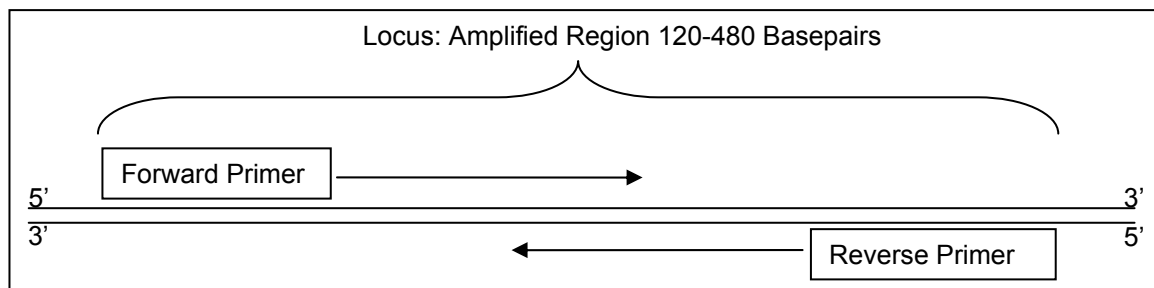


Steps for Locus Development

By Alisa Ramakrishnan, July 2004, updated May 2005

1. PCR clone
2. Sequence clone with forward and reverse primers (2 sequences)
3. Check sequence for microsatellites
 - a. Dinucleotide: 5 or more perfect repeats
 - b. Trinucleotide: 4 or more perfect repeats
 - c. Tetranucleotide: 4 or more perfect repeats
4. Check sequence for accuracy
5. Check for vector sequence and delete any vector
6. BLAST sequence (this will help find any leftover vector, too)
7. Do a local BLAST from BioEdit, using your own database, to make sure you don't already have this particular clone
8. Design primers (can use online 'Primer3' site if you want)
 - a. Region must have low repetitiveness and good sequence
 - b. Usually at least 50% GC
 - c. 3' end has at least one G/C
 - d. At least 20bp long
 - e. T_m 60°C-65°C (melting temperature, can check with IDT)
 - f. Amplified region greater than 120bp
 - g. No guanidine on 5' end of reverse primer (quenches fluorescence)
 - h. No single nucleotide repeats more than 3 (AAAA etc)
 - i. Run primer through IDT's Oligo Analyzer (<http://scitools.idtdna.com/Analyzer/>)
 - i. Check for hairpins, self-annealing, hetero-dimer



9. Test primers for amplification on 6-12 samples (or genotype mix)
 - a. Use the gradient block, 5°C on either side of T_m (less necessary if using HotStarTaq)
 - b. Run on 1-2% agarose gel
10. Test positive primers for polymorphism and null alleles
 - a. Amplify on 6 samples from each set (BRSY=OR/USDA, *Piri*=C,V,H)
 - b. Run on 4% metaphor gel (read instructions!)
11. For loci that amplify consistently, order fluorescent primers
 - a. 6-FAM, HEX or TAMRA on 5' end of Reverse primer, 100nmol scale