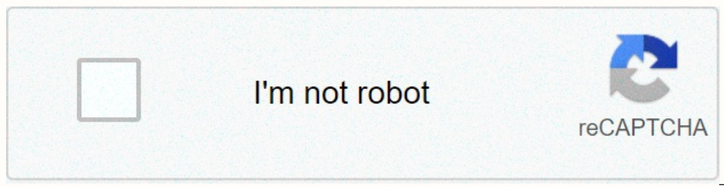

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When does independent assortment occur during

What helps ensure the survival of a species? Genetic variation. It is this variation that is the essence of evolution. Without genetic differences between individuals, survival of the fittest would not be likely. Either they all survive, or they all perish. Figure a ('PageIndex'{1}'): (CC BY 3.0; Profiles in Diversity Journal through wikimedia.org) Sexual reproduction results in endless possibilities of genetic variation. In other words, sexual reproduction results in offspring that are genetically unique. They differ from both parents and also from each other. This happens for several reasons. When the counterpart chromosomes form pairs during the prose I of meiosis I, the crossing may occur. Crossover is the exchange of genetic material between counterpart chromosomes. It results in new combinations of genes on each chromosome. When cells divide during meiosis, the counterpart chromosomes are randomly distributed to the child cells, and different chromosomes are secreted independently of each other. This is called a separate assortment. It results in gametes that have unique combinations of chromosomes. In sexual reproduction, two gametes come together to produce an offspring. But which of the millions of possible gametes will they be? This is likely to be a matter of chance. Obviously it's another source of genetic variation in offspring. This is known as random fertilization. All of these mechanisms that work together result in an incredible amount of potential variation. Each human partner, for example, has the potential to produce more than 64 billion genetically unique children. No wonder we're all different! The crossover occurs during prose I, and is the exchange of genetic material between non-sibling chromatids of counterpart chromosomes. I remember during prose I, the counterpart chromosomes are aligned in pairs, gene-by-gen along their entire length, forming a configuration with four chromatids, known as a tetrad. At this point, the chromatids are very close to each other and some two chromatid materials change chromosomes, i.e. the material breaks and reconnects in the same position on the counterpart chromosome (Figure .(' PageIndex'{2}')). This exchange of genetic material can occur many times within the same pair of counterpart chromosomes, creating unique combinations of genes. This process is also known as recombination. Figure ('PageIndex'{2}'): Crossing.o. A maternal DNA chain is shown in red. A paternal strand of DNA is shown in blue. The crossover produces two chromosomes that have not previously existed. The recombination process involves the breakage and re-application of parental chromosomes (M, F). This results in the generation of new chromosomes (C1, C2) that share DNA from both parents. FOR 2.5; David Eccles (Gringer) via Wikimedia). Figure ('PageIndex'{3}'): Crossing between counterpart chromosomes occurs among non-sibling chromatids of counterpart chromosomes. The result is an exchange of genetic material between counterpart chromosomes. (CC BY 4.0 via OpenStax College). During phase I, chromosomes condense and become visible within the nucleus. As the nuclear envelope begins to decompose, the counterpart chromosomes get closer. The synaptonemal complex, a lattice of proteins between the counterpart chromosomes, forms in specific places, extending to cover the entire length of the chromosomes. Tight pairing of counterpart chromosomes is called synapses. In synapses, genes in the chromatids of the counterpart chromosomes are aligned with each other. The synaptonemal complex also supports the exchange of chromosome segments between non-sibling counterpart chromatids in a process called crossing. Cross events are the first source of genetic variation produced by meiosis. A single crossover event between non-sibling counterpart chromatids leads to a DNA exchange between chromosomes. After the crossing, the synaptonemal complex decomposes and the cohesine connection between counterpart pairs is also eliminated. At the end of prose I, the pairs remain joined only in chiasmata; they are called tetrads because the four sibling chromatids of each pair of counterpart chromosomes are now visible. During metaphase I, tetrads move to the metaphasic plate with quinetocorous in front of opposite poles. The counterpart pairs are randomly oriented at the equator. This event is the second mechanism that introduces variation in gametes or spores. In each cell undergoing meiosis, the arrangement of tetrades is different. The number of variations depends on the number of chromosomes that make up a set. There are two orientation possibilities on the metaphasic plate. The possible number of alignments, therefore, is equal to 