Genetic test results

A clinical geneticist or genetic counsellor will explain which piece or pieces of genetic material is missing. The information given will include the location and size of the deletion as well as the known significance of any genes included in the change, and whether the same or a similar change has been seen before in another person.

Chromosomal deletions are commonly identified using a genetic test called microarray analysis (such as array CGH). The results of this test are likely to read something like the following example:

\[ \text{arr[hg19] 16p11.2 (29653028-30190538)x1 dn} \]

\[ \text{arr} \] This is the reference DNA sequence that the base pair numbers refer to, in this case human genome build 19

\[ \text{hg19} \] The test revealed a DNA change on the p arm of chromosome 16 in band 11.2

\[ \text{16p11.2} \] The DNA change is identified by its base pair numbers (the points where the chromosomal change has occurred).

\[ \text{(29653028-30190538)} \] This region covers 537,510 base pairs (=0.5 Mb)

\[ \text{x1} \] There is 1 copy of the piece of DNA specified. Since there should be 2 copies of chromosome 16, this indicates that the DNA change is a deletion

\[ \text{dn} \] The deletion occurred \textit{de novo} (as a ‘new event’).

If a deletion in a person is identified as \textit{de novo}, it is very unlikely to occur in any siblings of that person. If a test result is followed by \textit{mat}, the deletion has been inherited from the mother [maternal]; if it is followed by \textit{pat}, the deletion has been inherited from the father [paternal].

Genetic test results may also contain a list of \textit{morbid} genes. These are genes known to cause symptoms if they do not function as expected. Some morbid genes only cause symptoms if there are no functional copies, while others are “dose-sensitive” [may cause symptoms if there are usually two copies and one is lost or altered] or “imprinted” [one copy is already switched off].

Why did this happen and can it happen again?

Deletions can be inherited from an unaffected or affected parent, or happen as a new event (de novo).

Chromosome sections can be lost during the formation of eggs or sperm or during the complicated replication process that is needed to produce new cells as we grow and develop. Sometimes similar deletions occur in many unrelated people due to regions of repetitive DNA. It is important to know that nothing could have been done to prevent the deletion from happening. It was a natural event that no lifestyle, dietary or environmental factors are known to cause. There is nothing that anyone did before, during or after pregnancy to cause the deletion.

If a child has inherited the deletion, the chances of having another child with the same deletion is about 50%. If the deletion is \textit{de novo}, the chances are estimated at less than 1%. Your genetics centre should be able to offer counselling to all family members, including individuals with the deletion or microdeletion, regarding the chances of having another child with the same change.

Inform Network Support

Unique is a charity without government funding, existing entirely on donations and grants. If you can, please make a donation via our website at \text{www.rarechromo.org/donate}. Please help us to help you!

This information guide is not a substitute for personal medical advice. Families should consult a medically qualified clinician in all matters relating to genetic diagnosis, management and health.

Information on genetic changes is a very fast-moving field and while the information in this guide is believed to be the best available at the time of publication, some facts may later change. \text{Unique} does its best to keep abreast of changing information and to review its published guides as needed. This booklet was compiled by \text{Unique} (AP) and reviewed by Dr. Gregory Costain, Division of Clinical and Metabolic Genetics, The Hospital for Sick Children, Toronto, Canada.

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What are deletions and microdeletions?
A chromosomal deletion is the loss of a piece of genetic material from a chromosome. Deletions can vary in size and those that are too small to be seen under the microscope are sometimes called microdeletions.

What are chromosomes?
Our bodies are made up of many different types of cells, most of which contain our chromosomes. Chromosomes come in pairs; one member of each pair is usually inherited from each parent. Most cells have 23 pairs of chromosomes (a total of 46). Eggs and sperm, however, have a single copy of each chromosome pair; when a sperm fertilises an egg at conception, the number of chromosomes is restored to 46. We usually have 22 chromosome pairs called autosomes, numbered 1-22 roughly according to decreasing size, and two sex chromosomes that determine the characteristics associated with biological sex. Males usually have one X and one Y chromosome (XY), and females usually have two X chromosomes (XX).

Chromosomes can’t be seen with the naked eye but if cells are prepared in a specific way, the chromosomes can be stained and viewed under a microscope. This image shows the chromosomes present in a typical male (XY) cell.

How will a deletion affect me or my child?
Effects of chromosomal deletions vary greatly between individuals and are dependent on which chromosome is affected and what genetic material is missing. Deletions can affect intellectual abilities, and/or cause physical and functional changes to our bodies. Deletions thought to cause symptoms are called pathogenic, those that are thought to have no ill effect are called benign. There are also many deletions of uncertain significance that may be reclassified as benign or pathogenic when we’ve learnt more about them.

What are chromosome arms?
Each chromosome consists of two ‘arms’ joined together at a constricted part of the chromosome called the centromere. The shorter arm is called the ‘p’ arm, and the longer arm is known as the ‘q’ arm.

What are chromosome bands?
Each of our chromosomes can be identified as a series of bands visualised by specific laboratory staining techniques. The bands on each chromosome arm are numbered starting at the centromere (which has been assigned the number 10) and finishing at the telomere. Deletions are described by their band location on a chromosome arm. Descriptions start with the number of the chromosome e.g. chromosome 20 (as shown in the image below), followed by the arm letter, p or q. The number of the region e.g. 1 is then noted, followed by the band number e.g. 3, then any smaller sub-bands such as .2 or an even smaller division of a sub-band e.g. .33.

Deletion size
The size of a deletion is measured in bases or base pairs [bp]. The first base pair of each chromosome is at the tip (telomere) of the p arm, and the last is at the tip of the q arm. Since DNA sequences are so long, they are often measured in megabases [Mb’s]; 1 Mb = 1 million bp or kilobases (kb’s); 1 kb =1000 bp). Deletions smaller than 5 Mb (that’s 5,000,000 base pairs) are sometimes known as microdeletions.

Deletions can vary in size from one base pair [known as a sequence variant] to an entire chromosome [known as monosomy]. But the majority of deletions currently identified using standard technologies are between a few hundred kb and a few Mb. Such deletions are commonly known as copy number variants (CNVs) since the usual copy number of the piece of deleted DNA has been reduced by one. For autosomal chromosomes [1-22] this means the expected copy number of two (one from each chromosome pair), has been reduced to one, due to the deletion.