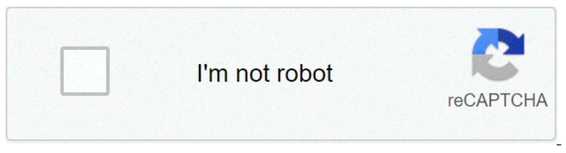

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How many sex chromosomes are in a human gamete

How many sex chromosomes are in a human gamete group of answer choices. How many sex chromosomes are normally in a human gamete quizlet. How many sex chromosomes are in a human gamete cell before fertilization. How many sex chromosomes are present in a human gamete. How many sex chromosomes are in a human gamete quizlet.

Photographic view of the total chromosomal complement in a cell A Karyotype is a preparation of the complete set of metaphase chromosomes in the cells of a species or in an individual organism, sorted by length, centromere position and other features. [1]: 544 2] [3] [4 and for a test that detects this complement or counts the number of chromosomes. Karyotyping is the process through which a karyotype is prepared by photographs of chromosomes, in order to determine the chromosomal complement of an individual, including the number of chromosomes and any anomalies. Karyotypes describe the chromosomal number of an organism and what these chromosomes seem under a light microscope. The focus is paid to their length, the position of the centrimeri, the bandage model, the differences between sexual chromosomes, and all other physical characteristics. [5] The preparation and study of Karyotypes is part of cytogenetic. This file demonstrates the basic knowledge needed to read a Karyotype Karyogram of the human male using the Giemsa color the study of entire chromosomes sets is sometimes known as Kariology. Chromosomes are depicted (resuming a photomicrograph) in a standard format known as Karyogram or Idiogram: in pairs, sorted by centromere size and position for chromosomes of the same size. The basic number of chromosomes in the somatic cells of an individual or a species is called the somatic number and is designated 2N. In the germline (sex cells) the chromosome number is N (human: n = 23). [3] P28 so, in human beings 2N = 46. So, in normal diploid organisms, autosomal chromosomes are present in two Copies. It can, or it can't, be sex chromosomes. The polyploid cells have more copies of chromosomes and aploid cells have single copies. Karyotypes can be used for many purposes; How to study chromosomal aberrations, cellular function, taxonomic relationships, medicine and collect information on past evolutionary events (karyosystematics). [6] History of Karyotype's studies Chromosomes were observed for the first time in vegetable cells by Carl Wilhelm von Nägeli in 1842. Their behavior in animal cells (Salamander) was described by Walther Flemming, the discoverer of mitosis , in 1882. The name was coined by another German anatomist, Heinrich von Waldeyer in 1888. It is new Latin from the ancient Greek Î¿î¬ï½ Karyon, kernel, seed, or core, and ï "ï ï ï € Î¿ï, Typos, "general form" The next phase took place after the development of genetics at the beginning of the 20th century, when it was appreciated that the chromosomes (which can be observed from the Karyotype) were the vector of the Genes. Lev Delaunay [RU] In 1922 it seems to have been the first person to define Karyotype as the phenotypic aspect of somatic chromosomes, in contrast with their gene content. [7] [8] The next story of the concept can be followed in the works of CD Darlington [9] and Michael JD White. [3] [10 The survey on human kariootype has requested many years to resolve the most fundamental question: how many Chromosomes does a human diploid human cell contain? [11] In 1912, Hans von WinIwarter reported 47 chromosomes in spermatogonia and 48 in Oogony, concluding a sex determination mechanism XX / XO. [12] The painter in 1922 was certainly not whether the diploid of human beings was 46 or 48, at first sight 46, [13] but was reviewed by him from 46 to 48, and insisted correctly on humans who had a system XX / XY. [14] Considering the techniques of time, these results were remarkable. Fusion of ancestral chromosomes has left distinctive remains of Telomeres, and a vestigial centromere Joe Hin Tjio who worked in the Albert Levan laboratory [15] found the number of chromosome to be 46 using new techniques available at the moment: using cells in culture Pretreat cells in an hypotonic solution, which inflates them and spreads the Arresting mitosis chromosomes in metaphase by a Squashing cholekin solution the preparation on the slide forcing chromosomes in a single planea Photomicrograph and organize the results in an indisputable Chancellor. The work has taken place in 1955 and was published in 1956. The