2n, where n is the number of chromosomes per set. Given these two mechanisms, it is highly unlikely that two haploid cells resulting from meiosis will have the same genetic makeup. Figure ('PageIndex'{4}'): Meiosis I guarantees unique Random gametes, independent assortment during metaphase that I can demonstrate considering a cell with a set of two chromosomes (n x 2). In this case, there are two possible arrangements on the equatorial plane in metaphase I. The total possible number of different gametes is 2n, where n is equal to the number of chromosomes in a set. In this example, there are four possible genetic combinations for gametes. With n 23 in human cells, there are more than 8 million possible combinations of paternal and maternal chromosomes. (CC BY 4.0 via OpenStax College). In humans, there are more than 8 million configurations in which chromosomes can align during meiosis metaphase I. It's the process meiosis, resulting in four unique haploid cells, which in these many combinations. This independent assortment, in which the chromosome inherited from the father or mother can be classified into any gamete, produces the potential for tremendous genetic variation. Along with random fertilization, there is a higher chance of genetic variation between any two people than the number of living individuals today. Sexual reproduction is the random fertilization of a female gamete using a male gamete. In humans, there are more than 8 million (223) combinations of chromosomes in the production of gametes in both men and females. A sperm cell, with more than 8 million chromosomal combinations, fertilizes an egg cell, which also has more than 8 million chromosomal combinations. That's more than 64 billion unique combinations, not counting the unique combinations produced by the crossing. In other words, each human partner could produce a child with over 64 billion unique chromosomal combinations! Sexual reproduction has the potential to produce tremendous genetic variation in offspring. During phase I, the counterpart chromosomes condense and become visible as the x-shape we know, pair to form a tetrad, and exchange genetic material across. In metaphase I, tetrads are aligned on the metaphasic plate and counterpart pairs are randomly oriented. This variation is due to the independent variety and crossover during meiosis, and the random binding of gametes during fertilization. What is the crossing and when does it happen? Describe how crossover, independent assortment and random fertilization lead to genetic variation. How many combinations of chromosomes are possible from sexual reproduction in humans? Create a diagram to show how the crossing occurs and how it creates new genetic combinations on each chromosome. Watch the video below to understand how genetic variations originate during sexual reproduction. Leeches look like disgusting creatures with little intelligence. But, in this Science Friday video, Dr. Mark Siddall discusses his research on leeches and some of their interesting properties. The independent assortment allows the calculation of genotypic and phenotypic proportions based on the probability of individual genetic combinations. Learning objectivesUse probability or forked line method to calculate the possibility of any particular genotype arising from a genetic cross From Mendel's independent assortment law states that genes do not influence each other with respect to the classification of alleles into gametes; all possible combinations of alleles for each gene are equally likely to occur. The of any particular genotypic combination of more than one gene

is therefore the probability of the desired genotype in the first locus multiplied by the probability of the desired genotype in the other loci. The forked fork method can be used to calculate the possibilities of all possible genotypic combinations of a cross, while the probability method can be used to calculate the possibility of any particular genotype that could result from that cross. Independent assortment key terms: Separate genes for separate traits are passed independently of each other from the parents to the offspring of Mendel's independent assortment law states that genes do not influence each other with respect to the classification of alleles in gametes: every possible combination of alleles for each gene is equally likely to occur. The independent assortment of genes can be illustrated by the dihybrid cross: a cross between two true breeding parents expressing different traits for two characteristics. Consider the characteristics of seed color and seed texture for two pea plants: one that has green, wrinkled seeds (yyrr) and one that has yellow and round seeds (YYRR). Because each parent is homozygote, the law of segregation indicates that the gametes for the green/wrinkled plant are years, while