

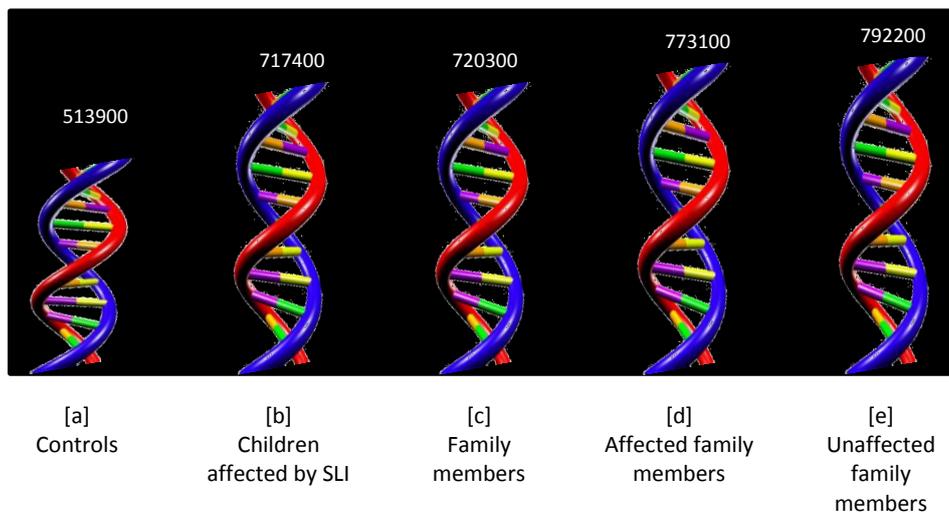
Amount of rearranged DNA in children affected by SLI.

Changes of DNA sequence (mutations) can involve the rearrangement of genetic material. Everyone has some rearrangements but some people have more than others. There is evidence that a higher number of rearrangements might put people at risk of developmental disorders.

In this study, we measured the level of DNA reorganisation in children affected by SLI and their family members and compared it to members of the general population.

We found that:

- Children affected by SLI had more DNA rearrangements than the general population ([a] compared to [b]).
- Family members of affected children also had more rearrangements ([a] compared to [c]).
- We found that this was true even when the family members did not have speech and language difficulties themselves ([a] compared to [e]).



*Amount of rearranged DNA in individuals affected by SLI and their family members.
The length of the DNA strand represents the average amount of rearranged DNA in the group shown.
The number above shows the number of base pairs of DNA that is rearranged.*

From this study, we think that families that are affected by SLI carry a higher number of DNA rearrangements. This puts all family members at an increased risk of developmental difficulties.

But it is not only the amount of reorganisation that is important. The location of the moved DNA also plays a role. If rearrangements do not disrupt any critical genes then it does not matter even if that person has lots of changes. If the rearrangement disrupts an important gene then the family member is more likely to develop speech and language difficulties. The fact that affected families have more rearrangements increases the chances of an important gene being disrupted but does not determine the speech and language difficulties directly.

If we can find out the location of important genes then this will help us to understand the biological basis of SLI.

This summary refers to the following research paper: Genome-wide analysis identifies a role for common copy number variants in specific language impairment. Simpson NH, Ceroni F, Reader RH, Covill LE, Knight JC; the SLI Consortium, Hennessy ER, Bolton PF, Conti-Ramsden G, O'Hare A, Baird G, Fisher SE, Newbury DF. Eur J Hum Genet. 2015 Jan 14. PMID:[25585696](https://pubmed.ncbi.nlm.nih.gov/25585696/) [[pdf](#)]