Karyotype of human includes only 46 chromosomes. [16] [17] The other great apes have 48 chromosomes. The human chromosome 2 is now known to be the result of a fusion end-to-end principle of two ancestral chromosomes APE. [18] [19] Observations of Karyotipi coloring studying karyotipi are made possible by staining. Usually, a suitable dye such as Giemsa, [20] it is applied after that the cells were arrested during cell division from a colchicine solution usually in metaphase or prometaphase when the majority has condensed. AffinchÂ © Giemsa stain to adhere properly, all proteins chromosomal â â must be digested and removed. For humans, the white blood cells are used more frequently because © are easily induced to divide and grow in tissue culture. [21] Sometimes the observations can be made of non-divided cells (interphase). The sex of an unborn fetus can be determined by observation of interphase cells (cfr. Hundredth and amniotic BAR Body). Observations Six different characteristics of Karyotypi are usually observed and compared: [22] Differences in absolute sizes of chromosomes. The chromosomes can vary in absolute measuring twenty times between family genres. For example, Lotus tenuis and Vicia Faba beans each have six pairs of chromosomes, but V. faba Chromosomes are many times larger. These differences probably reflect different amounts of DNA duplication. Differences in the position of the centromere. These differences are probably occurred through translocations. Differences in the relative size of the chromosomes. These differences are probably caused by segmental interchange of unequal lengths. Differences in the basic number of chromosomes. These differences could arise from unequal successive translocations that have removed all the essential genetic material from one chromosome, allowing its loss without penalty organism (the dislocation hypothesis) or through fusion. Humans have a pair of chromosomes in less than great apes. The human chromosome 2 appears to be a result from the fusion of two ancestral chromosomes, and many of the genes of these two original chromosomes were translocated in other chromosomes. Differences in the number and position of satellites. The satellites are small bodies attached to a chromosome by a thin thread. Differences in degree and distribution of heterochromatic regions. The spots heterochromatin darker than euchroomatina. The heterochromatin is packed tighter. The heterochromatin is mainly composed of DNA sequences genetically inactive and repetitive and partecipates © containing a greater amount of adenine-tymine pairs. The euchromatin is usually in the active transcription and stains much more reading since © has less affinity for the Giemsa stain. [23] The euchromatin regions contain large quantities of guanini-cytosine pairs. The staining technique which uses Giemsa Coloraing is Banding G call, and then produces the typical "G-Bands." [23] Therefore, a full account of a karyotipo can include the number, type, shape, and wrapping of chromosomes and partecipates © other cytogenetic information. It is often found the variation between the sexes, including the germ line and Soma (between gametes and the rest of the body), among members of a population (chromosomal polymorphism), the geographical specialization and mosaics or otherwise abnormal individuals. [10] Karyotype Karyotype human to human (male) Typical human canariti contain 22 pairs of autosomal chromosomes and a pair of sex chromosomes (allosomi). The karyotpi more common for females contain two X chromosomes and are denoted 46, XX; Males usually have one X chromosome and is denoted 46, XY. Approximately 1.7% of human beings are Intersex, sometimes due to variations in sex chromosomes. [24] [25] [unreliable source] Some variations of karyotype, if truck or allosomes, cause development abnormalities. Diversity and evolution of karyotypes thoughDNA replication and transcription are highly standardized in eukaryotes, one cannot say for their strings, which are highly variable. there is a variation between the species in the number of chromosomes and in detailed organization, despite their construction from the same macromolecules. This variation provides the basis for a series of studies in evolutionary cytology. in some cases there is a still significant variation within the species. in a review, enjoyfrey and masters conclude: In our opinion, it is unlikely that a process or another can take into account independently for the wide range of observed karyotype structures... but, used in combination with other phylogenetic