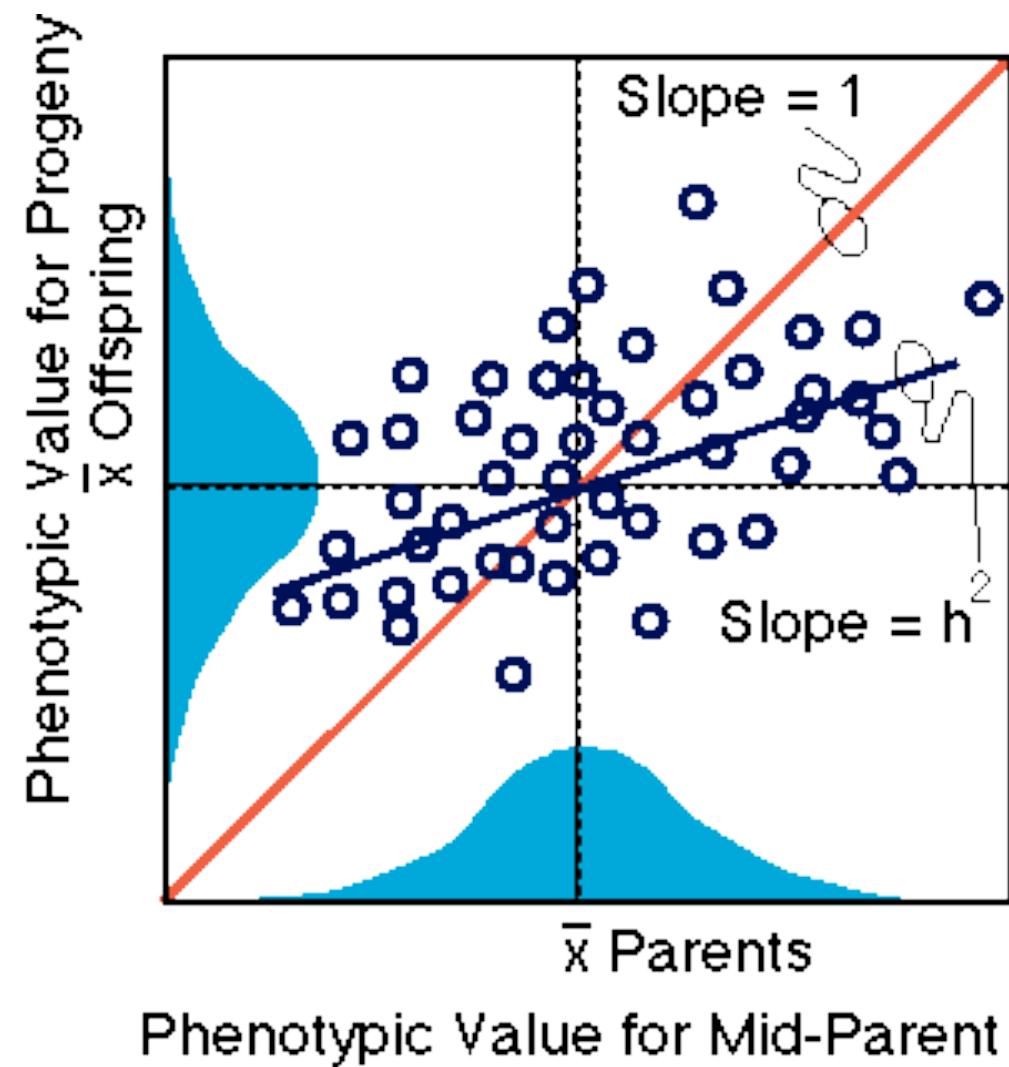
É o efeito médio dos genes dos pais que irá determinar o valor genotípico (fenotípico) médio da sua prole.

O valor de um indivíduo, avaliado pelo valor médio da sua prole é chamado **Valor de Acasalamento**. Portanto ao contrário do efeito médio de uma alelo (que em geral não é medido), o VA pode ser medido:

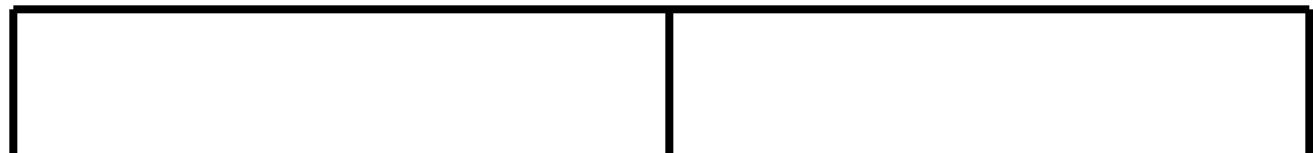
Valor de Acasalamento

“Se um indivíduo é acasulado ao acaso com um número de outros indivíduos tomados ao acaso da população, então seu valor de acasalamento é duas vezes o desvio médio da prole em relação á média da população”

O valor é multiplicado por 2 por que cada indivíduo parental contribui com metade dos genes da prole (outra metade vindo da população ao acaso)



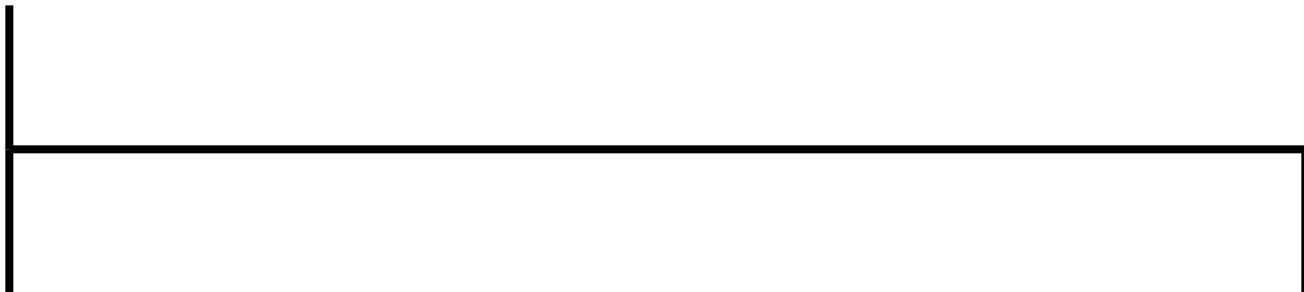
Efeito aditivo



O valor genotípico do heterozigoto é a média dos valores genotípicos dos homozigotos. Cada alelo “a” adiciona um valor constante, daí o nome.

Efeito de dominância

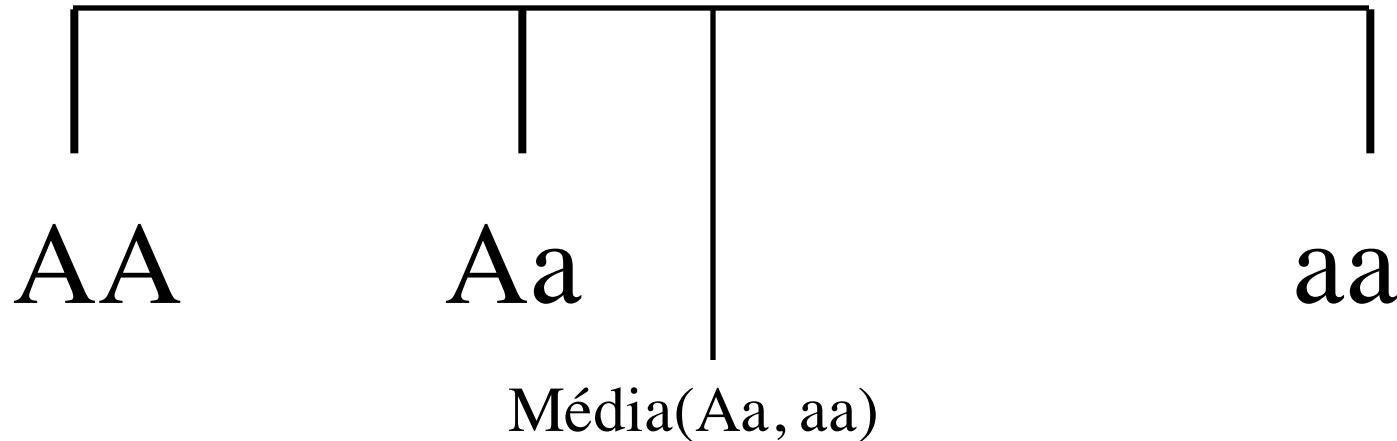
Aa



AA aa

O valor genotípico do heterozigoto é igual ao valor genotípico de um dos homozigotos. O alelo “A” domina sobre o alelo “a”, bastando haver um único “A” para a manifestação do fenótipo.

Efeito parcialmente dominante



O valor genotípico do heterozigoto está entre a média dos valores genotípicos dos homozigotos e o valor de um deles.

Variância fenotípica = Variância genética + Variância ambiental

$$V_p = V_g + V_e$$

$$V_g = V_a \text{ (aditiva)} + V_d \text{ (dominância)} + V_i \text{ (epistática)}$$

$$V_p = V_a + V_d + V_i + V_e$$

TABELA 11.1 Componentes da variação para quatro caracteres da *Drosophila melanogaster*. Cada componente é expresso como percentagem da variância fenotípica total (segundo Falconer, 1964).

	<i>Caráter</i>			
	1 cerdas	2 tórax	3 ovários	4 ovos
Variância fenotípica	100	100	100	100
Variância genética aditiva	52	43	30	18
Variância genética não aditiva	9	6	40	44
Variância ambiental	39	51	30	38

Caracteres:

1. número de cerdas nos 4.^º e 5.^º segmentos abdominais (Clayton, Morris e Robertson, 1957; Reeve e Robertson, 1954);
2. comprimento do tórax (Robertson, 1957);
3. tamanho dos ovários, isto é, número de ovariólos em ambos os ovários (Robertson, 1957);
4. número de ovos postos em 4 dias (4.^º ao 8.^º após a emergência) (Robertson, 1957).

Tipos de variância

Variância fenotípica: é a variância total da população. Inclui efeitos genéticos e não genéticos.

Variância genética: é a variância que é devida as diferenças genéticas existente entre os indivíduos da população. Exclui a variação causada por fatores ambientais.

Variância Aditiva = parte da variância genética que é devida aos efeitos individuais dos alelos

Variância de Dominância - surge da interação entre alelos de um locus (interação entre alelos de um mesmo locus)

Variância Epistática - surge da interação entre loci (interação entre alelos de diferentes loci)

Quadro 23.2 Proporção de variância aditiva (s_a^2) e variância de dominância (s_d^2) na covariância genética entre vários indivíduos relacionados

Parentes	Proporção estimada de	
	s_a^2	s_d^2
Cov (gêmeos idênticos)	1	1
Cov (pais-prole)	$\frac{1}{2}$	0
Cov (meio-irmãos)	$\frac{1}{4}$	0
Cov (irmãos)	$\frac{1}{2}$	$\frac{1}{4}$

$$COV(x, y) = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{n-1}$$

$$s^2 = \hat{\sigma}^2 = \frac{\sum (X_i - \bar{X})^2}{(n-1)}$$

$$r_{(x,y)} = \frac{COV(x,y)}{s_x s_y}$$

$$h^2 = Va/Vp = b = \text{COV}_{xy} / S_x^2$$

(VARIÂNCIA DOS PAIS X)

Onde x são as médias dos pais e y dos filhos

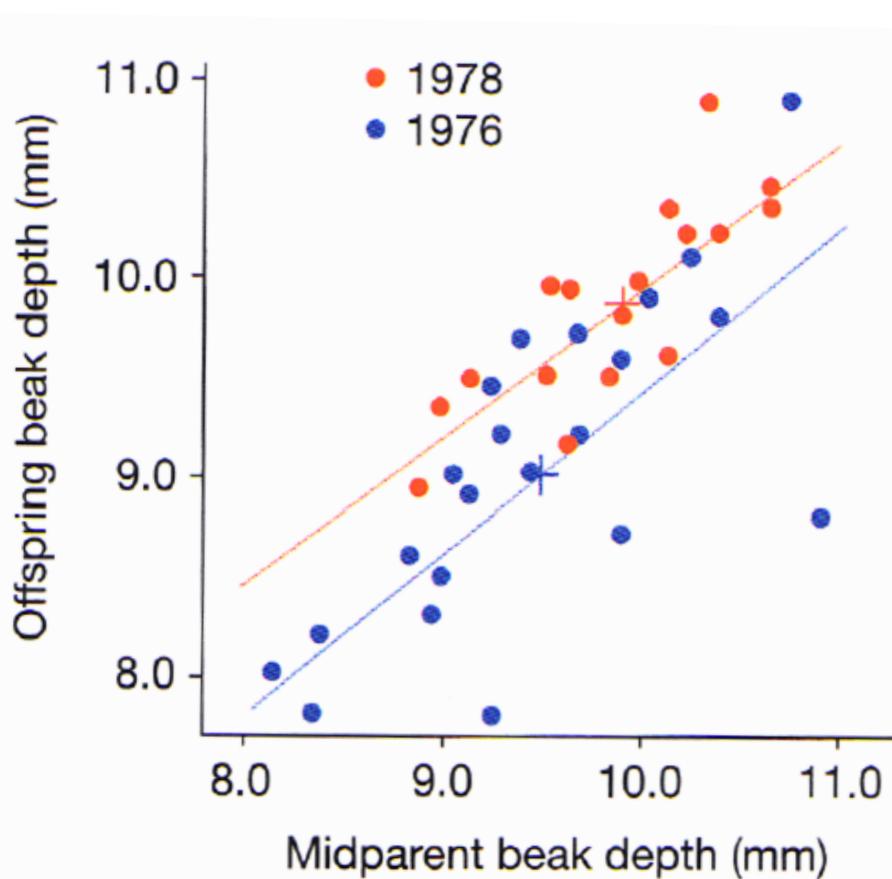
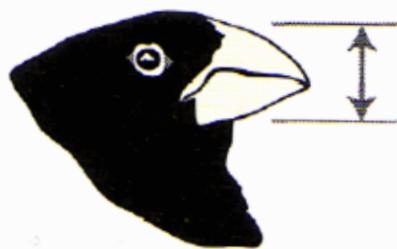


Figure 3.4 Heritability of beak depth in *Geospiza fortis* This graph shows the relationship between the beak depth of parents and their offspring. Midparent value is the average of the maternal and paternal measurements. Using this measurement is important because male *G. fortis* are bigger than females.

$$R = h^2 S$$

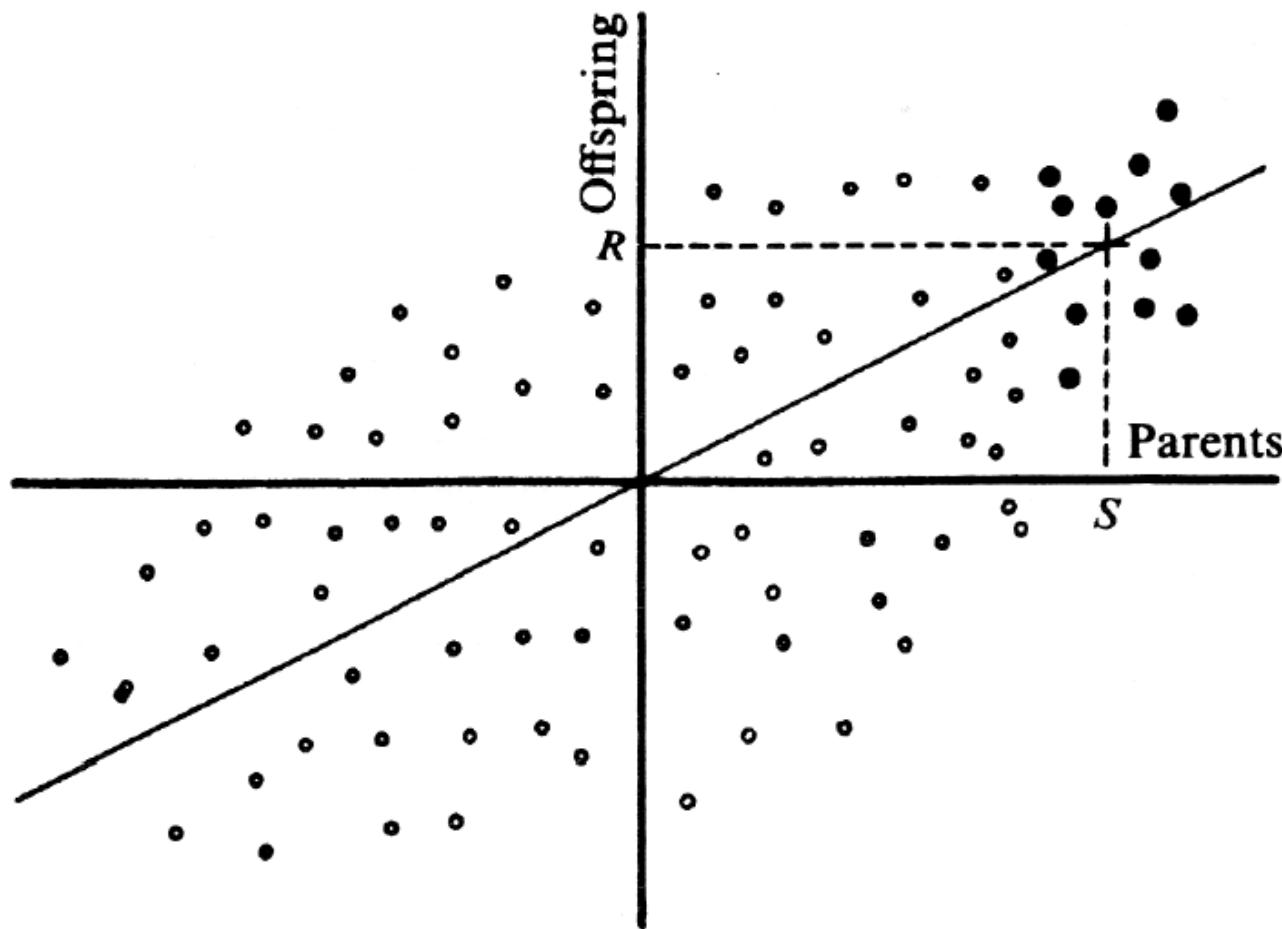
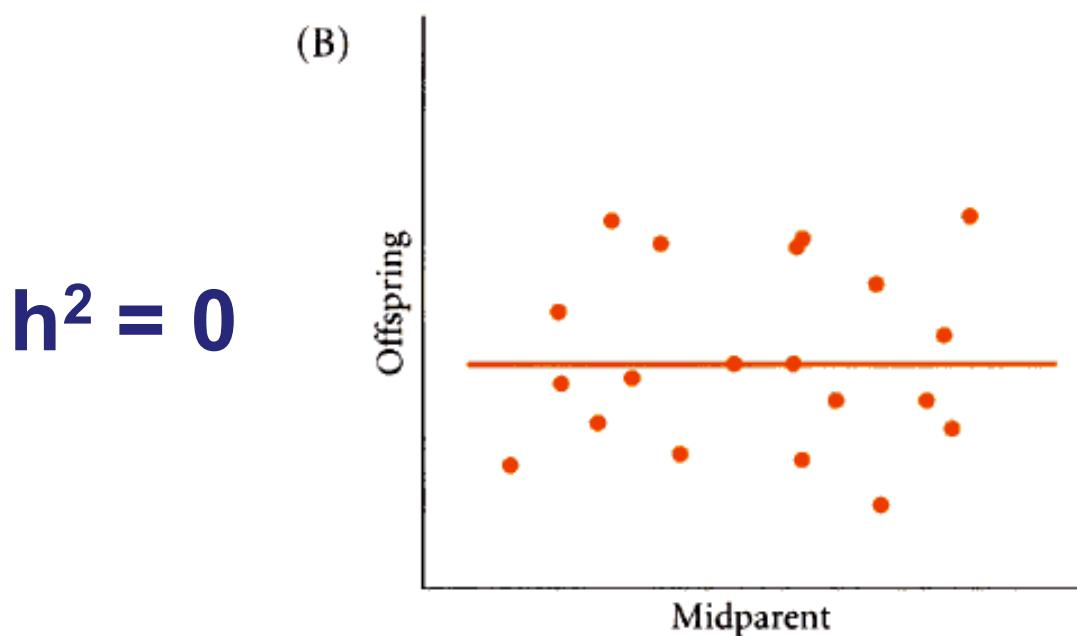
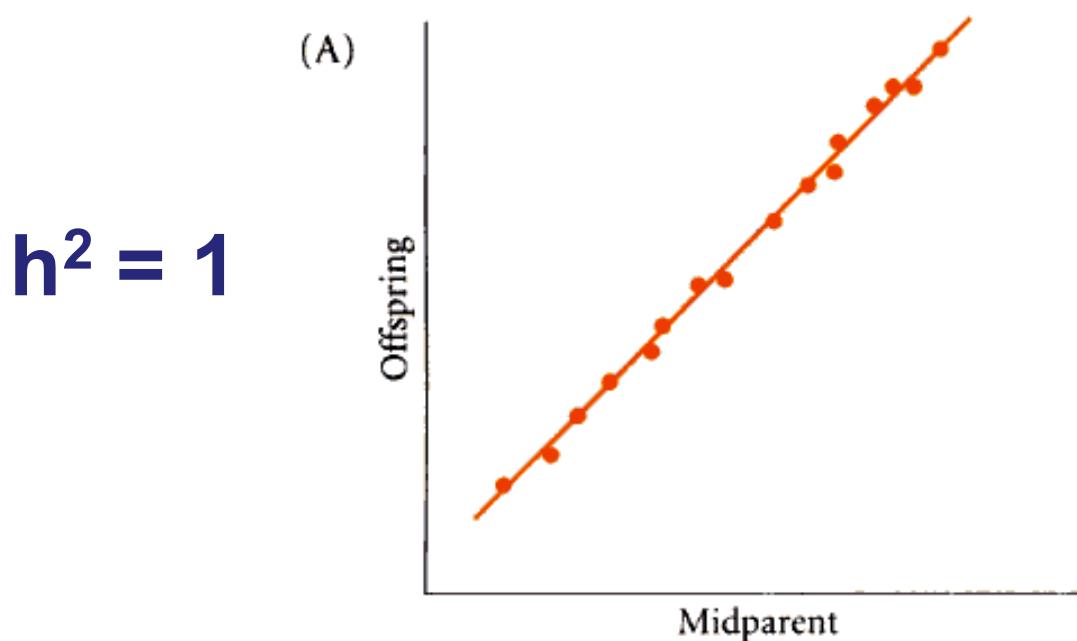
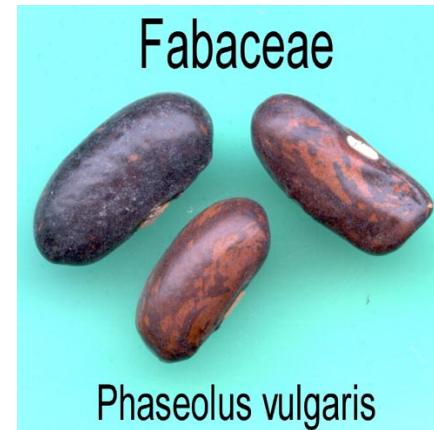


Fig. 11.1. Diagrammatic representation of the mean values of progeny plotted against the mid-parent values, to illustrate the response to selection, as explained in the text.



QTL = “Quantitative Trait Loci”

Une a Genética quantitativa com a biologia molecular na busca da identificação dos genes responsáveis pela variação fenotípica



Karl Sax – 1923 Genetics –

3 “marcadores fenotípicos”, 1 caráter continuo = peso do grão



Métodos para mapear QTL's

- Desenho experimental para estimar efeitos e posição de mapa de QTL's são extensões dos métodos utilizados para mapear "genes maiores" (= 3 x ou mais desvios padrões) ou "mendelianos" -----BASEADOS NO DESEQUILÍBRIO DE LIGAÇÃO
- Desequilíbrio entre alelos em locus ou loci "marcadores" e alelos no "gene(s) quantitativo" ligado a este marcadores.
- Precisamos então:
 - 1) Um mapa de ligação dos loci marcadores polimórficos que cubra o genoma totalmente
 - 2) Variação para o caráter contínuo dentro e entre populações ou linhagens

Escolha dos marcadores:

- 1) Altamente polimórficos (indivíduos diferentes provavelmente carregam alelos diferentes naquele locus)
- 2) Abundantes (assim cobrindo completamente o genoma)
- 3) Neutros (tanto sem efeito em relação ao caráter quantitativo quanto a aptidão)
- 4) co-dominantes (todos os genótipos podem ser identificados)

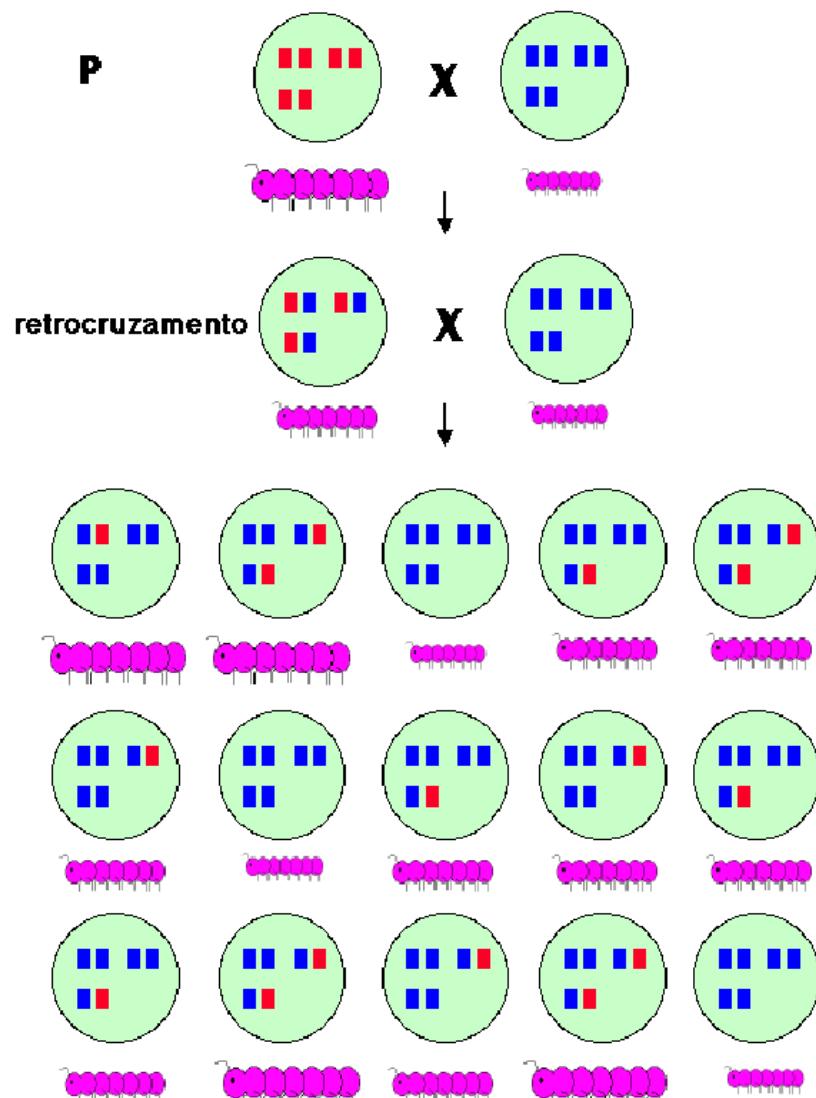
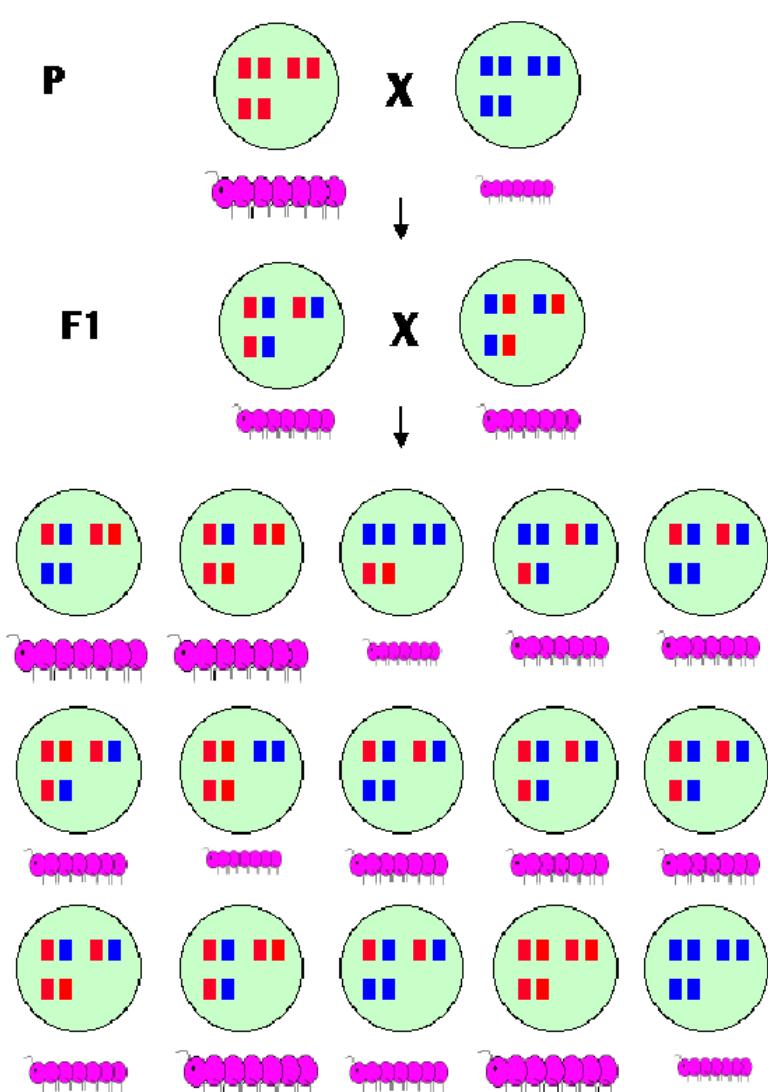
Até recentemente marcadores fenotípicos (como em Sax 1923) ou proteínas

----Mas não são exatamente “bons” marcadores

A partir da década de 80....

RFLP's, VNTR, Mini-satélites, micro-satélites, RAPD, etc

Cruzamento entre linhagens (populações) que diferem para o caráter em questão ou populações segregantes



Distância (arbitr.)	Média dos valores fenotípicos	
	para genótipo	para genótipo
0	24,7	24,7
10	24,7	24,7
20	24,0	25,4
30	22,1	27,3
40	19,3	30,1
50	19,3	30,1
60	22,1	27,3
70	24,0	25,4
80	24,7	24,7
90	24,7	24,7

Poucos ou muitos genes? Qual a intensidade dos efeitos???

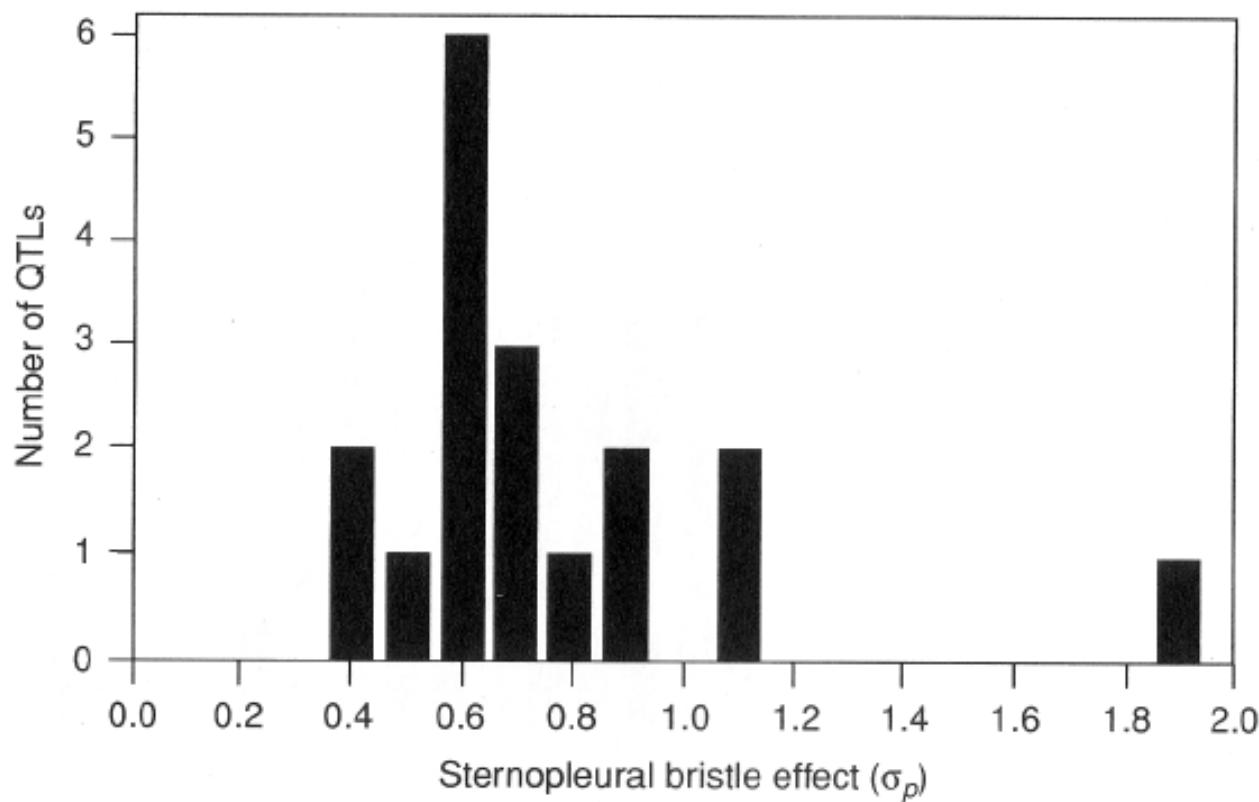


Fig. 21.3. Distribution of effects (a) of QTLs affecting sternopleural bristle number on Chromosome 3 of *Drosophila melanogaster*, in phenotypic standard deviation units. (Adapted from Shrimpton and Robertson, 1988b.)

São todos aditivos? Têm dominância? Completa ou parcial?

