Salmon Genomics

HYAK

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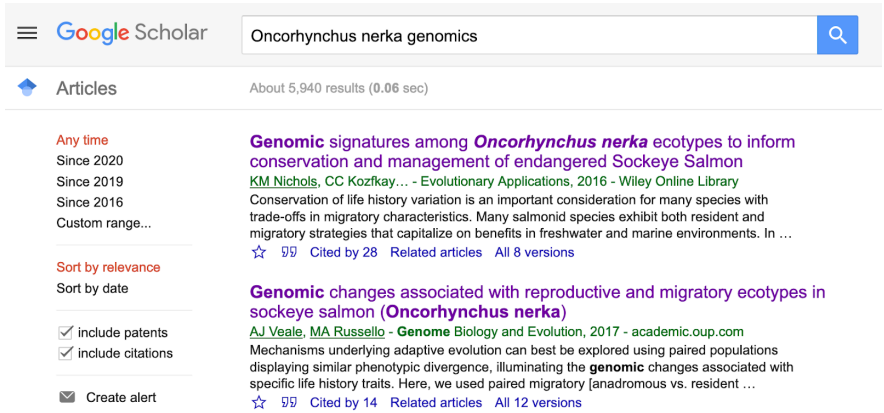
Recent Salmon Genomics Publications



GBE

Genomic Changes Associated with Reproductive and Migratory Ecotypes in Sockeye Salmon (*Oncorhynchus nerka*)

Andrew J. Veale[1,2] and Michael A. Russello[1,*]

[1]Department of Biology, The University of British Columbia, Kelowna, British Columbia, Canada

[2]Present address: Department of Environmental and Animal Sciences, Unitec, 139 Carrington Rd, Auckland, New Zealand

*Corresponding author: E-mail: michael.russello@ubc.ca.

Accepted: October 12, 2017

Data deposition: All Illumina raw reads are available from the NCBI sequence read archive (BioProject ID: PRJNA414118 All RADtag sequences are included in supplementary data file S1, Supplementary Material online and the final SNP data set in GENEPOP format is included as supplementary data file S8, Supplementary Material online.

Abstract

Mechanisms underlying adaptive evolution can best be explored using paired populations displaying similar phenotypic divergence, illuminating the genomic changes associated with specific life history traits. Here, we used paired migratory [anadromous vs. resident (kokanee)] and reproductive [shore- vs. stream-spawning] ecotypes of sockeye salmon (*Oncorhynchus nerka*) sampled from seven lakes and two rivers spanning three catchments (Columbia, Fraser, and Skeena) in British Columbia, Canada to investigate the

