Sequence-Tagged Sites (STS)

Introduction

Sequence-Tagged Site (STS)

is a relatively short, easily PCR-amplified sequence (200 to 500 bp) which can be specifically amplified by PCR and detected in the presence of all other genomic sequences and whose location in the genome is mapped.

The STS concept was introduced by Olson et al (1989). In assessing the likely impact of the Polymerase Chain Reaction (PCR) on human genome research, they recognized that single-copy DNA sequences of known map location could serve as markers for genetic and physical mapping of genes along the chromosome. The advantage of STSs over other mapping landmarks is that the means of testing for the presence of a particular STS can be completely described as information in a database: anyone who wishes to make copies of the marker would simply look up the STS in the database, synthesize the specified primers, and run the PCR under specified conditions to amplify the STS from genomic DNA.

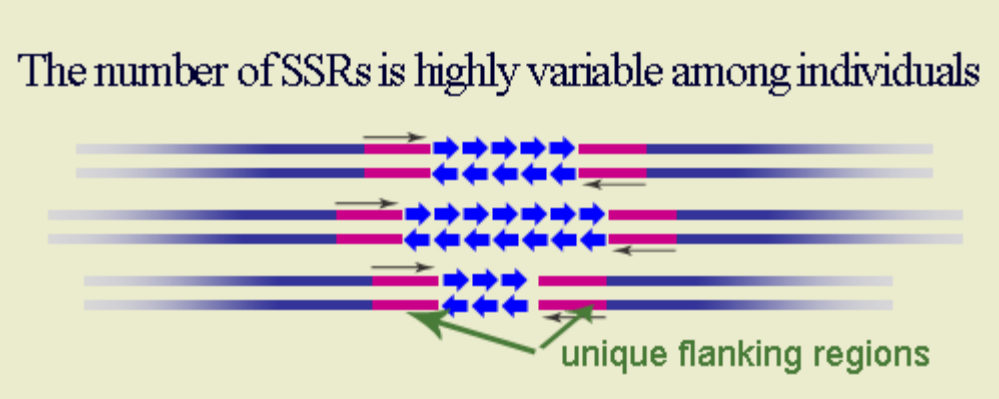
STS-based PCR produces a simple and reproducible pattern on agarose or polyacrylamide gel. In most cases STS markers are co-dominant, i.e., allow heterozygotes to be distinguished from the two homozygotes.

The DNA sequence of an STS may contain repetitive elements, sequences that appear elsewhere in the genome, but as long as the sequences at both ends of the site are unique and conserved, researches can uniquely identify this portion of genome using tools usually present in any laboratory.

Thus, in broad sense, STS include such markers as microsatellites (SSRs, STMS or SSRPs), SCARs, CAPs, and ISSRs.

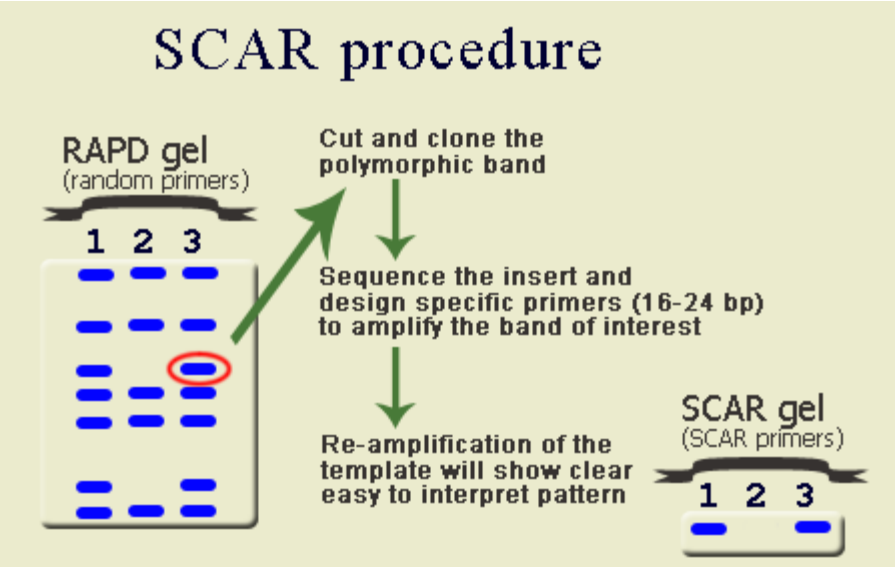
Microsatellites

Polymorphic loci present in nuclear DNA and organellar DNA that consist of repeating units of 1-10 base pairs, most typically, 2-3 bp in length, also called Simple Sequence Repeats (SSR), Sequence-Tagged Microsatellite Sites (STMS) or Simple Sequence Repeats Polymorphisms (SSRP). SSRs are highly variable and evenly distributed throughout the genome. This type of repeated DNA is common in eukaryotes. These polymorphisms are identified by constructing PCR primers for the DNA flanking the microsatellite region. The flanking regions tend to be conserved within the species, although sometimes they may also be conserved in higher taxonomic levels.



Sequence Characterized Amplified Region (SCAR)

DNA fragments amplified by the Polymerase Chain Reaction (PCR) using specific 15-30 bp primers, designed from nucleotide sequences established in cloned RAPD (Random Amplified Polymorphic DNA) fragments linked to a trait of interest. By using longer PCR primers, SCARs do not face the problem of low reproducibility generally encountered with RAPDs. Obtaining a co-dominant marker may be an additional advantage of converting RAPDs into SCARs.