the gametes for the yellow/round plant are all YR. Therefore, the F1 generation of offspring is all YyRr. For generation F2, the law of segregation requires that each gamete receive an R allele or an r allele along with a Y allele or a y allele. The independent assortment law states that a gamete in which an ordered r allele would be equally likely to contain a Y allele or a y allele. Therefore, there are four equally likely gametes that can form when the YyRr heterozygote is self-extracted as follows: YR, Yr, yr, and yr. Organizing these gametes along the top and left of a 4 × 4 square Punnett gives us 16 equally likely genotypic combinations. Of these genotypes, we infer a phenotypic ratio of 9 round/yellow:3 round/green:3 wrinkled/yellow:1 wrinkled/green. These are the proportions of offspring you would expect, assuming we make the crosses with a large enough sample size. Figure s(PageIndex{1}): Independent assortment of 2 genes: This dihybrid cross of pea plants involves genes for the color and texture of seeds. Due to independent assortment and dominance, the dihybrid phenotypic ratio 9:3:1 can collapse into two 3:1 proportions, characteristic of any monohybrid cross that follows a dominant and recessive pattern. Ignoring the color of the seed and considering only the texture of the seed on the anterior diabride cross, we would expect that three-quarters of the offspring of the F2 generation would be round and a quarter would be wrinkled. Similarly, by ingsing only the color of the seeds, we would assume that three-quarters of the F2offspring would be yellow and a quarter would be green. Classification of alleles for texture and color are separate events, so we can apply the product rule. Therefore, the ratio of round and yellow F2 offspring is expected to be (3/4) × (3/4) to 9/16, and the proportion of and the green offspring are expected to be (1/4) × (1/4) to 1/16. These proportions are identical to those obtained using a Punnett square. Round/green and wrinkled/yellow offspring can also be calculated using the product rule, as each of these genotypes includes a dominant phenotype and a recessive phenotype. Therefore, the ratio of each is calculated as (3/4) × (1/4) to 3/16. When more than two genes are being considered, the Punnett-square method becomes unsifiable. For example, examining a cross involving four genes would require a grid of 16 × 16 containing 256 boxes. It would be extremely cumbersome to manually introduce each genotype. For more complex junctions, forked line and probability methods are preferred. To prepare a forked line diagram for a cross between F1 heterozygous resulting from a cross between the AABBCC and aabbcc parents, we first create rows equal to the number of genes being considered and then segregate the alleles in each row into forked lines according to the probabilities of individual monohybrid crosses. Next, we multiply the values along each forked path to get the probabilities of F2 offspring. Note that this process is a diagram version of the product rule. Values along each forked track can be multiplied because each gene is associated independently. For a trihybrid cross, the F2fenotypic relationship is 27:9:9:9:3:3:3:1. Figure s('PageIndex'{1}': Independent assortment of 3 genes: The forked line method can be used to analyze a trihybrid cross. Here, the probability of color in generation F2 occupies the top row (3 yellow:1 green). The shape probability occupies the second row (3 round:1 wrinkled) and the height probability occupies the third row (3 high dwarves:1). The probability of each possible combination of traits is calculated by multiplying the probability for each individual trait. Therefore, the probability that the F2 offspring has yellow, round, and high features is 3 × 3 × 3, or 27. While the forked line method is a schematic approach to tracking probabilities on a cross, the probability method gives the proportions of offspring that each phenotype (or genotype) is expected to present without the added visual assistance. To fully demonstrate the power of the probability method, however, we can consider specific genetic calculations. For example, for a tetrahybrid cross between individuals who are heterozygous for all four genes, and in which the four genes are independently classified into a dominant and recessive pattern, what proportion of the offspring is expected to be recessive homozygous for the four alleles? Instead of writing possible genotypes, we can use the probability method. We know that for each gene the fraction of homozygote recessive offspring will be 1/4. Therefore, by multiplying this fraction for each of the four genes, (1/4) × (1/4) × (1/4) × (1/4), we determine that 1/256 1/256 the offspring will be recessive homozygotic quadrupedal. Recessive.

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