data, fissioning karyotypico can help explain dramatic differences in the diploid numbers between closely related species, which were previously unexplained. [26] although much is known about descriptive karyotypes, and it is clear that changes in the karyotype organization have had effects on the evolutionary course of many species, it is not clear what could be the general meaning. we have a poor understanding of the causes of karyotype evolution, despite many accurate investigations ... the general meaning of karyotype evolution is dark. "â€ ‰ maynard smith [27] changes during development instead of the usual gene repression, some organisms enter for a large-scale elimination of heterochromatin, or other types of adjustment visible to karyotype. elimination of chromosome. in some species, as in many swab flies, whole chromosomes are eliminated during development. [28] decrease in chromatin (founder father: theodor boveri.) in this process, found in some costumes and roundworms as ascaris suum, the portions of chromosomes are thrown away into particular cells. this process is a re-arrangement of the organized genome in which new telomeres are built and some heterochromatin regions are lost. [29] [30] in a. suum, all somatic cell precursors suffer a decrease in chromatin. [31] X-inactivation. the inactivation of a x chromosome occurs during the early development of mammals (see barr body and dosage compensation.) in placentali mammals, the inactivation is random as between the two xs; therefore the female of mammals is a mosaic against its x chromosomes. in marsupial is always the paternal x which is inactive. in human females, 15% of somatic cells to escape inactivation, [32] and the number of genes affected on the inactivated x chromosome varies between cells: in fibroblast cells on about 25% of the genes on the inactivation of body escape. [33] number of chromosomes in a set a spectacular example of variability among closely related species is the muntjac, which was studied by kurt benrschke and doris wurster. the diploid number of Chinese muntjac, muntiacus reevesi, was found to be 46, all telocentric. when they looked at the karyotype of Indian muntjac closely related, muntiacus muntjak, were amazed to find it with female = 6, male = 7 chromosomes. [34] they simply could not believe what they saw ... they kept quiet for two or three years because they thought something was not wrong in their culture of fabric ... but when they got a couple of other specimens that confirmed [their discoveries] ." â€ ‰ hsu p. 73-4 [17] the number of chromosomes in the karyotype among the unrelated species (relatively) is extremely variable. the low record is held by the unirelens nematode parascaris, where the aploid n = 1; and an ant: myrmecia pilosula. [35] the high record would be somewhere between the ferns, with the fake fern of the adder ophioglossum ahead with an average of 1262 chromosomes. [36] the highest score for animals could be the shortnose sturgeon acipenser brevirostrum achromosomes. [37] The existence of the innumerable chromosomes or B means that the number of chromosomes may vary even within an interbreeding population; and aneuploids are another example, although in this case they would not be considered normalof the population. The fundamental number, FN, of a karyotype is the number of main chromosomal arms visible for chromosome sets.[38][39] Thus, FN ≤ 2 x 2n, the difference depending on the number of chromosomes considered mono-armed (acrocentric or telocentric) present. Human beings have FN = 82,[40] for the presence of five acrocentric chromosomal couples: 13, 14, 15, 21, and 22 (human Y chromosome is also acrocentric). The autosomal base number or the autosomal base number, FNa[41] or AN,[42] of a karyotype is the number of main chromosomal arms visible by automi series (non-sex-linked chrome). Ploidy Ploidy is the number of complete sets of chromosomes in a cell. Polyploidia, where there are more than two sets of homologue chromosomes in cells, occurs mainly in plants. It was of great importance in plant evolution according to Stebbins.[43][46] The proportion of flowering plants that are polyploid has been estimated by Stebbins at 30-35%, but in the grasses the average is much higher, about 70%.