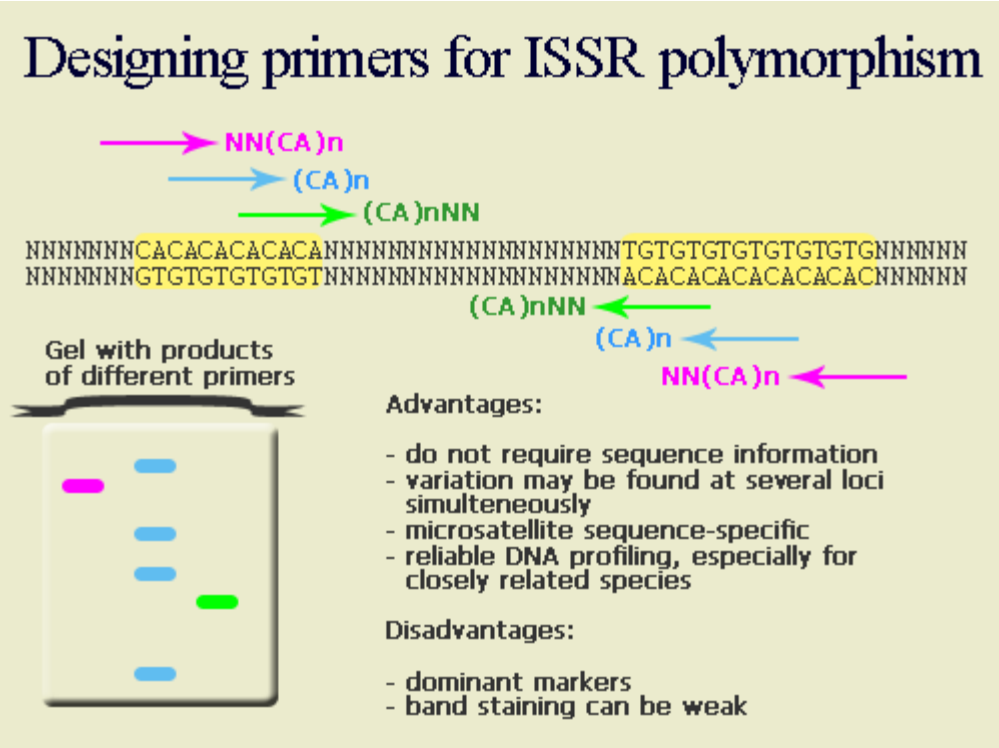


Cleaved Amplified Polymorphic Sequences (CAPS)

STS polymorphisms that can be detected by differences in restriction fragment lengths caused by SNPs or INDELs that create or abolish restriction endonuclease recognition sites in PCR amplicons produced by locus-specific oligonucleotide primers. In other words this technique aims to convert and amplified band that does not show variation by length of PCR product into a polymorphic one. More about CAPS in Overview of CAPS technology.

Inter-simple Sequence Repeats (ISSRs)

STS polymorphisms that are found between microsatellite repeats. Primers can be designed based on a microsatellite repeats exclusively, in which case this technique will target multiple loci due to known abundance of repeat sequences in the genome. Alternatively, primers can be extended outside or inside the ISSR in which case a unique region most likely will be amplified.



Sample Queries

Search Text	Probes
STS[probe type]	0
SCAR[probe type]	0
CAPS[probe type]	0
SSR[probe type]	0
SSR[probe type] AND unists[properties]	0

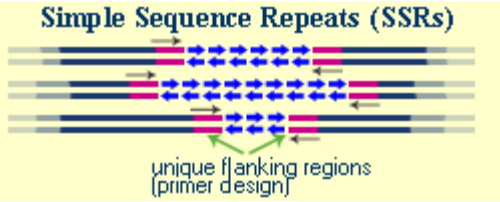
References

» Olson M et al. A common language for physical mapping of the human genome. Science. 1989 Sep 29;245(4925):1434-5. PMID: 2781285

Resources

» The NCBI Electronic PCR (e-PCR) compputational tool

» "Sequence Tagged Sites"[Majr] in PubMed



Disclaimer

Mention of specific products or vendors on this website does not constitute an endorsement by the U.S. government.

Help

- ProbeDB overview
- Announcements
- Downloading
- Glossary

Applications

- Gene Expression
- Gene Silencing
- Variation Analysis
- Genome Mapping

Technologies

- Bead Arrays
- Microarrays
- Morpholinos
- Overgo probes
- Resequencing
- RNAi
- PCR
- STS
- Real Time qRT-PCR
- SSO probes
- RAPD
- RFLP
- AFLP
- CAPS
- dCAPS
- MPSS
- MIP
- ISH

Projects

- GENSAT
- HapMap

- VariantSEQr
- TaqMan
- TRC
- RNAi Global

Distributors

- Open Biosystems
- Applied Biosystems

Simple NCBI Directory

Getting Started

- NCBI Education
- NCBI Help Manual
- NCBI Handbook
- Training & Tutorials
- Submit Data

Resources

- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy
- Variation

Popular

- PubMed
- Bookshelf
- PubMed Central
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

Featured

- Genetic Testing Registry
- GenBank
- Reference Sequences
- Gene Expression Omnibus
- Genome Data Viewer
- Human Genome
- Mouse Genome
- Influenza Virus
- Primer-BLAST
- Sequence Read Archive

- **NCBI Information**

- About NCBI
- Research at NCBI
- NCBI News & Blog
- NCBI FTP Site
- NCBI on Facebook
- NCBI on Twitter
- NCBI on YouTube
- Privacy Policy

NLM
NIH
DHHS
USA.gov

National Center for Biotechnology Information, U.S. National Library of Medicine 8600 Rockville Pike, Bethesda MD, 20894 USA

Policies and Guidelines | Contact

Last updated: 2017-11-09T11:33:30Z

HHS Vulnerability Disclosure