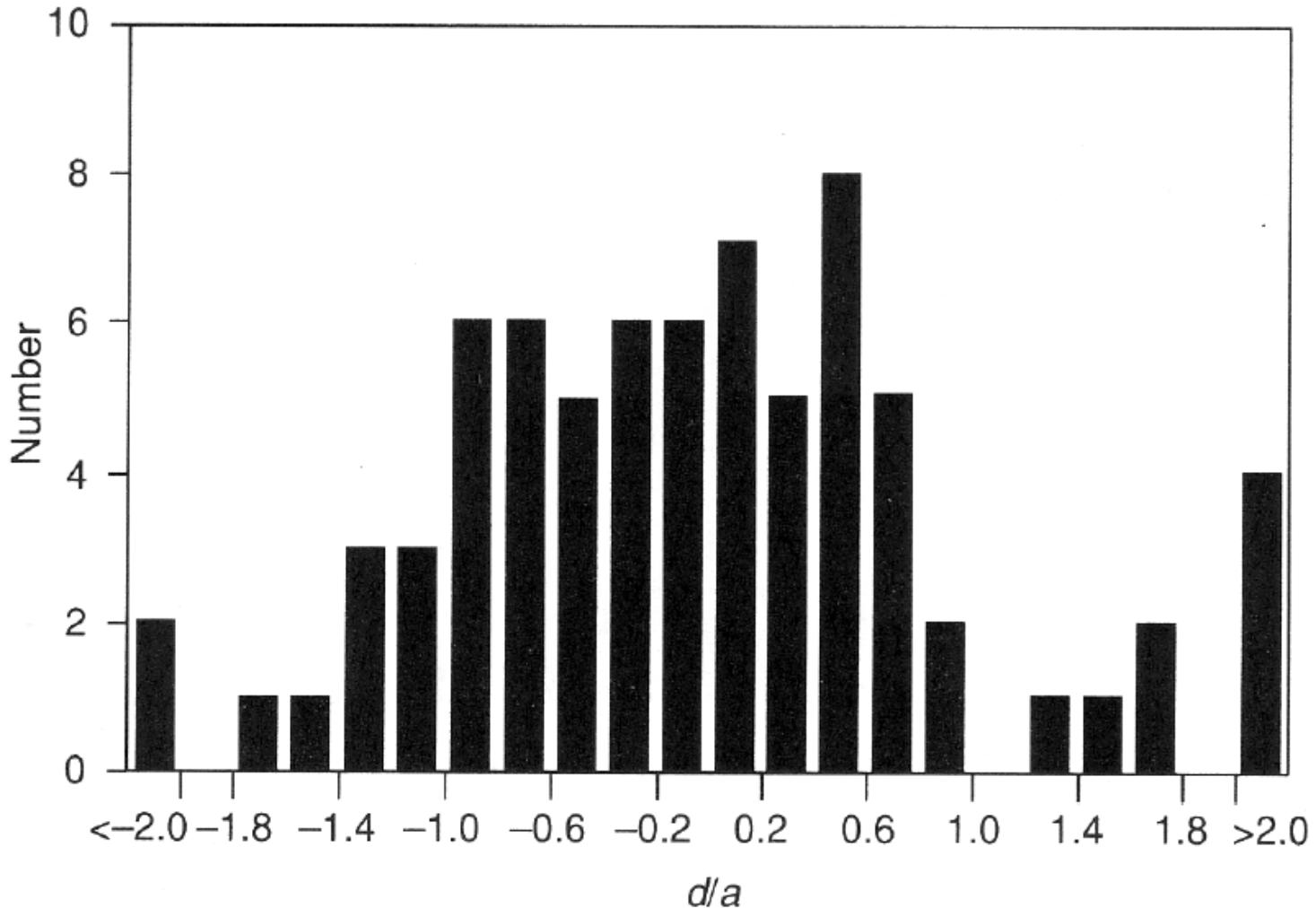
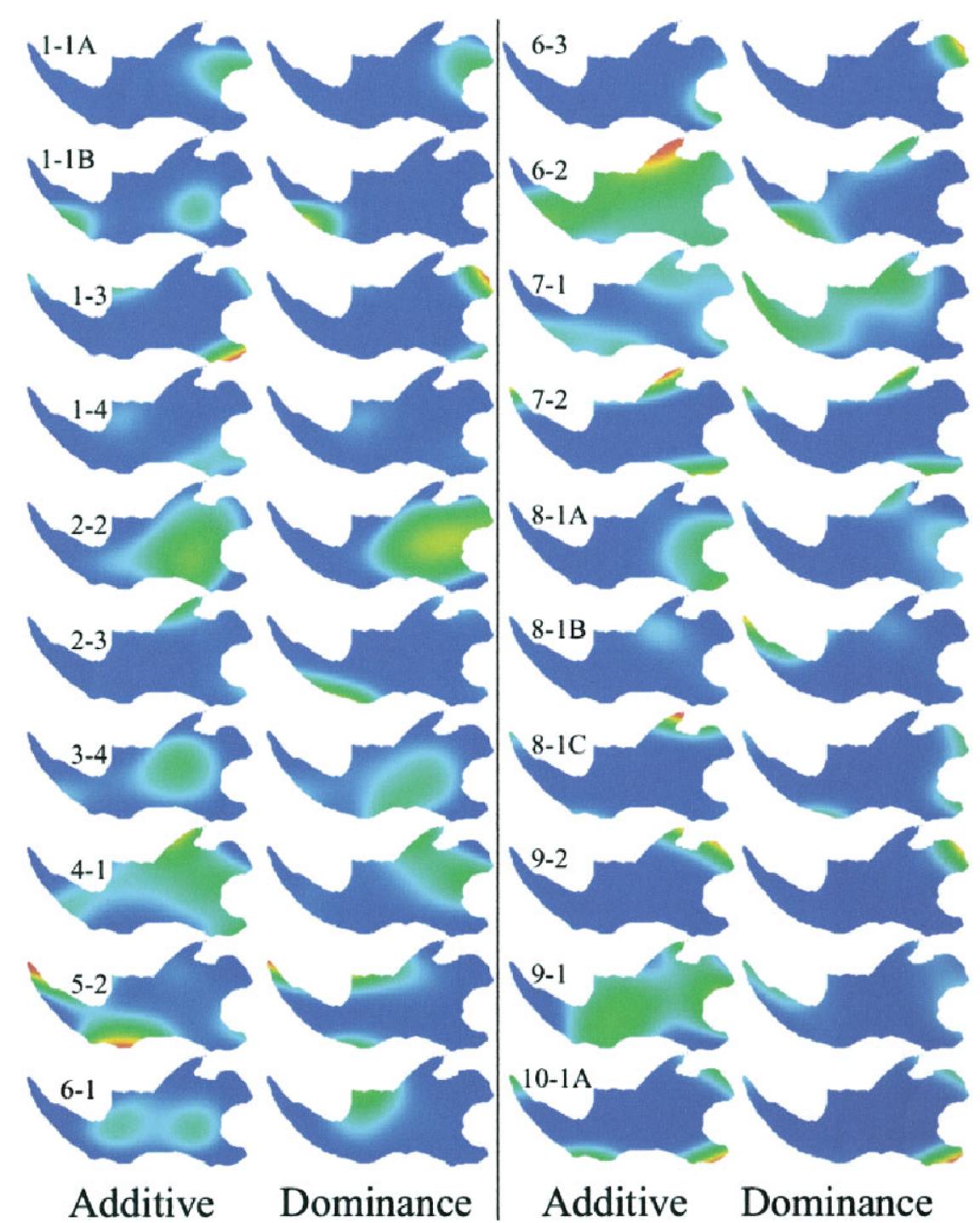
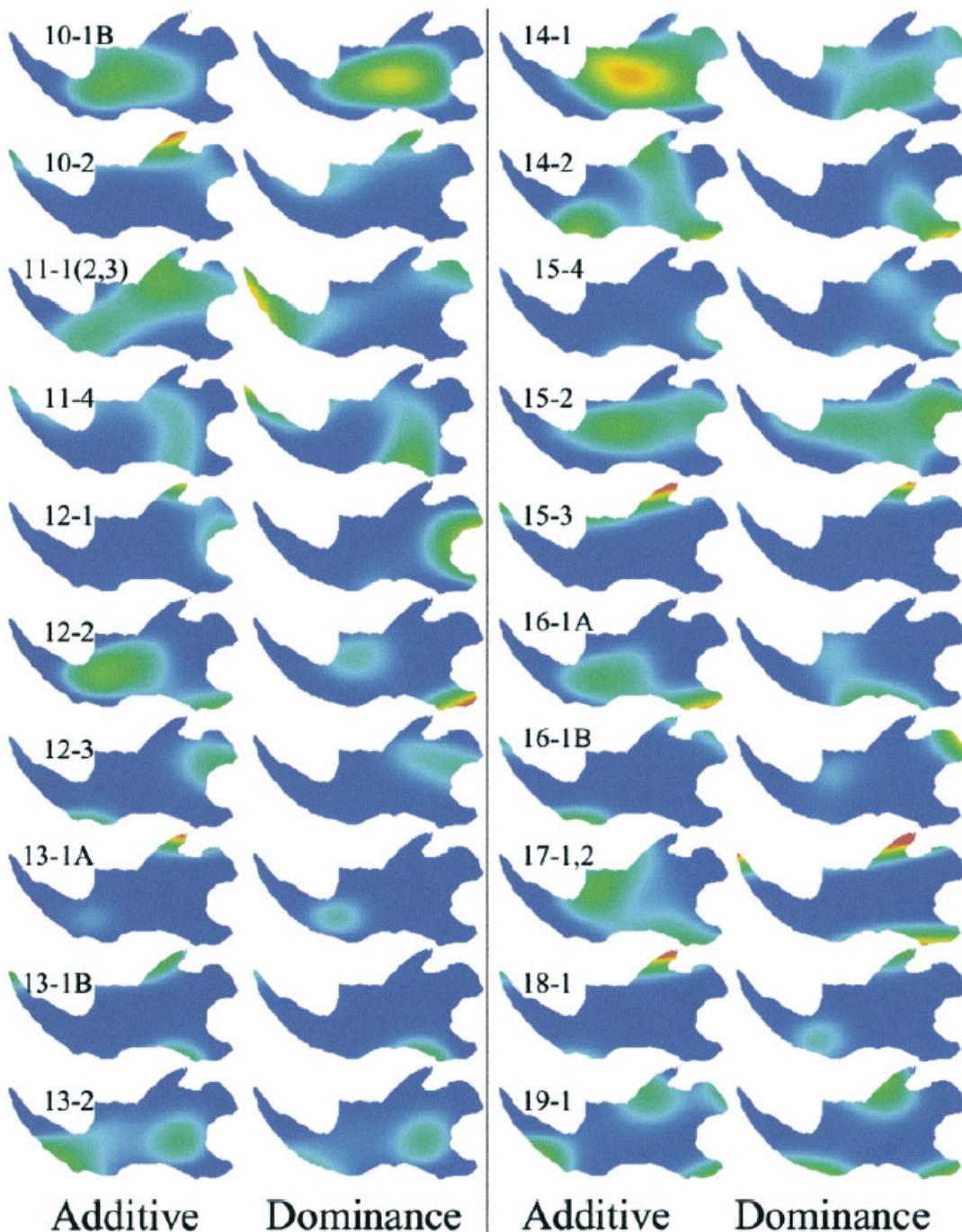


Fig. 21.4. Distribution of degrees of dominance (d/a) among 74 QTLs affecting vegetative traits of tomatoes, detected in the F_2 of a cross between the cultivated tomato and a wild species. (Adapted from deVicente and Tanksley, 1993.)



Têm pleiotropia?????



Pleiotropic Effects on Mandibular Morphology I. Developmental Morphological Integration and Differential Dominance

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ROBIN B. LINSEY, L. SUSAN PLETSCHER, AND JAMES M. CHEVERUD
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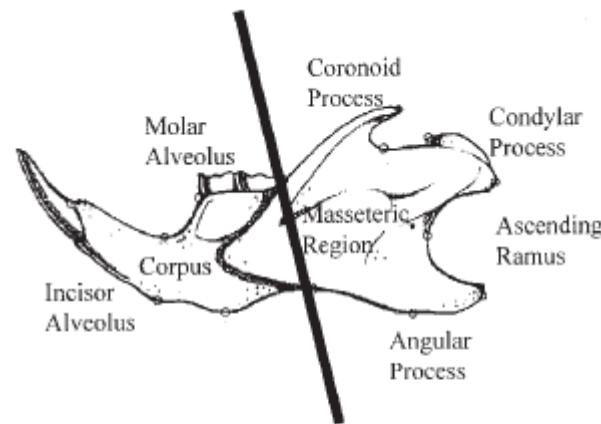


Fig. 1. Developmental regions of the mouse mandible (adapted from Atchley, '93). Each region derives from a different condensation of mesenchymal tissues and is affected by different associated tissues during development. See text for details.

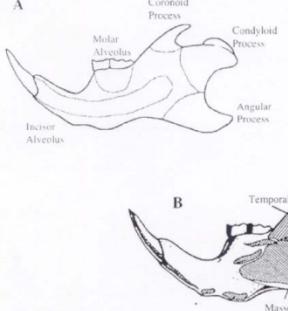


Fig. 7.3.—*A*, Mandibular condensations that coalesce to form the adult molar areas. (Modified from Atchley and Hall 1991.)

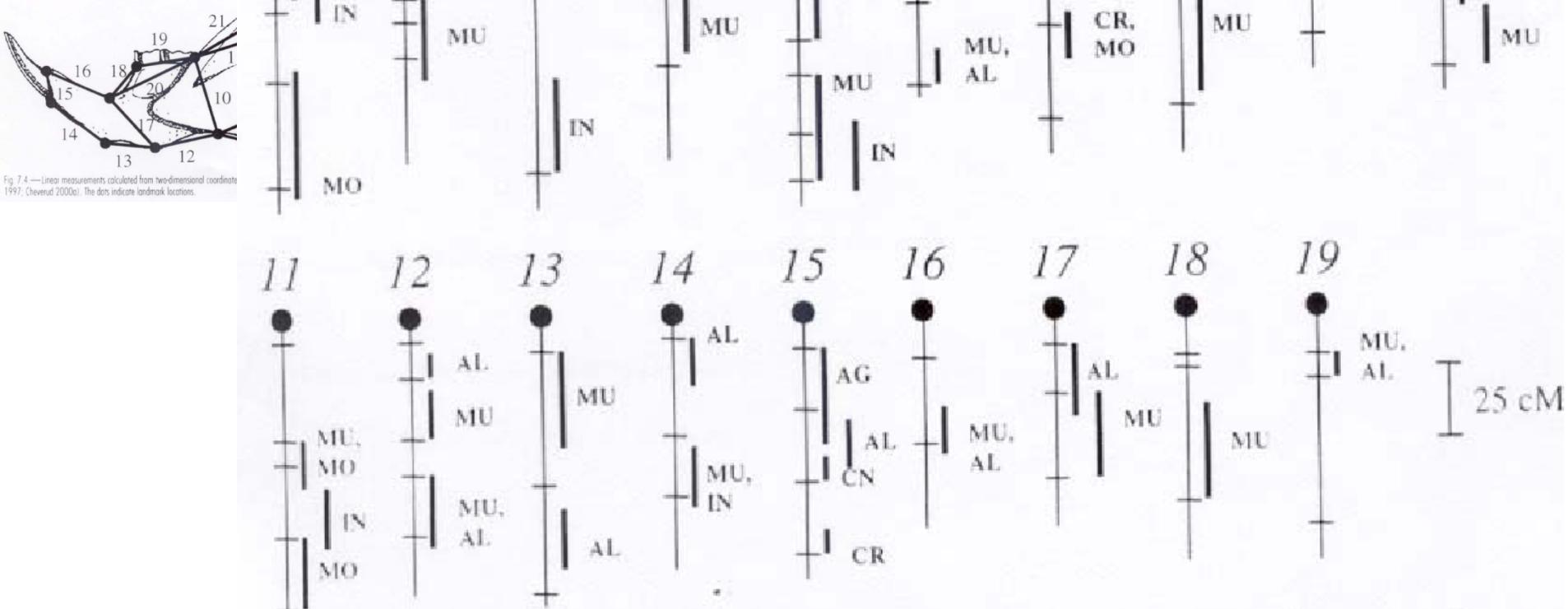


Fig. 7.5.—Genetic map positions of QTLs affecting mandibular morphology shown with 95% confidence regions. CR indicates that the QTL affects the coronoid process; CN, the condyloid process; AG, the angular process; MU, all the muscle attachment regions of the ascending ramus; IN, the incisor alveolus; MO, the molar alveolus; and AL, the total alveolar region. The dashed region on chromosome 2 indicates a region that was not sufficiently mapped in the first F_2 intercross to allow precise QTL placement. (After Cheverud 2000a.)

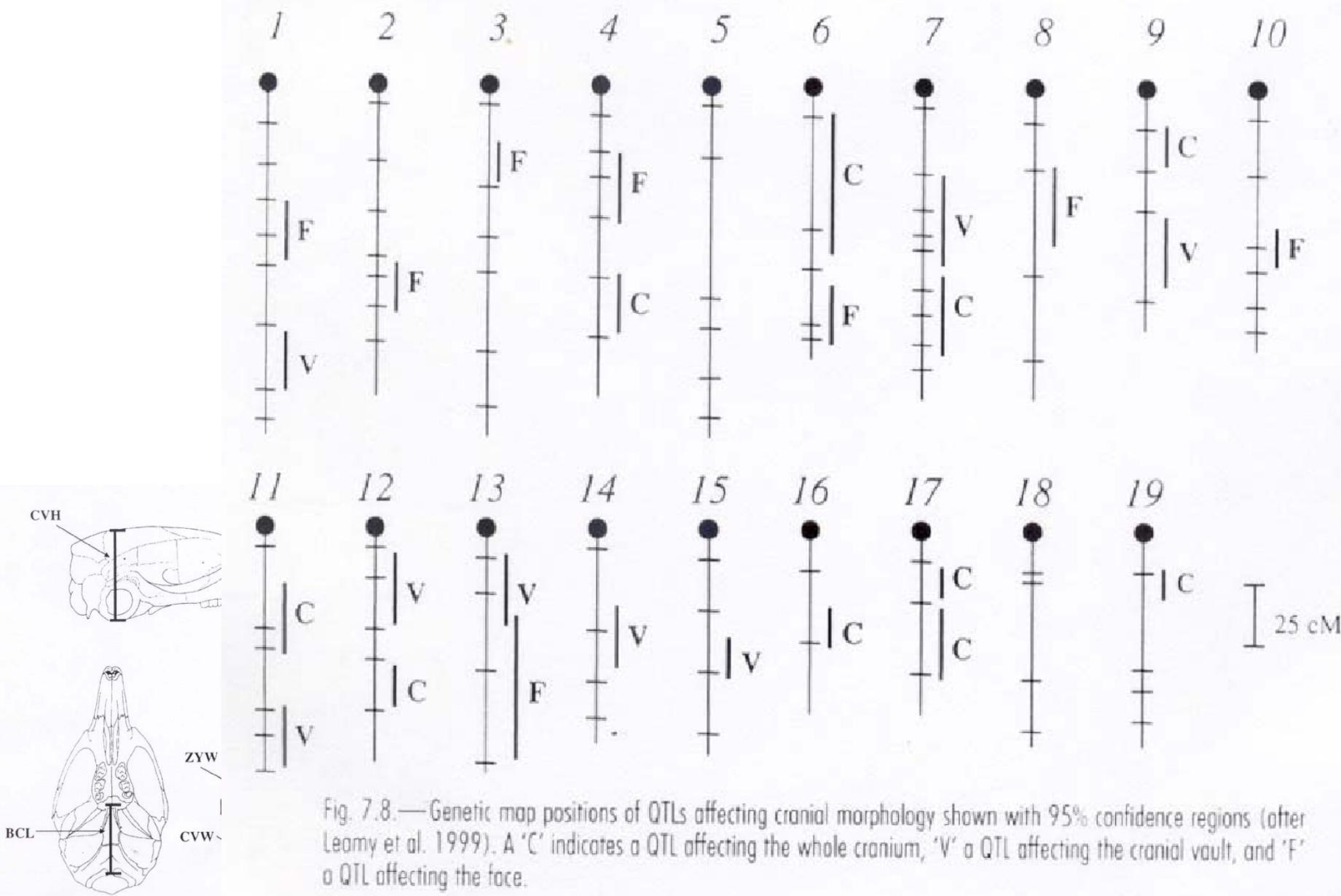


Fig. 7.7.—Measurements taken on the mouse skull (after Leamy et al. 1977). Measurements include cranial vault height (CVH), facial height (FCH), basicranial length (BCL), facial width (FCW), facial length (FL), cranial vault width (CVW), cranial vault length (CVL), zygomatic arch width (ZYW), and zygomatic arch length (ZYL).

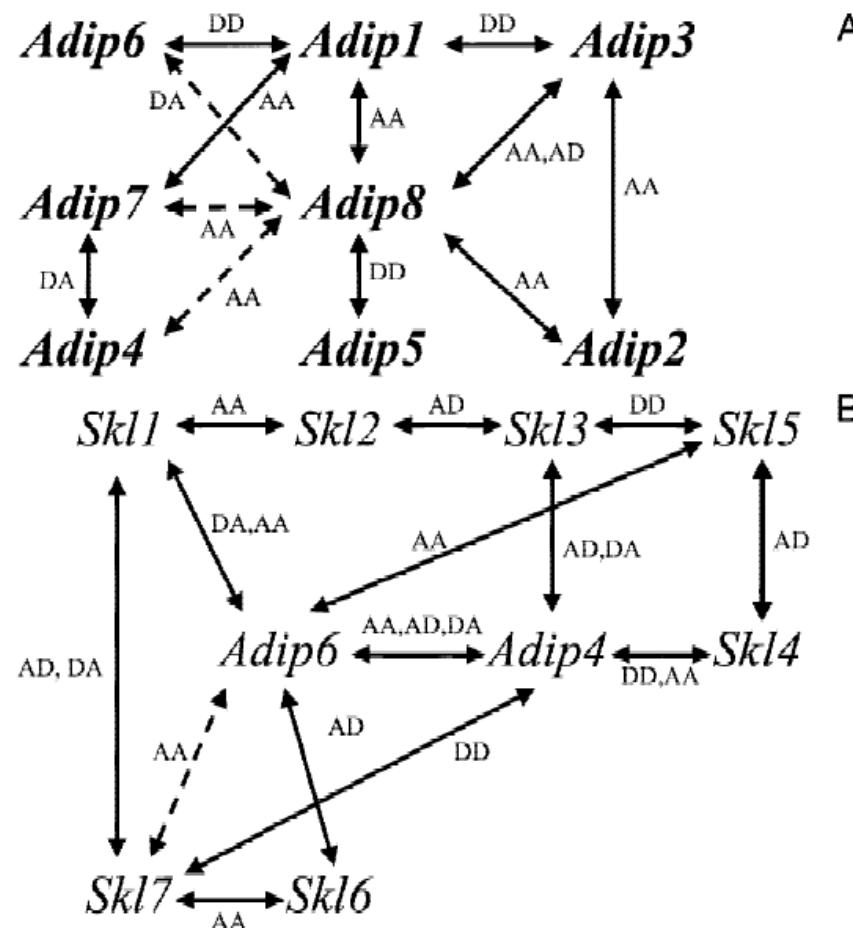


Fig. 2. Epistatic interaction patterns for adiposity (A) and tail length (B). Double-headed arrows indicate epistatic interactions labeled as additive by additive (AA), additive by dominance (AD), dominance by additive (DA), and/or dominance by dominance (DD) epistasis. Dashed lines indicate interactions significant at the 10% level, but not at the 5% level. *Adip4* and *Adip6* also have effects on tail length, and epistasis for these effects is portrayed in 2B.

Quantitative Trait Loci for Maternal Performance for Offspring Survival in Mice

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QTL for Matern

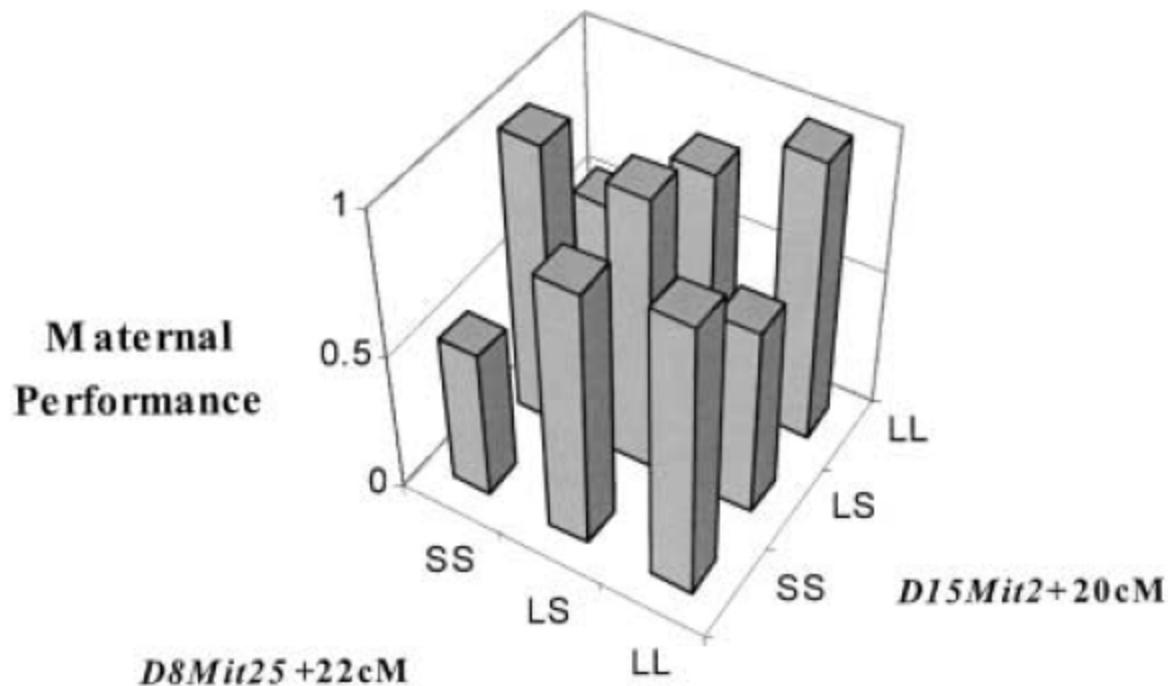


FIGURE 6.—Maternal performance genotypic values for the two-locus genotype at *D8Mit25 + 22 cM* and *D15Mit2 + 20 cM* illustrates additive-by-dominance interaction.

Arquitetura genética complexa

Vários genes, a maioria de pequeno efeito (menos ou até 1 desvio padrão)

Muita pleiotropia

Diversos graus de aditividade e dominância

Muita epistasia

Problemas e perspectivas

QTL's são uma subestimativa (2 QTL's próximos contam como 1; + x – cancelam o efeito)

Limite de resolução = 20 cM (ou 20.000.000 bp em humanos ou 40.000.000 em camundongos ou 10.000.000 em Drosophila)

QTL identificado é um segmento do cromossomo (pode conter vários loci) – mapeamento fino chega-se à 3 cM

Genes candidatos e clonagem de posição

Módulos

Mapa Genotípico-Fenotípico

ADAPTATION AND EVOLVABILITY

971

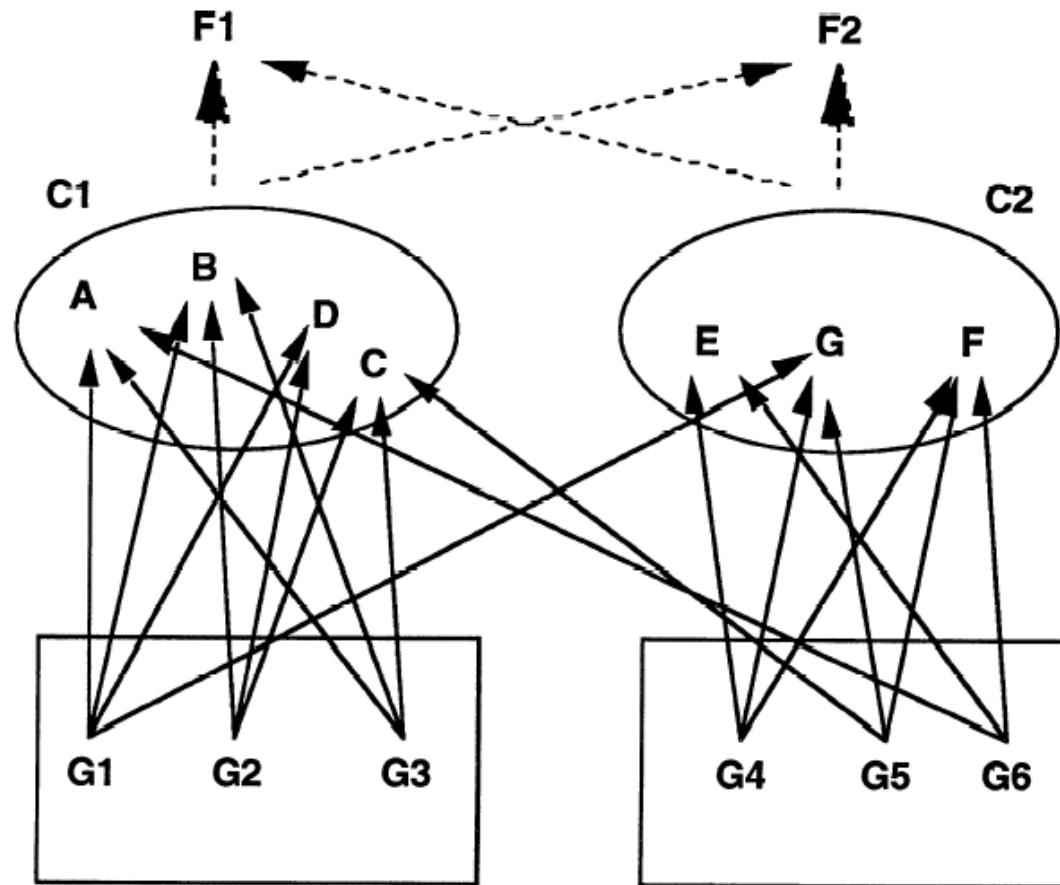


FIG. 1. Example of a modular representation of the character complexes $C_1 = \{A, B, C, D\}$ and $C_2 = \{E, F, G\}$ which serve to functions F_1 and F_2 . Each character complex has a primary function, F_1 for C_1 and F_2 for C_2 . Only weak influences exist of C_1 on F_2 and vice versa. The genetic representation is modular because the pleiotropic effects of the genes $M_1 = \{G_1, G_2, G_3\}$ have primarily pleiotropic effects on the characters in C_1 and $M_2 = \{G_4, G_5, G_6\}$ on the characters in complex C_2 . There are more pleiotropic effects on the characters within each complex than between them.

Seleção Natural & Adaptação

SE

- 1) Indivíduos dentro das espécies são variáveis
- 2) Uma parte desta variação é passada para a prole
- 3) A cada geração nascem mais filhotes do que podem sobreviver
- 4) Sobrevivência e reprodução não são ao acaso: Indivíduos que sobrevivem e depois se reproduzem (ou que se reproduzem mais do que os outros) são aqueles com as variações mais favoráveis naquele contexto ambiental. Estes são naturalmente selecionados. Em outras palavras, um relacionamento consistente entre uma certa característica e a capacidade de acasalamento, fertilidade, fecundidade e/ou sobrevivência (diferenças na aptidão darwiniana ou fitness).

ENTÃO

- A) A distribuição de frequências vai diferir entre gerações
- B) Esta distribuição pode ser prevista

Qual a diferença para deriva genética?



Rosemary Grant

Figure 3.2 The Galápagos islands Fourteen species of finch inhabit the Galapágos, and one finch resides on Cocos. On this map, Isla Daphne Major is a tiny speck between Santa Cruz and Santiago.



Peter Grant



The blue leg bands on this male medium ground finch mark it for study. Researchers have observed natural selection in action by studying this species on the Galápagos islands. (Peter R. Grant, Princeton University)

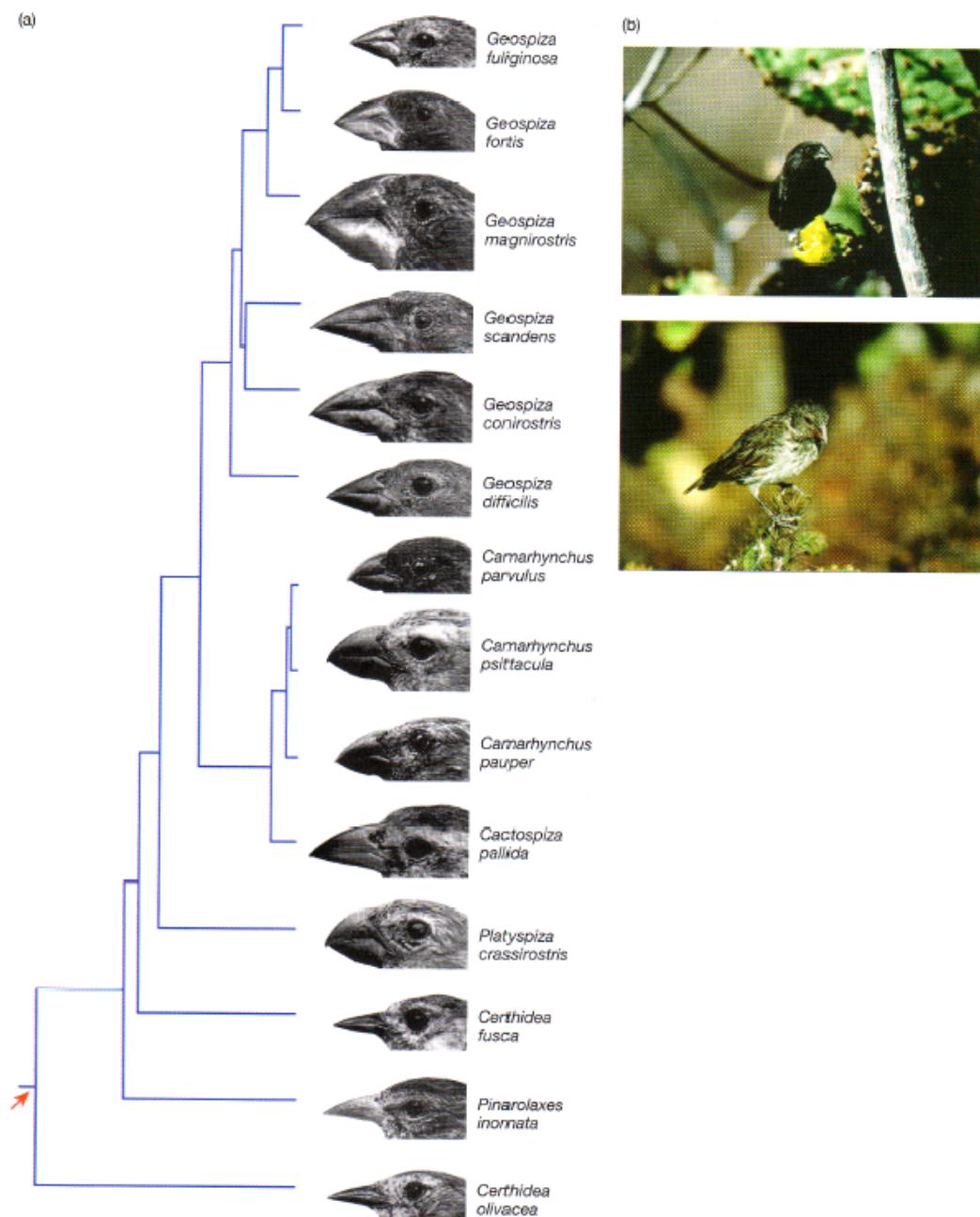
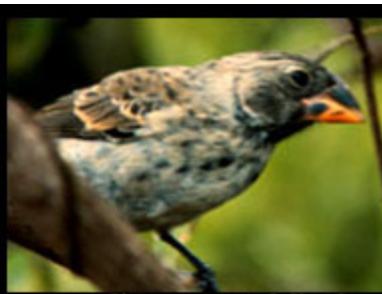


Figure 3.1 The Galápagos finches, and the medium ground finch *Geospiza fortis* (a) This phylogeny was estimated from similarities and differences in DNA sequences by Kenneth Petren and colleagues (1999), and shows the evolutionary relationships among 14 species of Darwin's finches. The photos show the extensive variation in beak size and shape among species. From Petren et al. (1999). (b) A male (top) and female (bottom) medium ground finch. (Photos: Peter R. Grant, Princeton University)



small ground finch



medium ground finch



large ground finch



sharp-beaked ground finch



cactus finch



large cactus finch



small tree finch



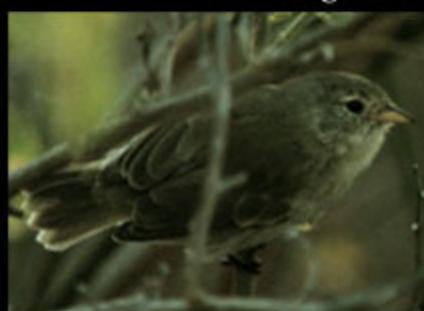
large tree finch?



vegetarian finch

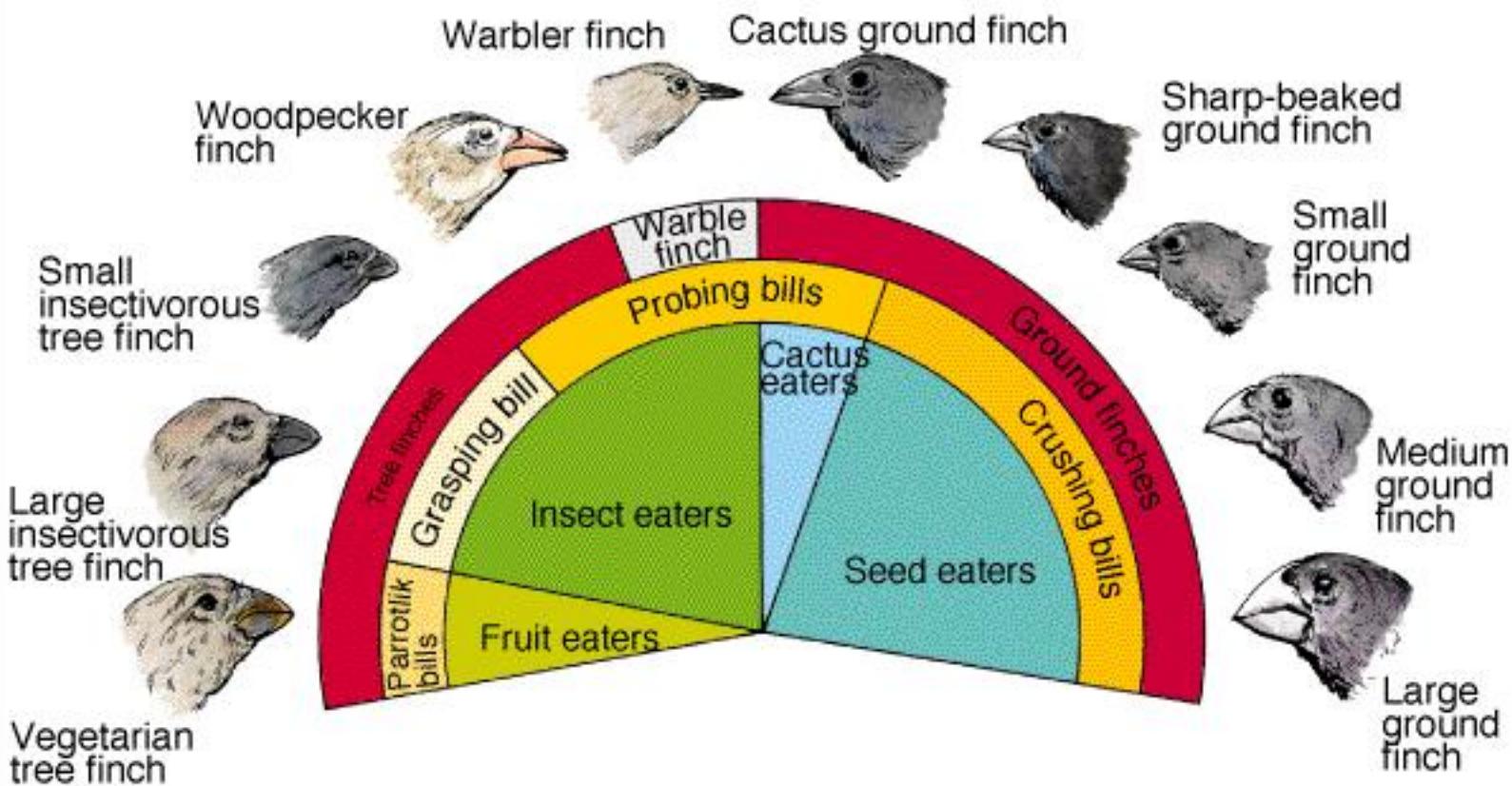


woodpecker finch



warbler finch

Darwin's Finches



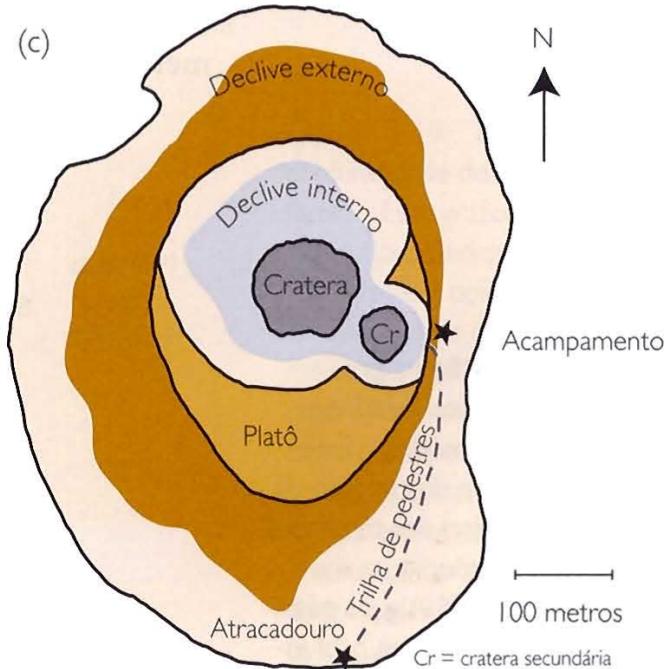
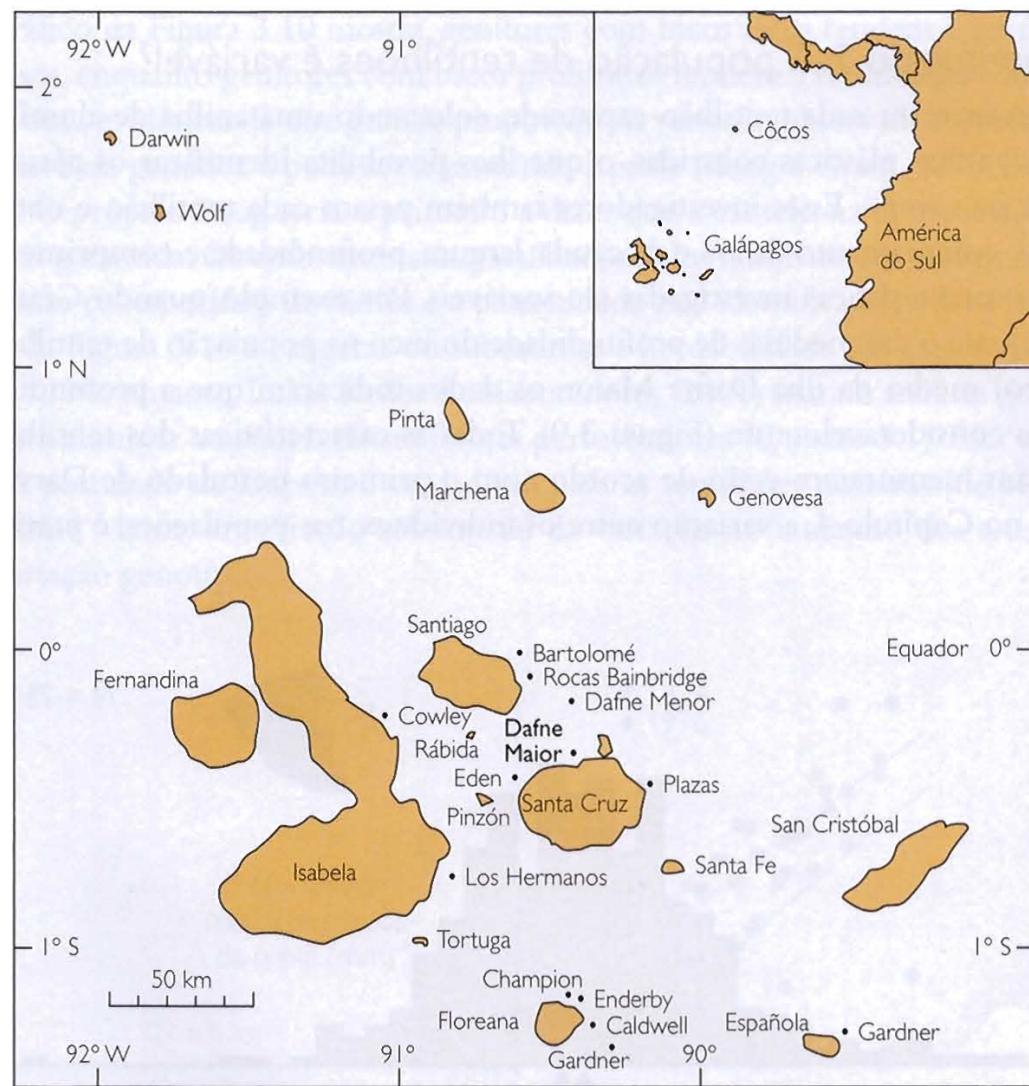


Figura 3.8 O Arquipélago das Galápagos e a Ilha Dafne Maior. (a) Ilha dos Côcos e Arquipélago das Galápagos, lar dos tentilhões de Darwin. A ilha Dafne Maior é uma ilha diminuta, situada entre Santa Cruz e Santiago. (b) Ilha Dafne Maior, vista de um barco que dela se aproxima. Visível como uma tênue linha branca ascendente, da esquerda para a direita, encontra-se a trilha de pedestres que se estende do atracadouro (no nível do mar) ao acampamento (na borda da cratera). (c) Mapa da ilha Dafne Maior. Observe o tamanho diminuto da ilha. Gentilmente cedidos por Boag e Grant (1984a).



