

Hands-on experience with PeanutBase

Goal: Identify potential peanut genes involved in abiotic stress using PeanutBase

Activity: The FASTA sequences given on page 2 and 3 are of two soybean transcripts that are associated with dehydration and salt stress (BMC Genomics 2014, 15:950). Use each of these sequences and report the following details:

1. Corresponding gene in peanut (Orthologous gene)

Hint: Use BLAT (under Browse & Search) and genome browser

2. Location (chromosome number, and start and end coordinates) of peanut gene

Hint: Use genome browser

3. Identify molecular marker(s) flanking the peanut gene

Hint: Use genome browser

4. Use the peanut gene and trace its gene family

Hint: Use “Gene Search” under “Browse and Search”

5. Use the gene family results, and report the Arabidopsis gene(s) in the same clade as of the peanut gene

6. Click on Arabidopsis gene(s) in the same clade as of the peanut gene (links to ThaleMine), and report the Arabidopsis gene function and tissue(s) with maximum gene expression.

7. Annotate the peanut gene based on soybean and Arabidopsis gene functions.

FASTA sequences of soybean transcripts

>Glyma.16g021000

CAGGACCAATGAGTTTTGGATATAAAGCCAACAATTGGGGACTTCACTCTGACCACCAT
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>Glyma.01g041700

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GAACCAAATTTTCCAACTCCTCAACTCTCATCAGATATCAACCTTCTCTCTCTCCAA
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