# HMB265:

# General & Human Genetics

Week 1

# Fall 2021

## Why do we care about genetics?

- 1) Medicine: treatment
  - diagnosis & prediction
  - gene therapy
  - pharmacogenomics
  - $\rightarrow$  Personalized medicine
- 2) Agriculture: genetic engineering help to improve traits, survival, etc.
- 3) Conservation
- 4) Biology

# Two hypotheses to explain inheritance (其实是错误的):

1) <u>Uniparental</u>: One parent contributes more

(Aristotle 认为是 male, 后代会长得和父亲一样)

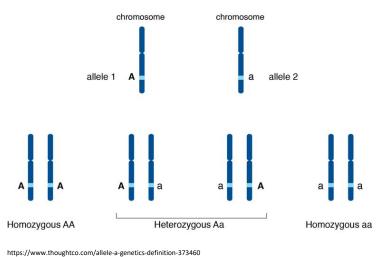
2) <u>Blended inheritance</u>: 1 + 6 = 8

(这个 hypothesis only explained single offspring, 但是无法解释 siblings 和 next generation)

# **Model Organism:**

- 1) short generation time
- 2) able to inbred (self-fertilize)
- 3) simple reproductive biology 并且一定要 discrete traits
- 4) easy to breed/grow (ex. Small in size)
- 5) large number of progeny

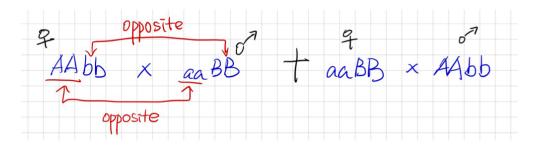
# **Terminology:**



我是重点啊!答应我一定要会好吗

- Locus genetically defined location, behave like one gene
- Allele alternative form at a given locus
- Dominant one allele that manifests itself regardless of the other allele that is present. (indicated by an uppercase letter)

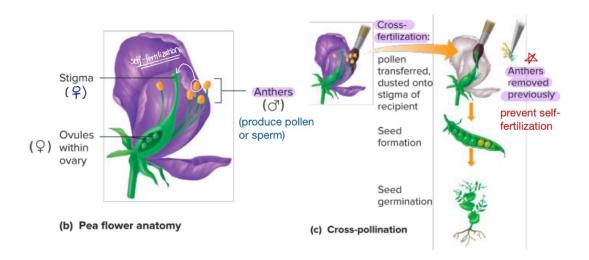
- Recessive an allele whose effect is "masked" when the dominant allele is present. For the recessive allele to manifest itself, all alleles at a locus must be Recessive (ex. aa) (indicated by a lowercase letter)
- Homozygous both alleles at a given diploid locus are the same (AA or aa)
- Heterozygous one dominant and one recessive at a diploid locus (Aa)
- Monohybrid one hybrid locus (e.g. AABBccDd)
- Dihybrid 2 hybrid loci (e.g. AaBbCCDD)
- True-breeding homozygous at the loci/locus (AA or aa)
- <u>Reciprocal crosses</u> cross 2 true-breeding lines that are opposite to each other and do another round that reverse the trait between the male and the female . Tell us that both parent contribute equally to offspring (independent).



• <u>Test Cross</u> – unknown genotype X homozygous recessive genotype (to find the unknown genotype (ex. aabb))

$$P:$$
 unknown × yy  
F1: if all  $y$  then unknown should be  $YY$ 

• Self-fertilization vs. cross-fertilization:



Mendel 最后选择了 Pisum sativum 来作为他的 model organism 因为:

- short generation time
- 可以 inbred

(得到一个 pure-breeding line (也叫 true-breeding, 就是紫花 self-fertilize always 得到紫花, 世世代代的 traits 都没有变化)

(可以把 2 个 pure-breeding lines cross-fertilized 来形成一个 hybrids (monohybrid cross))

- 可以做 reciprocal cross
- traits are discrete (7 antagonistic pairs: no intermediate form)
- easy to grow
- large number of progeny

