**Exercise 1:**

1)

Number of characters studied: 2 characters ( length of the stem, color of the stem) ( dihybridism ).

The result of crossing a pure line long green stemmed pea plant with a short white stemmed pea plant gave 102 long green stemmed pea plants (F1) thus:

Dominant characteristics: long stem, green color Recessive characters: short stem, white color

2)

**1st crossing** T = long stem

t = short stem G = green color g = white color

P Homozygous long X Homozygous short Homozygous green Homozygous white

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype of parents | TTGG | X | ttgg |
| G | TG |  | tg |

Genotype F1 TtGg

Phenotype F1 100% long and green stem

**2nd crossing F1 XF1 (self-cross between F1 ):**

P Heterozygous long X Heterozygous long Green heterozygous Green heterozygous

Genotype TtGg X TtGg

G 1 /4XL 1/4TG 1/4TG 1/4TG x 1/4XL 1/4TG 1/4TG 1/4TG

**F2**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | TG | Tg | tG | tg | Genotypes : Phenotypes : 1/16 TTGG: 1/16 long and green2/16 TTGg : 2/16 long, green4/16 TtGg 4/16 long and green2/16 TtGG 2/16 long, green1/16 TTgg 1/16 long and white 2/16 Ttgg 2/16 long and white1/16 ttGG 1/16 short and green2/16 ttGg 2/16 hort and green1/16 ttgg 1/16 short and whitePhenotypes :Long and green : 9/16 Long and white : 3 /16 Short and green: 3/16Short and white: 1/16 |
| TG | TTGG | TTGg | TtGG | TtGg |
| Tg | TTGg | TTgg | TtGg | Ttgg |
| tG | TtGG | TtGg | ttGG | ttGg |
| tg | TtGg | Ttgg | ttGg | ttgg |

3)

P Heterozygous long X Homozygous short Heterozygous green Homozygous white

Genotype TtGg X ttgg G 1/ 4TG 1 /4Tg 1/ 4TG 1 /4Tg x tg F1

|  |  |  |
| --- | --- | --- |
|  | tg | Genotypes : Phenotypes : 1/4 TtGg long and green: 1/4 Ttgg long, white:1/4 ttGg short, green:1/4 ttgg short and white:Phenotypes Obtained :26/102 long and green: = 1/4 (parental type) 25/102 long, and white: = 1/4 (recombinant type) 26/102 short and green: = 1/4 (recombinant type25/102 short and white: = 1/4 (parental type) |
| 1/4 TG | TtGg |
| 1/4 Tg | Ttgg |
| 1/4 tG | ttGg |
| 1/4 tg | ttgg |

-- What is this test called?

Dihybrid test-cross

-- It allows to see if the two genes studied are linked or not (located on the same chromosome or each on a different chromosome). Here the experimental results are in favor of the independent assortment of the characters (i.e. the two genes are carried by a different chromosome

4)

P Homozygous long X Heterozygous long Green heterozygous Green heterozygous

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype | TTGg | X | TtGg |
| G | 1/ 2XL 1 /2XL | x | 1/4XL 1/4XL 1/4TG 1/4XL |
| F1 |  |  |  |

|  |  |  |  |
| --- | --- | --- | --- |
|  | 1/2 TG | 1/2 Tg | Genotypes : Phenotypes :1/8 TTGG long and green 2/8 TtGg : long and green 1/8 TtGG long, green2/8 TTGg long, green 1/8 Ttgg long, white1/8 TTgg long and whitePhenotypes :Long green: 6/8 = 3/4 Long white: 2/8 = 1/4 |
| 1/4 TG | 1/8 TTGG | 1/8 TTGg |
| 1/4 Tg | 1/8 TTGg | 1/8 TTgg |
| 1/4 tG | 1/8 TtGG | 1/8 TtGg |
| 1/4 tg | 1/8 TtGg | 1/8 Ttgg |

**Exercise 2:**

**b+:** gray body

**b :** black body

**vg + :** normal wings

**vg :** vestigial wings

P Heterozygous gray body X Homozygous black body Heterozygous normal wings Homozygous vestigial wings

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype | b+ vg+ / bvg\_ | X | bvg / bvg\_ |
| G | b+vg + , b +vg , bvg + bvg | x | bvg |
| **F1** |  |  |  |

|  |  |  |
| --- | --- | --- |
|  | bvg | Genotypes : Phenotypes obtainedb+vg +/ bvg gray body , normal wings (450/1050, 43%) b+vg / bvg gray body , vestigial wings (90/1050, 8%)b vg +/ bvg black body , normal wings (85/1050, 8%) bvg / bvg black body, vestigial wings (425/1050, 41%)Phenotypes :gray body and normal wings + black body and vestigial wings > 50% (parental types) gray body and vestigial wings + black body and normal wings <50% (recombinant types) |
| b+vg + | b+vg +/ bvg |
| b+vg | b+vg / bvg |
| bvg + | b vg +/ bvg |
| bvg | bvg / bvg |

Given the proportions of the cross test, the 2 genes are linked (parental types >50% and recombinant types

<50%). We have 2 major categories (parental types) and not 4 equal types ( ¼ ).

1. The recombination frequency allows us to determine the distance between these 2 characters:

FR= number of recombinant types/total number=85+90/1050 X 100= 16.6% 16.6 cM= distance b- vg

1. genetic map

16cM 4cM

vg 20cM b cn

**Exercise 3:**

