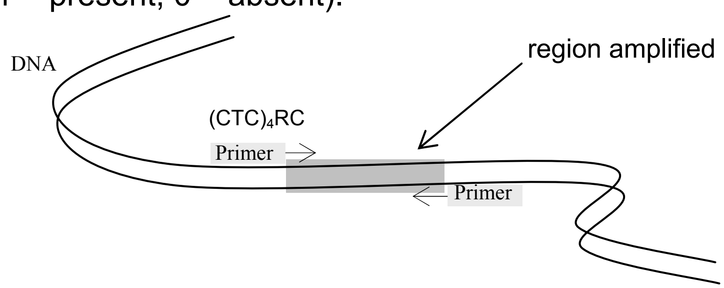
ISSR Information

What are they? ISSRs (**I**nter-**S**imple **S**equence **R**epeats) are segments of DNA found between two simple sequence repeats (usually dinucleotide or trinucleotide repeats).

e.g. 5-CTCTCTCTCTCT-GY-3’

ISSR techniques are nearly identical to RAPD techniques except that ISSR primers are designed from microsatellite regions and are longer (approximately 14 or more bp) than RAPD primers.

How is it done? The basic premise of ISSRs is that primer annealing sites are distributed evenly throughout the genome such that the primer will anneal to two sites orientated on opposing DNA strands. If these are within an appropriate distance of one another, the region between the two primers will be amplified through PCR. The region would not be amplified if there was divergence at the primer binding sites, if a binding site was lost, or if structural rearrangements of the chromosomes had occurred. The PCR products are run out on an agarose gel, stained with ethidium bromide, digitized, and bands are scored as diallelic (1 = present, 0 = absent).



Advantages:
1. Higher reproducibility than RAPDs
2. Bands are homologous (preliminary results)
3. Hypervariable enough for within-population studies

Disadvantages:
1. Dominant marker
2. Band absence can be due to a number of factors (must only compare shared bands)

History:
- The first ISSR studies were published in 1994 and focused on cultivated species (see Wolfe and Liston, 1998). These studies demonstrated the hypervariable nature of ISSR markers.
- ISSRs are now being applied to natural populations to address issues such as hybridization. In addition, several other studies from A. Wolfe's and D. Crawford's labs at Ohio State University, A. Liston's lab at Oregon State University, and H. Ballard's lab at Ohio University range from conservation biology to molecular ecology and systematics. These studies have demonstrated the utility of the technique in a wide range of applications and plant families (Asteraceae, Brassicaceae, Hippocastanaceae, Orchidaceae, Poaceae, Scrophulariaceae, Violaceae).

<u>Additional Sources:</u>

For a review of the ISSR technique, see:

Wolfe A.D. and Liston, A. 1998. Contributions of PCR-based methods to plant systematics and evolutionary biology. In: Plant Molecular Systematics II eds. D. E. Soltis, P. S. Soltis and J. J. Doyle. pp. 43-86. Kluwer.

Wolfe, A. D., Q-Y. Xiang, and S. R. Kephart. 1998. Assessing hybridization in natural populations of *Penstemon* (Scrophulariaceae) using hypervariable intersimple sequence repeat (ISSR) bands. Molecular Ecology 7: 1107-1125.

For detailed information on the technique and to also find helpful internet links, visit the **ISSR Resource Website** at:

http://www.biosci.ohio-state.edu/~awolfe/ISSR/ISSR.html