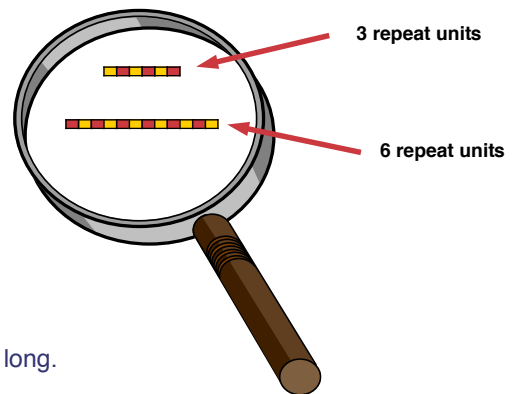


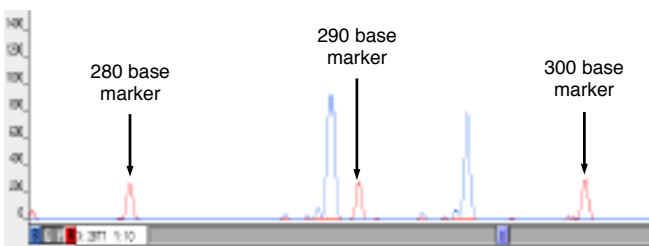
Like ourselves, fish inherit two copies of each gene, one from each parent.

This is equally true of microsatellite sequences
So each individual is likely to harbour two versions of each microsatellite and it is likely that they will be of different lengths.



Following PCR, we can detect these size differences using the DNA sequencer.

The output below tells us that this individual has two copies of this particular microsatellite, one 289 bases long and the other 295 bases long.



If we have previously determined the genotypes of all the parents in a breeding programme, we can use this information to assign an individual fish to its most probable parents.

For example, this pair of parents could quite possibly give rise to the individual in the example above: one parent providing the 289 allele, the other the 295 allele.....



.....whereas we can rule this pair out, since neither could have provided the 295 allele.

From this example it is clear that, using a single microsatellite marker we can rule some parents out with certainty.

Of course, this is not the same as assigning one individual to one set of parents with confidence. But we can increase our level of confidence by examining each individual at more than one microsatellite locus simultaneously. The electropherogram below shows a genotype produced using a novel marker system developed at LNS for analysis of rainbow trout, which uses 10 microsatellite markers. With this number of markers we can assign individuals to their parents in almost every case.