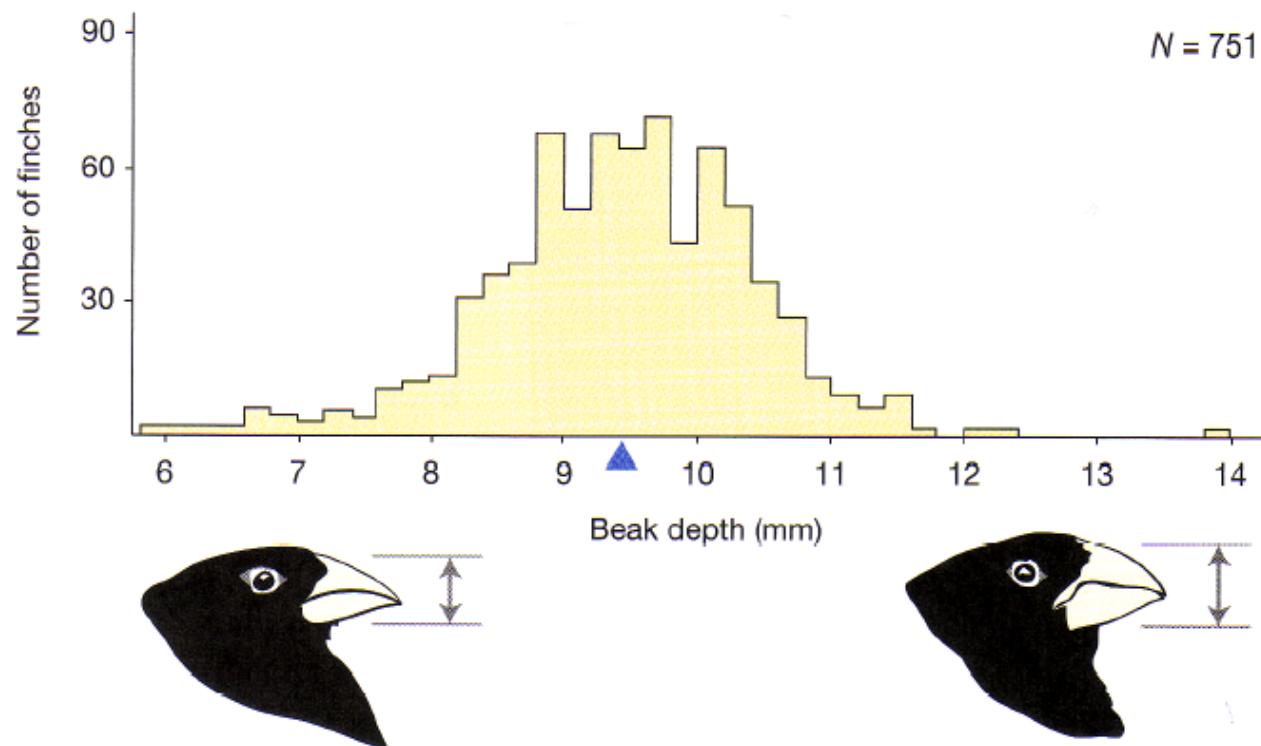




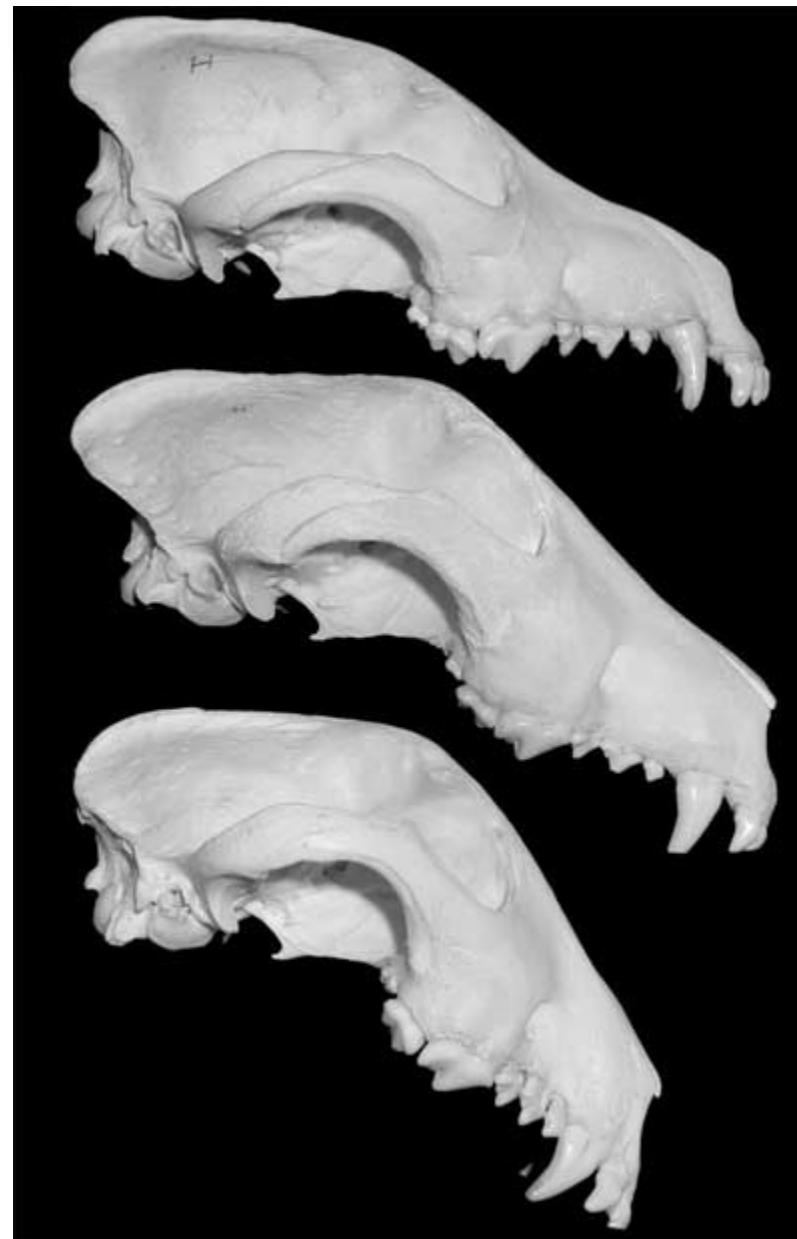
1) Indivíduos dentro das espécies são variáveis

Figure 3.3 Beak depth in medium ground finches This histogram shows the distribution of beak depth in medium ground finches on Daphne Major in 1976, at the start of the Grant study. A few birds have shallow beaks, less than 8 mm deep. Most birds have medium beaks, 8 to 11 mm deep. A few birds have deep beaks, more than 11 mm deep. (N stands for sample size; the blue arrow along the x axis indicates the mean, or average.)

When variation in the characteristics of organisms is plotted, it is common to observe a bell-shaped curve like the one formed by this histogram. The extent, cause, and nature of variation in traits is a focus of Chapter 4 and Chapter 7.

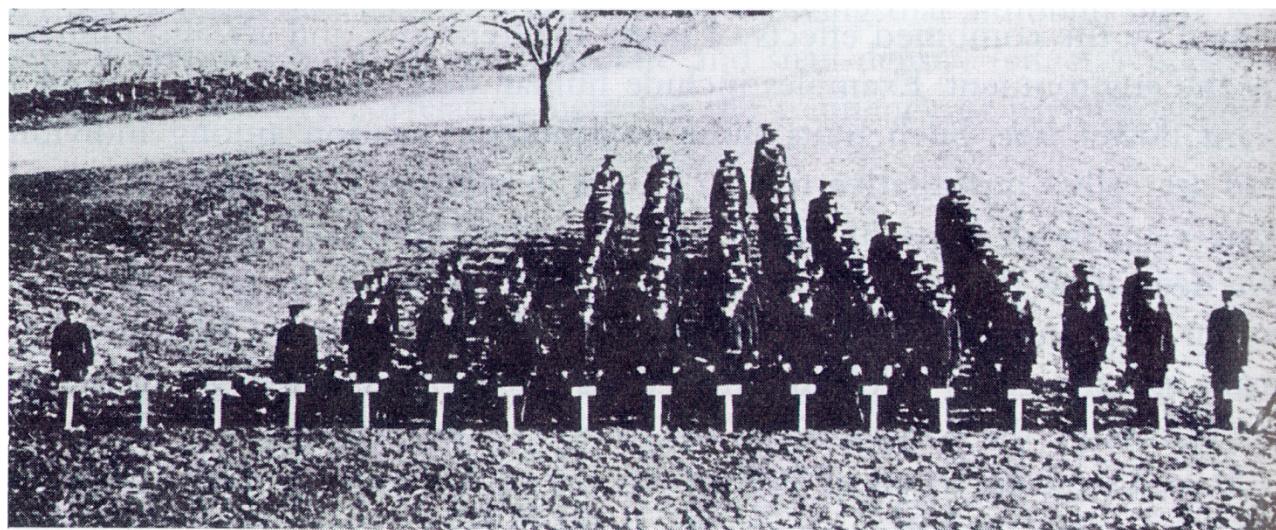


1) Indivíduos dentro das espécies são variáveis



1) Indivíduos dentro das espécies são variáveis

(a)



(b)

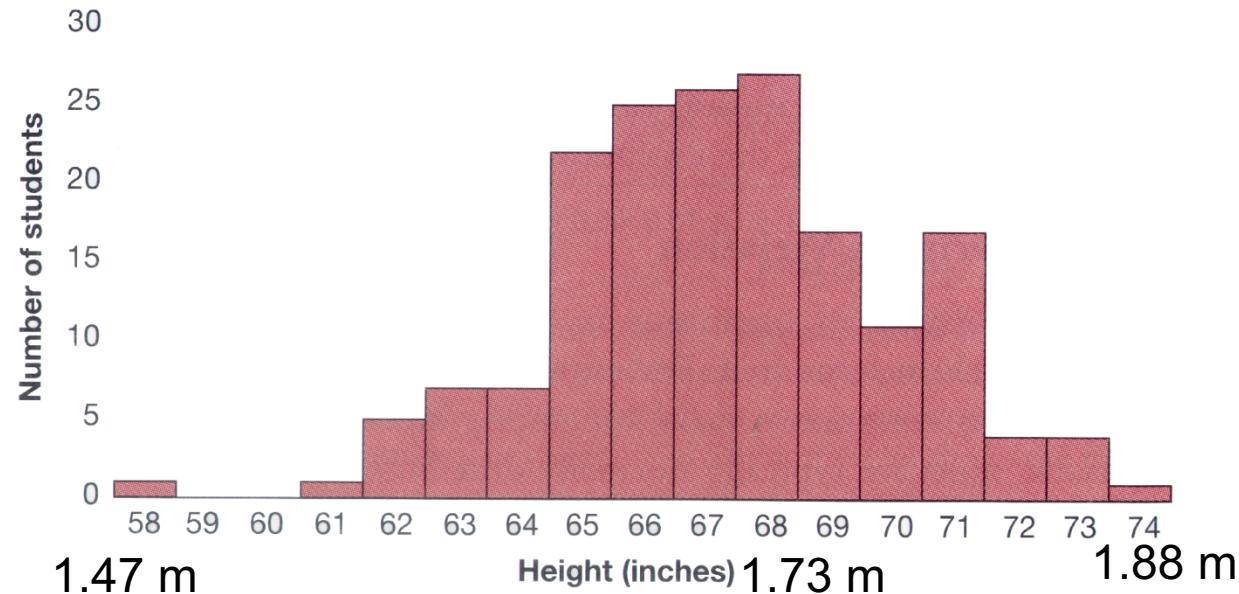
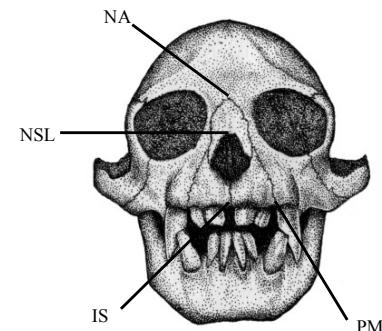
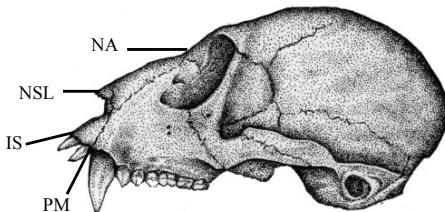
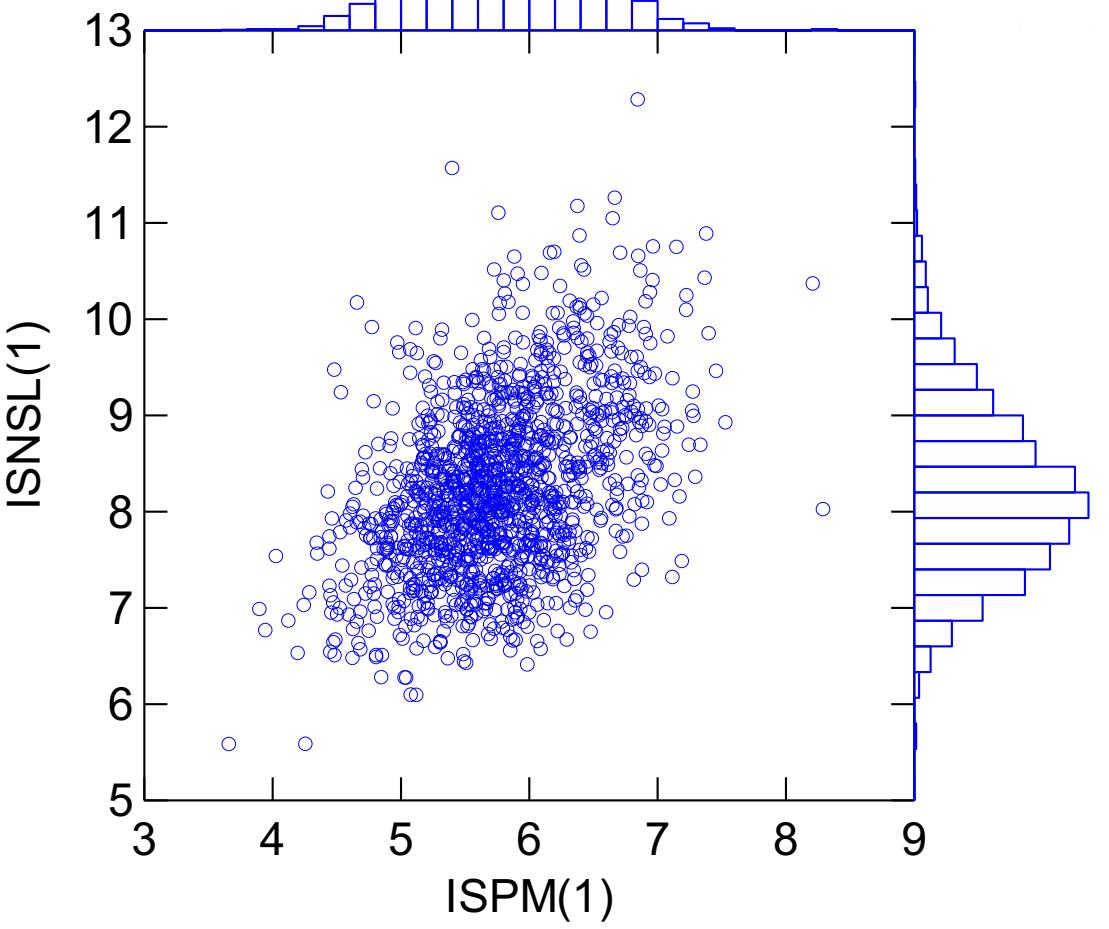
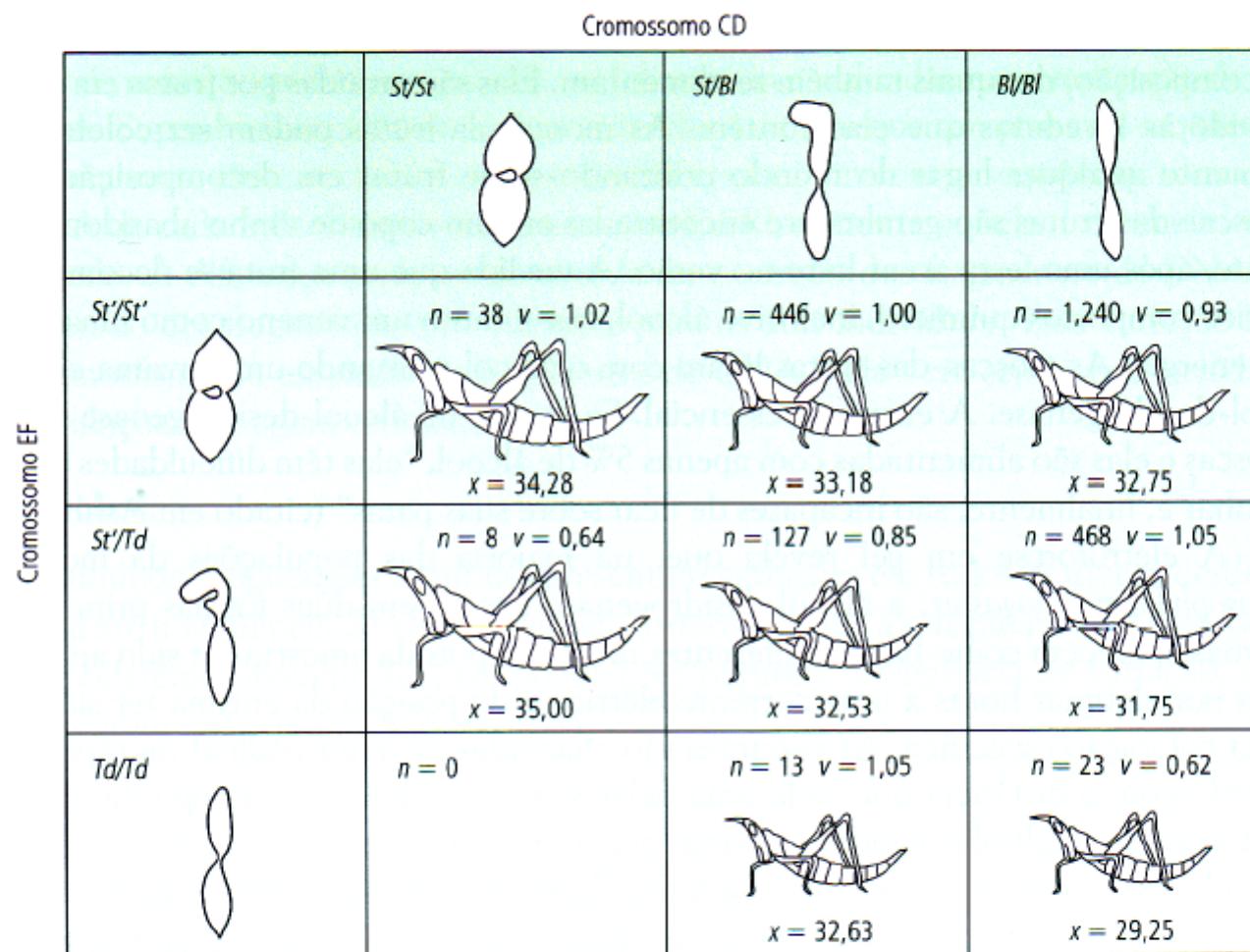


Figure 6.11 Normally distributed variation in a trait

(a) A photograph, published in the Journal of Heredity in 1914 by Albert Blakeslee, of a group of students at Connecticut Agricultural College sorted by height. The arrangement of the students forms a living histogram. (b) A graphical histogram representing the distribution of heights among the students shown in (a).



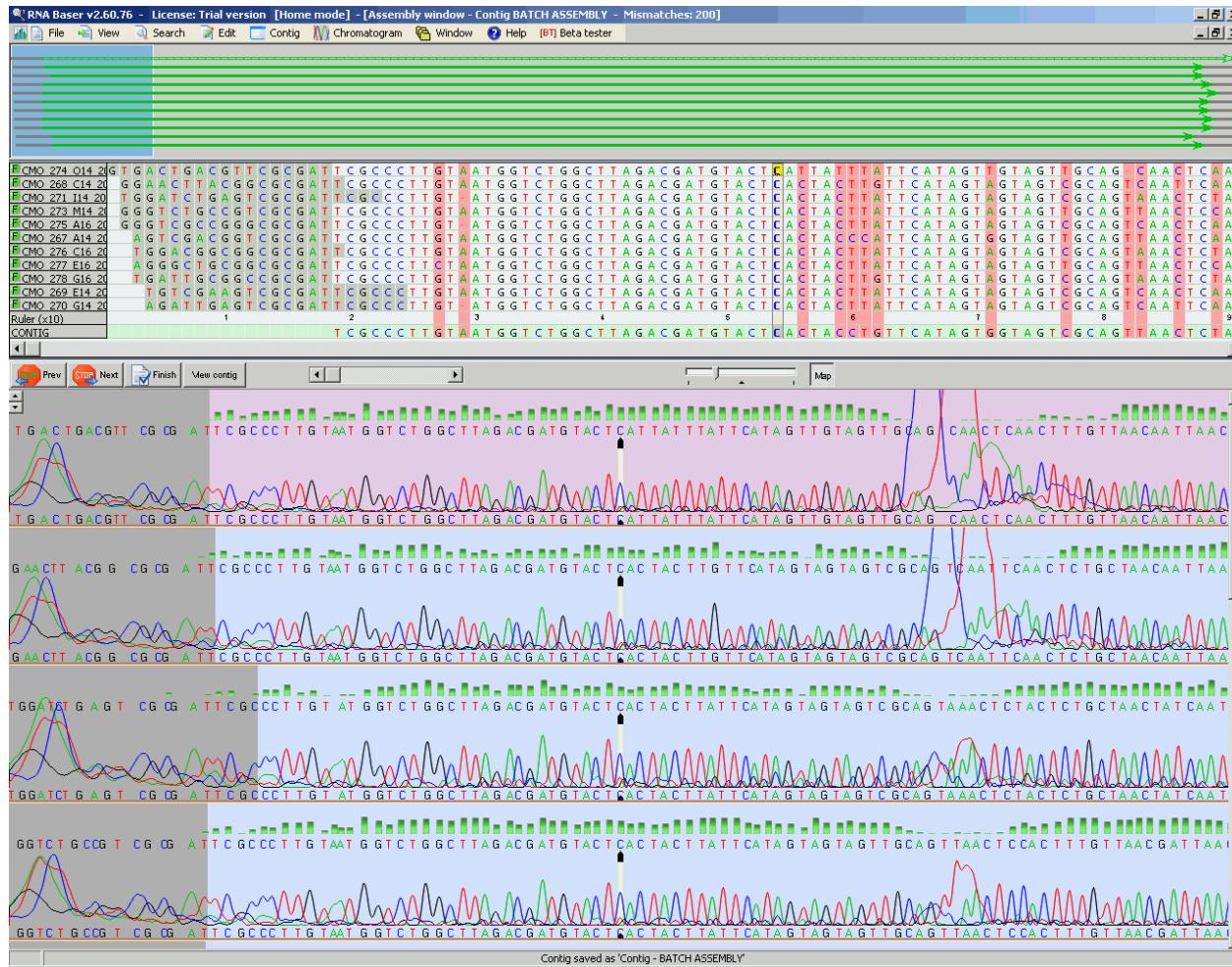
**Figura 4.7**

O gafanhoto australiano *Keyacris scurra* é polimórfico para inversões de dois cromossomos. Os dois cromossomos são chamados de CD e EF, respectivamente. As formas padrão e invertida do cromossomo CD são chamadas de St e Bl; as formas padrão e invertida do cromossomo EF são chamadas de St' e Td. v é a viabilidade relativa em um sítio em Wombat, Nova Gales do Sul, expressada em relação à viabilidade da forma St/Bl St'/St', a qual foi arbitrariamente estabelecida como sendo 1. n é o tamanho da amostra, x é o peso vivo médio. As figuras ilustram o tamanho relativo dos gafanhotos. De White (1973).

Comportamento



Variação entre indivíduos no DNA



2) Uma parte desta variação é passada para a prole

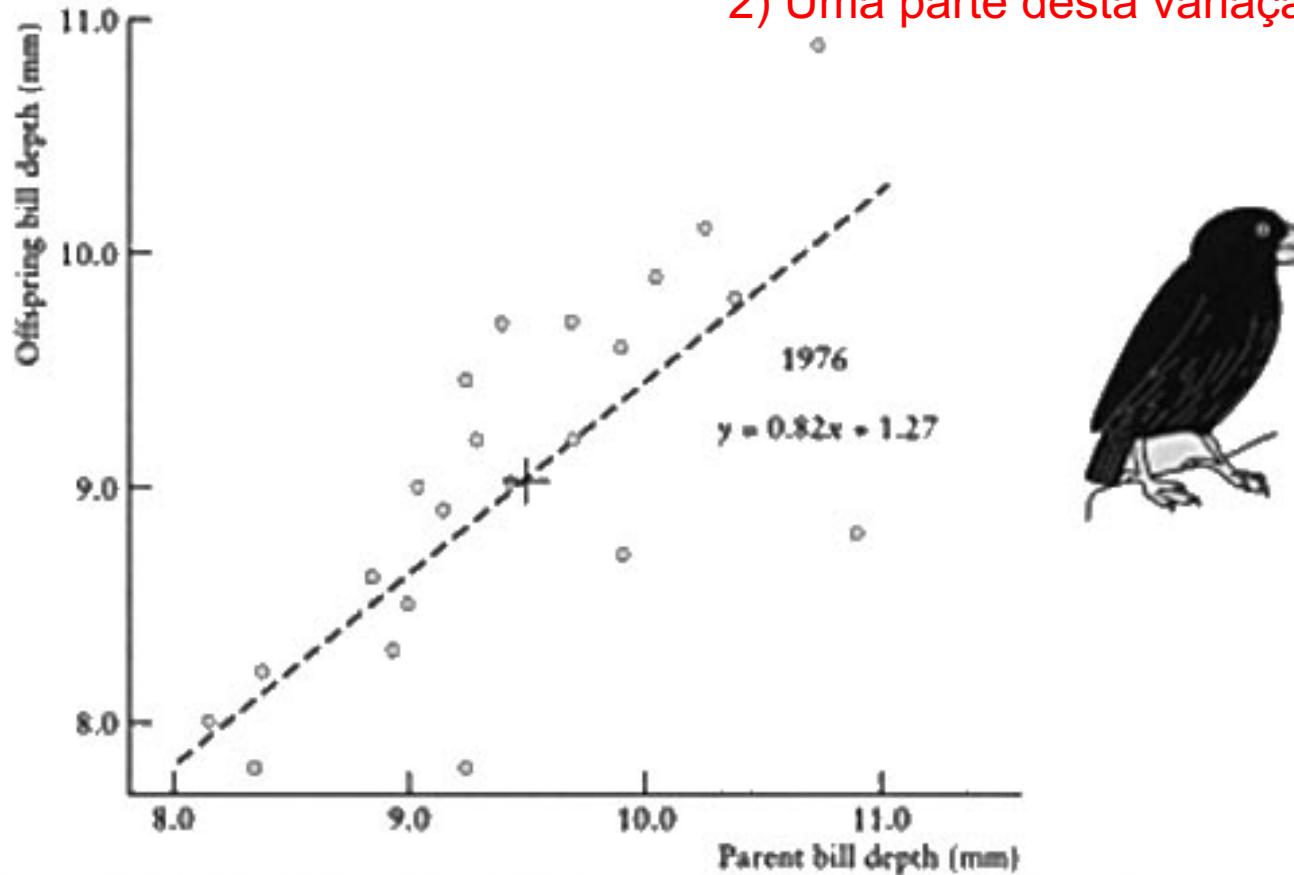
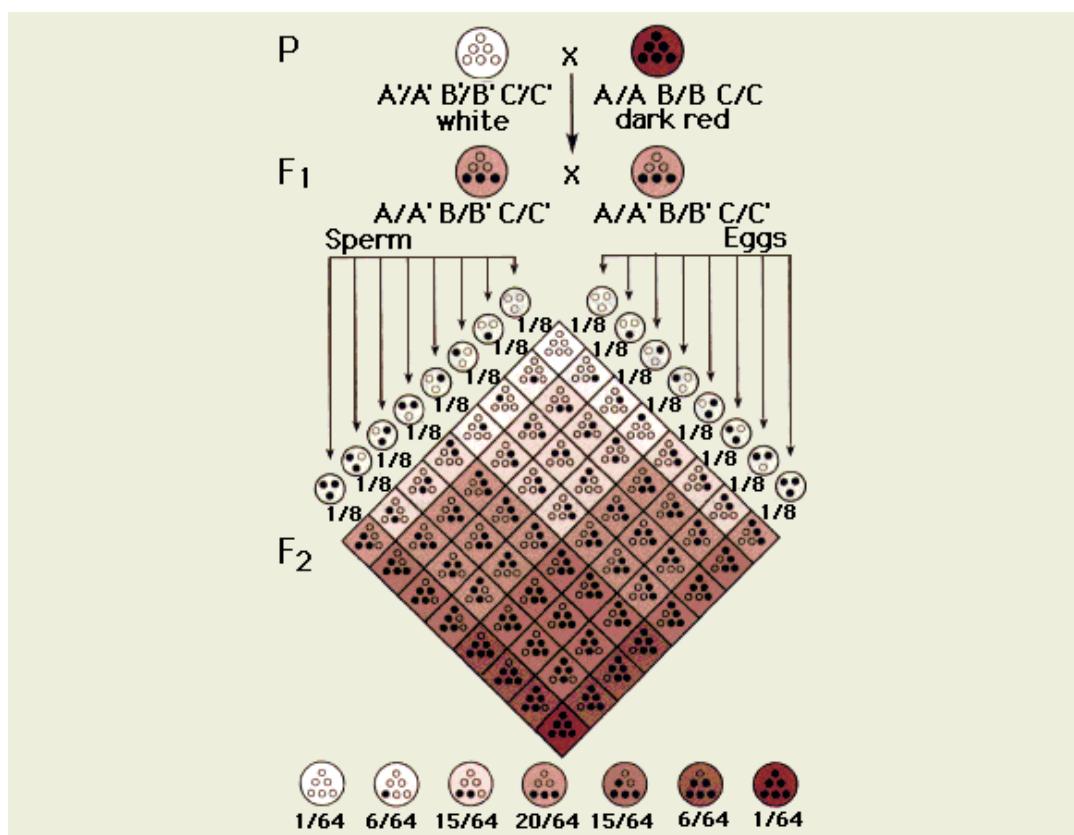
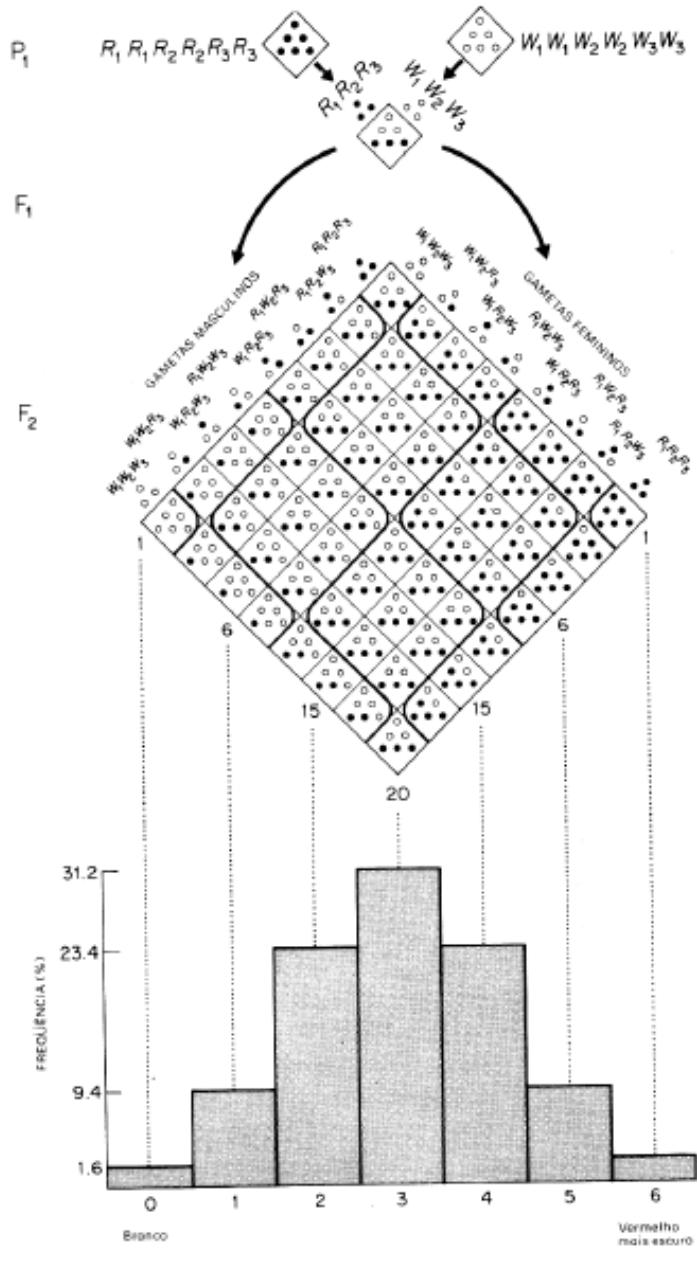


Figure 13.21 Heritability of beak depth in one of Darwin's finches, *Geospiza fortis*. The slope of the regression line is an estimate of heritability, which can range from 0 (no heritability) to 1 (perfect heritability). (Modified from Boag 1983.)

The correlation between beak size of offspring and their midparent value (the average of parents) is 0.90 both in 1976 (open circles) and 1978 (closed circles), even though the mean beak size increases due to a drought in 1978. This correlation shows constant high heritability independent of environmental change. Note that high heritability does not mean that a trait is constant: beak size is highly variable (note range of axes), and can vary across time (displacement of slopes).



Nilsson-Ehle cruzamento tri-gênico de trigo

FIGURA 11.1 Herança da cor do grão no trigo. Cada ponto preto representa um gene "vermelho". (Redesenhado com pequena modificação e com permissão da Macmillan Publishing Co., Inc., de *Genetics*, por Monroe W. Strickberger.)

2) Uma parte desta variação é passada para a prole

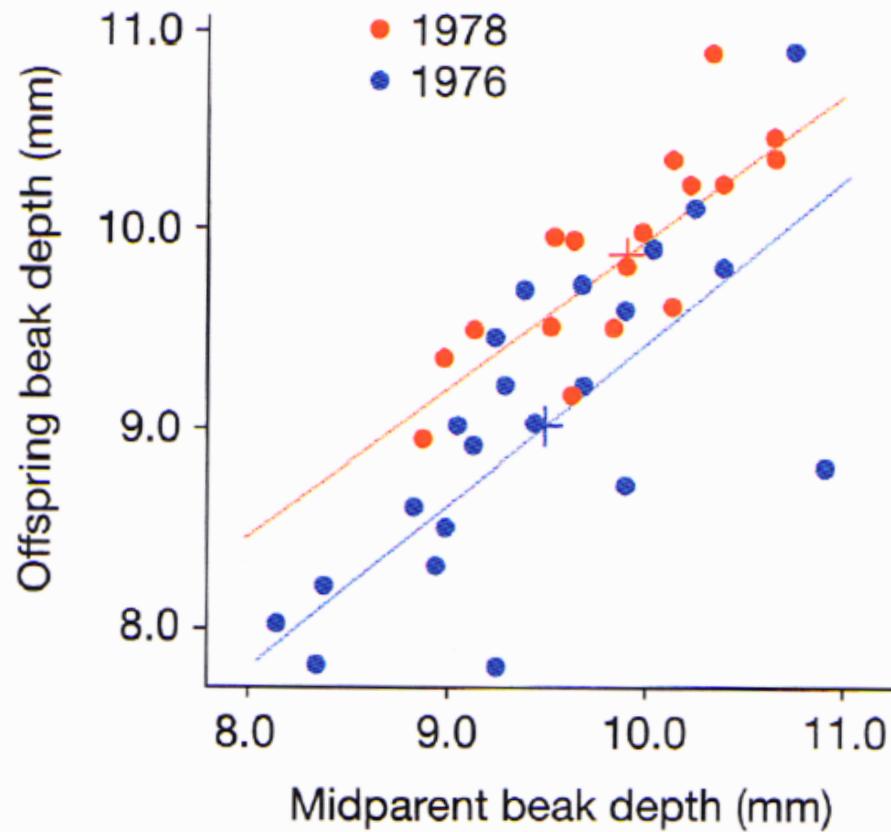
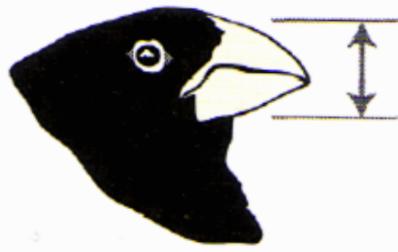


Figure 3.4 Heritability of beak depth in *Geospiza fortis* This graph shows the relationship between the beak depth of parents and their offspring. Midparent value is the average of the maternal and paternal measurements. Using this measurement is important because male *G. fortis* are bigger than females.