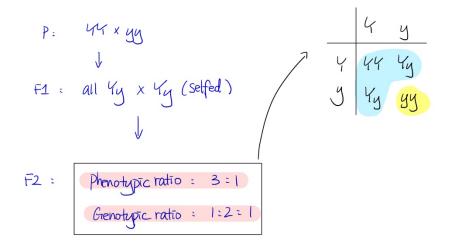
# **Monohybrid Cross:**

- Examining only one single trait
- YY x yy
- All F1 generation show the dominant phenotype
- F2 generation: phenotype ratio = 3 : 1

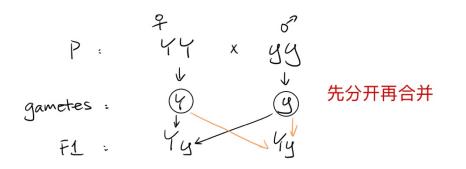
## genotype ratio = 1:2:1

- Law of Segregation = explains how genes are transmitted:
  - Two members of a gene pair segregate from each other into the gametes
    Then unite at random)
  - 先分开再合并 (在 gamete formation 的时候分开, fertilization 的时候合并)

# 灵魂画手时间: Punnett Square:



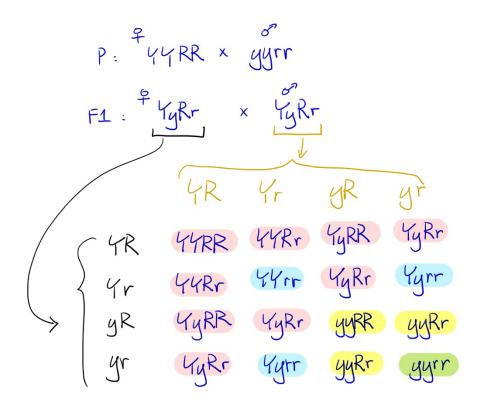
Law of Segregation:



# **Dihybrid Cross:**

- Examining two traits
- ex) RRYY X rryy
- All F1 generation show dominant phenotype
- F2 generation show 9:3:3:1 phenotypic ratio
- Law of Independent Assortment = During gamete formation, the segregation of alleles at one locus is independent of the segregation of alleles at another locus (分开找 Yy, Rr 各自的 prob. 然后再乘起来)

灵魂画手时间:



# Law of Probability for multiple genes:

- 2<sup>n</sup> = number of possible gamete combinations for each parent Thus, 2<sup>n</sup> X 2<sup>n</sup> = number of genotypes
- "and" events = multiplication (product rule)
  "or" events = addition (sum rule)

(一般情况下题目问到 what is the prob. of obtaining the genotype RrYyTtss? 用 product rule; 而问到 prob. of obtaining either RRYYTTSS or rryyttss 则要用 sum rule)

1) P: RrYyTtSs X RrYyTtSs What is the prob. of obtaining the genotype RrYyTtss?

2) P: RrYyTtSs X RrYyTtSs What is the prob. of obtaining the genotype RRYYTTSS or rryyttss?

3) Female: AaBbccDDEe X Male: aaBbCcddEe What proportion of the progeny will phenotypically resemble the female parent?

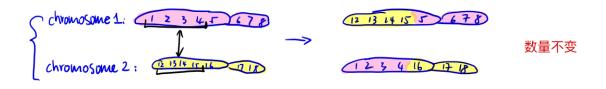
# **LECTURE 3: Molecular Basis of Genetic Polymorphisms & Their Detection**

#### **Mutations:**

- Genes change from one allelic form to another
- Genes mutate randomly and spontaneously, or can be induced by a mutagen
- 只有在 germline cells 里的 mutations 才会被遗传,而在 somatic cells 里的不会
- Mutations are the source of allelic variation
- Mutate allele has a frequency of <1%
- 不同的 genes 有着不同的 mutation rate
- Mutations affecting phenotype occur very rarely
- <u>Wild-type allele</u>: frequency  $\geq 1\%$
- <u>Mutant allele</u>: frequency < 1%
- <u>Monomorphic</u>: gene with only one wilt-type allele
- <u>Polymorphic</u>: gene with more than one wild-type allele
- <u>Forward mutation</u>: change wild-type to a different allele
- <u>Reverse mutation</u>: change from mutate allele back to wild-type allele
- Forward mutation 的 rate almost always 高于 reverse mutation 的 rate

