Difference Between Heterochromatin and Euchromatin



The major difference between heterochromatin and euchromatin is that **heterochromatin** is such part of the chromosomes, which is a firmly packed form and are **genetically inactive**, while **euchromatin** is an uncoiled (loosely) packed form of chromatin and are **genetically active**.

When the non-dividing cells of the nucleus were observed under the light microscope, it exhibited the two regions, on the ground of concentration or intensity of staining. The **dark stained** areas are said as heterochromatin and **light stained** areas are said as euchromatin.

Around **90%** of the total human genome is euchromatin. They are the parts of chromatin and participate in the protection of DNA in the genome present inside the nucleus. **Emil Heitz** in the year 1928, coined the term Heterochromatin and Euchromatin.

By focussing on the few more points, we will be able to understand the difference between both types of chromatin. Given below is the comparison chart along with the brief description of them.

Content: Heterochromatin Vs Euchromatin

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Comparison Chart

BASIS FOR COMPARISON	HETEROCHROMATIN	EUCHROMATIN
Meaning	The tightly packed form of DNA in the chromosome is called as heterochromatin.	The loosely packed form of DNA in the chromosome is called as euchromatin.
DNA density	High DNA density.	Low DNA density.
Kind of stain	Stained dark.	Lightly stained.
Where they are present	These are found at the periphery of the nucleus in eukaryotic cells only.	These are found in the inner body of the nucleus of prokaryotic as well as in eukaryotic cells.
Transcriptional activity	They show little or no transcriptional activity.	They actively participate in the process of transcription.
Other features	They are compactly coiled.	They are loosely coiled.
	They are late replicative.	They are early replicative.
	Regions of heterochromatin are sticky.	Regions of euchromatin are non- sticky.
	Genetically inactive.	Genetically active.
	Phenotype remains unchanged of an organism.	Variation may be seen, due to the affect in DNA during the genetic process.

It permits the gene expression regulation and also maintains the structural integrity of the cell. It results in genetic variations and permits the genetic transcription.

Definition of Heterochromatin

The area of the chromosomes which are **intensely stained** with DNA-specific strains and are relatively condensed is known as **heterochromatin**. They are the **tightly packed** form of DNA in the nucleus.

The organization of heterochromatin is so highly compact in the way that these are inaccessible to the protein which is engaged in gene expression. Even the chromosomal crossing over is not possible due to the above reason. Resulting them to be transcriptionally as well as genetically inactive.



Heterochromatin is of two types: Facultative heterochromatin and constitutive heterochromatin. The genes which get silenced through the process of **Histone methylation or siRNA** through **RNAi** are called as **facultative heterochromatin**. Hence they contain inactive genes and is not a permanent character of every nucleus of the cells.

While the **repetitive and structurally functional genes** like telomeres or centromeres are called as **Constitutive heterochromatin**. These are the continuing nature of the cell's nucleus and contains no gene in the genome. This structure is retainable during the interphase of the cell.

The **main function** of the heterochromatin is to protect the DNA from the endonuclease damage; it is due to its compact nature. It also prevents the DNA regions to get accessed to proteins during gene expression.

Definition of Euchromatin

That part of chromosomes, which are **rich in gene** concentrations and are loosely packed form of chromatin is called as **euchromatin**. They are active during transcription.

Euchromatin covers the maximum part of the dynamic genome to the inner of the nucleus and is said that euchromatin contains about **90% of the entire human genome**.

To allow the transcription, some parts of the genome containing active genes are loosely packed. The wrapping of DNA is so loose that DNA can become readily available. The structure of euchromatin resembles the nucleosomes, which consist of histones proteins having around 147 base pairs of DNA wrapped around them.

Euchromatin actively participates in transcription from DNA to RNA. The **gene regulating mechanism** is the process of transforming euchromatin into heterochromatin or vice versa.

The active genes present in euchromatin gets transcribed to make mRNA whereby further encoding the functional proteins is the **main function** of euchromatin. Hence they are considered as genetically and transcriptionally active. **Housekeeping** genes are one of the forms of euchromatin.