3) A cada geração nascem mais filhotes do que podem sobreviver

Afídeo	524 bilhões em 1 ano
Elefante	19 bilhões em 750 anos
Mosca doméstica	191×10^{18} em 5 meses
Mosca do cogumelo	60000 por metro quadrado a cada 35 dias
Staphylococcus aureus (bactéria)	Celulas iriam cobrir a terra com 2 metros de profundidade em 48 horas

19 milhões em 750 anos



$>10^{79}$ em 16 anos
= Número estimado de elétrons no universo visível

3) A cada geração nascem mais filhotes do que podem sobreviver

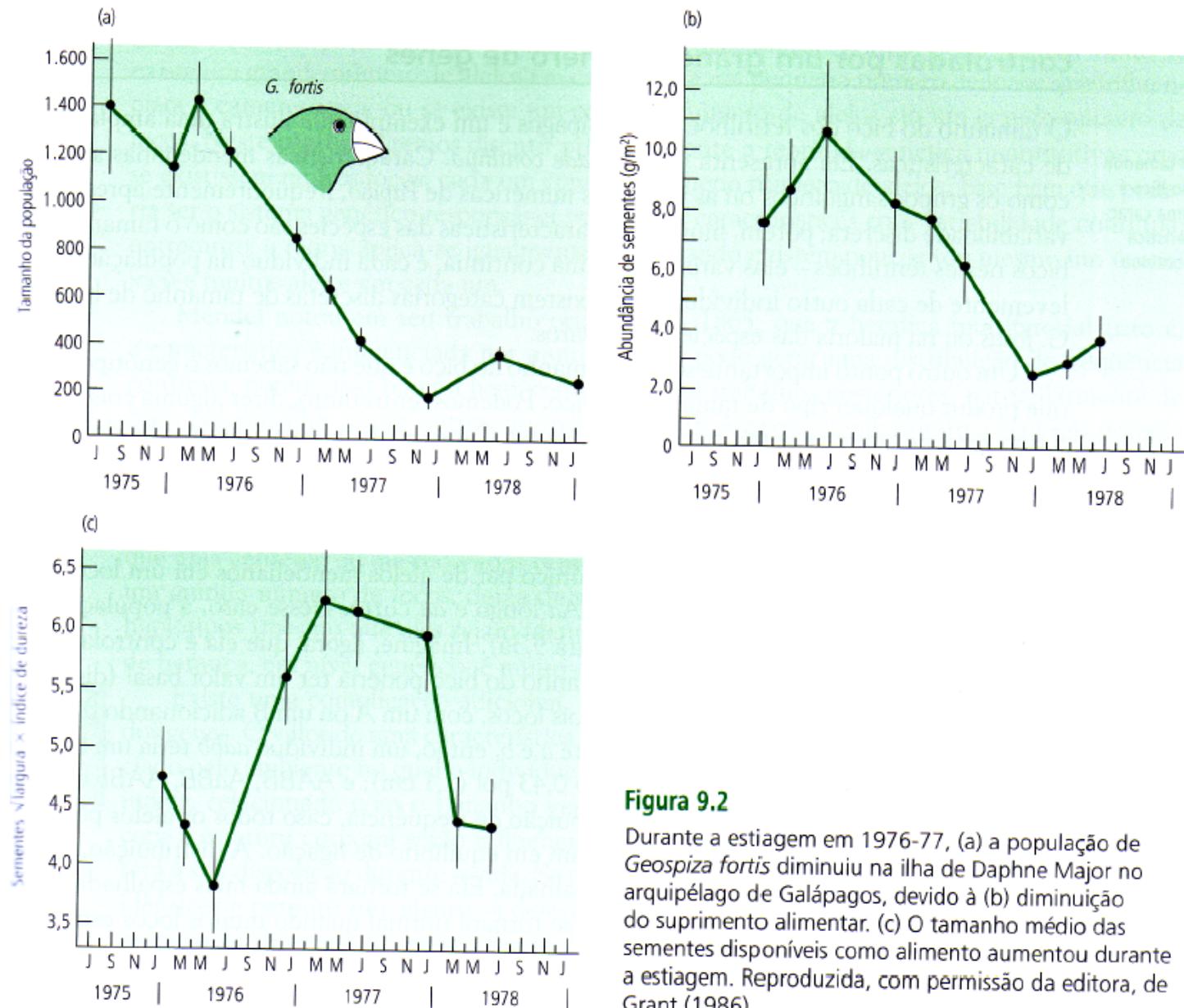


Figura 9.2

Durante a estiagem em 1976-77, (a) a população de *Geospiza fortis* diminuiu na ilha de Daphne Major no arquipélago de Galápagos, devido à (b) diminuição do suprimento alimentar. (c) O tamanho médio das sementes disponíveis como alimento aumentou durante a estiagem. Reproduzida, com permissão da editora, de Grant (1986).



4) Sobrevida e reprodução não são ao acaso: Indivíduos que sobrevivem e depois se reproduzem (ou que se reproduzem mais do que os outros) são aqueles com as variações mais favoráveis naquele contexto ambiental.

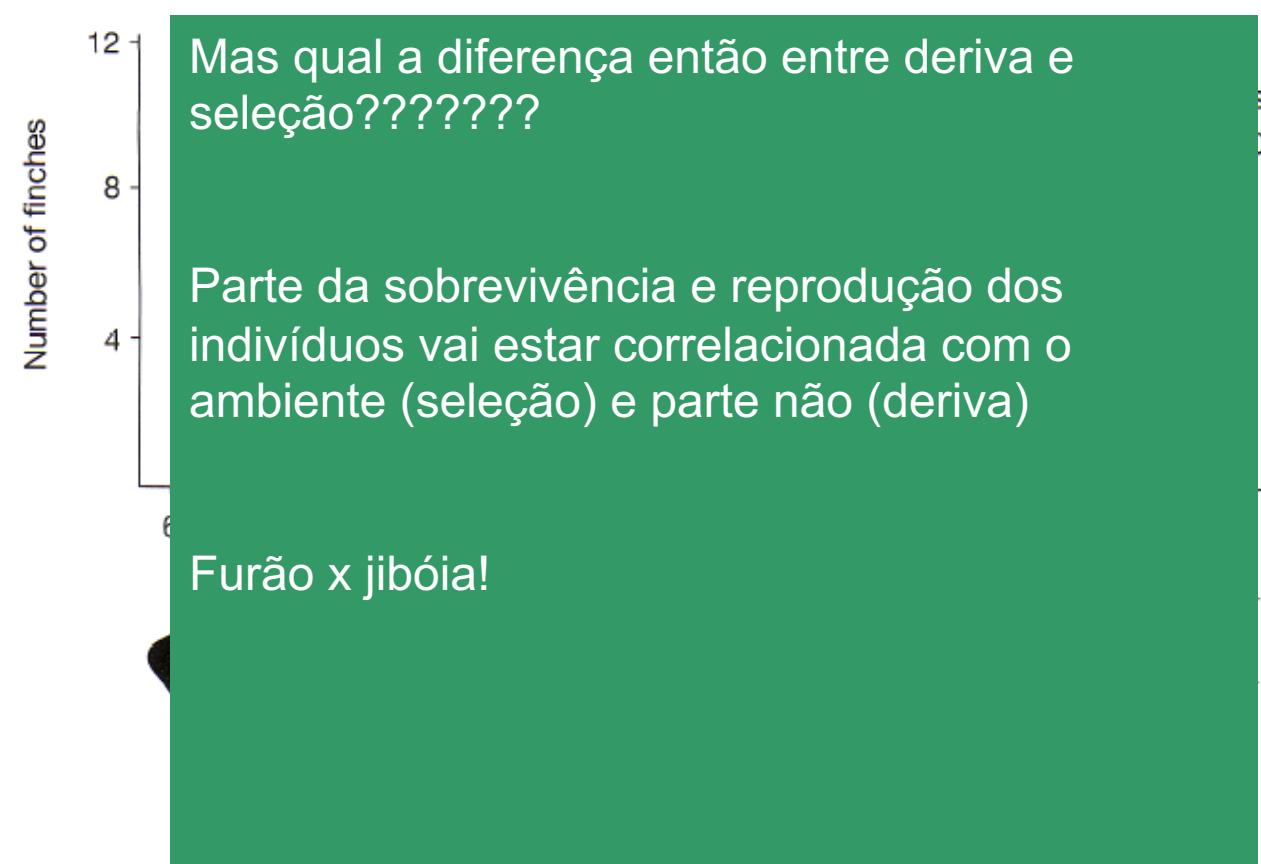
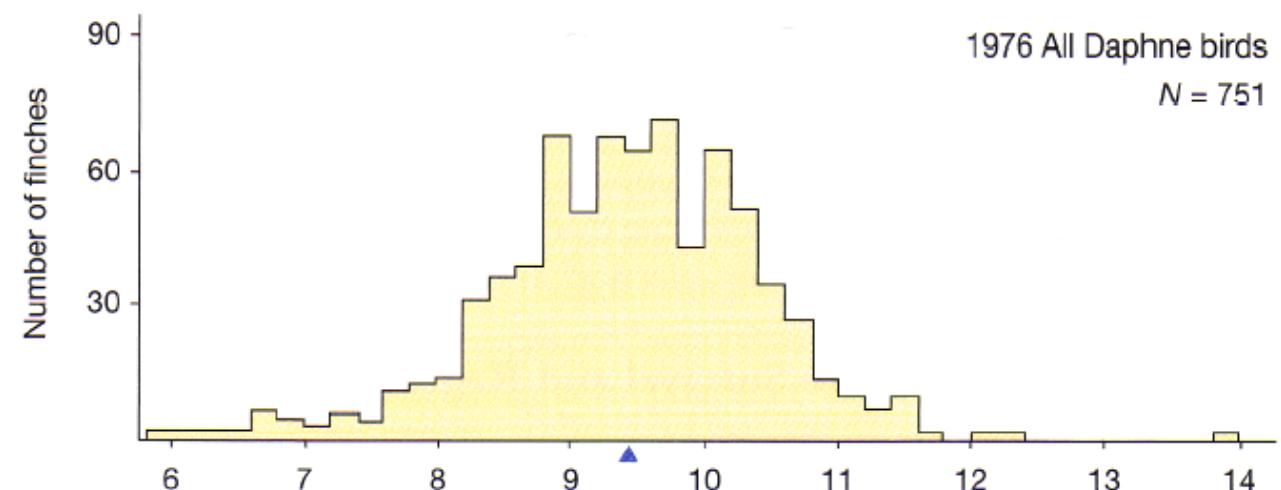


Figure 3.6 Beak depth before and after natural selection These histograms show the distribution of beak depth in medium ground finches on Daphne Major, before and after the drought of 1977 (Grant 1986). Copyright © 1986, Princeton University Press. Reprinted by permission of Princeton University Press.

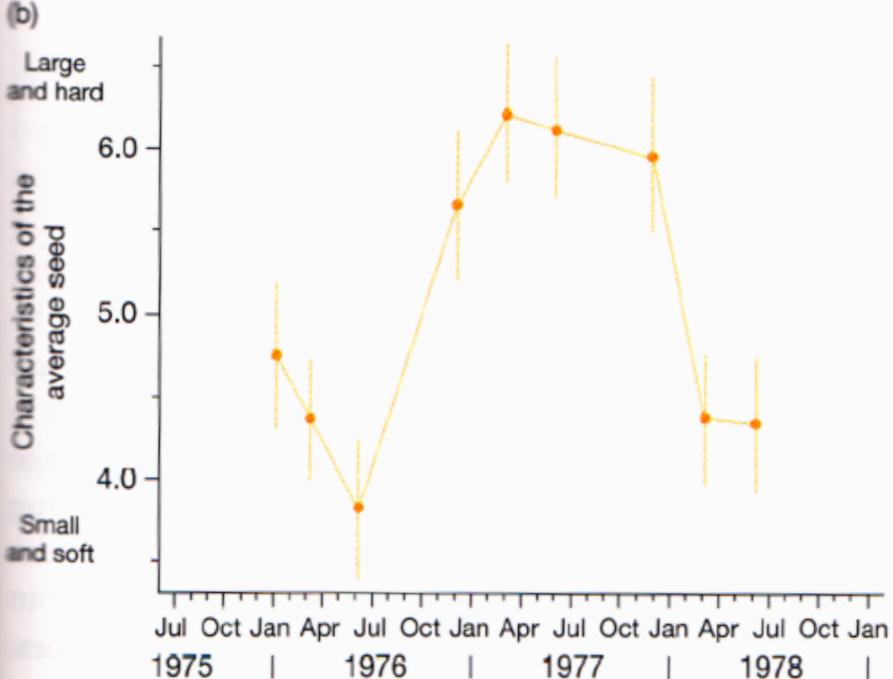
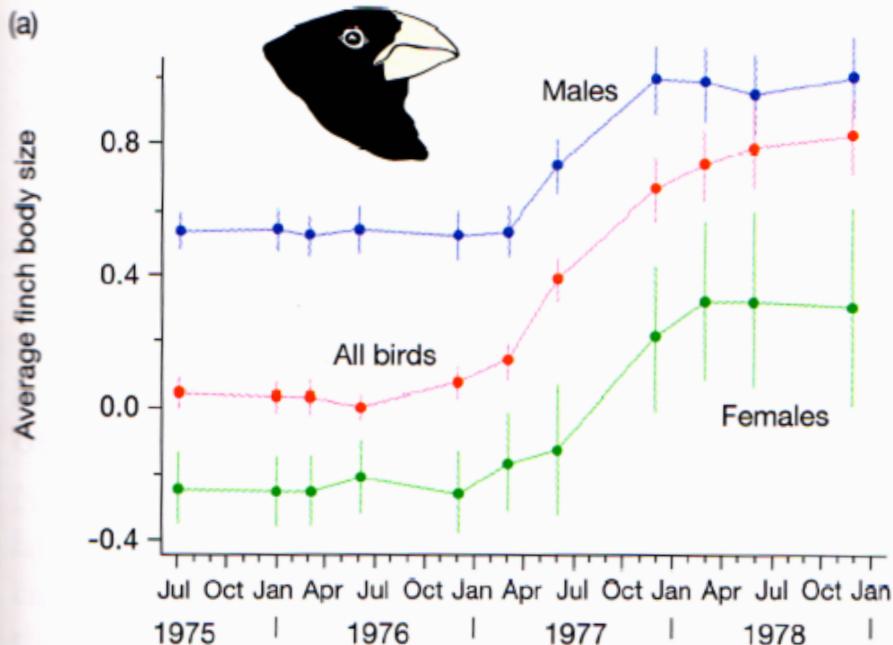


Figure 3.7 Changes in the overall body size of ground finches and in seed characteristics (a) These plots show the overall body size of finches caught before, during, and after the drought on Daphne Major. (The axis has no units because body size was calculated as a composite measure called a principal component score.) The "All birds" line represents the average of males and females. As in Figure 3.5, the data points represent population means, the vertical lines represent standard errors, and the horizontal lines are drawn between data points simply to make the trends easier to see. (b) This graph shows changes in the hardness of seeds available on Daphne Major before, during, and after the drought. The hardness index plotted on the y-axis is a special measure created by Boag and Grant (1981). Reprinted with permission. Copyright © 1981, American Association for the Advancement of Science.

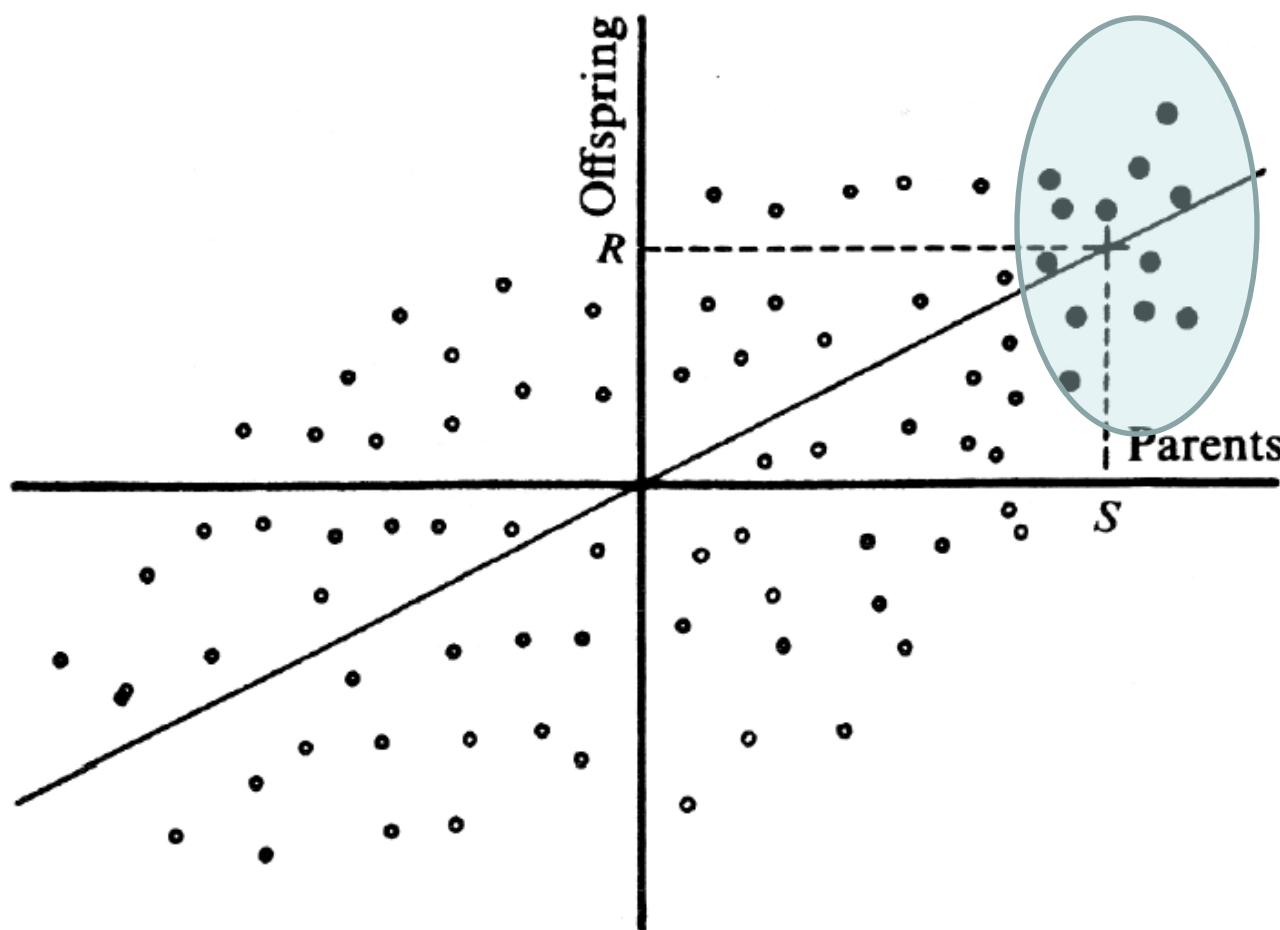


Fig. 11.1. Diagrammatic representation of the mean values of progeny plotted against the mid-parent values, to illustrate the response to selection, as explained in the text.

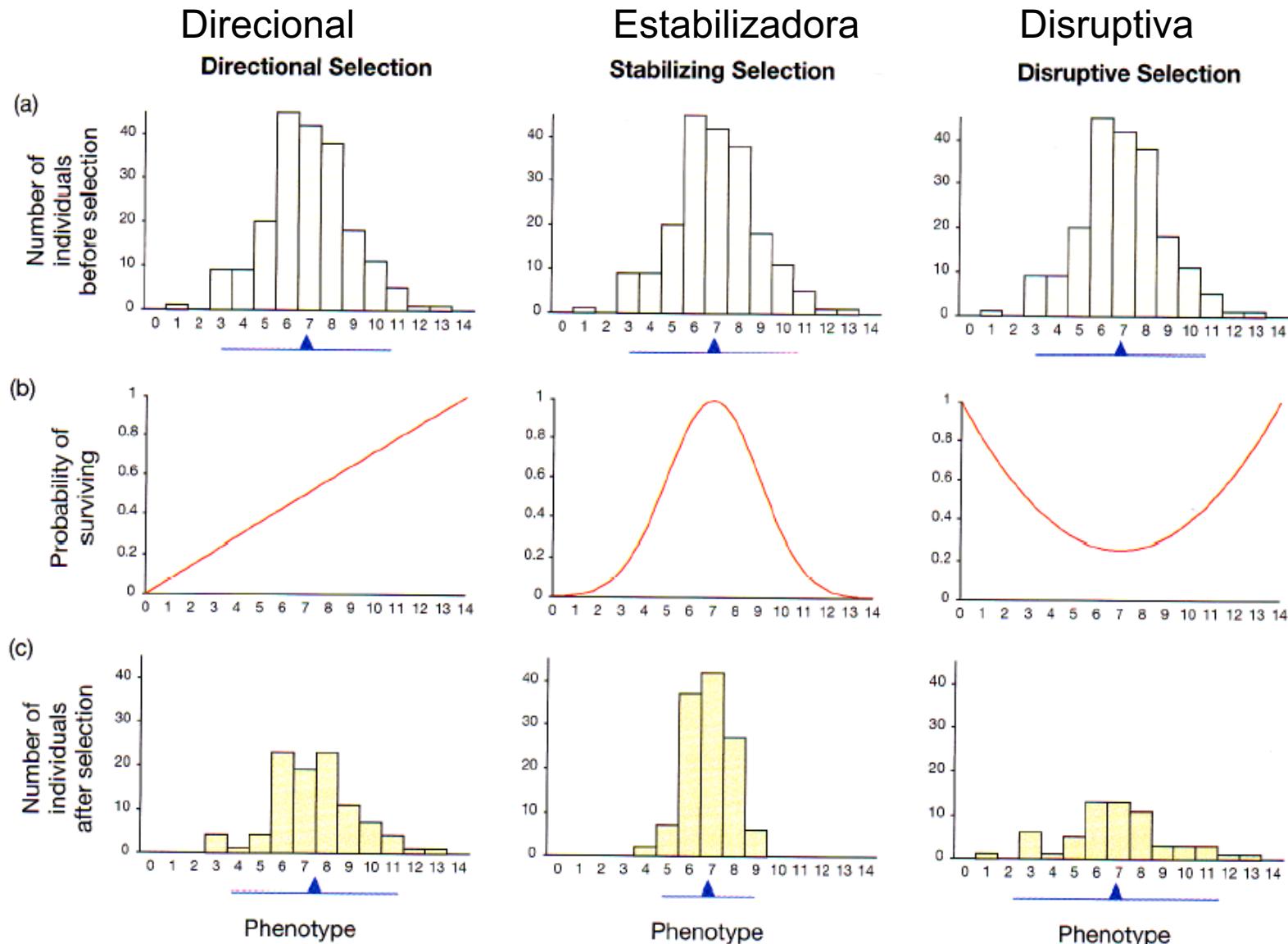


Figure 7.34 Three modes of selection Each column represents a mode of selection. The graphs in row (a) are histograms showing the distribution of a phenotypic trait in a hypothetical population before selection. The graphs in row (b) show different patterns of selection; they plot the probability of survival (a measure of fitness) as a function of phenotype. The graphs in row (c) are histograms showing the distribution of the phenotypic trait in the survivors. The blue triangle under each histogram shows the mean of the population. The blue bar under each histogram shows the variation (± 2 standard deviations from the mean). After Cavalli-Sforza and Bodmer (1971).

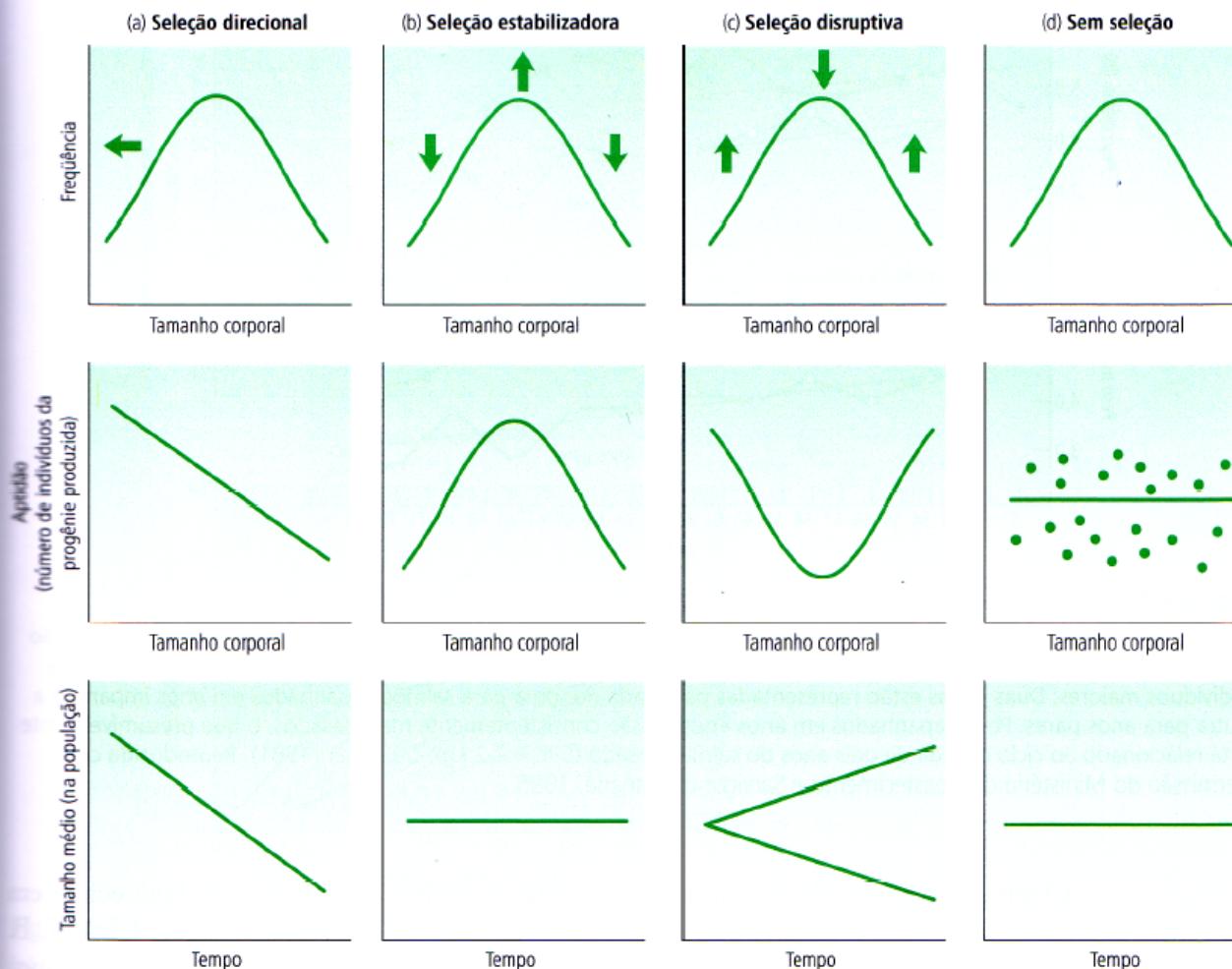
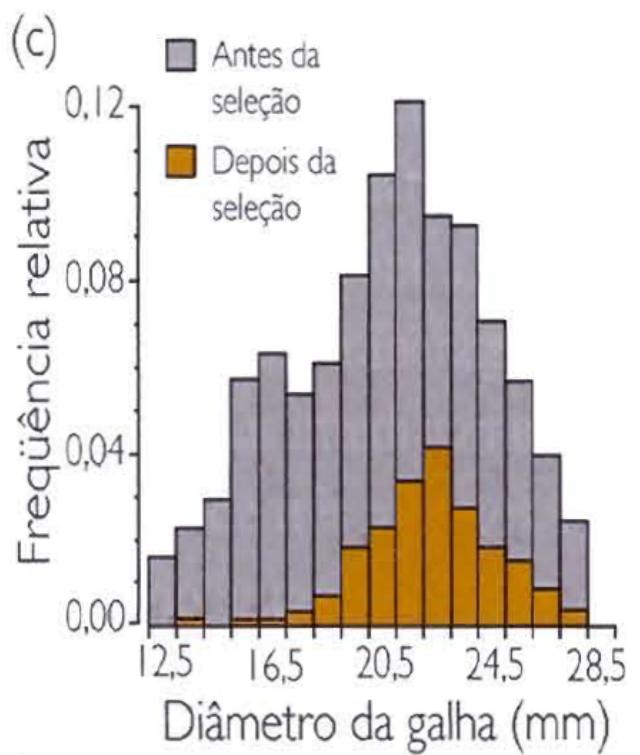
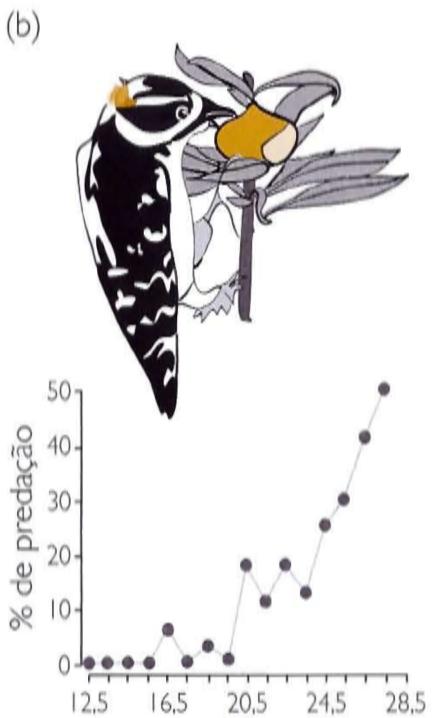
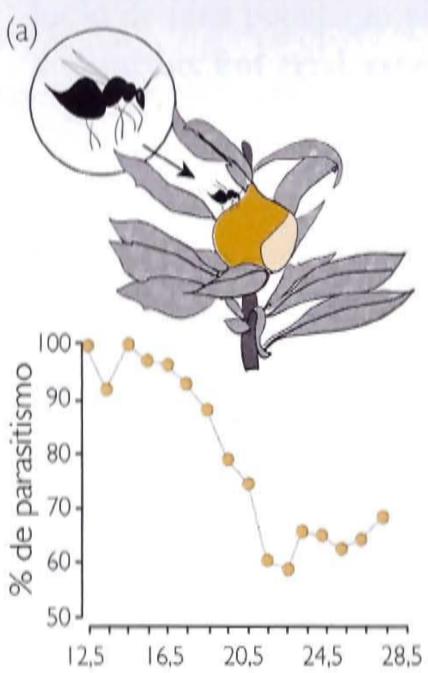
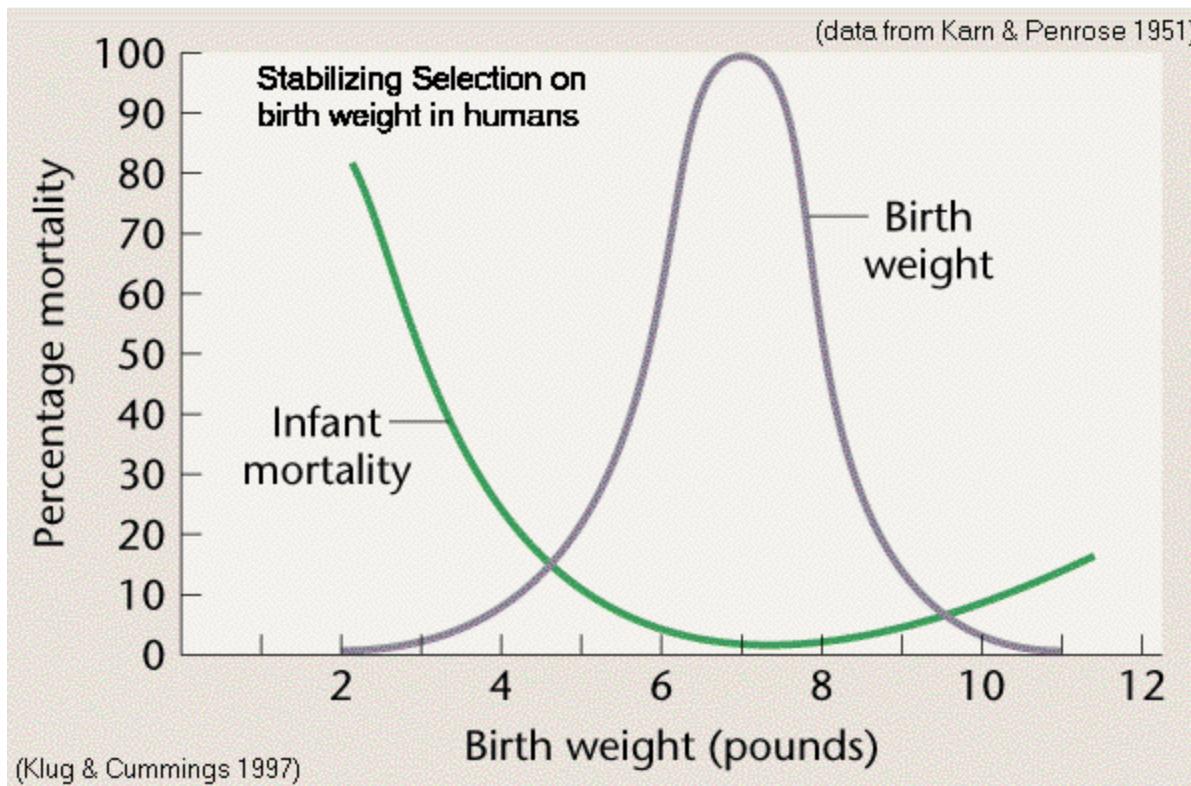


Figura 4.2

Os três tipos de seleção. A linha superior mostra a freqüência de distribuição do caráter (tamanho corporal). Para muitos caracteres na natureza, essa distribuição possui um pico central, próximo à média, e é menor nos extremos. (A distribuição normal, ou “curva em forma de sino”, é um exemplo particular desse tipo de distribuição.) A segunda linha mostra a relação entre o tamanho corporal e a aptidão, em uma geração, e a terceira mostra a alteração esperada na média do caráter ao longo de muitas gerações (se o tamanho corporal é herdável). (a) Seleção direcional. Indivíduos menores têm uma maior aptidão, e a espécie tem o seu tamanho corporal médio diminuído ao longo do tempo. A Figura 4.3 é um exemplo. (b) Seleção estabilizadora. Indivíduos de tamanho intermediário têm uma maior aptidão. A Figura 4.4a é um exemplo. (c) Seleção disruptiva. Ambos os extremos são favorecidos e, se a seleção é forte o suficiente, a população divide-se em duas. A Figura 4.5 é um exemplo. (d) Nenhuma seleção. Se não há relação entre o caráter e a aptidão, a seleção natural não age nesse caso.

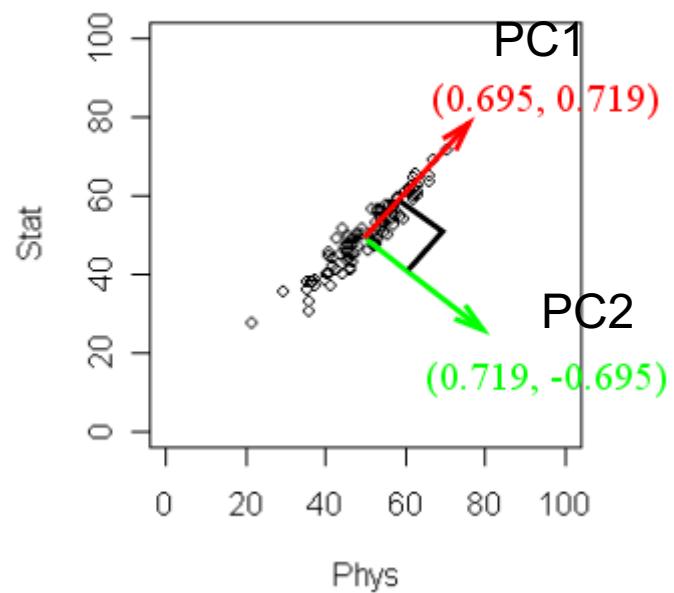
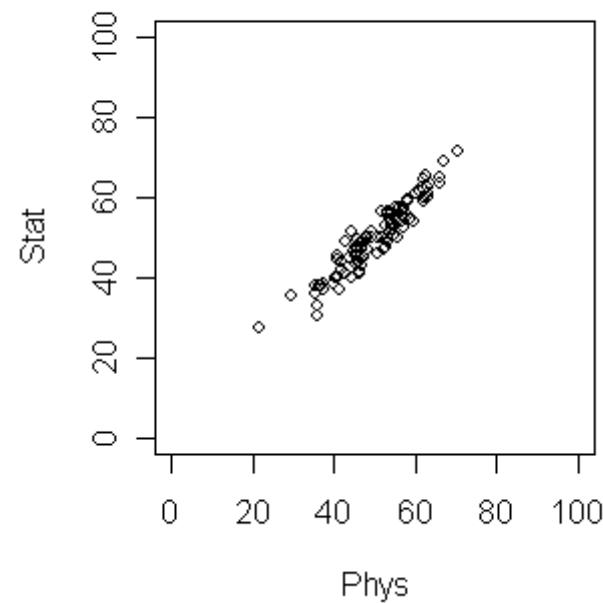
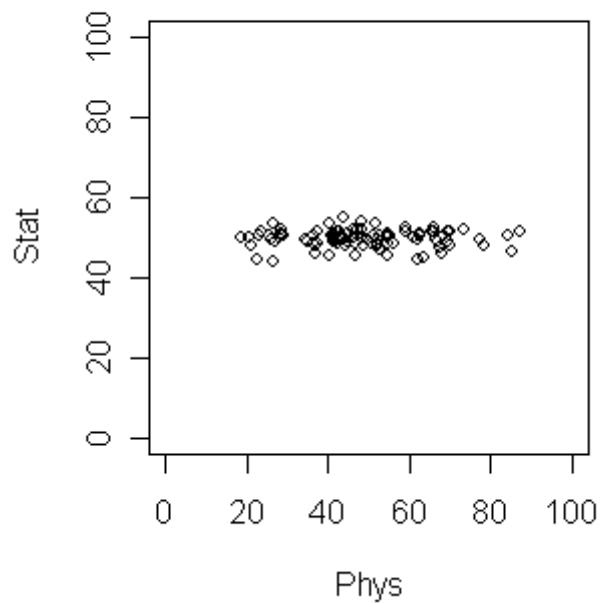




Karn & Penrose (1951) showed that birth weight follows a normal distribution, that mortality for newborns is greater for those either under- or over-weight, and that the mean birth weight (7 lbs) coincides with that showing minimum mortality. That is, natural selection reduces the variance in birthweight, in such a way that the distribution has become stabilized around the optimum size for maximum survival.