## Classification of mutations by effect on DNA molecule:

- 1) Substitution: = point mutation = single nucleotide polymorphism (SNP) Change in only one nucleotide
- 2) Deletion: one or more DNA pairs is lost
- 3) Insertion: one or more DNA pairs is added
- 4) Inversion: rotate a piece of DNA
- 5) Reciprocal translocation: parts of nonhomologous chromosomes change places



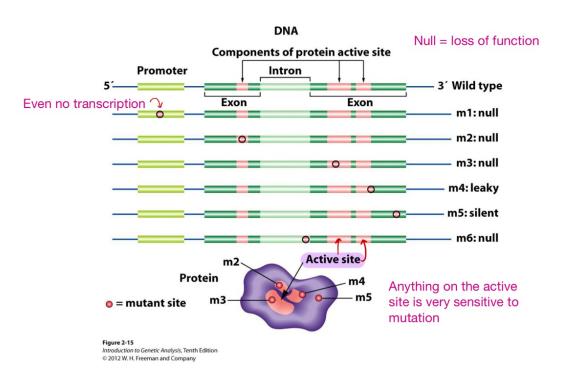
6) Chromosomal rearrangements: affect many genes at one time

#### **Effects of Mutations:**

- Mutations will produce two different alleles of a gene
- Causing changes in DNA (gene) expression (affect transcription, splicing, translation and folding)
- Affect protein function
- Thus, affect phenotype

#### Classification of mutations by effect on gene expression:

- 1) Null Mutation: cause non-functional protein (最严重)
- 2) Leaky Mutation: cause loss of function (还能工作)
- 3) Silent Mutation: does not affect the function of protein (没影响)



- Note: 在 promoter 上的 mutation 连 transcription 都没有, 直接 loss of function
  - 在 active site 上的也都是 null, 因为 active site is very sensitive to mutation
  - 在 intron 的头或尾的 mutation 也比较严重,因为会导致无法 recognize splice site

#### The gene basis of Mendel's "antagonistic pairs":

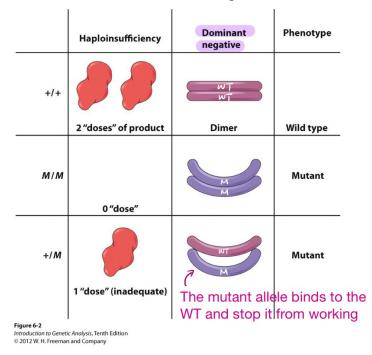
- a) Pea shape:
  - R有 Sbe1, r没有 Sbe1
  - RR和 Rr都会 produce Sbe1, 从而 produce Amylopectin (round shape)
  - rr 不会 produce Sbe1, produce non-functional starch (wrinkled shape)
- b) Pea stems:
  - LE can produce high activity of gibberellin (GA)  $3\beta$ -hydroxylase  $\rightarrow$  long stems
  - le produce low activity of gibberellin (GA)  $3\beta$ -hydroxylase  $\rightarrow$  short stems

## Genetic basis of single-gene disorders: PKU

- PKU is caused by mutations in the PAH gene
- Resulting in low level of enz. phenylalanine hydroxylase production
- Causing a build up of toxic compound phenylpyruvic acid.
- Phenylpyruvic acid can interfere with nervous system development.
- Normally phenylalanine will be convert into tyrosine.

#### Classification of mutations by <u>effect on phenotype:</u>

- 1) Haplosufficiency
  - 50% of the protein product is sufficient to give wt phenotype.
  - Mutation is recessive
- 2) Haploinsufficiency
  - 50% of the protein product is not enough to give wt phenotype.
  - Mutation is dominant
- 3) Dominant negative
  - Mutant allele will produce a mutant protein that bind and inactivate a wt protein in a dimer. Function like an antagonist.



## Detection of allelic polymorphism at the molecular level:

- 1) PCR & DNA sequencing
  - 我们一般先用 PCR 来做 amplification, 再做 DNA sequencing
  - Use SNP detection approaches at identified SNP to screen at-risk relatives
- 2) New Technologies:
  - Next-generation sequencing: cheaper & can allow massive amounts of sequencing

#### **Principles of allele detection:**

- 1) Attempting to visualize allelic polymorphism
- 2) At the level of DNA sequence
- 3) Can detect polymorphism from DNA to protein level
- 4) Analysis performed on diploid nuclear genome