Key differences between Heterochromatin and Euchromatin

Following are the substantial points to differentiate among heterochromatin and euchromatin:

- 1. The tightly packed form of DNA in the chromosome is called as **heterochromatin**, while the loosely packed form of DNA in the chromosome is called as **euchromatin**.
- 2. In heterochromatin, the **density of DNA** is **high** and are **stained dark**, whereas in euchromatin the density of DNA is **little** and are **lightly stained**.
- 3. Heterochromatin is **found** at the periphery of the nucleus in eukaryotic cells only, and Euchromatin is **located** in the inner body of the nucleus of prokaryotic as well as in eukaryotic cells.
- 4. Heterochromatin shows little or **no transcriptional activity** as well they are **genetically inactive**, on the other hand, Euchromatin **actively** participates in the process of transcription and are **genetically active** also.
- 5. Heterochromatin is **compactly coiled** and is **late replicative**, whereas Euchromatin is **loosely coiled** and **early replicative**.
- 6. **Regions** of heterochromatin are sticky, but the areas of Euchromatin are non-sticky.
- 7. In Heterochromatin part, the **phenotype** remains unchanged of an organism, though variation may be seen, due to the effect in DNA during the genetic process in the Euchromatin.
- 8. Heterochromatin permits the **gene expression regulation** and also maintains the structural integrity of the cell though Euchromatin results in **genetic variations**, and allows the genetic transcription.

Conclusion

From the above information regarding chromatin – their structure and types. We can say that only Euchromatin is vigorously involved in the transcription process although heterochromatin and its types do not play such significant role.

Constitutive heterochromatin contains the satellite DNA, and it surrounds the centromere, and facultative heterochromatin is disbanded. So apparently it can be said that the eukaryotic cells and their inner structure are relatively complex.

Heterochromatin

From Wikipedia, the free encyclopedia Jump to navigationJump to search **Heterochromatin** is a tightly packed form of <u>DNA</u> or <u>condensed DNA</u>, which comes in multiple varieties. These varieties lie on a continuum between the two extremes of <u>constitutive heterochromatin</u> and <u>facultative heterochromatin</u>. Both play a role in the <u>expression of genes</u>. Because it is tightly packed, it was thought to be inaccessible to polymerases and therefore not transcribed, however according to Volpe et al. (2002),^[1] and many other papers since,^[2] much of this DNA is in fact transcribed, but it is continuously <u>turned over</u> via <u>RNA-induced transcriptional silencing</u> (RITS). Recent studies with <u>electron microscopy</u> and <u>OsO₄</u> staining reveal that the dense packing is not due to the chromatin.^[3]

Constitutive heterochromatin can affect the genes near itself (e.g. <u>position-effect</u> <u>variegation</u>). It is usually <u>repetitive</u> and forms structural functions such as <u>centromeres</u> or <u>telomeres</u>, in addition to acting as an attractor for other gene-expression or repression signals.

Facultative heterochromatin is the result of genes that are <u>silenced</u> through a mechanism such as <u>histone deacetylation</u> or <u>Piwi-interacting RNA</u> (piRNA) through <u>RNAi</u>. It is not repetitive and shares the compact structure of constitutive heterochromatin. However, under specific developmental or environmental signaling cues, it can lose its condensed structure and become transcriptionally active.^[4]

Heterochromatin has been associated with the di- and tri-methylation of <u>H3K9</u> in certain portions of the genome.^[II] <u>H3K9me3</u>-related <u>methyltransferases</u> appear to have a pivotal role in modifying heterochromatin during lineage commitment at the onset of <u>organogenesis</u> and in maintaining lineage fidelity.^[II]



The nucleus of a human cell showing the location of heterochromatin

Note that the informal diagram shown here may be in error as to the location of heterochromatin. An inactivated X-chromosome (a.k.a. <u>Barr body</u>) migrates to the nuclear membrane alone, leaving the active X and other chromosomes within the nucleoplasm (away from the membrane in general). Other heterochromatin appear as

particles separate from the membrane, "Heterochromatin appears as small, darkly staining, irregular particles scattered throughout the nucleus ...".

 \Box

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Structure[edit]

<u>Chromatin</u> is found in two varieties: <u>euchromatin</u> and heterochromatin.^{III} Originally, the two forms were distinguished cytologically by how intensely they stained – the euchromatin is less intense, while heterochromatin stains intensely, indicating tighter packing. Heterochromatin is usually localized to the periphery of the <u>nucleus</u>. Despite this early dichotomy, recent evidence in both animals^{III} and plants^{IIII} has suggested that there are more than two distinct heterochromatin states, and it may in fact exist in four or five 'states', each marked by different combinations of <u>epigenetic</u> marks.