	<i>Antes da seleção - 1976</i>		<i>Depois da seleção - 1978</i>		
	<i>Média</i>	<i>SE</i>	<i>Média</i>	<i>SE</i>	<i>deltaz</i>
peso (g)	16.06	0.06	17.13	0.13	1.07
Asa	67.88	0.1	68.87	0.2	0.99
Tarso	19.08	0.03	19.29	0.07	0.21
Comprimento do bico	10.63	0.03	10.95	0.06	0.32
Profundidade do bico	9.21	0.03	9.7	0.06	0.49
largura do bico	8.58	0.02	8.83	0.05	0.25
Tamanho da amostra	634		135		

Como fica a evolução sob seleção quando ligamos isto a ocorrência de módulos?



O estudo de longo prazo realizado por Grant e Grant demonstra que o mecanismo de evolução de Darwin pode ser registrado em populações naturais. Quando os quatro postu-

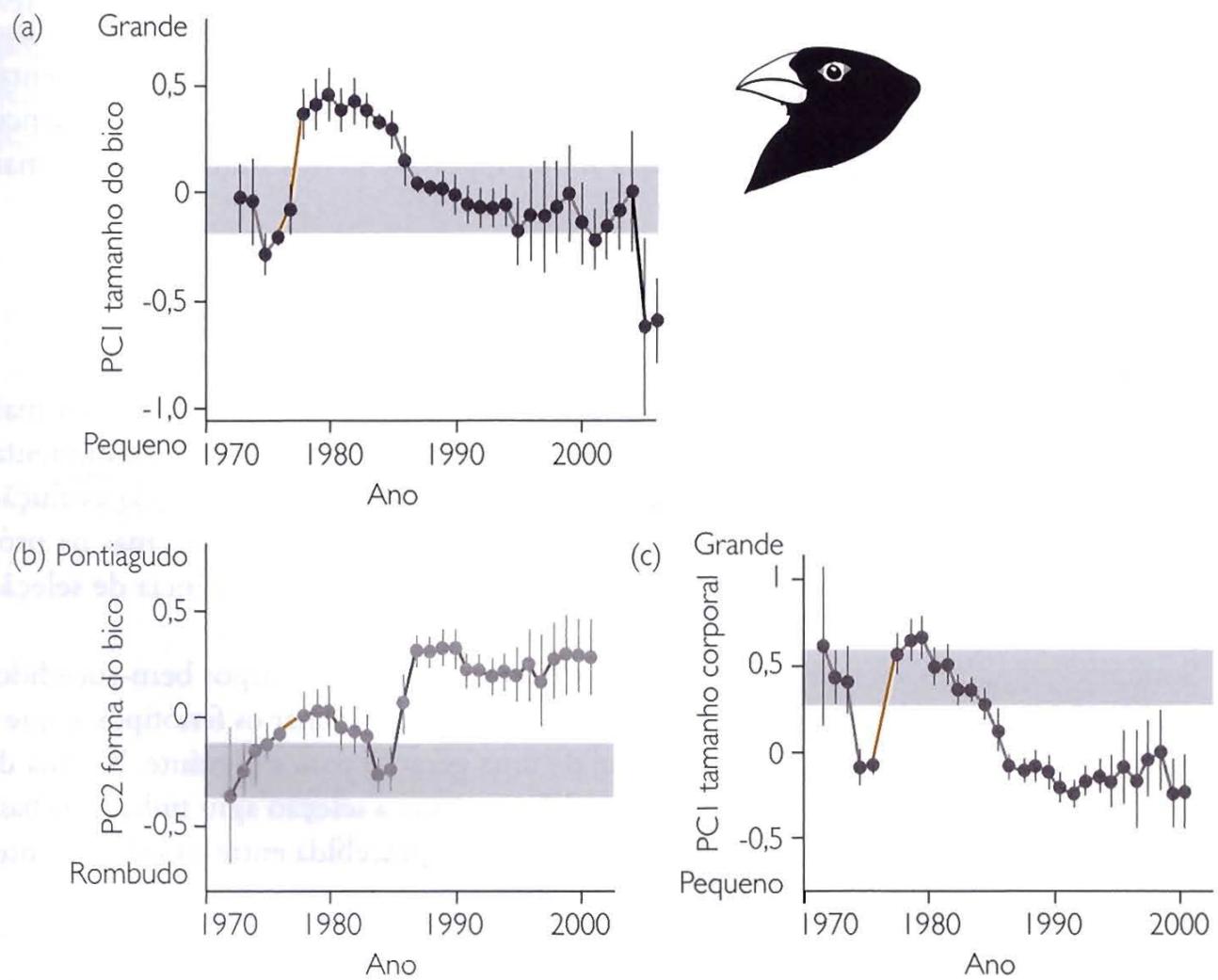


Figura 3.15 Trinta anos de evolução na população de tentilhões rasteiros [de bico] médio da ilha Dafne Maior. Esses gráficos rastreiam os valores adultos médios de tamanho e forma do bico e de tamanho corporal entre os *Geospiza fortis* da ilha de Dafne Maior, do início da década de 1970 aos anos 2000. As linhas verticais representam o intervalo de confiança de 95% para a média estimada. Se não tivesse ocorrido evolução, os intervalos de confiança para todos os pontos teriam recoberto a faixa cinza, correspondente ao intervalo de confiança de 95% para 1973, o primeiro ano com dados completos. As mudanças que ocorreram durante a estiagem de 1977 são indicadas em laranja. Em (a), a mudança ocorrida durante a estiagem de 2004 é indicada em preto. A população mostrou evolução significativa nas três características. (a) Gentilmente cedido por Grant e Grant (2006). (b e c) Gentilmente cedidos por Grant e Grant (2002).

Como fica a evolução sob seleção quando ligamos isto a ocorrência de módulos?

The road to modularity

Günter P. Wagner*, Mihaela Pavlicev† and James M. Cheverud‡

Abstract | A network of interactions is called modular if it is subdivided into relatively autonomous, internally highly connected components. Modularity has emerged as a rallying point for research in developmental and evolutionary biology (and specifically evo–devo), as well as in molecular systems biology. Here we review the evidence for modularity and models about its origin. Although there is an emerging agreement that organisms have a modular organization, the main open problem is the question of whether modules arise through the action of natural selection or because of biased mutational mechanisms.

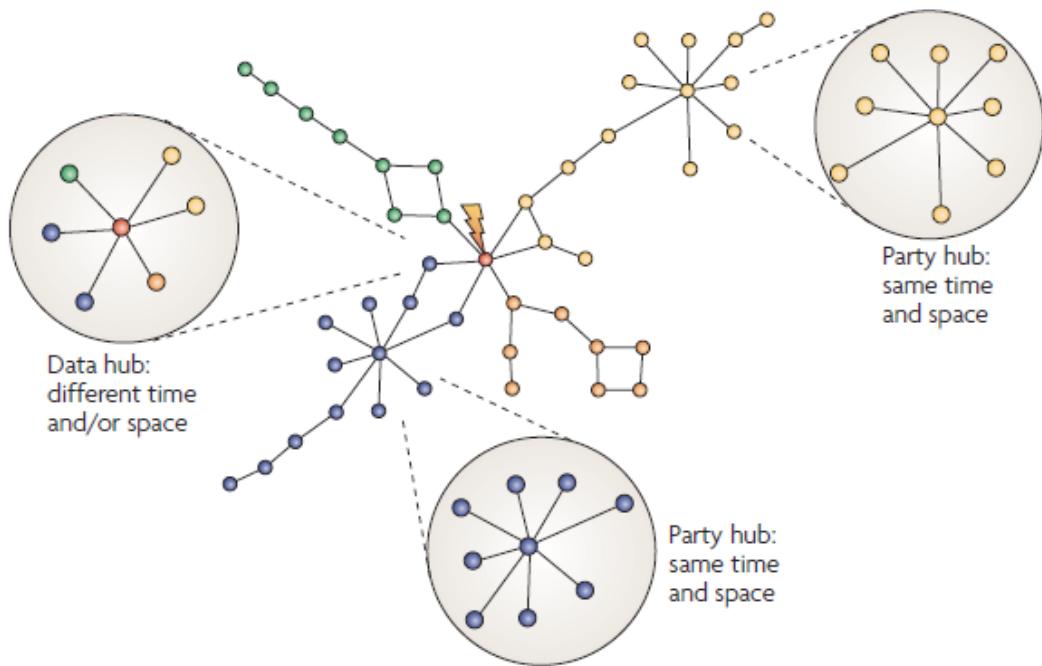


Figure 1 | A protein network with two types of highly connected nodes (protein).
‘Party’ hubs interact simultaneously with many partners, whereas ‘date’ hubs interact with their partners at different times and/or locations. The interactions are inferred from mRNA coexpression patterns. The coloration reflects the mRNA expression similarity.
The figure is reproduced from *Nature* REF. 13 © (2004) Macmillan Publishers Ltd.

Módulos

Mapa Genotípico-Fenotípico

ADAPTATION AND EVOLVABILITY

971

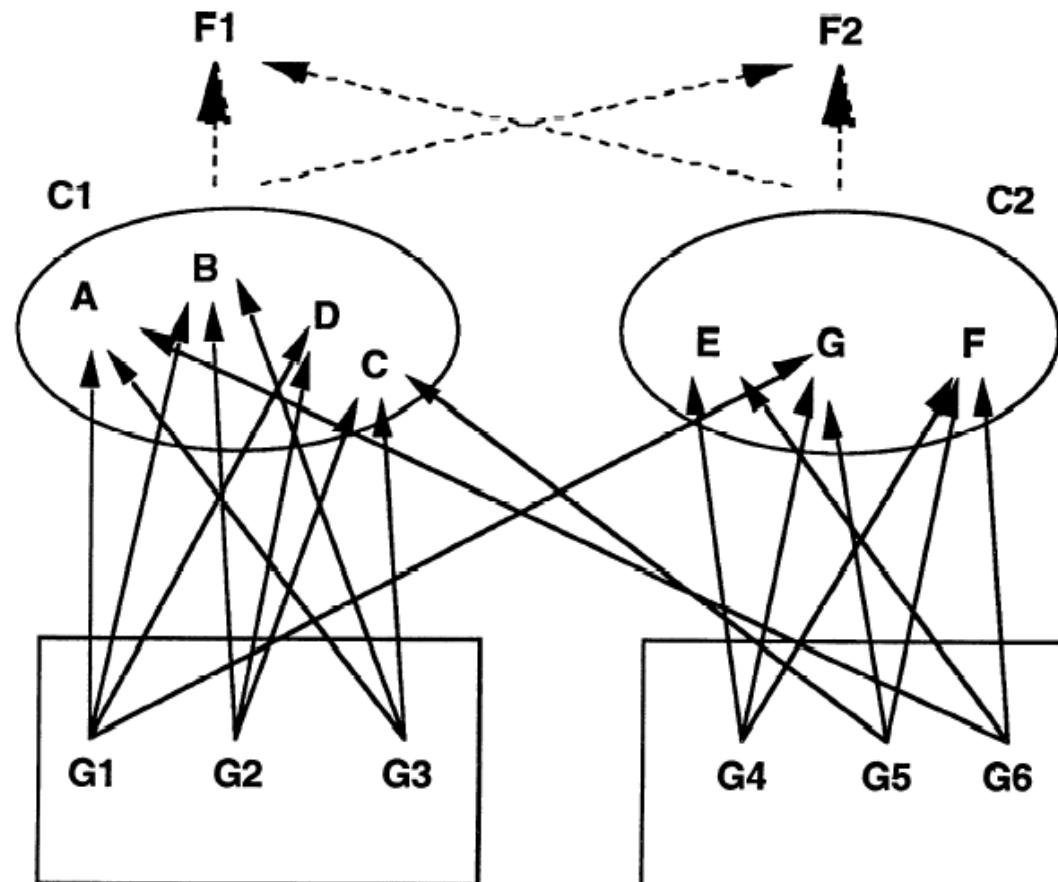


FIG. 1. Example of a modular representation of the character complexes $C_1 = \{A, B, C, D\}$ and $C_2 = \{E, F, G\}$ which serve to functions F_1 and F_2 . Each character complex has a primary function, F_1 for C_1 and F_2 for C_2 . Only weak influences exist of C_1 on F_2 and vice versa. The genetic representation is modular because the pleiotropic effects of the genes $M_1 = \{G_1, G_2, G_3\}$ have primarily pleiotropic effects on the characters in C_1 and $M_2 = \{G_4, G_5, G_6\}$ on the characters in complex C_2 . There are more pleiotropic effects on the characters within each complex than between them.



Raisa L'vovna Berg
(March 27, 1913–March 1, 2006)

The presence of correlations between, for instance, the dimensions of some parts of an organism and the absence of correlations between the dimensions of these and the other parts of the same organism indicate the independence of certain developmental processes with respect to other processes within the organism. The pleiades are thus a manifestation of differentiation.

EVOLUTION 14: 171-180. June, 1960

THE ECOLOGICAL SIGNIFICANCE OF
CORRELATION PLEIADES¹

R. L. BERG

Leningrad State University, Leningrad, USSR

Received October 12, 1959

Pleiades = Modularity / Morphological Integration

While the concept of morphological integration describes the association among parts, the concept of modularity emphasizes the dissociability of parts.

Organisms are build upon modules and traits are integrated within modules while modules are also integrated at upper levels

Desenvolvimento ocorre através de uma série de módulos discretos que interagem.

Organismos são construídos de unidades que são coerentes dentro delas mesmas (correlacionadas) e ainda assim fazem parte de uma unidade maior (células em tecidos, tecidos em órgãos, órgãos em sistemas, ...)

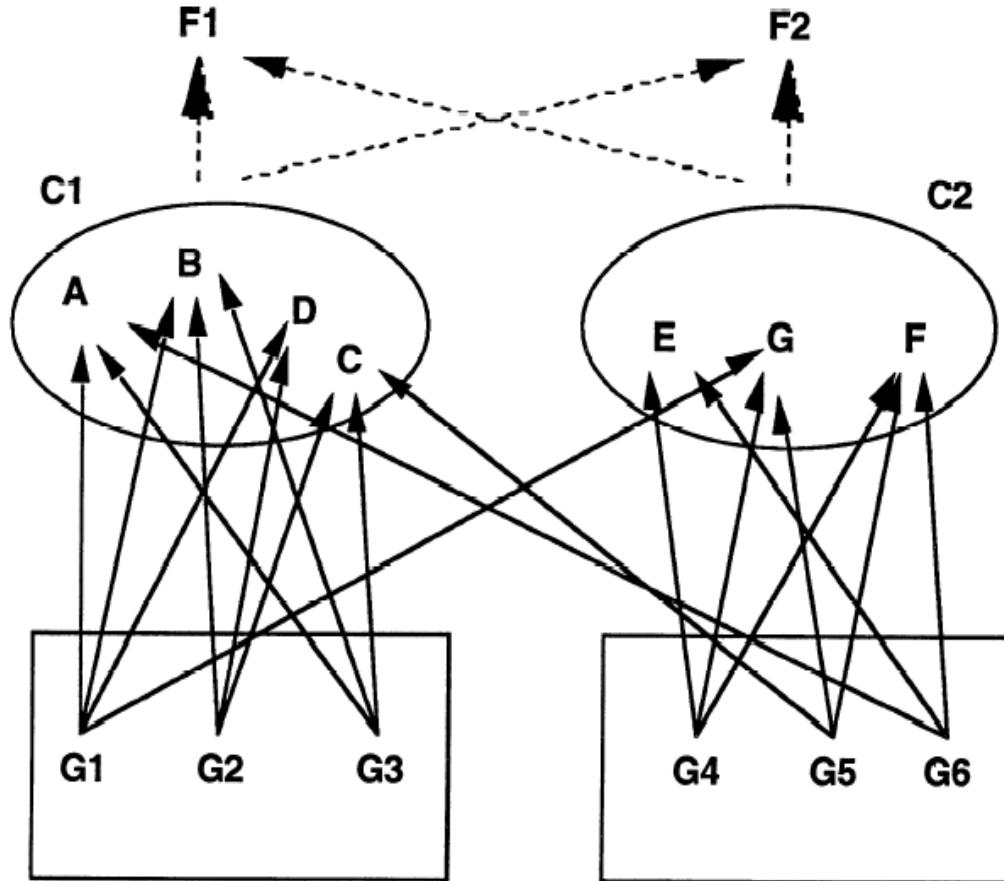
No desenvolvimento estes módulos incluem campos morfogenéticos, vias metabólicas, linhagens celulares, etc.

Morphological Integration/Modularity

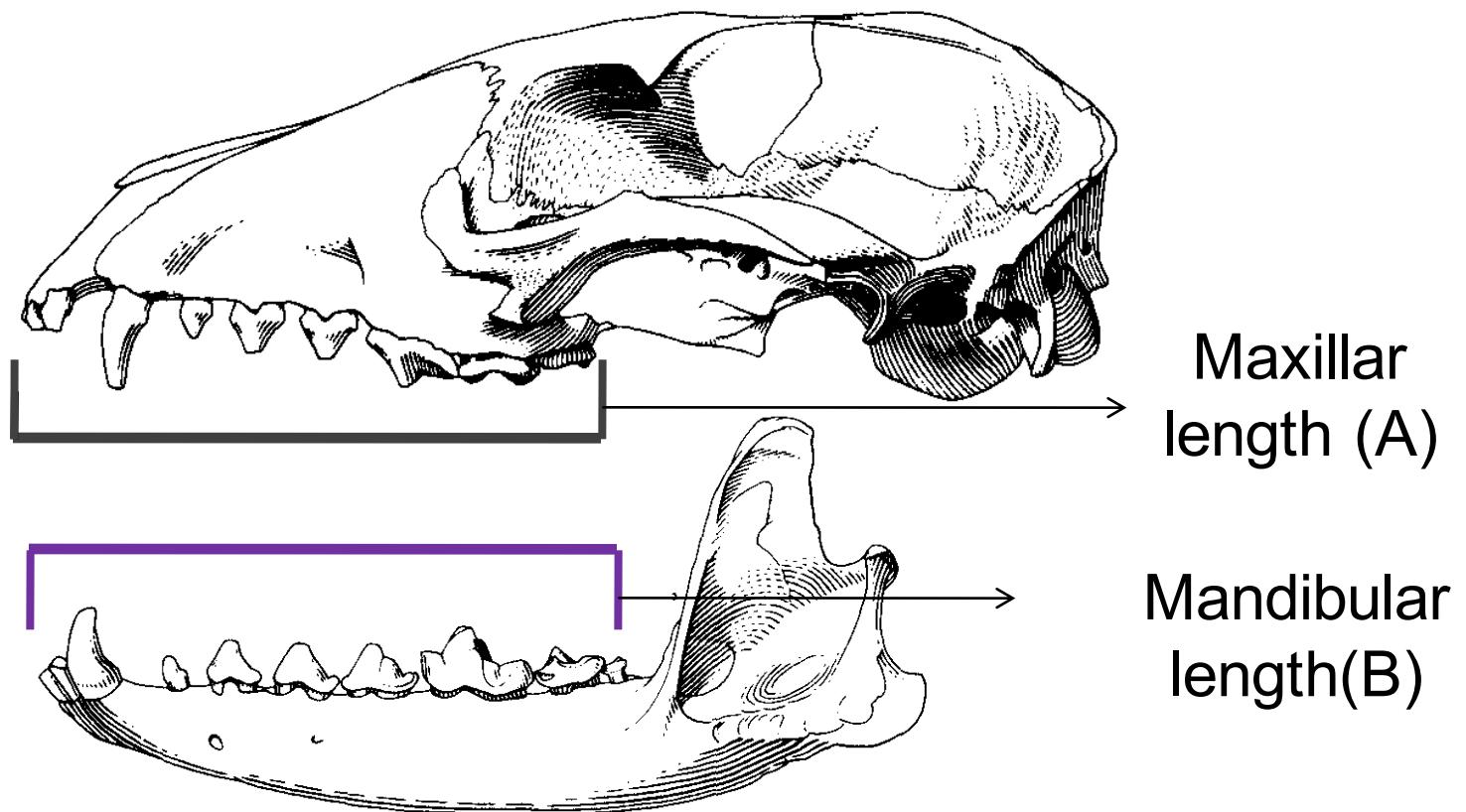
- 1) Function and development establish a interdependence relationship between traits
- 2) This relationship expresses in the phenotype. The degree of association in the phenotype reflects the association of these units via development and function
- 3) Traits morphologically integrated within modules evolve conjointly while traits in different modules can evolve to some extent independently

Modularity

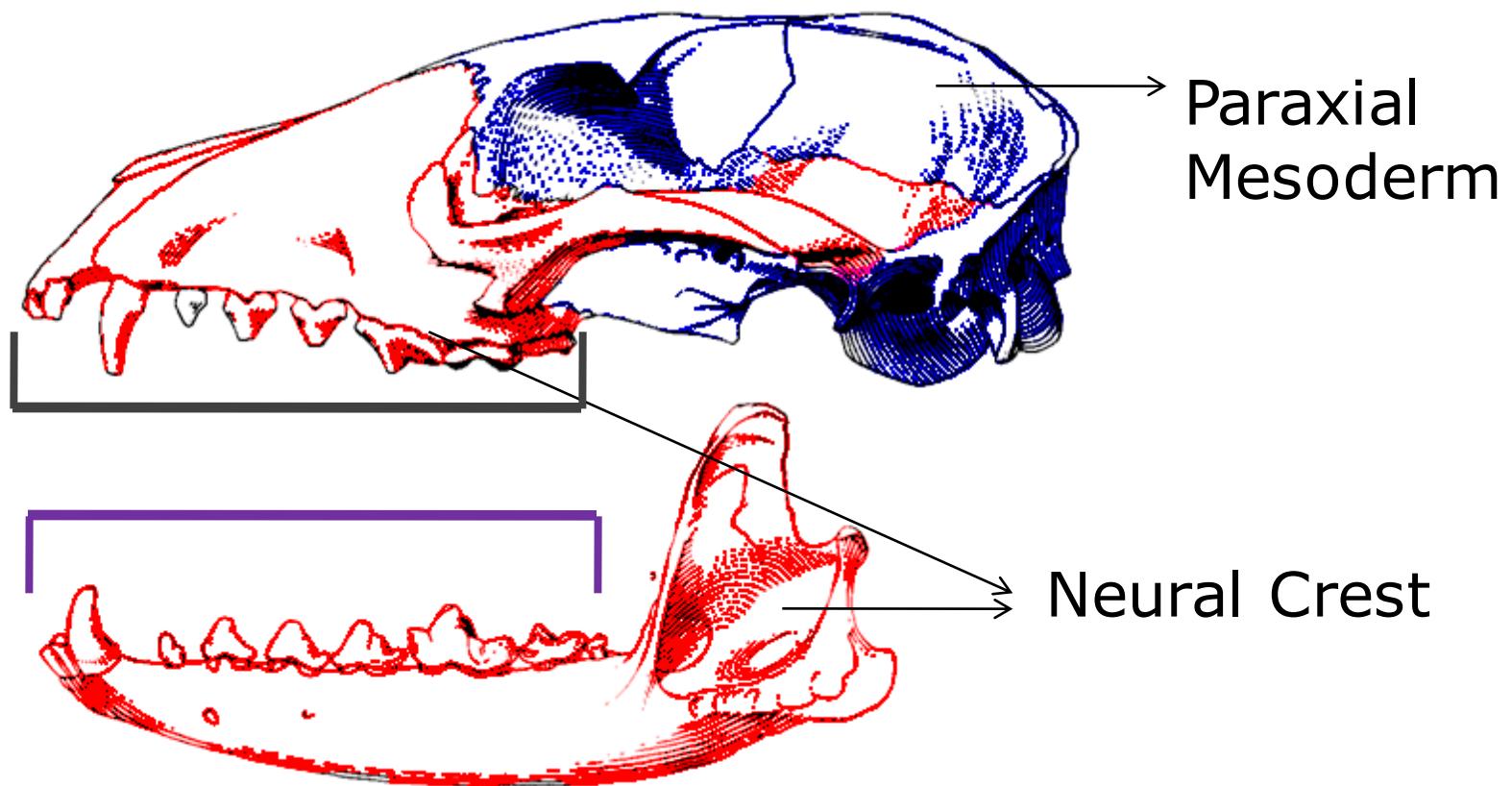
Genotype-Phenotype map

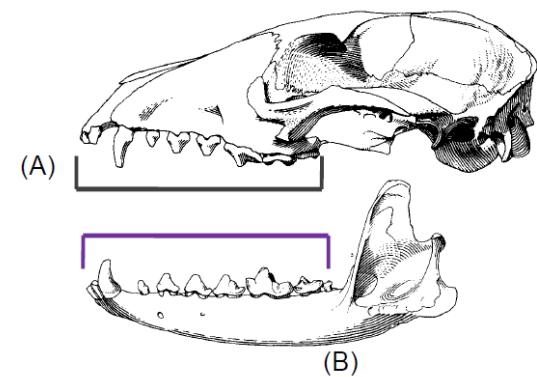
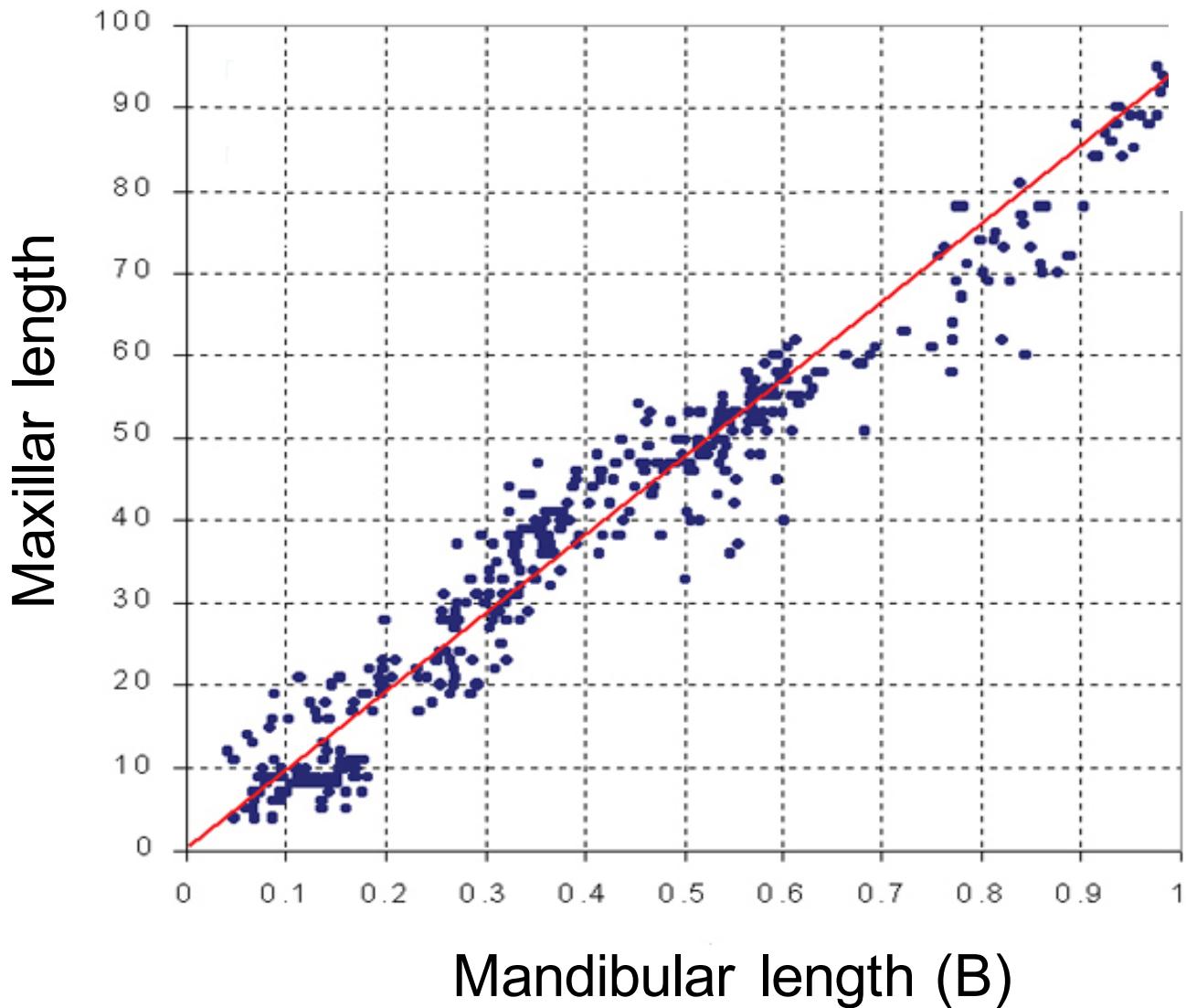


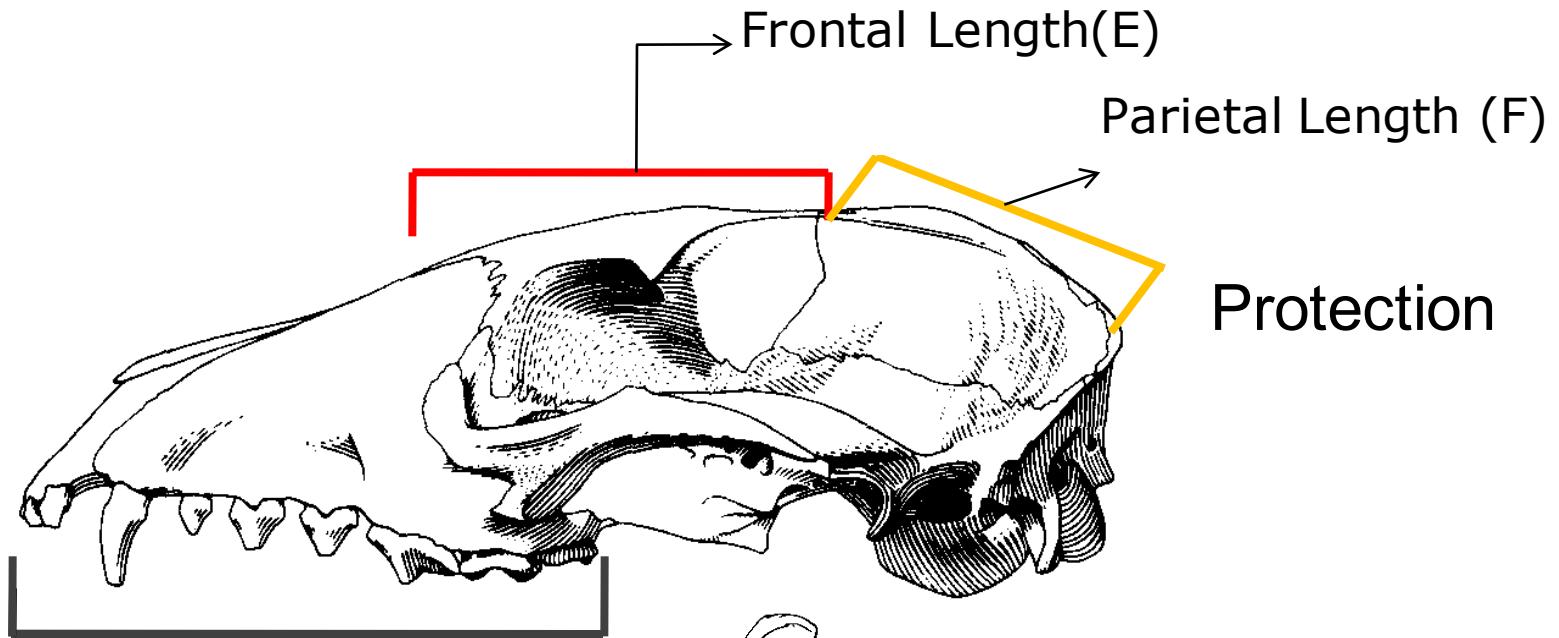
Let's take a look on this...



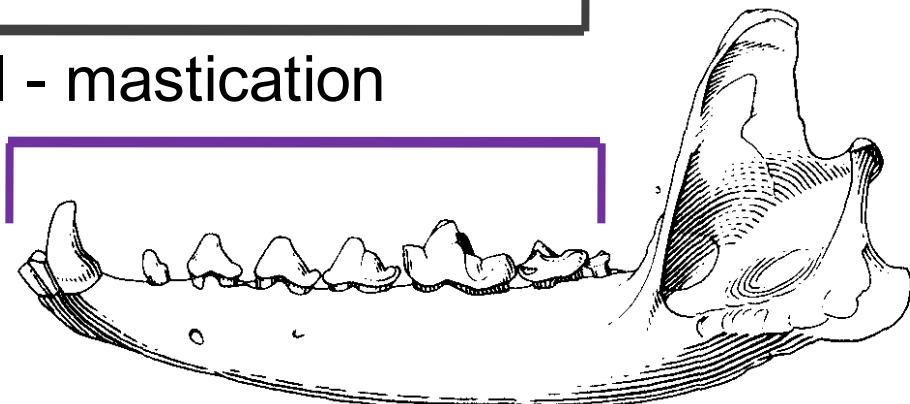
Common developmental origin





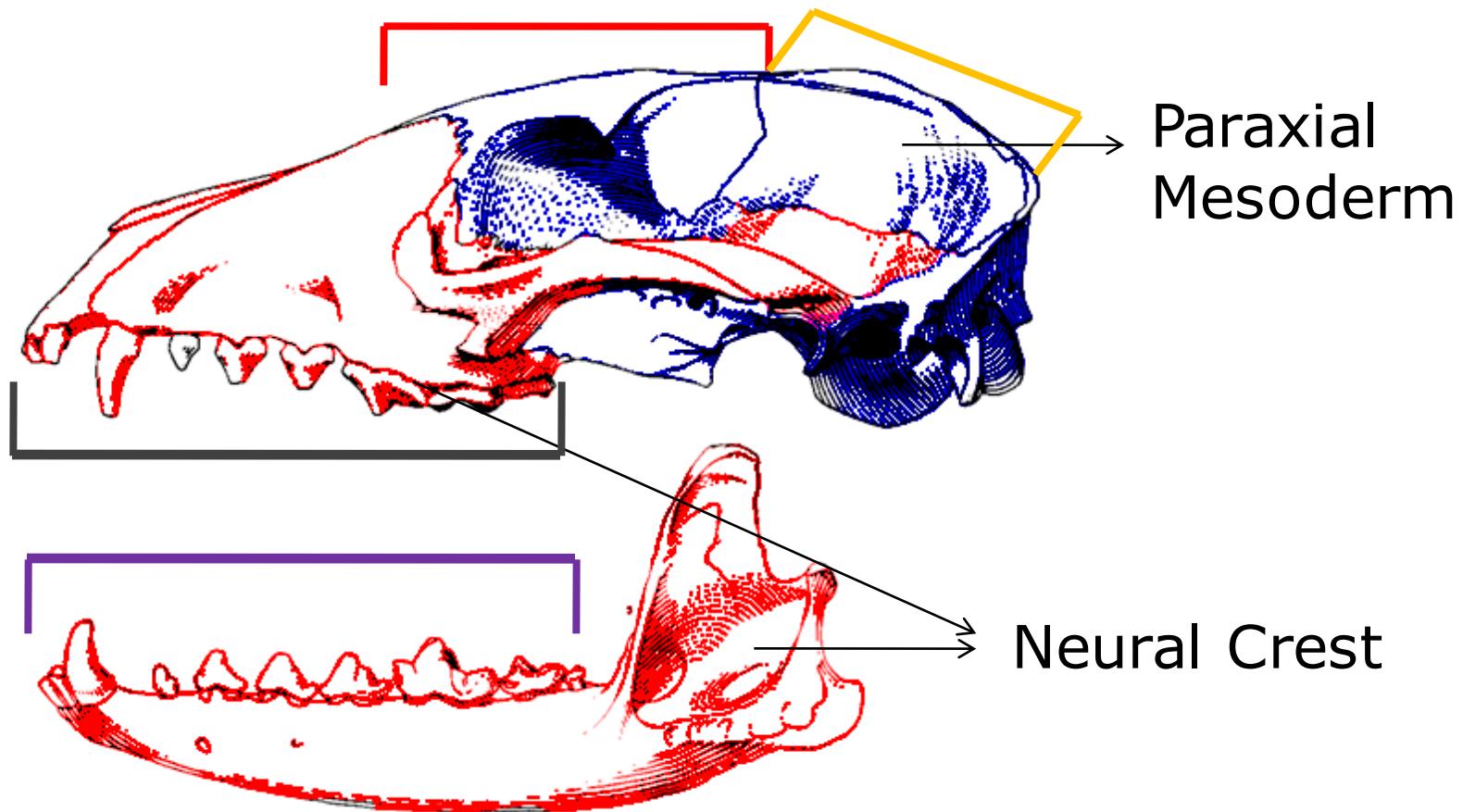


Oral - mastication

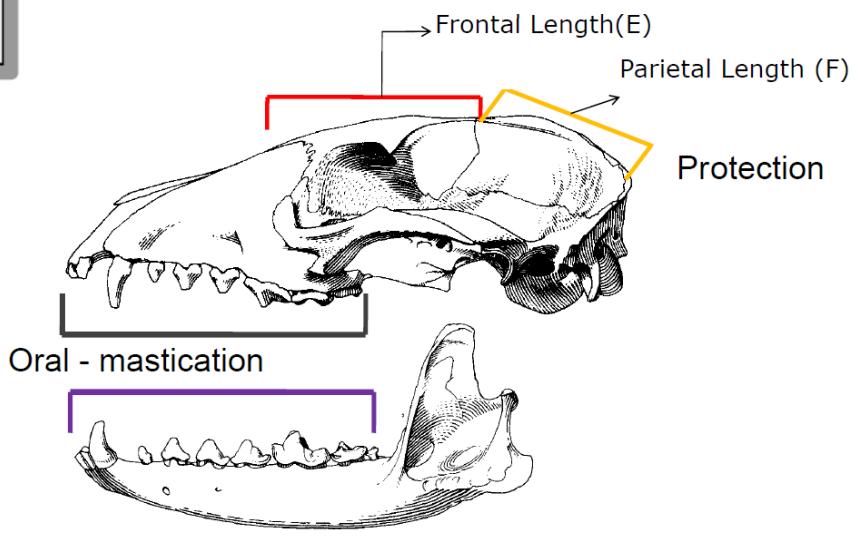
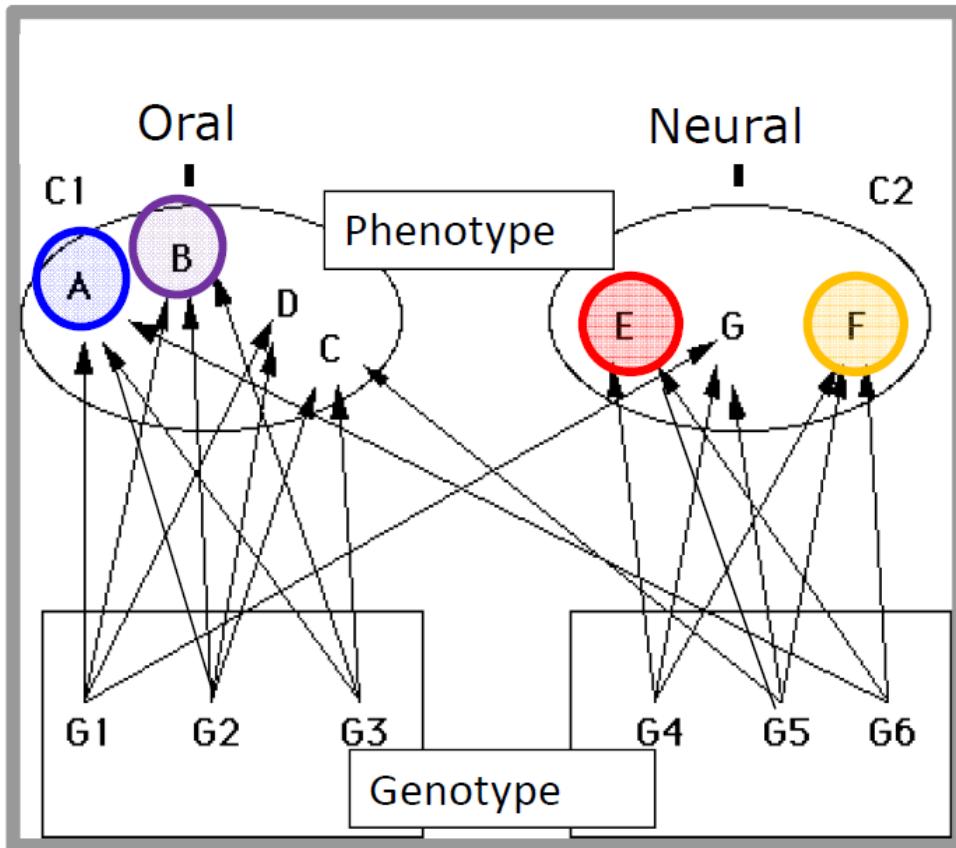