Restriction site associated DNA markers

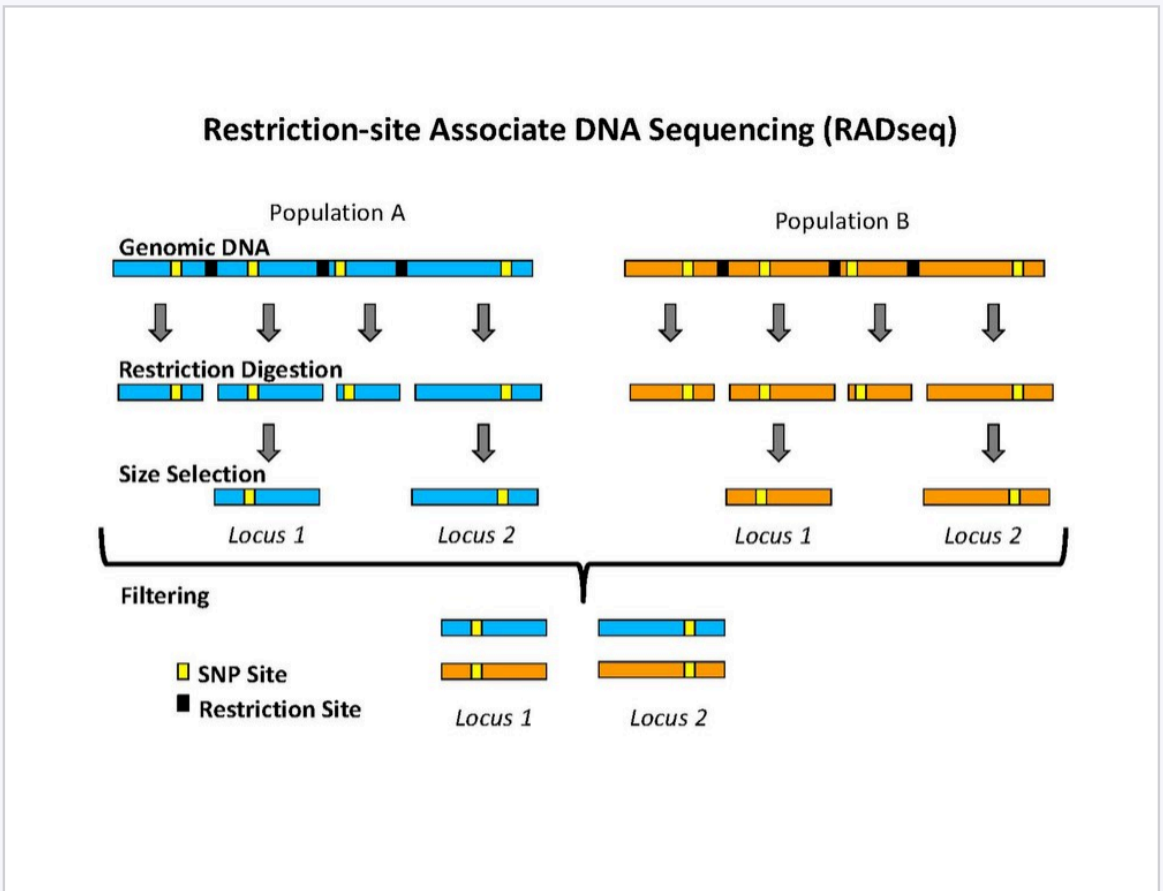
From Wikipedia, the free encyclopedia

Restriction site associated DNA (RAD) markers are a type of genetic marker which are useful for association mapping, QTL-mapping, population genetics, ecological genetics and evolution. The use of RAD markers for genetic mapping is often called RAD mapping. An important aspect of RAD markers and mapping is the process of isolating RAD tags, which are the DNA sequences that immediately flank each instance of a particular restriction site of a restriction enzyme throughout the genome.[1] Once RAD tags have been isolated, they can be used to identify and genotype DNA sequence polymorphisms mainly in form of single nucleotide polymorphisms (SNPs).[1] Polymorphisms that are identified and genotyped by isolating and analyzing RAD tags are referred to as RAD markers.

Contents [hide]

Isolation of RAD tags [edit]

The use of the flanking DNA sequences around each restriction site is an important aspect of RAD tags.[1] The density of RAD tags in a genome depends on the



Genomic DNA is first digested with a specific restriction enzyme(s) to fragment the DNA. For restriction fragment length polymorphism (RFLP) analysis, these fragments are then visualized by gel electrophoresis. For RADseq, restriction fragments are ligated to an

Some Tools from the Paper

- Download data from NCBI SRA [download] [howto] [data]
  - build, login, and compute nodes
  - gscratch, scrubbed, lab, and home directories

- STACKS: pipeline for building loci from RAD-seq data [site] [code]
  - build node, modules (gcc)

- BayesScan: detecting natural selection from population-based genetic data [code] [container] [blastn]
  - Singularity [shub] [docs]

- diveRsity: estimation and exploration of population genetics parameters and their associated errors [paper]
- pcadapt: detect genetic markers involved in biological adaptation [code]
  - Install R packages

Appendix

Additional Links

- This is a SLURM scheduled managed cluster [docs].
- Also mentioned environment modules [docs].

Command Reference

```
# interactive / build node
$ srun -p build --time=4:00:00 -n 4 --mem=30G --pty $0

# load singularity module
$ module load singularity

# grab R docker container
$ singularity pull docker://r-base:4.0.2

# grab BayeScan from singularity hub
$ singularity pull shub://MarissaLL/singularity-containers:bayescan_2.1
```