Heterochromatin mainly consists of genetically inactive <u>satellite sequences</u>,^[11] and many genes are repressed to various extents, although some cannot be expressed in euchromatin at all.^[12] Both <u>centromeres</u> and <u>telomeres</u> are heterochromatic, as is the <u>Barr body</u> of the second, inactivated <u>X-chromosome</u> in a female.

Function[edit]

Heterochromatin has been associated with several functions, from gene regulation to the protection of chromosome integrity;^[13] some of these roles can be attributed to the dense packing of DNA, which makes it less accessible to protein factors that usually bind DNA or its associated factors. For example, naked double-stranded DNA ends would usually be interpreted by the cell as damaged or viral DNA, triggering <u>cell</u> cycle arrest, <u>DNA repair</u> or destruction of the fragment, such as by <u>endonucleases</u> in bacteria.

Some regions of chromatin are very densely packed with fibers that display a condition comparable to that of the chromosome at <u>mitosis</u>. Heterochromatin is generally clonally inherited; when a cell divides, the two daughter cells typically contain heterochromatin within the same regions of DNA, resulting in <u>epigenetic inheritance</u>. Variations cause heterochromatin to encroach on adjacent genes or recede from genes at the extremes of domains. Transcribable material may be repressed by being positioned (in *cis*) at these boundary domains. This gives rise to expression levels that vary from cell to cell,¹¹⁴ which may be demonstrated by <u>position-effect variegation</u>.¹¹⁵ Insulator sequences

may act as a barrier in rare cases where constitutive heterochromatin and highly active genes are juxtaposed (e.g. the 5'HS4 insulator upstream of the chicken β -globin locus,^[16] and loci in two <u>Saccharomyces</u> spp.^{[17][18]}).

Constitutive heterochromatin[edit]

Main article: Constitutive heterochromatin

All cells of a given species, package the same regions of DNA in <u>constitutive</u> <u>heterochromatin</u>, and thus in all cells, any genes contained within the constitutive heterochromatin will be poorly <u>expressed</u>. For example, all human chromosomes <u>1</u>, <u>9</u>, <u>16</u>, and the <u>Y-chromosome</u> contain large regions of constitutive heterochromatin. In most organisms, constitutive heterochromatin occurs around the chromosome centromere and near telomeres.

Facultative heterochromatin[edit]

The regions of DNA packaged in facultative heterochromatin will not be consistent between the cell types within a species, and thus a sequence in one cell that is packaged in facultative heterochromatin (and the genes within are poorly expressed) may be packaged in euchromatin in another cell (and the genes within are no longer silenced). However, the formation of facultative heterochromatin is regulated, and is often associated with morphogenesis or differentiation. An example of facultative heterochromatin is X chromosome inactivation in female mammals: one X chromosome is packaged as facultative heterochromatin and silenced, while the other X chromosome is packaged as euchromatin and expressed.

Among the molecular components that appear to regulate the spreading of heterochromatin are the <u>Polycomb-group proteins</u> and non-coding genes such as <u>Xist</u>. The mechanism for such spreading is still a matter of controversy.^[19] The polycomb repressive complexes <u>PRC1</u> and <u>PRC2</u> regulate <u>chromatin</u> compaction and gene expression and have a fundamental role in developmental processes. PRC-mediated <u>epigenetic</u> aberrations are linked to <u>genome instability</u> and malignancy and play a role in the <u>DNA damage</u> response, <u>DNA repair</u> and in the fidelity of <u>replication</u>.^[20]

Yeast heterochromatin[edit]

<u>Saccharomyces cerevisiae</u>, or budding yeast, is a model <u>eukaryote</u> and its heterochromatin has been defined thoroughly. Although most of its genome can be characterized as euchromatin, *S. cerevisiae* has regions of DNA that are transcribed very poorly. These loci are the so-called silent mating type loci (HML and HMR), the rDNA (encoding ribosomal RNA), and the sub-telomeric regions. Fission yeast (<u>Schizosaccharomyces pombe</u>) uses another mechanism for heterochromatin formation at its centromeres. Gene silencing at this location depends on components of the <u>RNAi</u> pathway. Double-stranded RNA is believed to result in silencing of the region through a series of steps.