[47] Polyploidia in the lower plants (fernes, cups and psilotales) is also common, and some species of ferns have reached levels of polyploids much higher than the highest levels known in flowering plants. Polyploidia in animals is much less common, but has been significant in some groups. [48] The polyploid series in related species which consists entirely of multiples of a single base number is known as euploid. Haplo-diploidy, where a sex is diploid, and the other haploid. It is a common agreement in Imenoptera, and in some other groups. Endopolyploidy occurs when in adult differentiated tissues cells ceased to divide by mitosis, but nuclei contain more than the original somatic number of chromosomes. [49] In the endomitosis or endoreduplication, chromosomes in a "religious" nucleus undergo the reduplication, the chromosomes of the daughter separating each other within an intact nuclear membrane. [50] In many cases, endopolyploid nuclei contain tens of thousands of chromosomes (which cannot be accurately counted). The cells do not always contain exact multiples (powers of two), which is why the simple definition 'an increase in the number of chromosomal sets caused by replication without cell division' is not accurate enough. This process (especially studied in insects and in some higher plants such as corn) can be a development strategy to increase the productivity of tissues that are highly active in biosynthesis.[51] The phenomenon occurs sporadically throughout the Eucharistic kingdom from protozoa to human beings; is varied and complex, and serves differentiation and morphogenesis in many ways. [52] See palaeopolyploidy for the investigation of ancient karyotype duplications. Aneuploidy Aneuploidy is the condition in which the chromosome number in the cells is not the typical number for the species. This would give rise to a chromosome anomaly like an extra chromosome or one or more lost chromosomes. The abnormalities in the chromosome number usually cause a defect in development. Down syndrome and Turner syndrome are examples of this. The anauploidy can also occur within a group of closely related species. Classical examples in plants are the genus Crepis, where the gametic numbers (= haploid) form the series x = 3, 4, 5, 6 and 7; and Crocus, where each number from x = 3 to x = 15 is represented by at least one species. The proof of various types shows that trends in evolution have gone in different directions in different groups. [53] In primates, the great monkeys have 24x2 chromosomes while humans have 23x2. Human chromosome 2 was formed by a fusion of ancestral chromosomes, reducing the number. [54] Chromosomal polymorphism Some species are polymorphic for different chromosomal structural forms. [55] The structural change mayassociated with different numbers of chromosomes in different individuals, which occurs in the Coccinella Chilocinus CholoCinus Some mantides of the genus Ameles, [citation necessary] the European Shrew Sorex Araneus. [56] There are some evidence of the case of the Molluss Thais Lapillus (the Whelk dog) on the coast of Brittany, that the two chromosomal morphs are adapted to different habitats. [57] Species Trees The detailed study of chromosome band in insects with polytene chromosomes can reveal relations between closely related species: The classic example is the study of the chromosome band in the Hawaiian drosophiids of Hampton L. Carson. In about 6,500 square meters (17,000 km2), the Hawaiian Islands have the largest collection of Drosophilid flies in the world, living from rain forests to subalpine meadows. These species of Drosophilid of about 800 Hawaiian are usually assigned to two genera, Drosophila and Scaptomiza, in the drosophilidae of the family. The Polytene band of the "Wing Wing" group, the most studied group of Hawaiian drosophilia, allowed Carson to process the evolutionary tree long before genome analysis was feasible. In a way, gene agreements are visible in the wrapping patterns of each chromosome. The rearrangements of chromosome, in particular the inversions, allow to see which species are closely related. The results are clear. Inversions, if traced in the form of the tree (and independent of all other information), show a clear "flow" of species from older to the most recent islands. There are also cases of colonization to the elderly islands and jumping the islands, but these are much less frequent. Using the K-AR dating, the current islands date back from 0.4 million years ago (mya) (Mauna Kea) to 10mya (Necker). The oldest member of the Hawaiian archipelago still above the sea is Kure Atollo, which can be dated to 30 mya. The archipelago itself (produced from the Pacific dish that moves on a hot spot) has existed for much longer, at least in the Cretaceous. Previous islands now under the sea (Guyots) form the Emperor's Seamount chain. [58] All native species Drosophila and