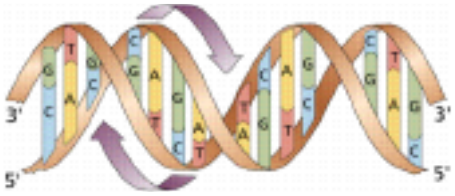
LANDCATCH Natural Selection

# Why Genetic Markers?

Within the cells of every living creature is the entire hereditary blueprint for building and maintaining the organism. This information is carried by DNA. DNA is a long chain of subunits (bases) linked together and whilst there are only four possible bases: C, A, G and T, they may be linked together in any order to form chains many millions of bases long.

**TTCTGGTATTCTCGATACGTCAGTCACTAGTTCGCACTAGTCAAGCTACTACGCATGTCAGGCAG**

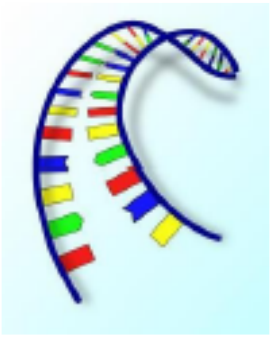



It is within this sequence of bases, that the hereditary instructions are encoded and it is slight variations in this sequence that make every individual unique.
In some organisms the DNA blueprint contains as many as 100 billion bases and so it is difficult to identify these differences directly: genetic markers are a tool we can use to take a 'snapshot' of the DNA sequence.
There are a number of different types and which type we choose will depend on what question we want answered. LNS has pioneered the use of one particular type: microsatellite markers, for parentage assignment in farmed fish species.

## WHAT IS A MICROSATELLITE?

Microsatellites are stretches of short sequences, usually 1-6 bases long, repeated many times. For example a common type of microsatellite is a dinucleotide repeat such as:

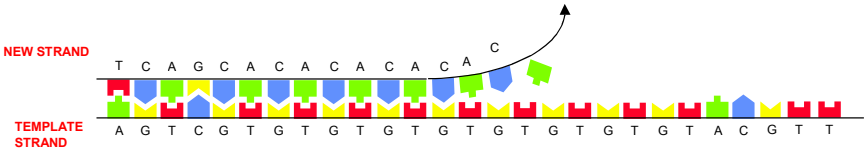
**CACACACACACACACACACACACA**



To understand why they are so useful as genetic markers we need to think about how DNA replicates in a living organism.
Most of us are familiar with the 'double helix' structure of DNA. This double helix is formed from two chains like the example above, wound around each other.

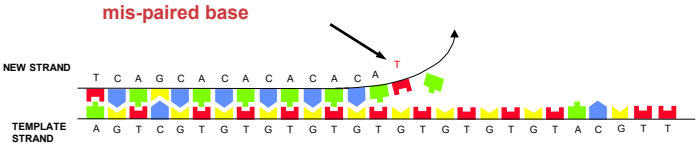
Each of the chains is enormously strong and very stable, but the two individual strands can separate and come back together with relative ease. However in order to fit together as a double helix, it is necessary that a C always sits opposite a G whilst a T will only fit opposite an A.

The important consequence of this is that, given a supply of C's, A's, G's and T's, each of the separated strands can act as a template for the construction of a faithful copy of the original double helix.




In a living cell this process is catalysed by an enzyme, DNA polymerase, that starts at one end of each single strand and adds bases in turn to a growing complementary strand, until two complete double stranded molecules have been assembled.

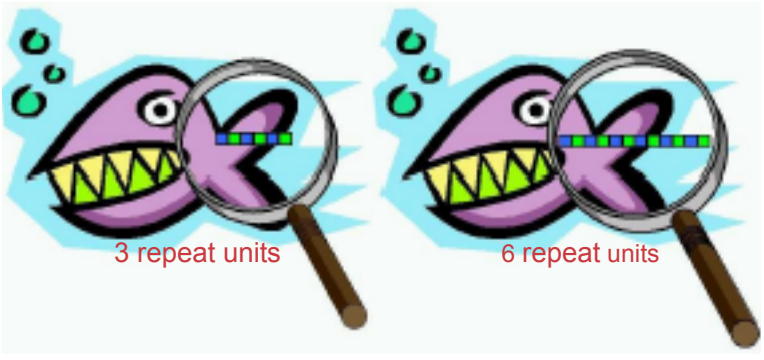
However, like a typist copying text, sometimes mistakes are made and it is these rare mistakes - mutations – that give rise to the variation we see between individuals.




What if a typist came to a series of repeated 'and's in the text? Mistakes would not be so rare, since it would be very easy to miss out or add in one or more 'and'.

A similar thing happens when the polymerase comes to a repeated sequence: it is relatively easy to add in or miss out a repeat unit and as a result, microsatellites vary far more within a species than regular sequences do.

These stepwise alterations accumulate over evolutionary time and so, within a species each microsatellite is likely to exist in a number of different forms (alleles).




Moreover the differences are <u>length</u> polymorphisms: we can identify each allele on the basis of its length alone, we do not need to know the sequence and we can identify length polymorphisms far more easily than sequence polymorphisms. How we go about this is described in the third poster, but first, how do we pick out our microsatellite from the millions of other sequences in our DNA sample?