

Caps markers to genome

Noëlle Schenk

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Compare with *P. axillaris* caps markers (caps)

Caps markers are markers which have been associated with a chromosome. Align caps to new genome version of *P. exserta* and check if scaffold-to-chromosome classification can be validated.

Make database of genome for blastn.

```
makeblastdb -in /home/exserta/Documents/master_project_noelle/data/P.EXSERTA.v.2.0/P.exserta.v.2.0.fasta
```

Blast caps marker sequences

The script below blasts all files in the folder “path”/“chr” that end with .fa or .fasta and blasts them against the reference genome database created above. To run it for all chromosomes, the variable chr needs to be changed to “chr_1”, then to “chr_2”, ... This is not automated yet because the path and folder names of chromosomes could change.

The blast output is in outformat 6.

```
path="/home/exserta/Documents/master_project_noelle/data/caps/"
chr="chr_7"
outpath="out_align_caps_markers/"
for f in ${path}${chr}/*.fa*
do
    f=${f##*/}
    echo "Processing ${path}${chr}/${f}"
    blastn -db /home/exserta/Documents/master_project_noelle/data/P.EXSERTA.v.2.0/P.exserta.v.2.0.fasta -q
    echo "results written to ${outpath}${chr}${f%.*}.out"
done
```

Analysis

For marker chr_4PM74caps, there was no blast result.

Results are documented in results_align_caps_markers.ods.