Modified from Berta, 1982

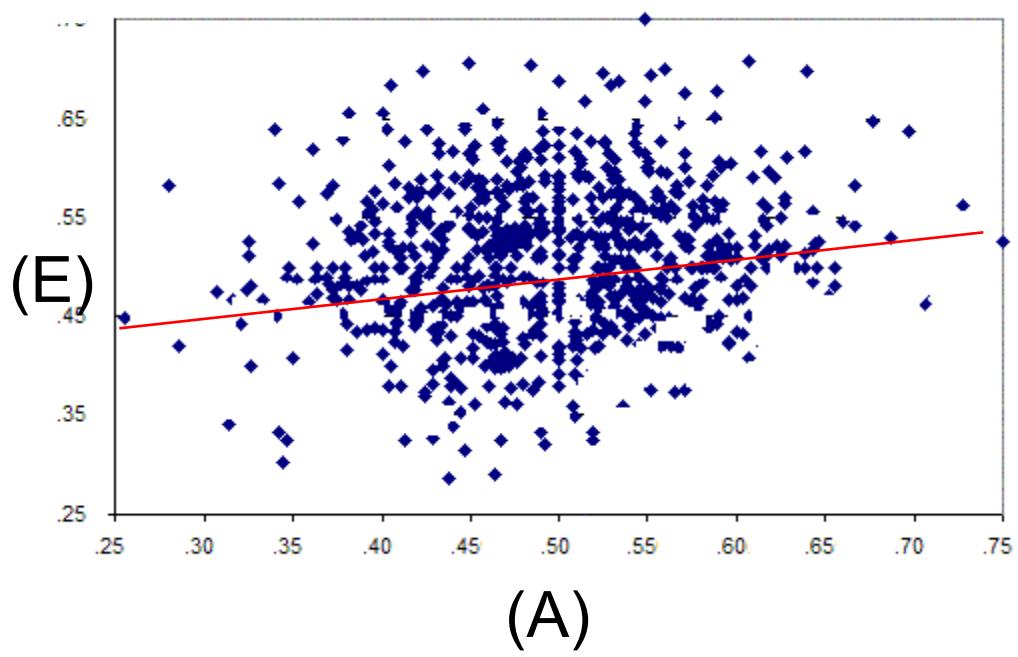
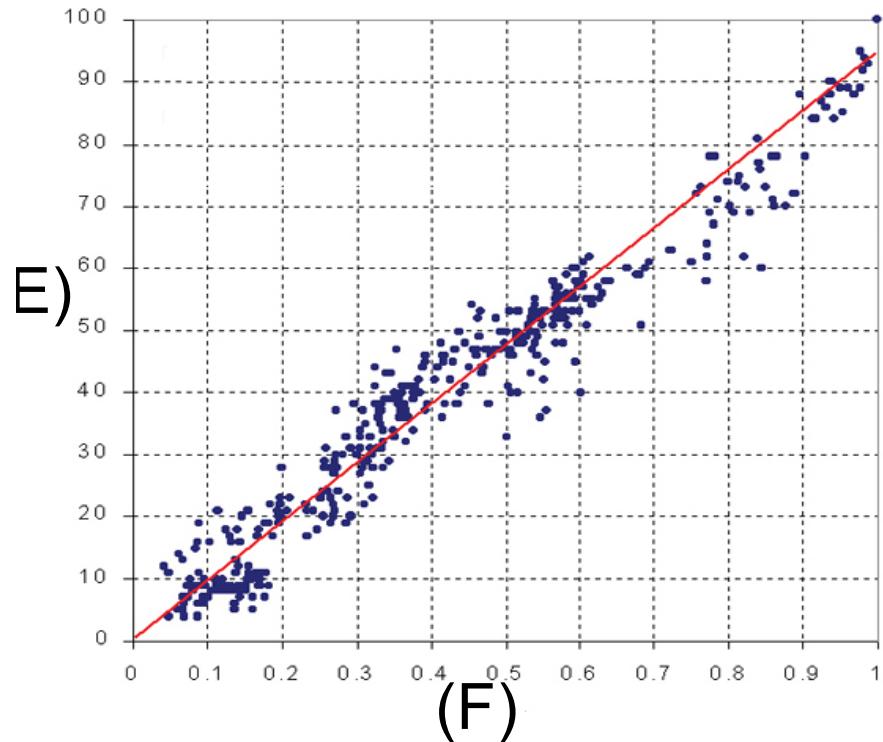
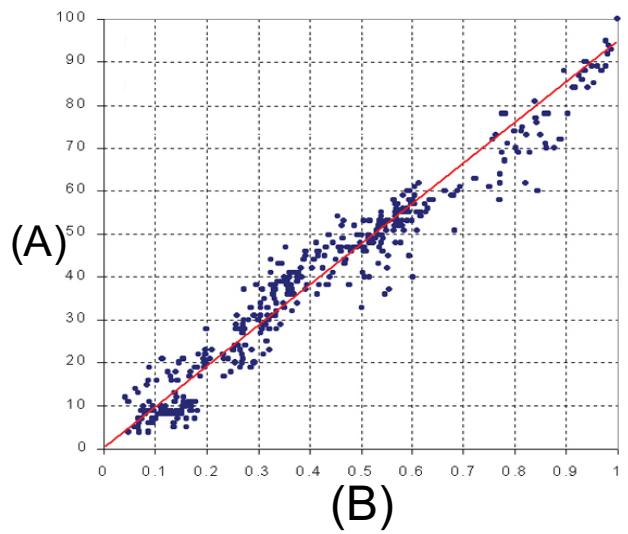
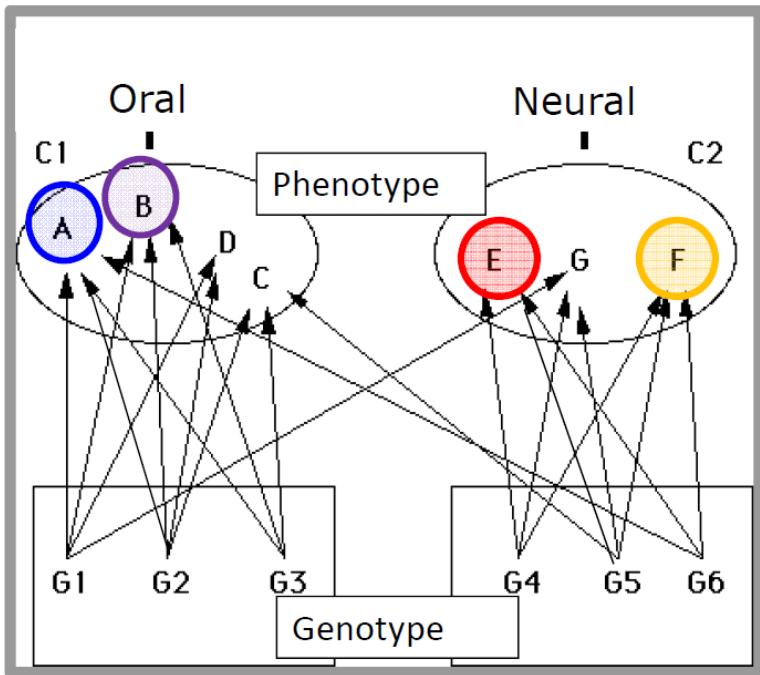
Developmental Origin and Function



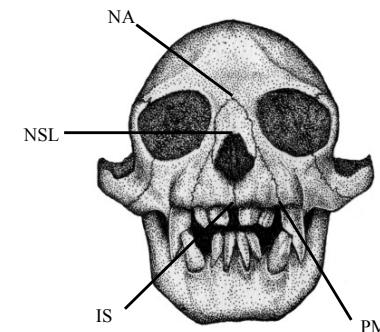
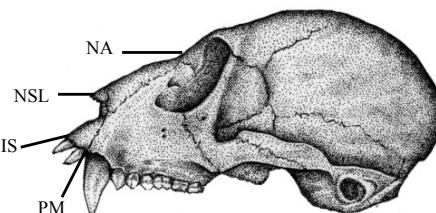
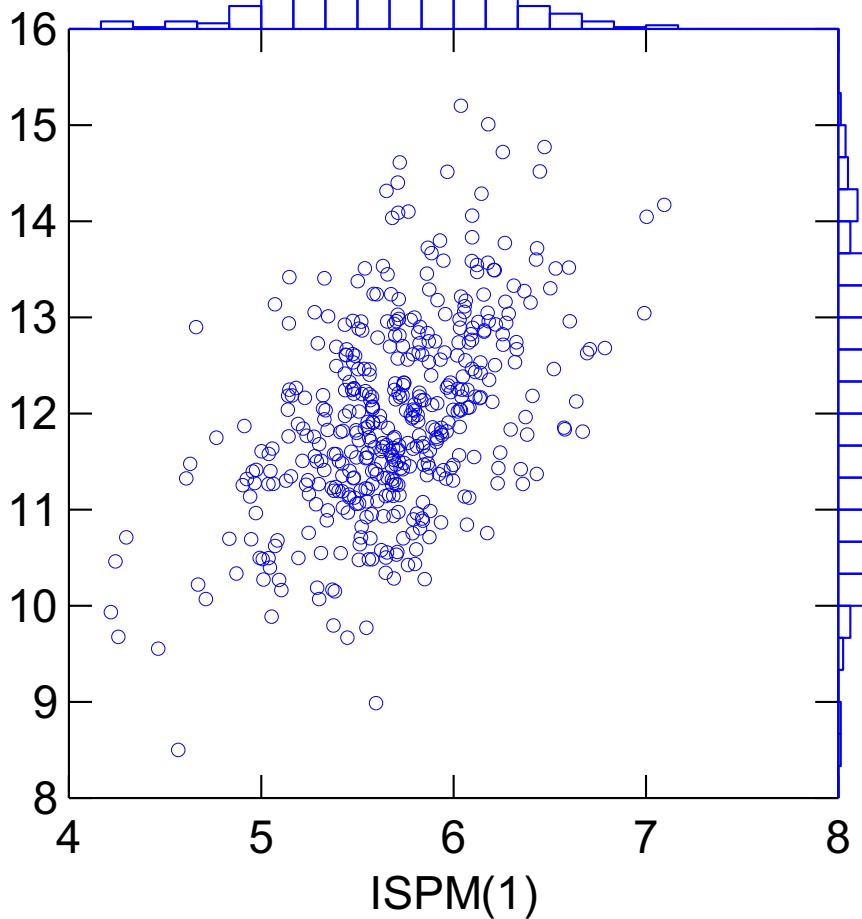
Pleiotropy and Epistasis are key elements of the genetic architecture underlying morphological integration and modularity



Modified from Berta, 1982



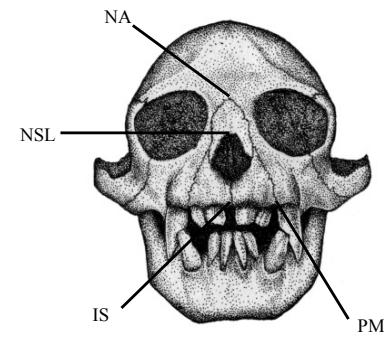
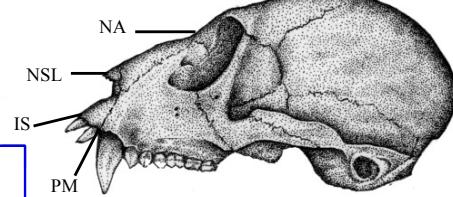
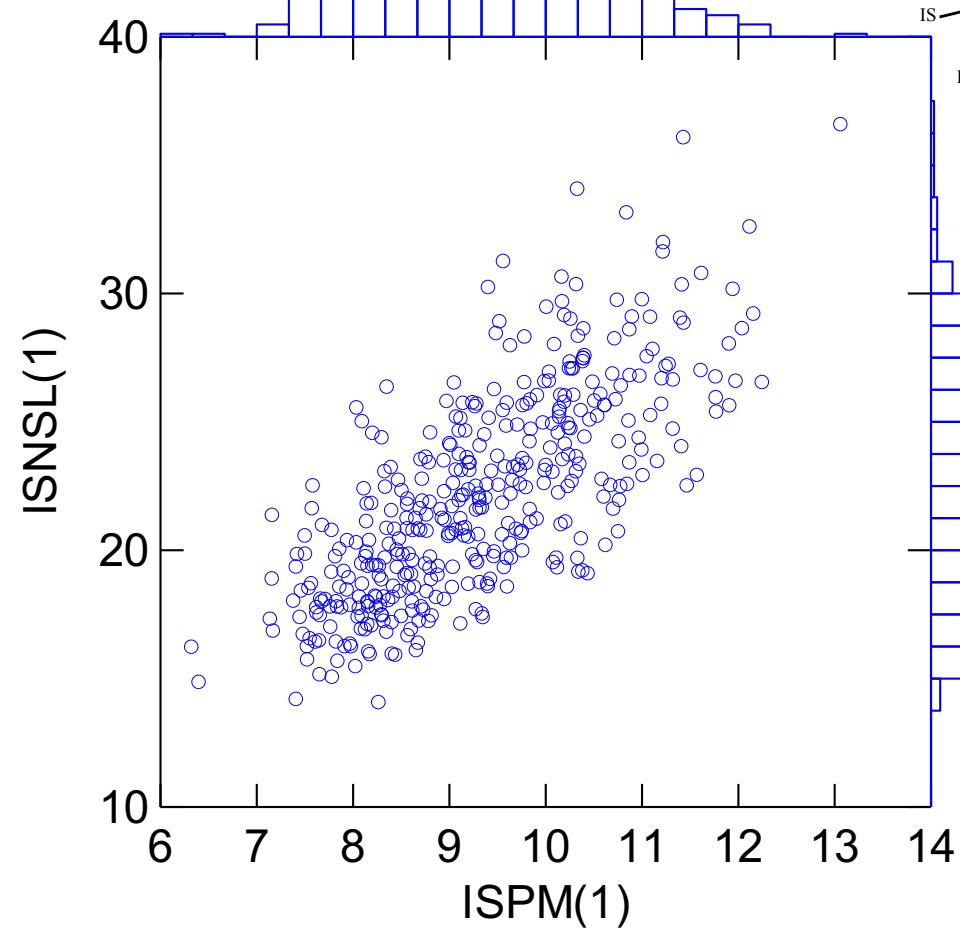
ISNSL(1)



Callicebus (sauás or guigós)



Alouatta (bugios or roncadores)



Variância fenotípica = Variância genética + Variância ambiental

$$V_p = V_g + V_e$$

$V_g = V_a$ (aditiva) + V_d (dominância) + V_i (epistática)

$$V_p = V_a + V_d + V_i + V_e$$

$$COV(x, y) = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{n-1}$$

$$s^2 = \hat{\sigma}^2 = \frac{\sum (X_i - \bar{X})^2}{(n-1)}$$

$$r_{(x,y)} = \frac{COV(x,y)}{s_x s_y}$$

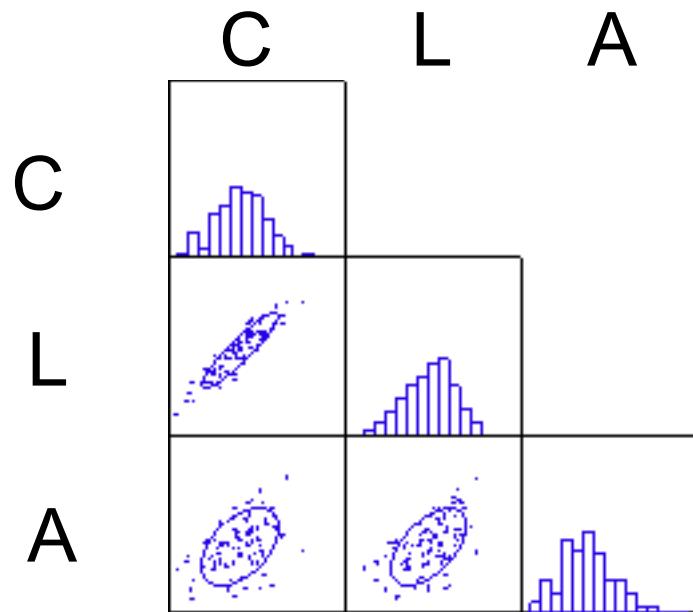
Genetic Correlation and Covariance

- phenotypic correlation = genetic + environmental correlation
- $r_P = r_A + r_D + r_E$
- $r_P = h_x h_y r_A + e_x e_y r_E$

$$\text{COV}_{P_{xy}} = \text{COV}_{A_{xy}} + \text{COV}_{E_{xy}}$$

Variance/Covariance and Correlation Matrices

Represent the pattern and magnitude of modularity and integration



$$\begin{matrix} & \text{C} & \text{L} & \text{A} \\ \text{C} & \mathbf{v}_C & & \\ \text{L} & \mathbf{CV}_{C-L} & \mathbf{v}_L & \\ \text{A} & \mathbf{CV}_{C-A} & \mathbf{CV}_{L-A} & \mathbf{v}_A \end{matrix}$$

$$\begin{bmatrix} 1 \\ \text{Corr}_{C-L} & 1 \\ \text{Corr}_{C-A} & \text{Corr}_{L-A} & 1 \end{bmatrix}$$

Why should we care about those variance/covariance patterns ?

- Patterns of genetic and developmental variation might either constrain or facilitate the evolution of morphological complexes and direct the pathways and pace of evolutionary change.
- Also, those MI (morphological integration) patterns are a product of development, genetic architecture and previous history of a lineage

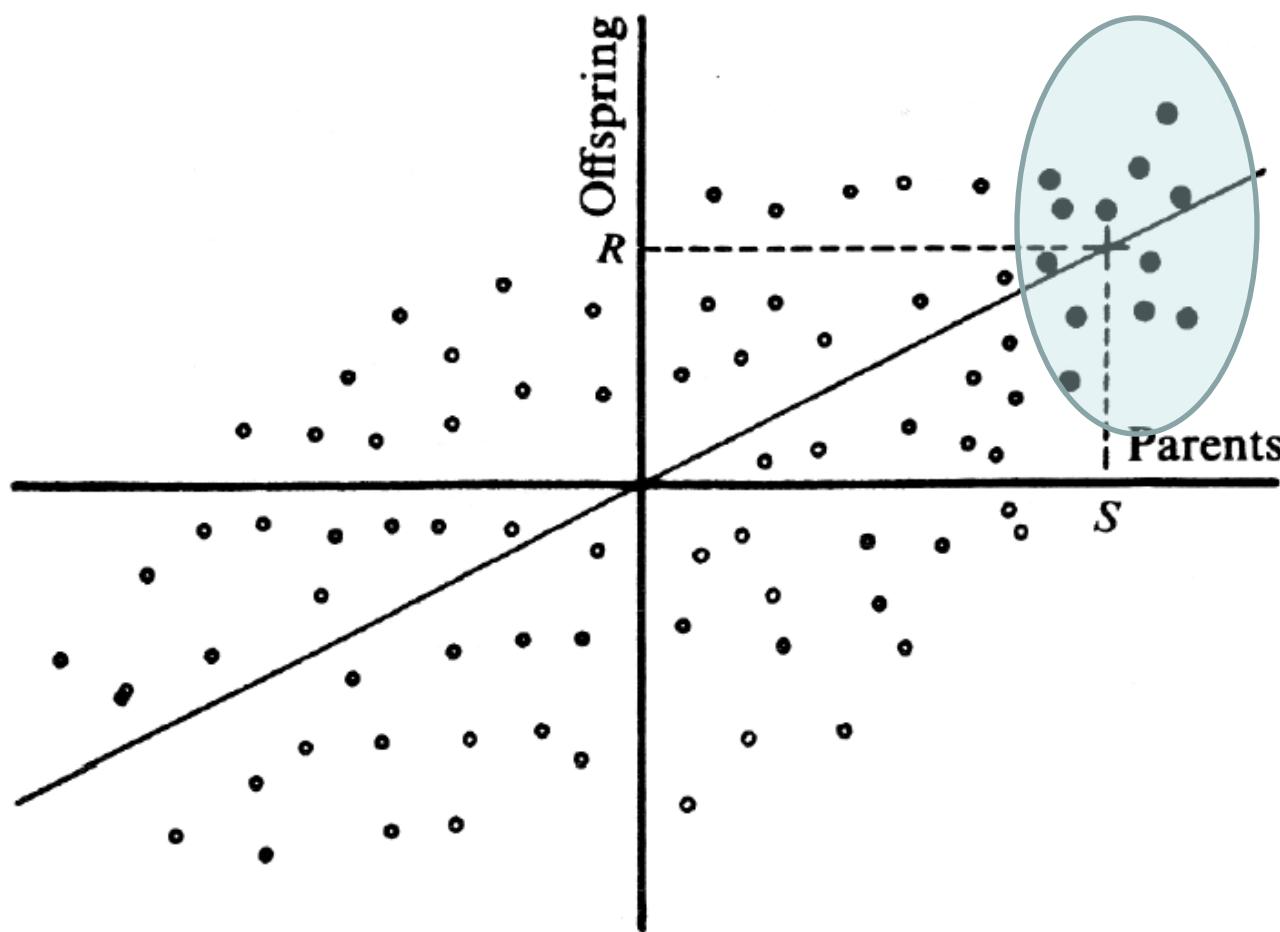


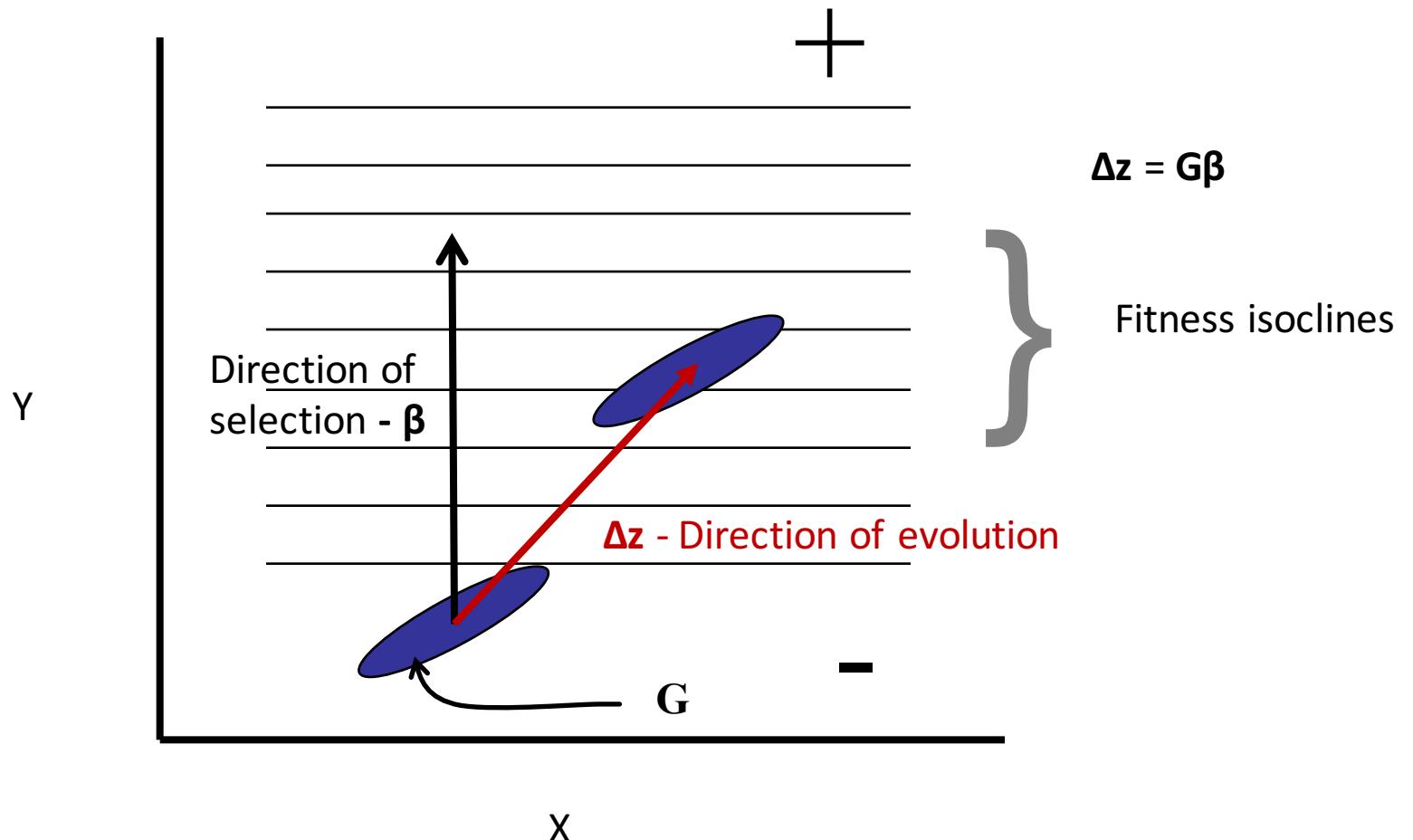
Fig. 11.1. Diagrammatic representation of the mean values of progeny plotted against the mid-parent values, to illustrate the response to selection, as explained in the text.

Darwinian Evolution

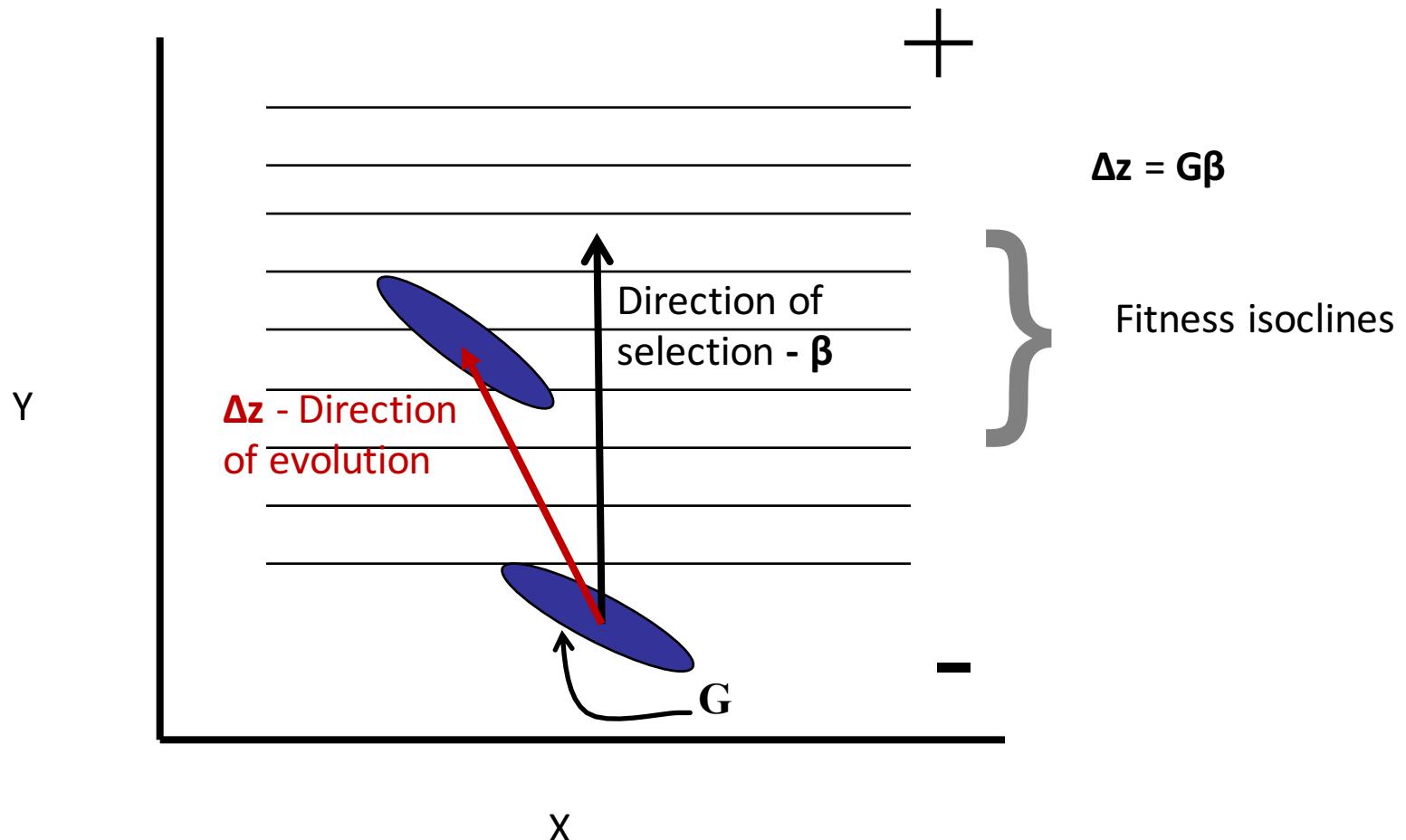
$$\Delta z = G\beta$$

Evolutionary Change = Heritable Genetic X Selection
Variation/Covariation

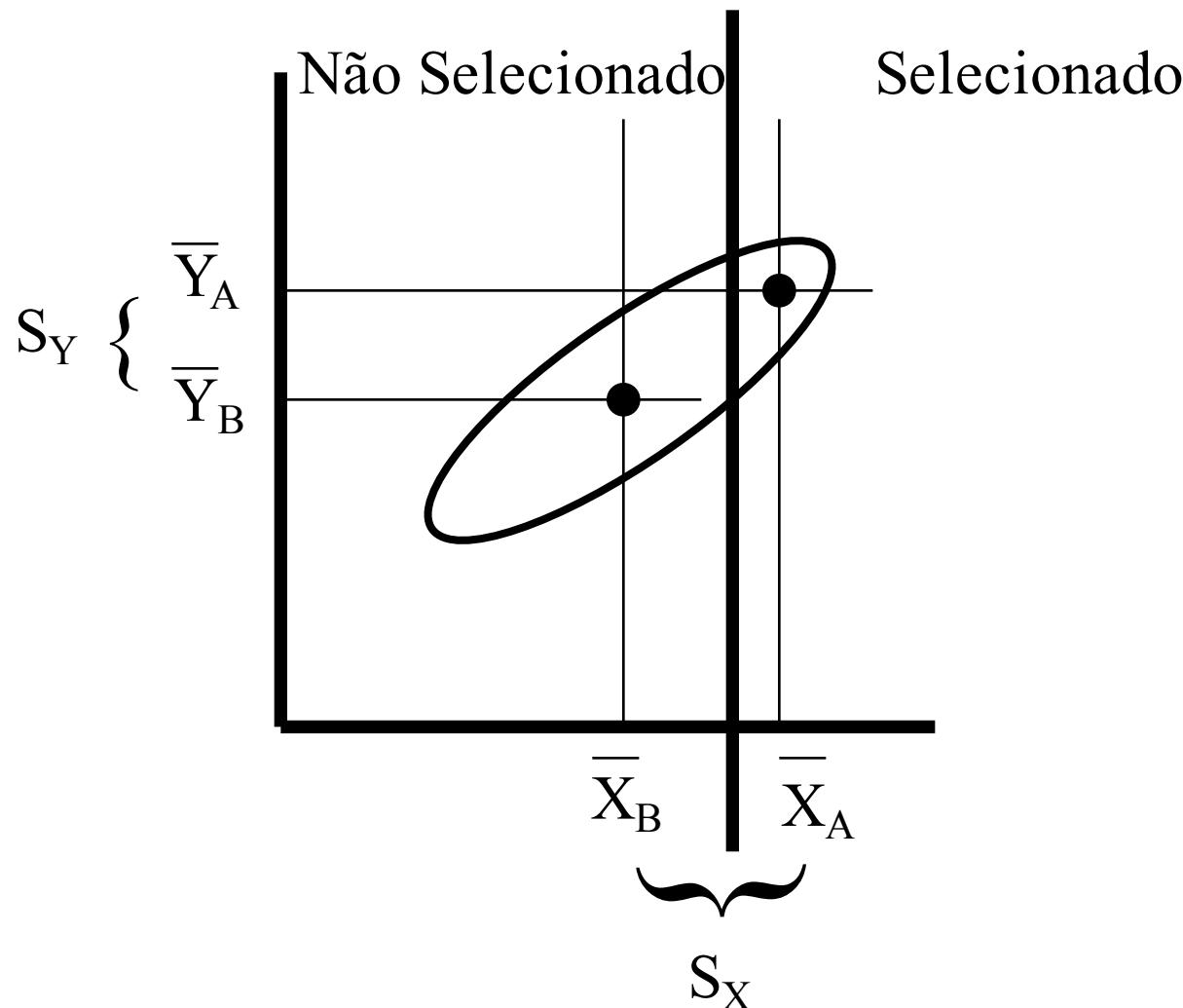
Evolutionary response to selection (Δz) deviates from the direction of selection (β) because of the pattern of the genetic variance/covariance matrix (G)



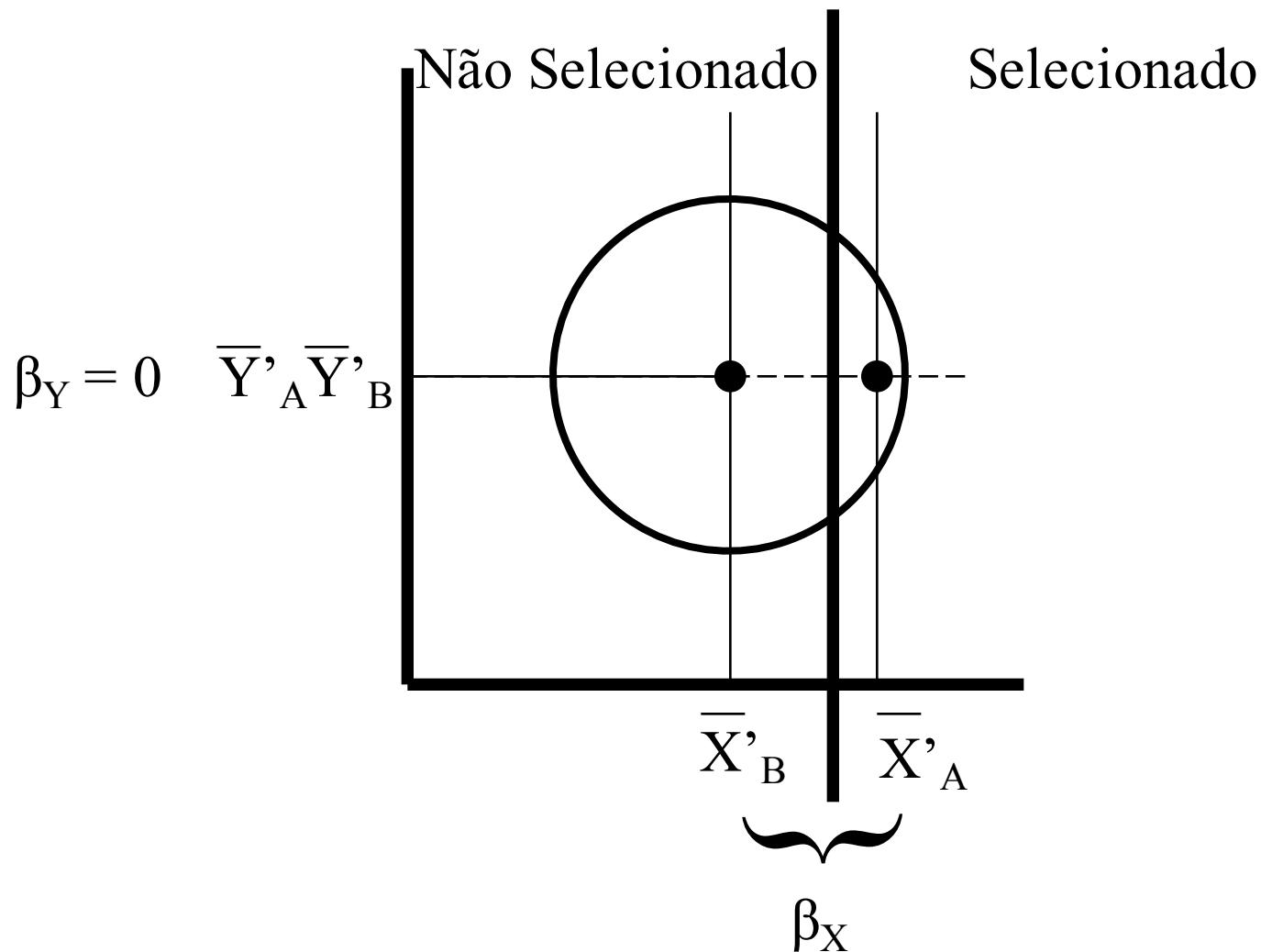
Evolutionary response to selection (Δz) deviates from the direction of selection (β) because of the pattern of the genetic variance/covariance matrix (G)

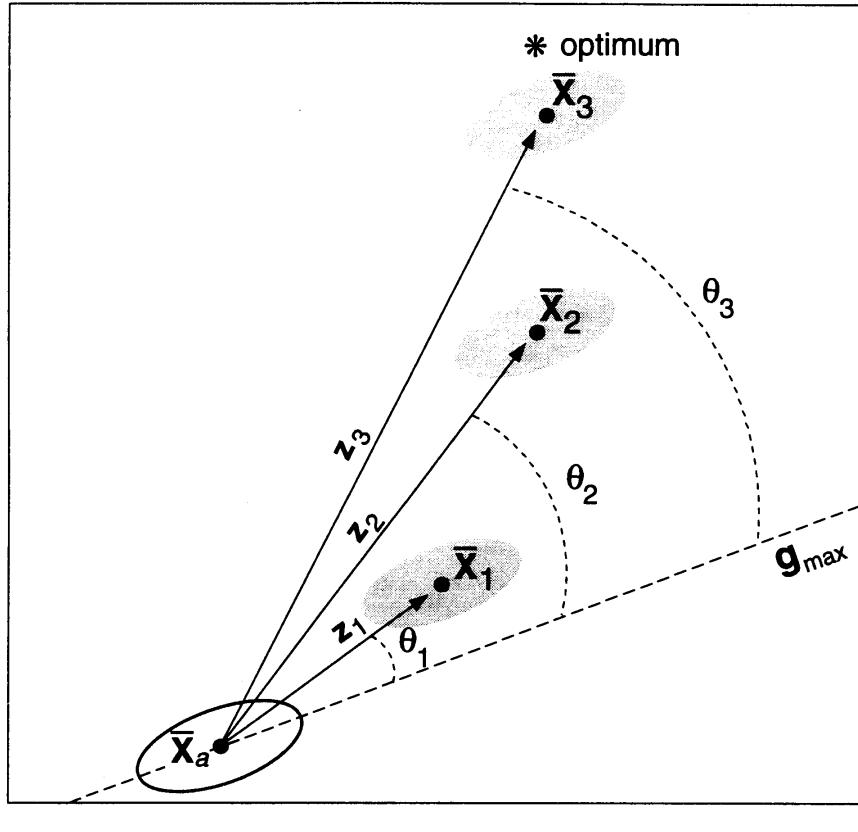


Seleção aparente em Y com seleção direta no caráter correlacionado X



Seleção direta em X Independente da Seleção direta no Caráter Correlacionado Y





Trait 1

FIG. 1. The path of divergence between two species when traits are genetically correlated. Ellipses outline the additive genetic ("breeding") values of individuals within each population. The long axis of the ellipse is the direction of greatest genetic variance, \mathbf{g}_{\max} . To simplify the illustration, the position of one of the species is assumed to be fixed at the ancestral value ($\bar{\mathbf{X}}_a$; unshaded). The second species (shaded) is diverging from the first because of continuous directional selection toward a new optimum. Three stages of divergence ($\bar{\mathbf{X}}_1 - \bar{\mathbf{X}}_3$) illustrate the curved path taken; $\mathbf{z}_1 - \mathbf{z}_3$ are directions of the difference between ancestor and descendant at each stage; θ measures the angle between \mathbf{g}_{\max} and the line separating species means, \mathbf{z} .