In the fission yeast *Schizosaccharomyces pombe*, two RNAi complexes, the RITS complex and the RNA-directed RNA polymerase complex (RDRC), are part of an RNAi

machinery involved in the initiation, propagation and maintenance of heterochromatin assembly. These two complexes localize in a <u>siRNA</u>-dependent manner on chromosomes, at the site of heterochromatin assembly. <u>RNA polymerase II</u> synthesizes a transcript that serves as a platform to recruit RITS, RDRC and possibly other complexes required for heterochromatin assembly.^[21]22] Both RNAi and an exosomedependent RNA degradation process contribute to heterochromatic gene silencing. These mechanisms of *Schizosaccharomyces pombe* may occur in other eukaryotes.^[23] A large RNA structure called <u>RevCen</u> has also been implicated in the production of siRNAs to mediate heterochromatin formation in some fission yeast.^[24]

See also[edit]

• Centric heterochromatin

References[edit]

- Volpe TA, Kidner C, Hall IM, Teng G, Grewal SI, Martienssen RA (September 2002). <u>"Regulation of heterochromatic silencing and histone H3 lysine-9 methylation by RNAi"</u>. Science. 297 (5588): 1833–7. <u>doi:10.1126/science.1074973</u>. <u>PMID 12193640</u>.
- 2. <u>A</u> <u>"What is the current evidence showing active transcription withinin..."</u>www.researchgate.net. Retrieved 2016-04-30.
- Ou HD, Phan S, Deerinck TJ, Thor A, Ellisman MH, O'Shea CC (July 2017). <u>"ChromEMT:</u> <u>Visualizing 3D chromatin structure and compaction in interphase and mitotic</u> <u>cells"</u>. Science. **357** (6349): eaag0025. doi:10.1126/science.aag0025. PMC 5646685. PMID 28751582.
- ▲ Oberdoerffer P, Sinclair DA (September 2007). <u>"The role of nuclear architecture in genomic instability and ageing</u>". Nature Reviews. Molecular Cell Biology. 8(9): 692–702. <u>doi:10.1038/nrm2238</u>. <u>PMID 17700626</u>.
- <u>A</u> Rosenfeld JA, Wang Z, Schones DE, Zhao K, DeSalle R, Zhang MQ (March 2009). <u>"Determination of enriched histone modifications in non-genic portions of the human genome"</u>. BMC Genomics. **10** (1): 143. <u>doi:10.1186/1471-2164-10-143</u>. <u>PMC 2667539</u>. <u>PMID 19335899</u>.
- A Nicetto D, Donahue G, Jain T, Peng T, Sidoli S, Sheng L, et al. (January 2019). <u>"H3K9me3-heterochromatin loss at protein-coding genes enables developmental lineage specification"</u>. Science. **363** (6424): 294–297. doi:10.1126/science.aau0583. PMC 6664818. PMID 30606806.
- 7. Shown here: Electron microscope image of nucleus with heterochromatin particles annotated [1]
- Elgin, S.C. (1996). "Heterochromatin and gene regulation in Drosophila". <u>Current Opinion in Genetics & Development</u>. 6 (2): 193–202. <u>doi:10.1016/S0959-437X(96)80050-5</u>. <u>ISSN 0959-437X</u>. <u>PMID 8722176</u>.
- 9. <u>^</u> van Steensel B (May 2011). <u>"Chromatin: constructing the big picture"</u>. The EMBO Journal. **30** (10): 1885–95. <u>doi:10.1038/emboj.2011.135</u>. <u>PMC</u> <u>3098493</u>. <u>PMID</u> <u>21527910</u>.
- <u>A</u> Roudier F, Ahmed I, Bérard C, Sarazin A, Mary-Huard T, Cortijo S, et al. (May 2011). <u>"Integrative epigenomic mapping defines four main chromatin states in Arabidopsis</u>". The EMBO Journal. **30** (10): 1928–38. <u>doi:10.1038/emboj.2011.103</u>. <u>PMC 3098477</u>. <u>PMID 21487388</u>.
- <u>^</u> Lohe AR, Hilliker AJ, Roberts PA (August 1993). <u>"Mapping simple repeated DNA sequences in heterochromatin of Drosophila melanogaster"</u>. Genetics. **134** (4): 1149–74. <u>PMC</u> 1205583. <u>PMID</u> 8375654.
- Lu BY, Emtage PC, Duyf BJ, Hilliker AJ, Eissenberg JC (June 2000). <u>"Heterochromatin protein 1 is required for the normal expression of two heterochromatin genes in Drosophila"</u>. Genetics. **155** (2): 699–708. <u>PMC</u> <u>1461102</u>. <u>PMID</u> <u>10835392</u>.
- <u>A</u> Grewal SI, Jia S (January 2007). "Heterochromatin revisited". Nature Reviews. Genetics. 8 (1): 35–46. <u>doi:10.1038/nrg2008</u>. <u>PMID 17173056</u>. An up-to-date account of the current understanding of

repetitive DNA, which usually doesn't contain genetic information. If evolution makes sense only in the context of the regulatory control of genes, we propose that heterochromatin, which is the main form of chromatin in higher eukaryotes, is positioned to be a deeply effective target for evolutionary change. Future investigations into assembly, maintenance and the many other functions of heterochromatin will shed light on the processes of gene and chromosome regulation.