Scaptomiza in Hawaiê »I have apparently descended from a single ancestral species that colonized the islands, probably 20 million years ago. Subsequent adaptive radiation was spurned by a lack of competition and a wide variety of niches. Although it would be possible for a single pregnant female to colonize an island, it is more likely that it was a group from the same species. [59] [60] [61] There are other animals and plants on the Hawaiian archipelago that have undergone similar radiation, if less spectacular, adaptive. [63] [64] Chromosome chromosome chromosome chromosome chromosomes show a band pattern when treated with some stains. Bands are alternating light and dark stripes that appear along the lengths of chromosomes. Exclusive band models are used to identify chromosomes and to diagnose chromosome aberrations, including chromosome break, loss, duplication, translocation or inverted segments. A range of different chromosomal treatments produce a range of band models: bands G, bands G, bands R, c-bands, bands Q-Band, T-Bands and Nor-Band. The representation of the types of cytogenetic wrapping karyotypes uses different techniques to display different aspects of chromosomes: [21] Banda G is obtained with Giemsa Macchia after the digestion of chromosomes with trypsin. Brings a series of bands slightly and obscurely spotted - dark regions tend to be heterochromatic, replicating and rich. Bright regions tend to be euchromatic, precise and rich replicas of GC. This method will normally produce 300 400 groups in a normal and human genome. R-Bandaggio is the opposite of the G band (the R stands for "reverse"). The dark regions are euchromatic (regions rich in guanine-cytosine) and the bright regions are heterochromatic (regions rich in tymine-adenine). C-Banding:It is linked to constituent heterochromate, then stain centromeri. The name derives from centromeric or constitutive heterochromatin. The preparations undergo alkaline denaturation before the color that lead to an almost complete complete DNA. After washing the probe, the remaining DNA is re-stitched and stained with the Giemsa solution composed of methylene azure, methylene violet, methylene blue and ethylene eosine. The heterochromatous binds much of the dye, while the rest of the chromosomes absorb only little. C-bonding has been particularly suitable for plant chromosomes. Q-banding is a fluorescent model obtained using quinacrine for coloring. The band model is very similar to that seen in G-banding. They can be recognized by a yellow fluorescence of different intensity. Most of the colored DNA is heterochrome. Quinacrin (athebrine) binds both regions rich in AT and GC, but only the AT-quinacrin-complex fluoresces. Because the rich regions of AT are more common in heterochromatin than in euchromatin, these regions are preferably labeled. The different intensity of each band reflects the different AT content. Other fluorochromes such as DAPI or Hoechst 33258 also lead to characteristic and reproducible models. Each of them produces its own specific model. In other words: the properties of bonds and the specificity of fluorochromes are not based solely on their affinity with regions rich in AT. Rather, the distribution of AT and the association of AT with other molecules such as istons, for example, influences binding properties of fluorochromes. T-banding: displays telomeres. Silver color: Silver nitrate spot the nucleolar organization associated region protein. This produces a dark region in which silver is deposited, indicating the activity of rRNA genes within the classic Karyogram karyotype NOR. Citogenetics by a human probed female lymphocyte for the Alu sequence using FISH. In the "classic" karyotype (depilate), a colorant, often Giemsa (G-banding), less frequently mepacrine (quinacrino), is used for band stains on chromosomes. Giemsa is specific for phosphate DNA groups. Quinacrine binds to regions rich in adenine-thymines. Each chromosome has a characteristic banding pattern that helps identify them; both chromosomes in a couple will have the same model of banding. The Karyotipi are arranged with the short arm of the chromosome on the top, and the long arm on the bottom. Some karyotypes call short and long arms p and q respectively. In addition, the regions and subregions are given numerical names from proximal to distal on chromosomal arms. For example, the Cri du chat syndrome involves a short arm deletion of chromosome 5. It is written as 46,XX,5p-. The critical region for this syndrome is the deletion of p15.2 (the locus on chromosome), which is written as 46,XX, of(5)(p15.2).