LINES OF LEAST RESISTANCE

ER

Research, University of British Columbia,
V6T 1Z4, Canada
evolution.ubc.ca

ful for predicting long-term adaptive evolution? To reatest additive genetic variance within populations. genetic measurements from other vertebrates, show ed in the direction of \mathbf{g}_{\max} for at least four million ntiation. This bias toward the direction of evolution een species is inversely proportional to θ , the angle netic variation. The direction of greatest phenotypic is successful at predicting the direction of species es and covariances constrain adaptive change in ve hypothesis, however, cannot be ruled out: that se divergence and \mathbf{g}_{\max} are both shaped by the same ve differentiation occurs principally along "genetic

relation, genetic variance, heritability, natural se-

Received March 19, 1996.

Restrições Evolutivas = qualquer coisa que altere a direção, taxa e magnitude da mudança evolutiva -> capturada na Matriz **G** (matriz de variância/covariância genética aditiva)

* While constraints sometimes are perceived as an obstacle to evolution in some directions they might also be envisaged as facilitating the adaptive process along what Schlüter (1996) called “genetic lines of least evolutionary resistance”.

Evolution, 50(5), 1996, pp. 1766–1774

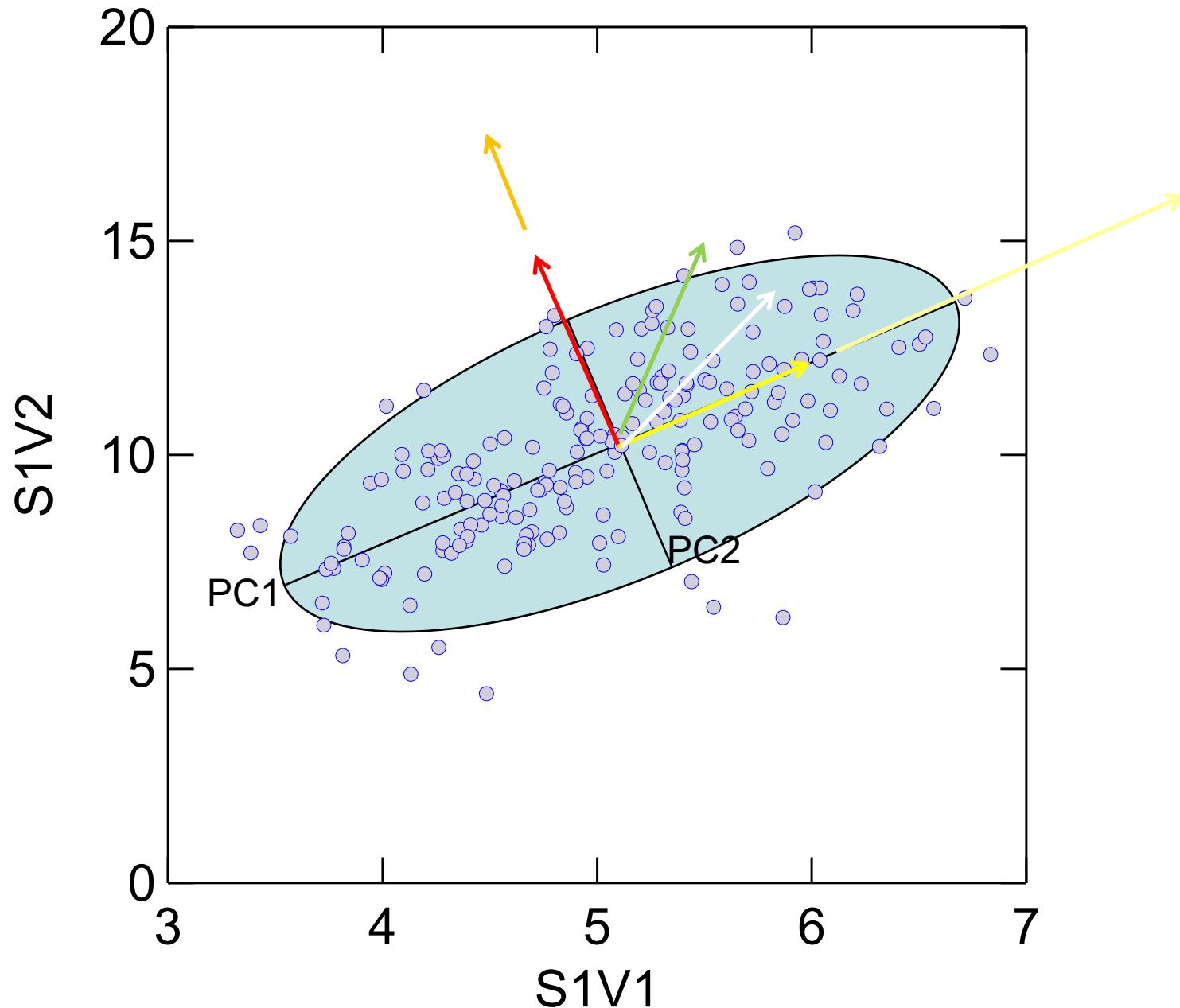
ADAPTIVE RADIATION ALONG GENETIC LINES OF LEAST RESISTANCE

DOLPH SCHLUTER

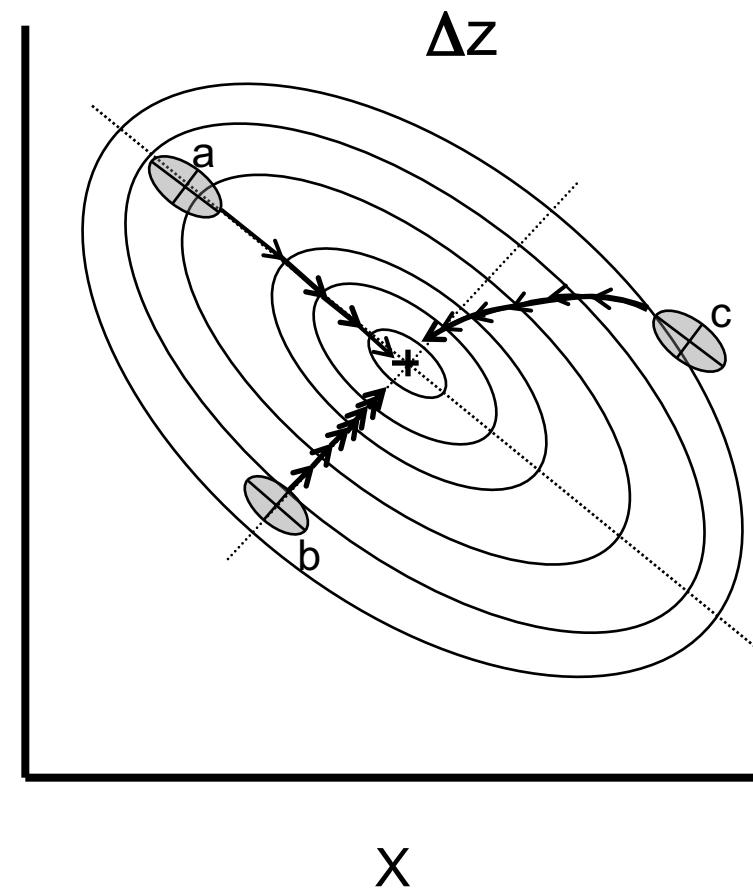
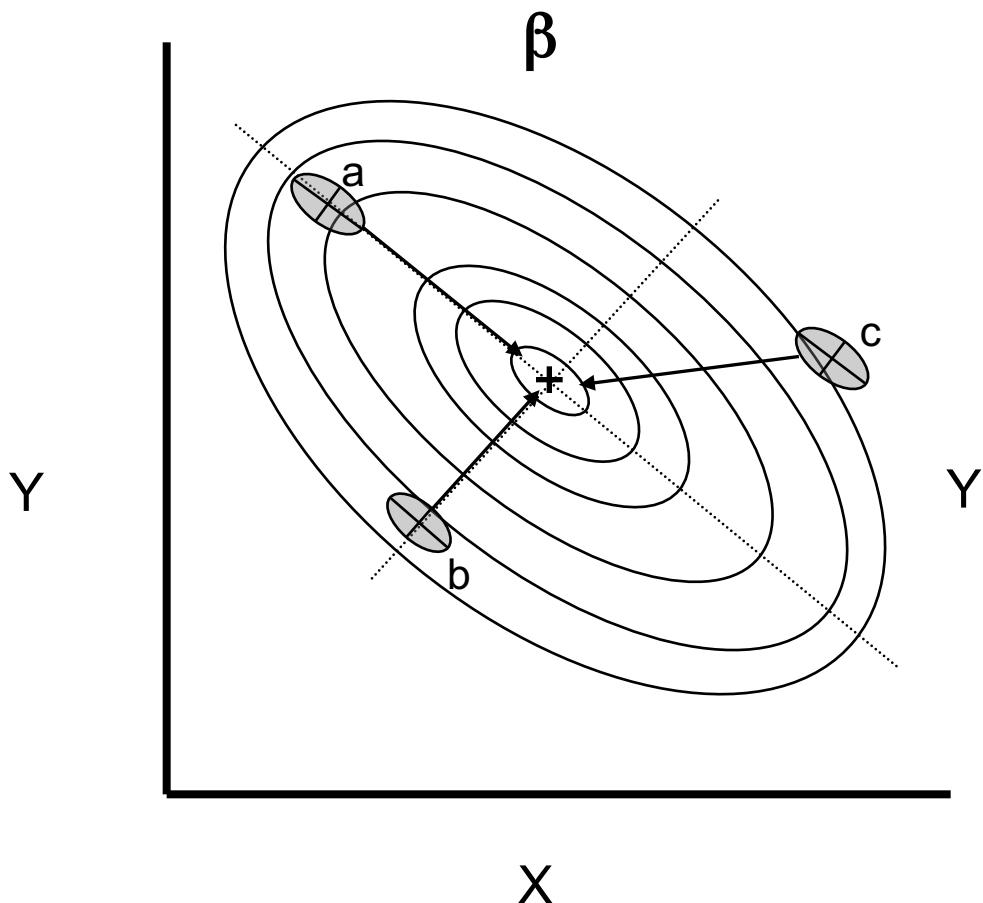
*Department of Zoology and Centre for Biodiversity Research, University of British Columbia,
Vancouver, British Columbia V6T 1Z4, Canada
E-mail: schluter@zoology.ubc.ca*



Cores escuras = gradientes de seleção
Cores claras = respostas evolutivas

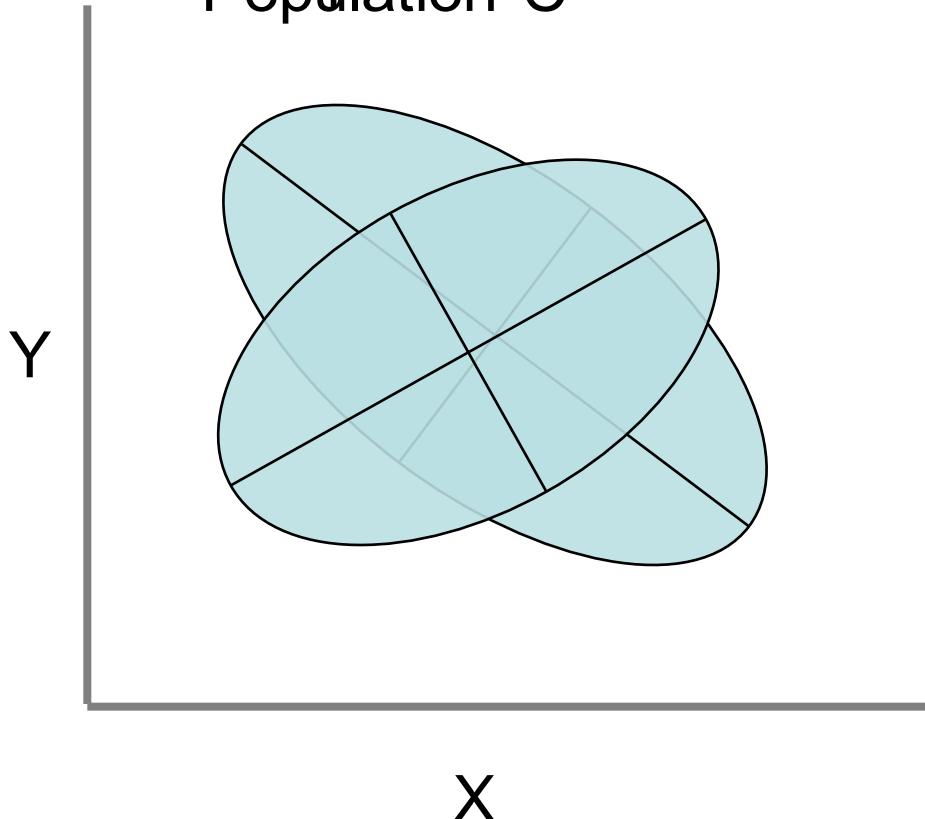


Paisagem Adaptativa

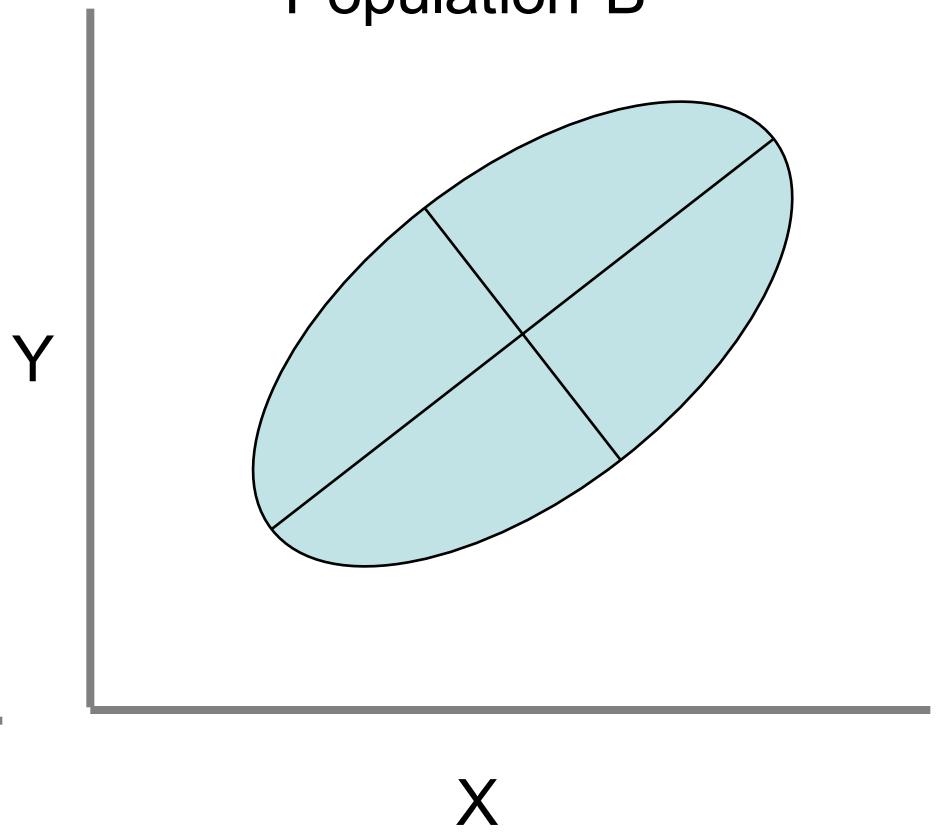


Critical issue ! Are those V/CV patterns similar among groups? – should be evaluated empirically

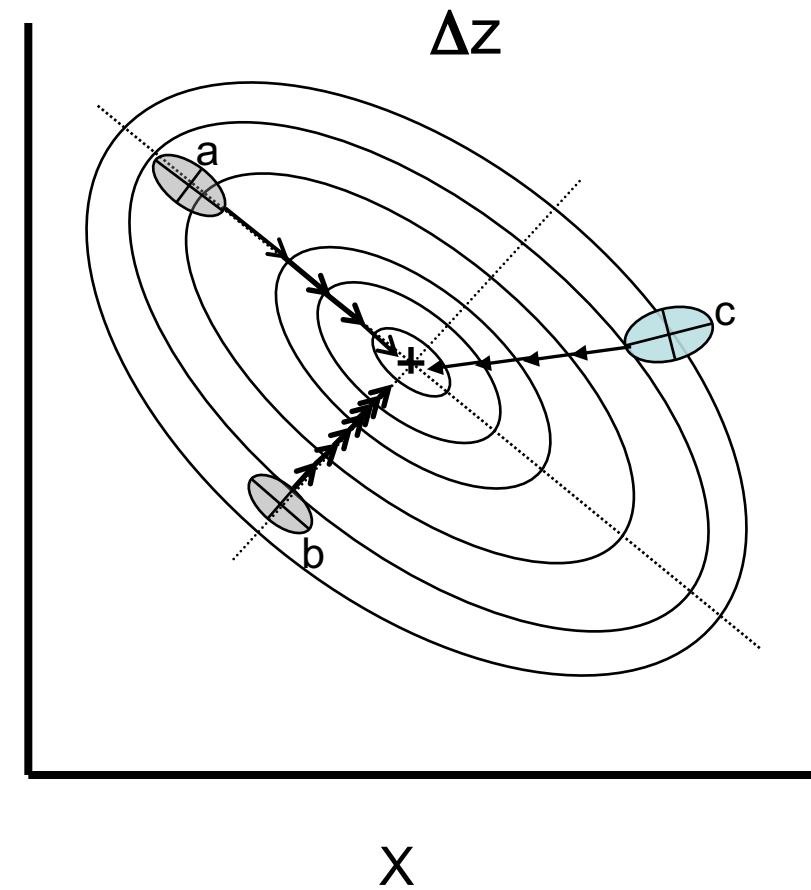
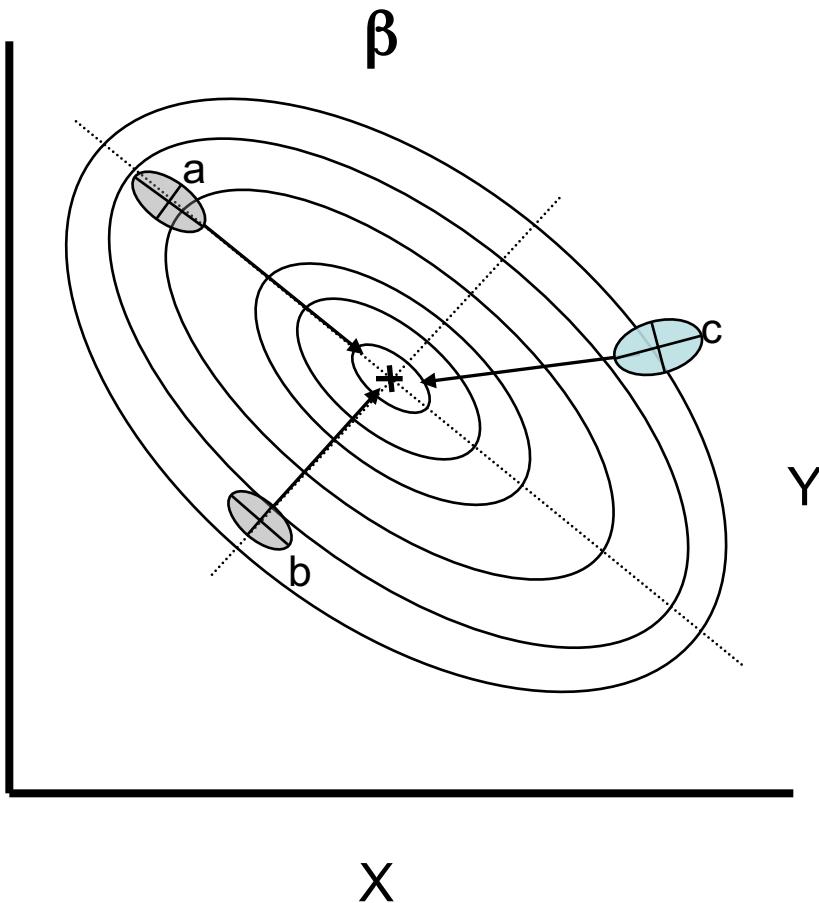
Population A



Population B



Paisagem Adaptativa



Em matemática, o produto de duas matrizes é definido somente quando o número de colunas da primeira matriz é igual ao número de linhas da segunda matriz. Se A é uma matriz m -por- n e B é uma matriz n -por- p , então seu **produto** é uma matriz m -por- p definida como AB (ou por $A \cdot B$). O produto é dado por

$$(AB)_{ij} = \sum_{r=1}^n a_{ir} b_{rj} = a_{i1}b_{1j} + a_{i2}b_{2j} + \cdots + a_{in}b_{nj}.$$

para cada par i e j com $1 \leq i \leq m$ e $1 \leq j \leq p$.

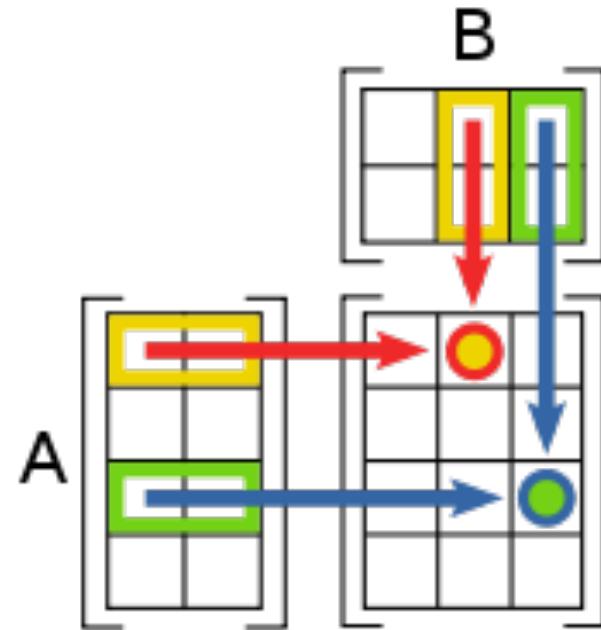
$$P = AB$$

$$P_{rc} = \sum_{\alpha} A_{r\alpha} B_{\alpha c}$$

Example:

$$\begin{bmatrix} 3 & 1 \\ -2 & 5 \end{bmatrix} \begin{bmatrix} 6 & 2 \\ 1 & 9 \end{bmatrix} = \begin{bmatrix} 19 & 15 \\ -7 & 41 \end{bmatrix}$$

$$\begin{bmatrix} 4 & 1 & -3 \\ 5 & 2 & 2 \end{bmatrix} \begin{bmatrix} 2 & 7 \\ 1 & -3 \\ 6 & 4 \end{bmatrix} = \begin{bmatrix} -9 & 13 \\ 24 & 37 \end{bmatrix}$$

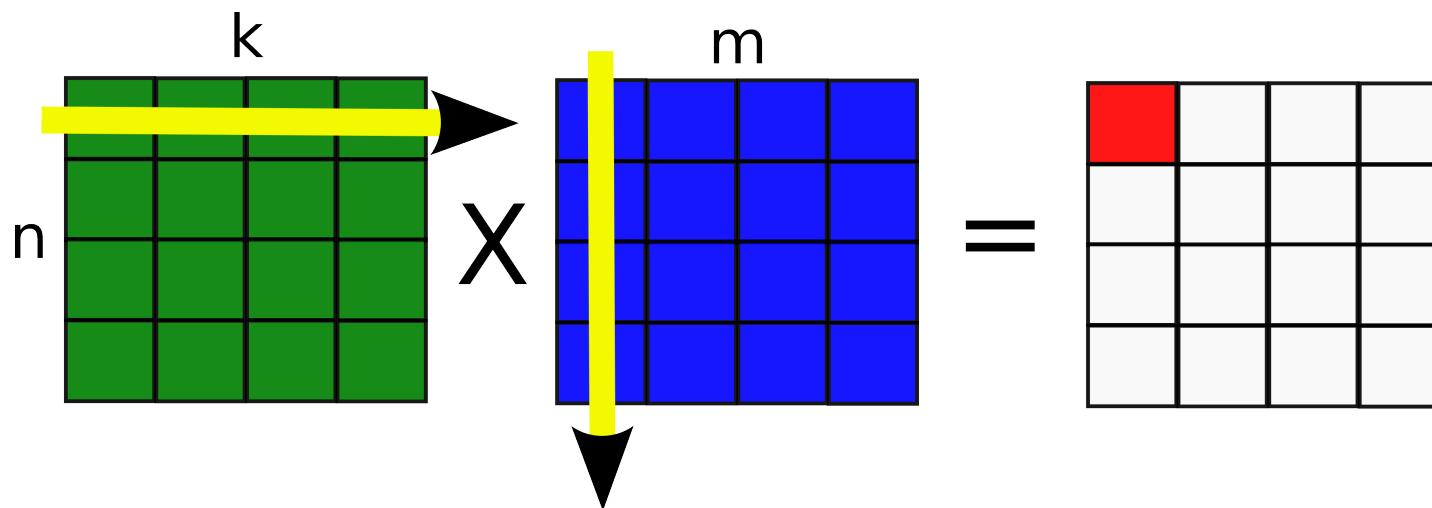


$$\begin{bmatrix} \frac{1}{-1} & 0 & \frac{2}{1} \end{bmatrix} \times \begin{bmatrix} 3 & \frac{1}{2} \\ 2 & \frac{1}{1} \\ 1 & 0 \end{bmatrix} = \begin{bmatrix} 5 & \frac{1}{2} \\ 4 & 2 \end{bmatrix}.$$

$$\begin{bmatrix} 2 & 3 \\ 1 \times 2 \end{bmatrix} \begin{bmatrix} 2 \\ 4 \\ 2 \times 1 \end{bmatrix} = \begin{bmatrix} 16 \\ 1 \times 1 \end{bmatrix}$$

$$\begin{bmatrix} 1 & 3 & 2 \\ 1 \times 3 \end{bmatrix} \begin{bmatrix} 1 & 0 \\ 2 & 4 \\ 5 & 1 \\ 3 \times 2 \end{bmatrix} = \begin{bmatrix} 17 & 14 \\ 1 \times 2 \end{bmatrix}$$

$$\begin{bmatrix} 2 & 5 & 1 \\ 4 & 3 & 1 \\ 2 \times 3 \end{bmatrix} \begin{bmatrix} 1 & 0 & 0 \\ 0 & 2 & 0 \\ 2 & 3 & 1 \\ 3 \times 3 \end{bmatrix} = \begin{bmatrix} 4 & 13 & 1 \\ 6 & 9 & 1 \\ 2 \times 3 \end{bmatrix}$$



$$\mathbf{S} = \mathbf{A} + \mathbf{B}$$

$$S_{rc} = A_{rc} + B_{rc}$$

Example:

$$\begin{bmatrix} 3 & 1 \\ -2 & 5 \end{bmatrix} + \begin{bmatrix} 6 & 2 \\ 1 & 9 \end{bmatrix} = \begin{bmatrix} 9 & 3 \\ -1 & 14 \end{bmatrix}$$

Addition

Two matrices can be added only if both have the same number of columns and the same number of rows. If this criterion is met, then

Evolução Darwiniana

$$\Delta z = G\beta$$

EVOLUÇÃO = VARIAÇÃO * SELEÇÃO
HERDADA

Box 7.7 Continued

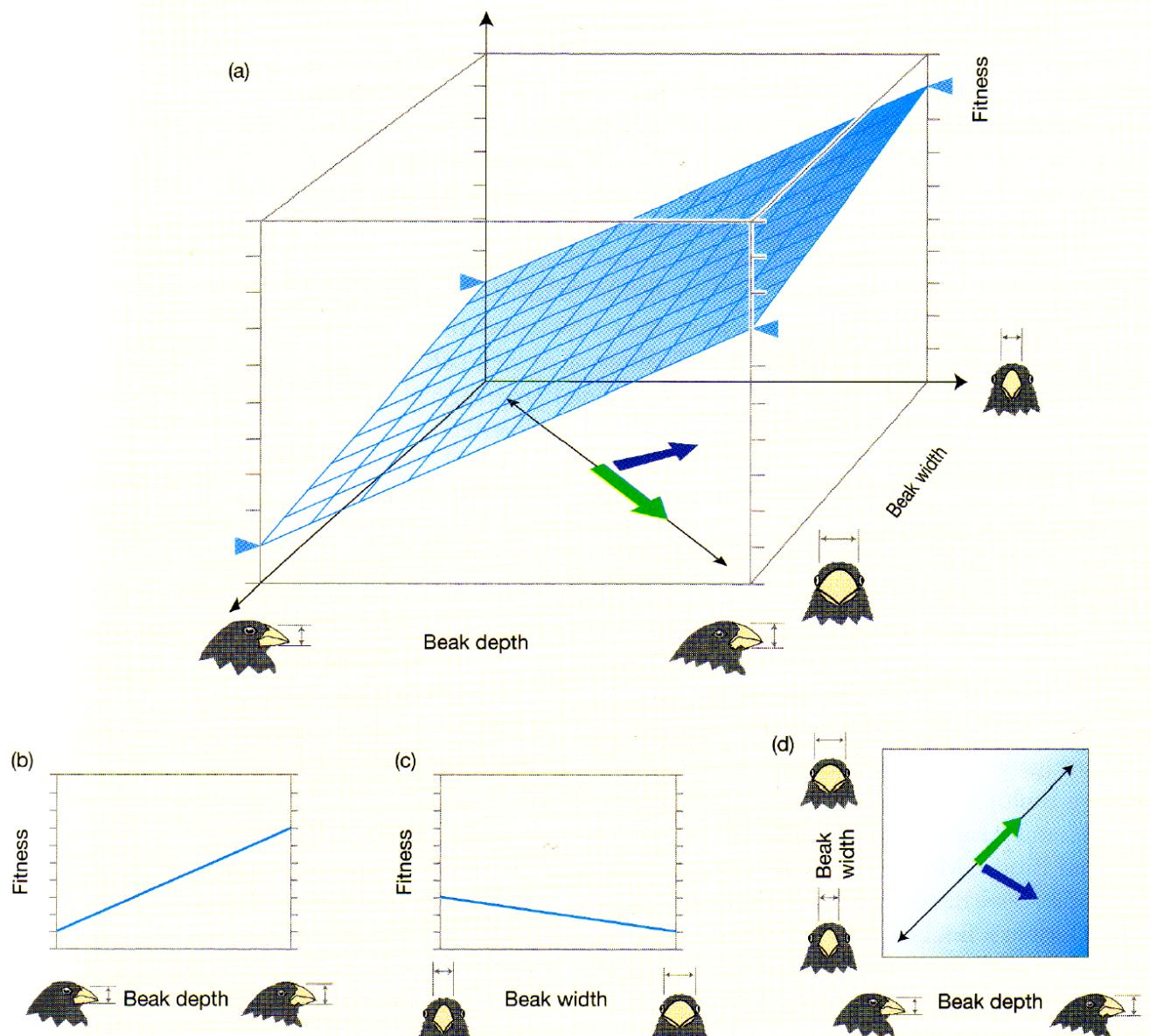
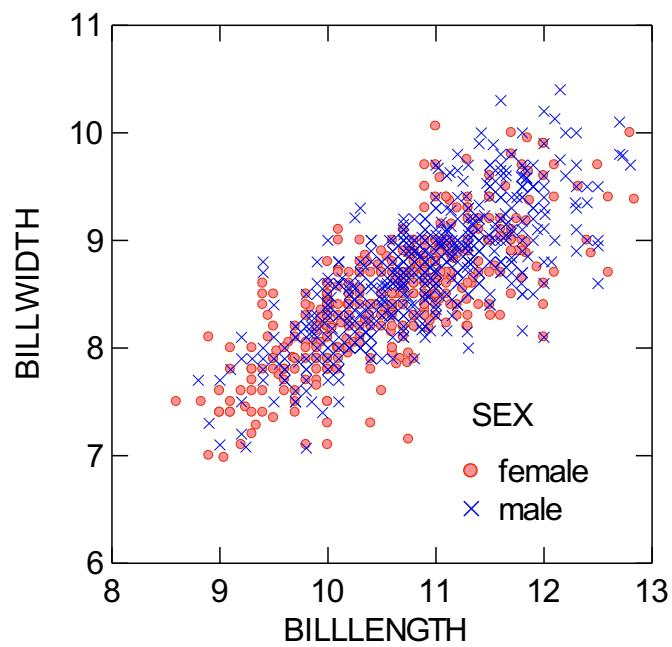
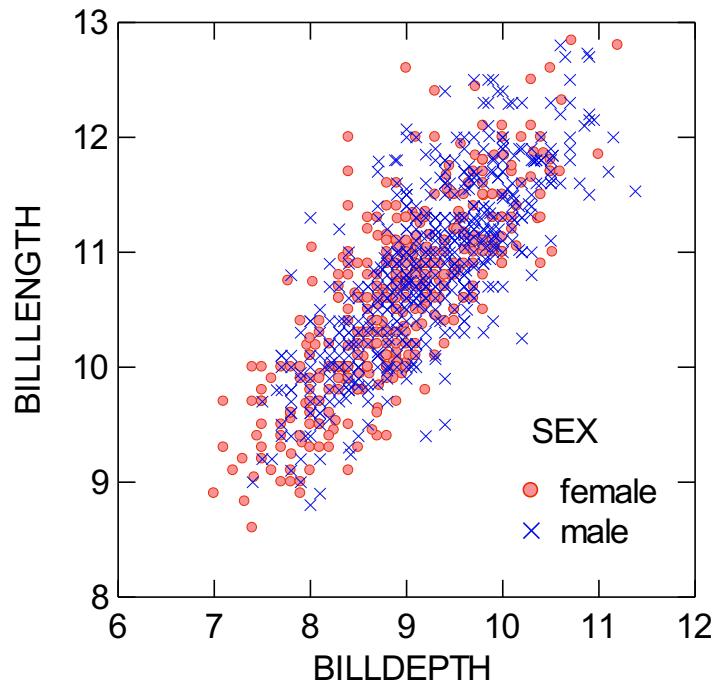
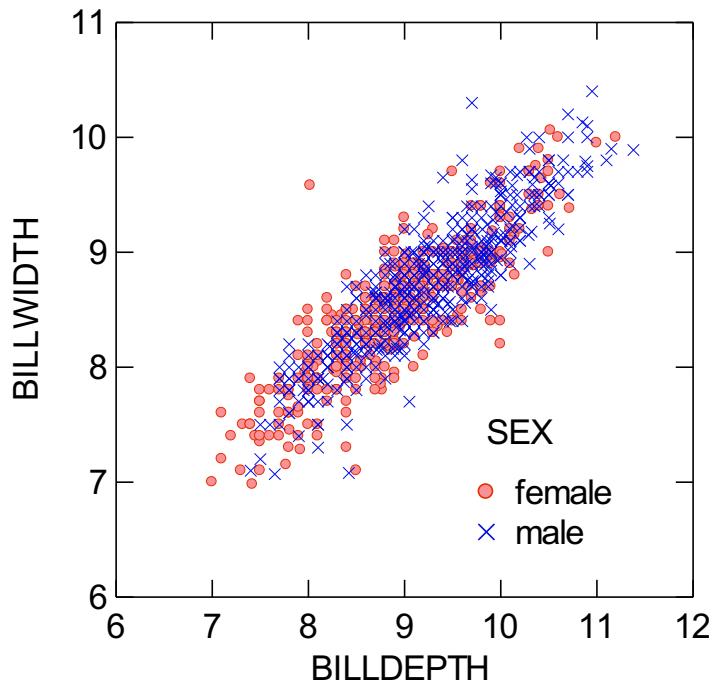
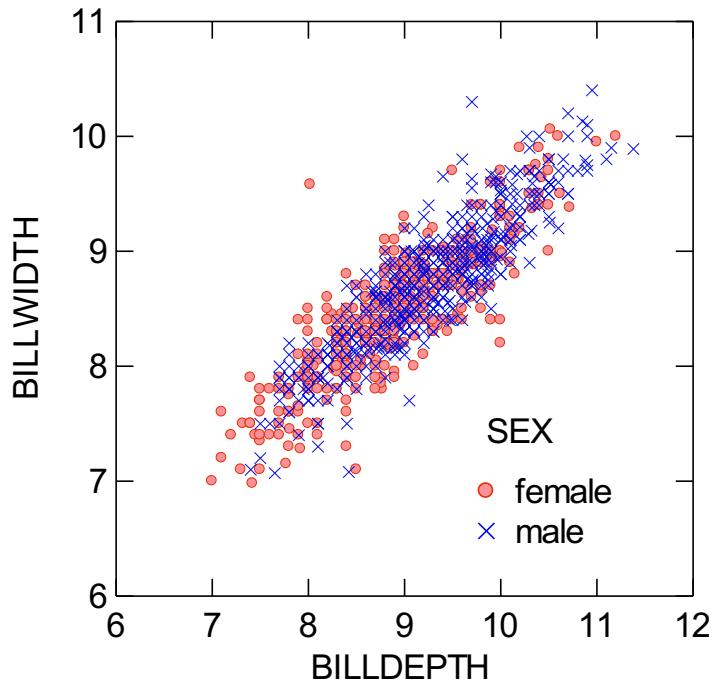


Figure 7.24 A multidimensional analysis of selection on beak size in medium ground finches (a) The gridded plane shows the relationship between fitness and both beak depth and beak width. Birds with deep and narrow beaks had highest fitness. (b), (c), and (d) show the same scenario in two-dimensional graphs.