- <u>^</u> Fisher AG, Merkenschlager M (April 2002). "Gene silencing, cell fate and nuclear organisation". Current Opinion in Genetics & Development. **12** (2): 193–7. <u>doi:10.1016/S0959-437X(02)00286-1</u>. <u>PMID 11893493</u>.
- <u>A Zhimulev, I.F.</u>; et al. (December 1986). "Cytogenetic and molecular aspects of position effect variegation in Drosophila melanogaster". <u>Chromosoma</u>. 94 (6): 492– 504. doi:10.1007/BF00292759. ISSN 1432-0886.
- <u>A</u> Burgess-Beusse B, Farrell C, Gaszner M, Litt M, Mutskov V, Recillas-Targa F, et al. (December 2002). <u>"The insulation of genes from external enhancers and silencing chromatin"</u>. Proceedings of the National Academy of Sciences of the United States of America. 99 Suppl 4 (Suppl 4): 16433– 7. <u>doi:10.1073/pnas.162342499</u>. <u>PMC 139905</u>. <u>PMID 12154228</u>.
- Allis CD, Grewal SI (August 2001). "Transitions in distinct histone H3 methylation patterns at the heterochromatin domain boundaries". Science. 293(5532): 1150– 5. <u>doi:10.1126/science.1064150. PMID</u> 11498594.
- <u>^</u> Donze D, Kamakaka RT (February 2001). <u>"RNA polymerase III and RNA polymerase II promoter complexes are heterochromatin barriers in Saccharomyces cerevisiae"</u>. The EMBO Journal. 20 (3): 520–31. <u>doi:10.1093/emboj/20.3.520</u>. <u>PMC 133458</u>. <u>PMID 11157758</u>.
- <u>A</u> Talbert PB, Henikoff S (October 2006). "Spreading of silent chromatin: inaction at a distance". Nature Reviews. Genetics. 7 (10): 793–803. <u>doi:10.1038/nrg1920</u>. <u>PMID</u> <u>16983375</u>.
- 20. ▲ Veneti Z, Gkouskou KK, Eliopoulos AG (July 2017). <u>"Polycomb Repressor Complex 2 in Genomic Instability and Cancer"</u>. International Journal of Molecular Sciences. **18** (8): 1657. <u>doi:10.3390/ijms18081657</u>. <u>PMC 5578047</u>. <u>PMID 28758948</u>.
- <u>A</u> Kato H, Goto DB, Martienssen RA, Urano T, Furukawa K, Murakami Y (July 2005). "RNA polymerase II is required for RNAi-dependent heterochromatin assembly". Science. **309** (5733): 467–9. <u>doi:10.1126/science.1114955</u>. <u>PMID 15947136</u>.
- Djupedal I, Portoso M, Spåhr H, Bonilla C, Gustafsson CM, Allshire RC, Ekwall K (October 2005). <u>"RNA Pol II subunit Rpb7 promotes centromeric transcription and RNAi-directed chromatin silencing</u>". Genes & Development. **19** (19): 2301–
 <u>doi:10.1101/gad.344205</u>. <u>PMC 1240039</u>. <u>PMID 16204182</u>.
- Vavasseur; et al. (2008). <u>"Heterochromatin Assembly and Transcriptional Gene Silencing under the Control of Nuclear RNAi: Lessons from Fission Yeast"</u>. RNA and the Regulation of Gene Expression: A Hidden Layer of Complexity. Caister Academic Press. <u>ISBN 978-1-904455-25-7</u>.
- <u>^</u> Djupedal I, Kos-Braun IC, Mosher RA, Söderholm N, Simmer F, Hardcastle TJ, et al. (December 2009). <u>"Analysis of small RNA in fission yeast; centromeric siRNAs are potentially generated through a structured RNA</u>". The EMBO Journal. **28** (24): 3832–44. <u>doi:10.1038/emboj.2009.351</u>. <u>PMC 2797062</u>. <u>PMID 19942857</u>.