[65] Multicolor FISH (mFISH) and spectral karyotype (KY technique) The spectral karyogram of a human female Multicolor FISH and the oldest spectral karyotyping are molecular cytogenetic techniques used to simultaneously visualize all pairs of chromosomes in an organism in different colors. Fluorescent probes labeled for each chromosome are made by labeling the specific chromosome DNA with different fluorophers. Since there are a limited number of spectrally distinct fluorophores, a combinatorial labeling method is used to generate many different colors. Fluophoro combinations are captured and analyzed by a fluorescence microscope using up to 7 narrow band fluorescence filters or, in the case of spectral karyotyping, using a interferometer attached to a fluorescence microscope. In the case of a mFISH image, each combination of fluorochrome from the resulting original images is replaced by a pseudo-color in a dedicated image analysis software. Thus, chromosomal or chromosomal sections can be viewed and identified,The analysis of chromosomal rearrangements. [66] In the case of spectral karyotyping, the image processing software assigns a pseudo color to each spectrally different combination, allowing the display of the single single chromosomes. [67] Spectral Kiaryotype Human Karyotype Pescolor is used to identify structural chromosomal aberrations in cancer cells and in other conditions of the disease when Giemsa Banding or other techniques are not accurate enough. Digital Karyotyping Digital Karyotyping is a technique used to quantify the DNA copy number on a genomic scale. The short DNA sequences from specific locies of the whole genome are isolated and enumerated. [68] This method is also known as virtual Karyotyping. Chromosomal abnormalities Main article: Chromosome abnormalities can be numerical, such as in the presence of extra or missing chromosomes or structural, such as in derived chromosomes, translocations, inversions, deletions or large-scale duplications. Numerical abnormalities, also known as aneuploidy, often occur as a result of non-destruct during meiosis in the formation of a gamete; Trisomies, in which there are three copies of chromosomes instead of the usual two, are common numerical abnormalities. Structural abnormalities often result from errors in homologated recombination. Both types of abnormalities may occur in gametes and therefore will be present in all cells of the affected person's body, or may occur during mitosis and give rise to a genetic mosaic individual that has some normal and some abnormal cells. In the chromosome abnormalities of human beings leading to disease in humans include Turner's syndrome is from a single X chromosome (45, X or 45, X0). Klinefelter syndrome, the most common male chromosomal disease, otherwise known as 47, XXY, is caused by an extra x chromosome. Edwards syndrome is caused by trisomy (three copies) of chromosome 18. Down syndrome, a common chromosomal disease, is caused by chromosome 21 trisomy. Patau syndrome is caused by chromosome 13 trisomy. Trisomy 9, considered the 4th most common Trisomy, has many individuals affected by long lived, but only in a form other than a complete trisomy, such as Trisomy 9P syndrome or mosaic trisomy 9. often work pretty well, but they tend to have problems with speech. Also documented are Trisomy 8 and Trisomy 16, although they generally do not survive at birth. Some disturbances arise from the loss of one piece of a chromosome, including Cri du chat (cat's scream), from a short arm truncated on chromosome 5. The name comes from the distinctive cry of children, caused by abnormal formation of larynx. 1P36 Cancellation syndrome, from the loss of part of the short arm of chromosome 1. Angelman Syndrome - 50% of cases have a long arm segment of the missing 15 chromosome; A deletion of maternal genes, example of imprinting disorder. Prader-Willi syndrome â€ "50% of cases have a long arm segment of the missing 15 chromosome; A cancellation of paternal genes, example of imprinting disorder. Chromosome abnormalities may also occur in cancerous cells of a completely genetically normal individual; A well-documented example is the Philadelphia chromosome, a mutation of translocation commonly associated with chronic myelogen leukemia and less often with acute lymphocerate leukemia. See also references to the screen of the cytogenetic notation genome Judd, walter s.; Campbell, Christopher S.; Kellogg, Elizabeth a.; Stevens, peter f.; Donoghue, Michael J. (2002). 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