Column1	BILLLENGTH	BILLDEPTH	BILLWIDTH
BILLLENGTH	1		
BILLDEPTH	0.787	1	
BILLWIDTH	0.762	0.877	1



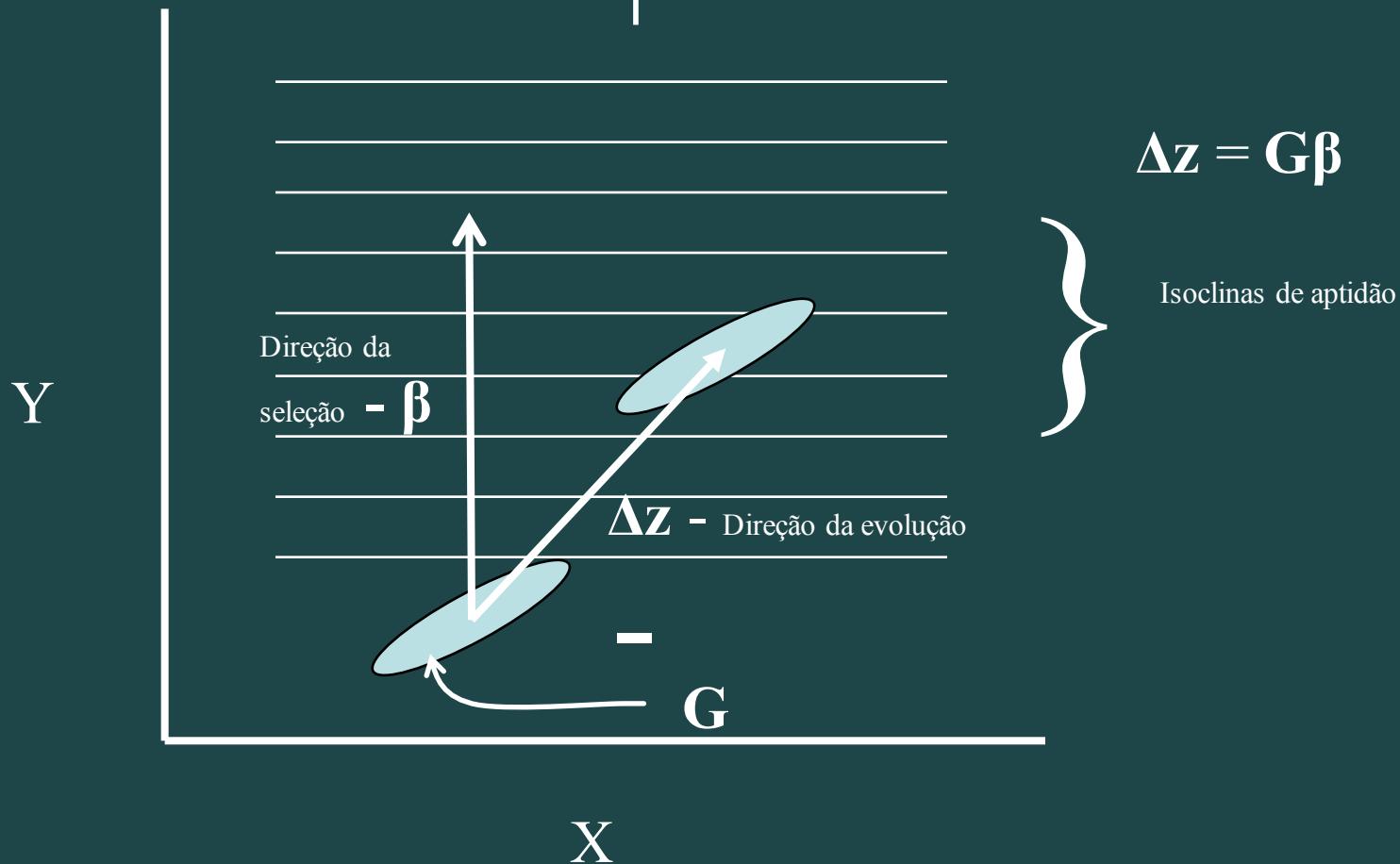
Number of observations: 537

Males	BILLLENGTH	BILLDEPTH	BILLWIDTH
BILLLENGTH	0.564		
BILLDEPTH	0.438	0.567	
BILLWIDTH	0.324	0.379	0.323

Females	BILLLENGTH	BILLDEPTH	BILLWIDTH
BILLLENGTH	0.623		
BILLDEPTH	0.48	0.594	
BILLWIDTH	0.342	0.38	0.335

Number of observations: 387

- Resposta evolutiva à seleção (Δz) desvia da direção da seleção (β) por causa do padrão da matriz de variância/covariância genética (G = faz o papel da h^2 na equação univariada $R = h^2 S$, e portanto e devido primordialmente aos efeitos dos alelos em todos os genes individuais afetando os caracteres em questão)

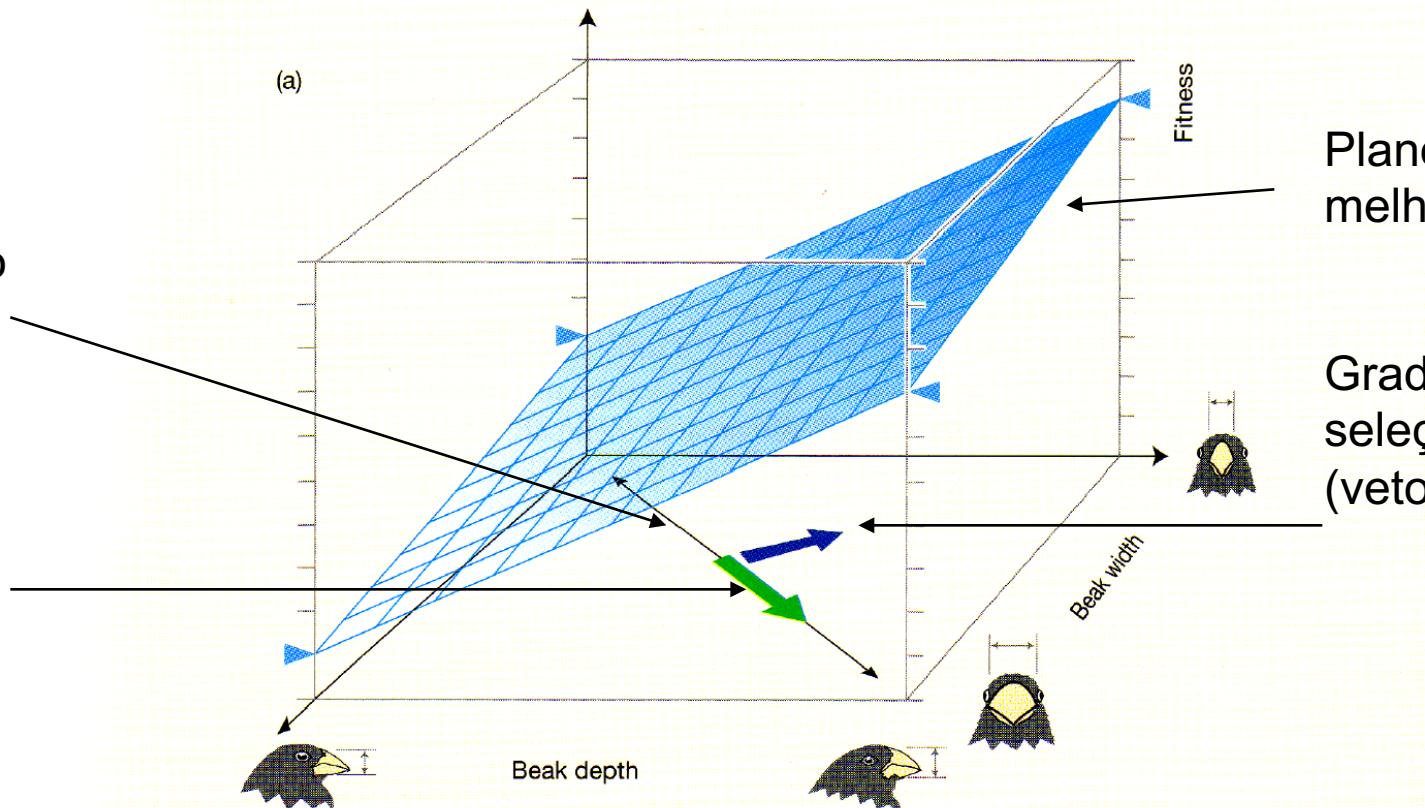


Plano de melhor ajuste

Correlação entre x e y

Gradiente de seleção (vetor)

Resposta



Removem a correlação para estes graficos

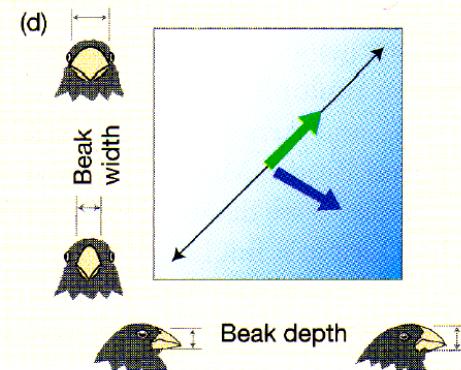
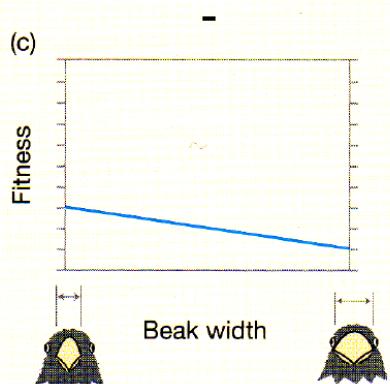
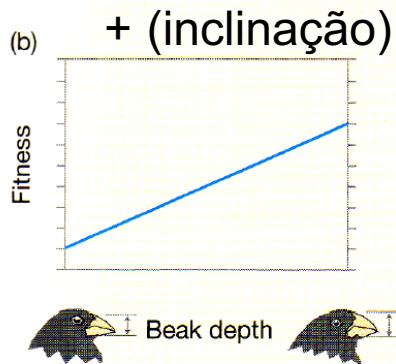


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E sob deriva genética?

Vamos ver o que acontece com as frequências gênicas?

Assumindo que a matriz G permanece relativamente estável o que aconteceria com as médias das populações oriundas de uma população ancestral?

E sob deriva genética?

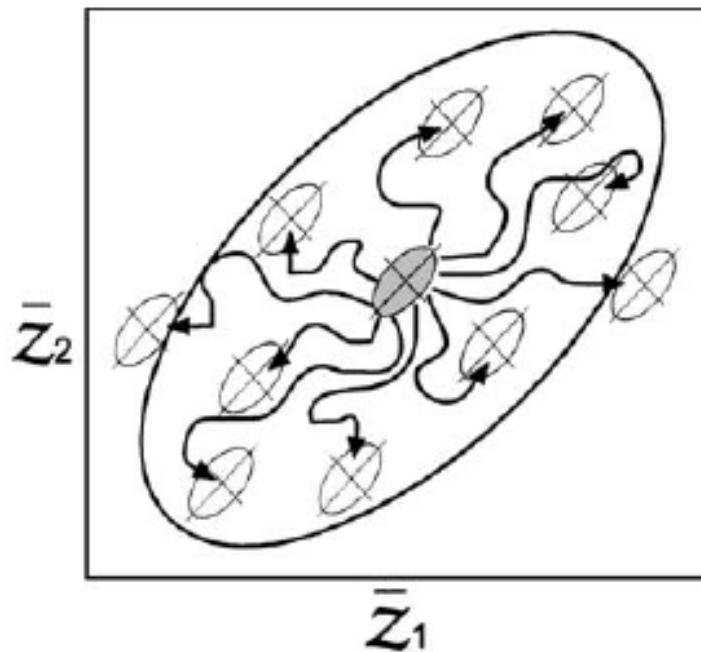


Figure 6. Bivariate drift on a flat adaptive landscape. The small ellipse at the center represents the G-matrix of the ancestral population. The large, outer ellipse represents 95% confidence ellipse for the means of replicate, descendant populations. Solid curved lines show representative evolutionary trajectories. Other conventions as in Figure 5.

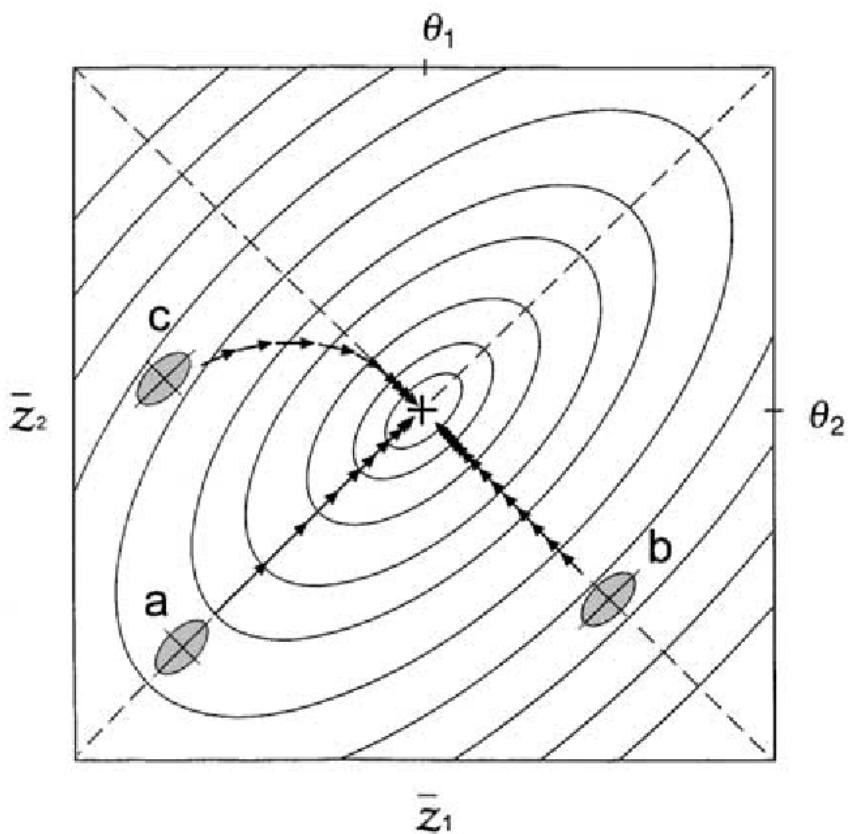


Figure 5. Evolution on an adaptive landscape depends on the alignment of the axes (principal components) of genetic variation (shaded ellipses) with the axes (principal components) of the adaptive landscape. Evolution follows straight trajectories when major (lower left) or minor (lower right) axes are aligned. In general, axes are out of alignment (upper left) and evolution follows a curved trajectory. The small ellipses around each of the three population means represent genetic variation around each mean (the eigenvectors and eigenvalues of the **G**-matrix) and hence are on a different scale of measurement.

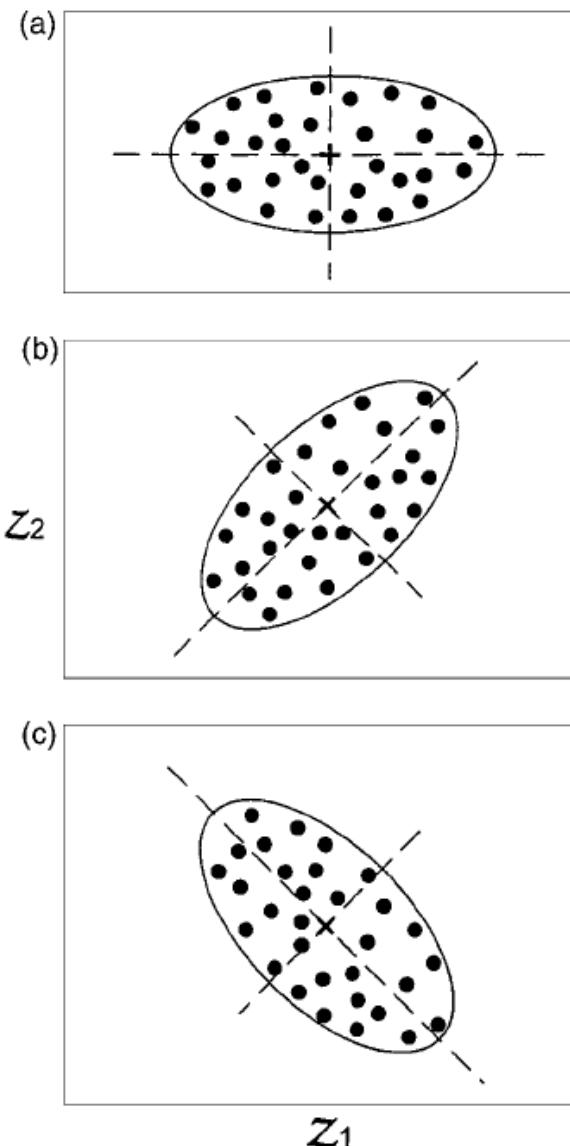


Figure 4. Bivariate distributions of breeding (additive genetic) values representing different patterns of genetic variance and covariance. (a) Large genetic variance in trait 1, small genetic variance in trait 2 and no genetic covariance. (b) Positive genetic covariance. (c) Negative genetic covariance.

Evolução da modularidade – Note que o conceito de módulos se aplica a vários níveis na hierarquia biológica (do molecular ao organismal)

ADAPTATION AND EVOLVABILITY

973

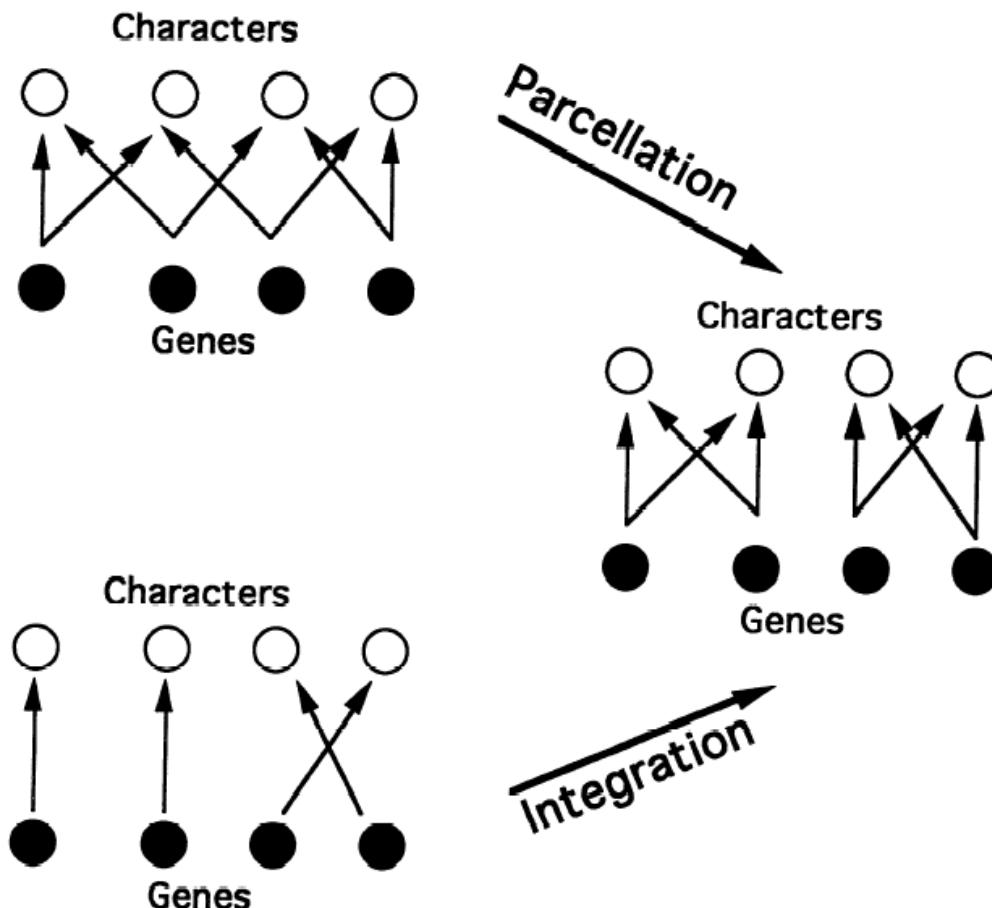
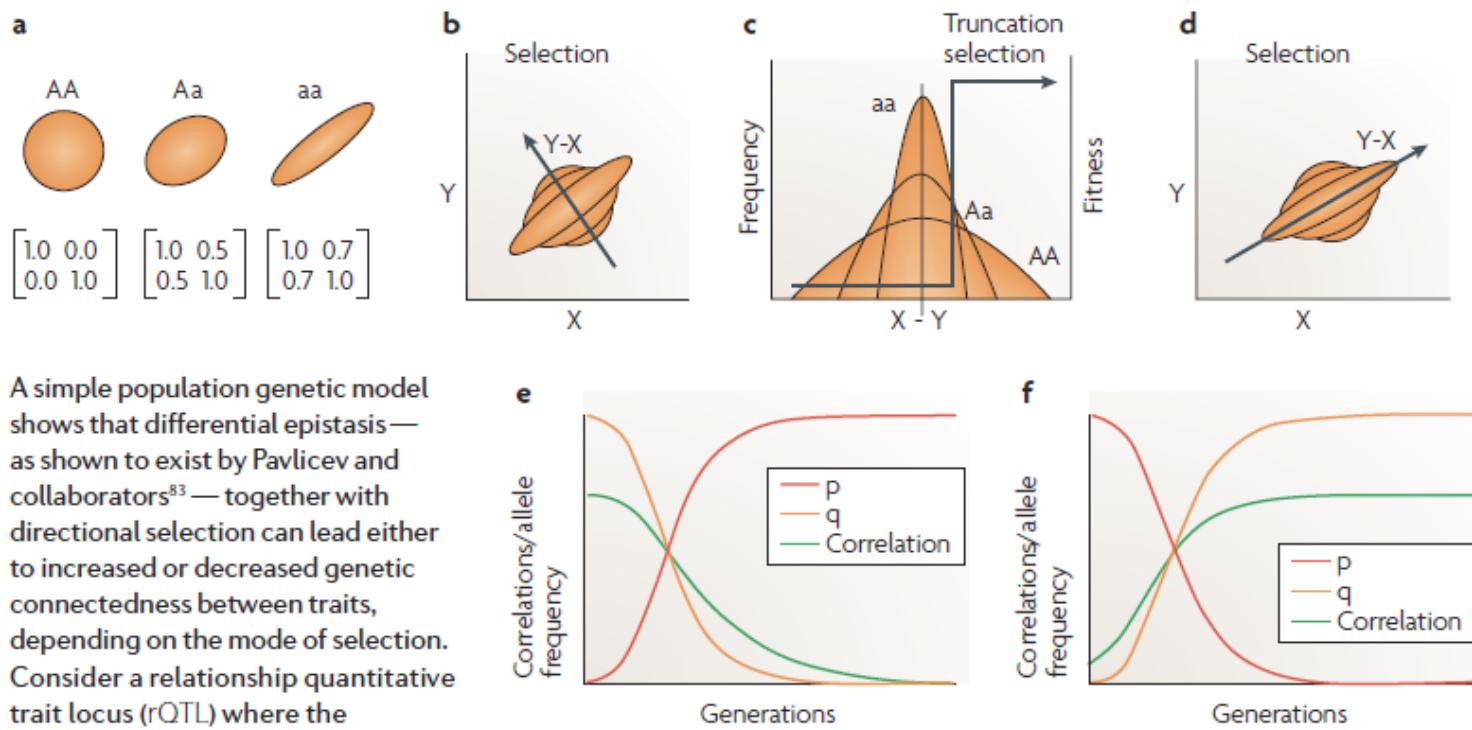


FIG. 2. Two ways of obtaining modularity. Parcellation consists of a differential suppression of pleiotropic effects between groups of characters. Modularity through integration consists in the selective acquisition of pleiotropy among characters from the same group.

Box 3 | A simple model for the evolutionary modification of pleiotropic effects



A simple population genetic model shows that differential epistasis—as shown to exist by Pavlicev and collaborators⁸³—together with directional selection can lead either to increased or decreased genetic connectedness between traits, depending on the mode of selection. Consider a relationship quantitative trait locus (rQTL) where the phenotypic correlation between

traits X and Y, but not the means, vary with the genotype (part a), so that the three genotype-specific distributions are superimposed one on the other (part b). Phenotypic correlations vary from 0.0 for the AA homozygotes, 0.5 for the heterozygote, and 0.7 for the aa homozygotes. Consider the situation in which the A allele first appears in a population that is fixed for the a allele. This population will have a high positive correlation between X and Y of 0.70. Threshold directional selection in the Y-X direction with greater than 50% of the population on the low side of the threshold (part c) favours the A allele and a lower phenotypic correlation. The A allele will increase in frequency towards 1 and the correlation will decrease towards 0 (part e), dismantling the original XY module. Likewise, if the a allele invades a population that is fixed for the A allele and there is selection in the X+Y direction (part d), the a allele will increase in frequency and the correlation will increase from 0.0 to 0.7, creating a module of coordinated, co-selected, traits (part f). Thus, directional selection can either integrate previously independent traits or dismantle existing modules, depending on the direction of selection relative to the existing pattern of integration by acting on the genetic variation in intertrait relationships at relationship loci. This re-organization of modules will also lead to an increase in genetic variation in the direction of selection owing to epistatic interaction between the rQTL and other loci that affect trait means, thus accelerating the rate of evolution in the population. Selection can lead to a modular configuration that fits the patterns of correlated selection among traits so that traits that are selected together will become integrated with each other, losing their connections with other non-selected or contrarily selected traits.



Saguinus G-matrix against P-matrices of all NWM ****P < 0.0001

	V/CV similarity with G-matrix
Alouatta	0.88
Ateles	0.80
Brachyteles	0.84
Lagothrix	0.85
Cacajao	0.92
Chiropotes	0.90
Pithecia	0.96
Callicebus	0.94
Cebus	0.88
Saimiri	0.91
Aotus	0.93
Leontopithecus	0.66
Saguinus	0.99
Callimico	0.81
Callithrix	0.87
Cebuella	0.83

Evolution, 59(5), 2005, pp. 1128–1142

SIZE AS A LINE OF LEAST EVOLUTIONARY RESISTANCE: DIET AND ADAPTIVE MORPHOLOGICAL RADIATION IN NEW WORLD MONKEYS

GABRIEL MARROIG^{1,2} AND JAMES M. CHEVERUD^{3,4}

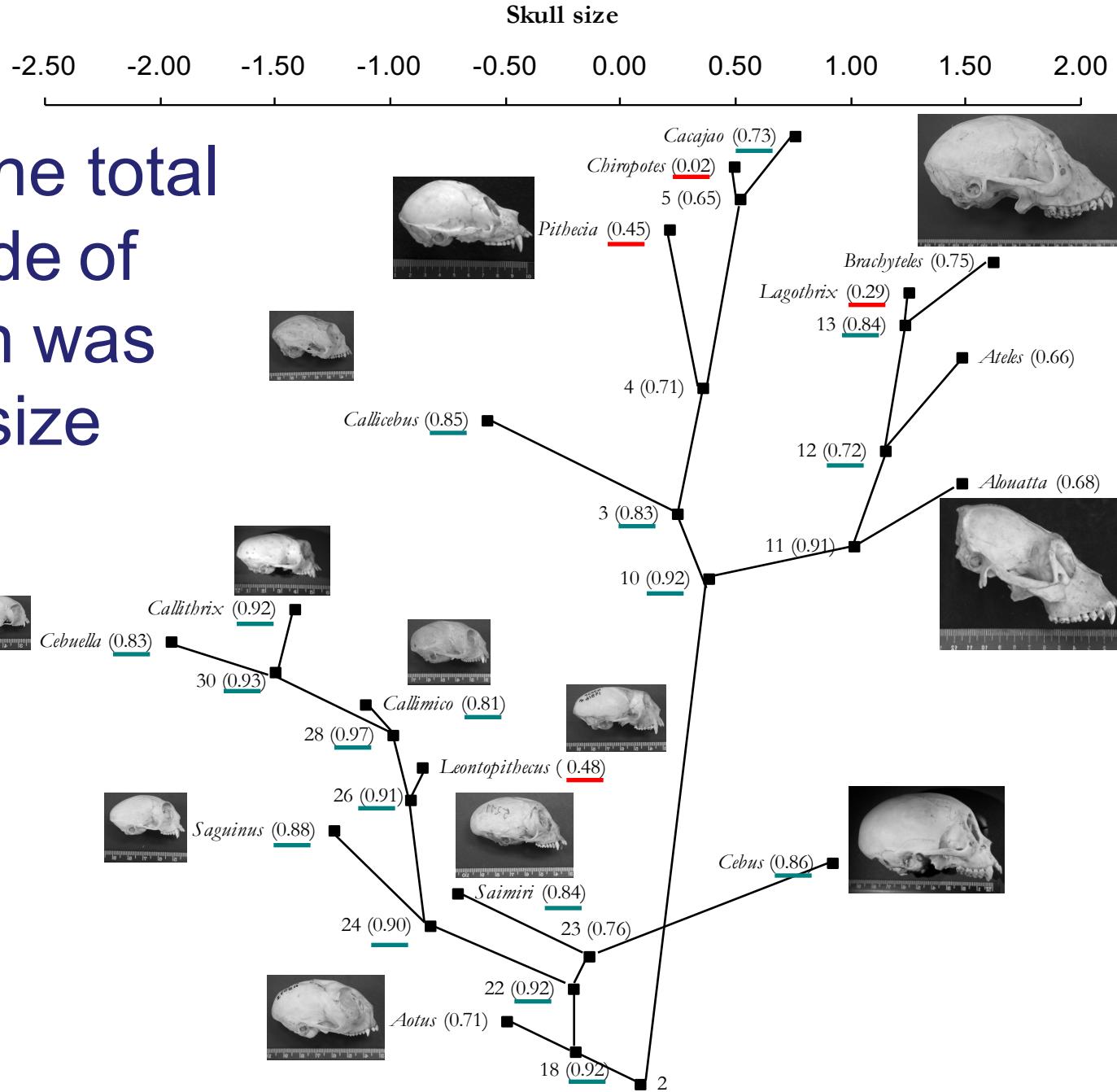
¹*Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, CP 11.461, CEP 05422-970, São Paulo, SP, Brazil*

²*E-mail:* gmarroig@ib.usp.br

³*Department of Anatomy and Neurobiology, Washington University School of Medicine, 660 South Euclid Avenue, Campus Box 8108, Saint Louis, Missouri, 63110*

⁴*E-mail:* cheverud@pcg.wustl.edu

93% of the total
magnitude of
evolution was
aligned size



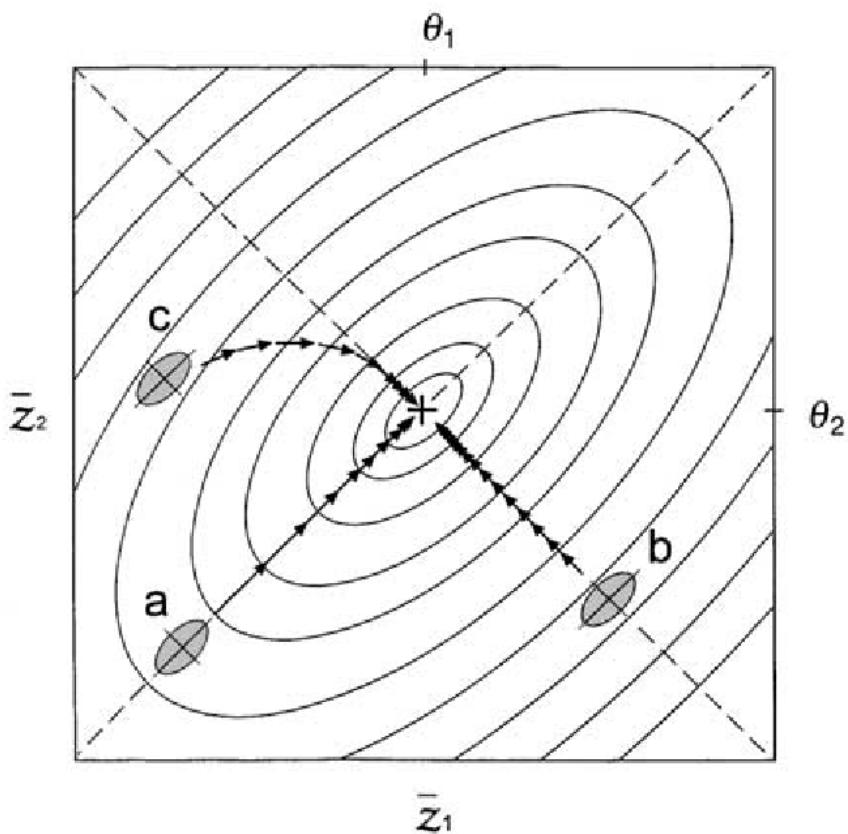


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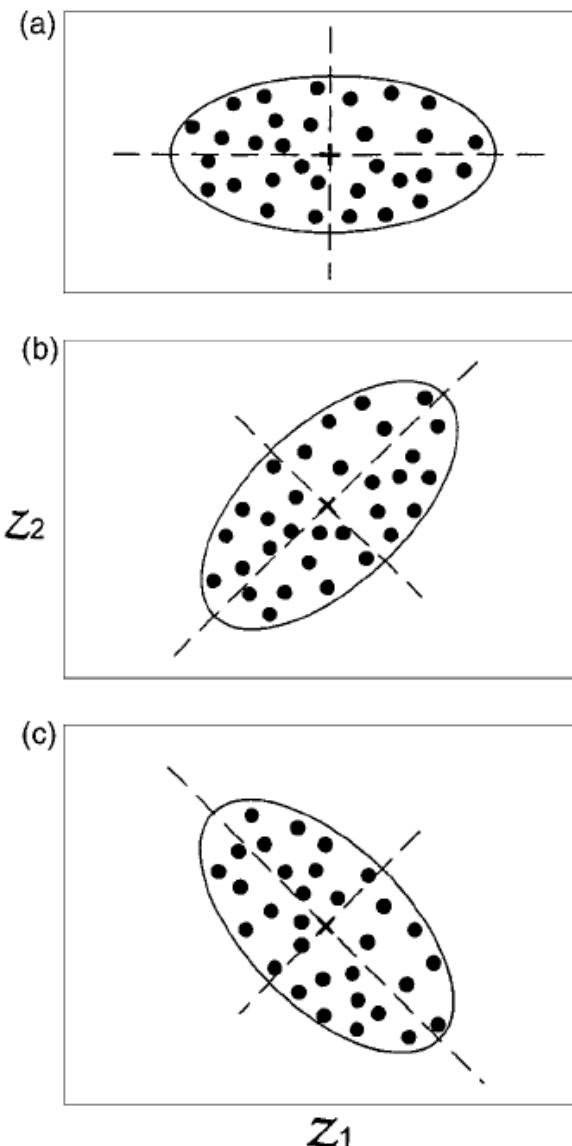


Figure 4. Bivariate distributions of breeding (additive genetic) values representing different patterns of genetic variance and covariance. (a) Large genetic variance in trait 1, small genetic variance in trait 2 and no genetic covariance. (b) Positive genetic covariance. (c) Negative genetic covariance.

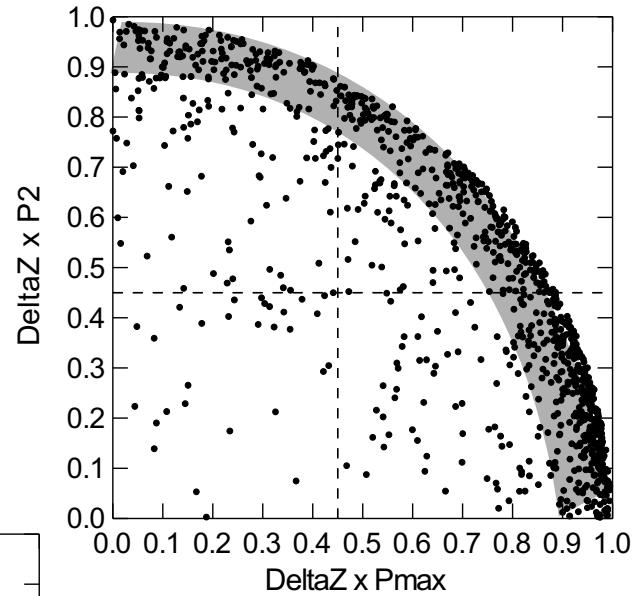
Skull Modularity in Neotropical Marsupials and Monkeys: Size Variation and Evolutionary Constraint and Flexibility

LEILA T. SHIRAI AND GABRIEL MARROIG*

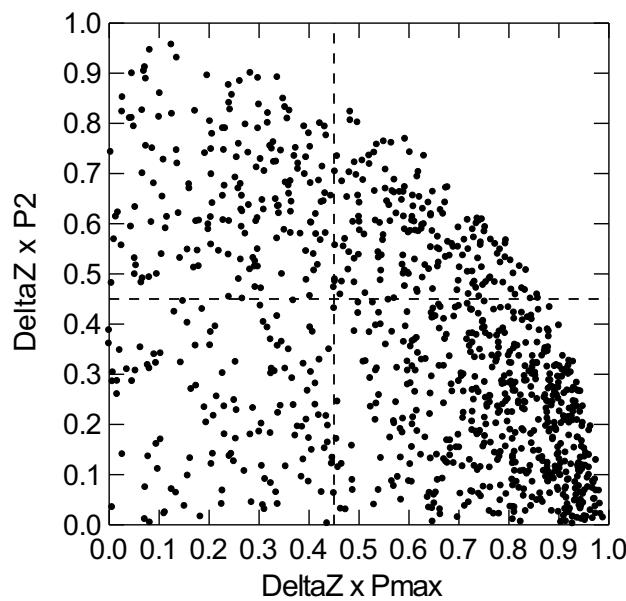
Laboratório de Evolução de Mamíferos, Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil



Metachirus – moderate integration but a lot of variation in both PC1 and 2



Cebuella _low
integration



Didelphis – high
integration

