DOCUMENTATION

BLOSSOM STTM HUB:

The Blossom STTM Hub is a tool which designs STTM sequences from miRNA and insert the designed STTM into the required DNA vectors to plot the plasmid map and to get the features and sequencing of the resulting vector. It also display the transgenic lines varying in different characteristics both genotypic and phenotypic. The species mainly under consideration here are rice, maize, arabidopsis and poplar. The customers can purchase the required vectors and plasmids after STTM modification by selecting from the transgenic lines display shown through the Michigan Tech Blossom STTM store.



Targeting Small RNAs for Destruction in Crops by Short Tandem Target Mimic (STTM)

This project aims to develop microRNA (miRNA) knockdown populations in selected crops using our recently developed small tandem target mimic (STTM) technology. This is the first attempt to systematically generate such genetic resources for the plant community, representing a critical step towards comprehensive characterization of miRNA functions. We will further use these mutant populations to investigate the functional conservation and diversification of highly conserved plant miRNAs, and to study the regulatory role of miRNAs in plant-microbe interactions. Hundreds to thousands of miRNAs have been identified from dozens of plant species including agriculturally important crops such as rice, maize, wheat, and soybean. However, their roles in plant development and response against various pathogens and other stresses are largely unknown. The STTM technology is a powerful tool that can robustly trigger the degradation of specific miRNAs in plants, making it possible to dissect miRNA functions. Here, we propose to systemically silence miRNAs in crops by STTM. These miRNA knockdown libraries will be of great use for understanding miRNA functions and will set up genetic basis for crop improvement. Therefore, it is worth making an effort to explore the following specific aims:

DESIGN STTM STEP 1:

The STTM Hub application's Design_STTM phase first accepts miRNA sequence along with a name from the user. Then, the user is given an option to select a DNA vector sequence from a plausible list. The application is automated to design the STTM sequence using the miRNA input provided by the user. The designed STTM is to be inserted into the DNA vector chosen. The user is then given an option whether to transfer the designed STTM into another binary vector. Based on the selection made, the user is made to proceed to STEP 2.

STEP 1:		
Enter a name for miRNA sequence :		Example input : miRNA166
Enter the miRNA sequence :		Example input: GGGGGAUGAAGCCUGGUCCGA (RNA) GGGGGATGAAGCCTGGTCCGA (DNA)
Select vector to insert the designed STTM: pOT2 ▼		
We design and insert the STTM into pOT2 vector first, then we transfer it to a binary vector called pFGC5941 through PCR amplification. The primers containing PacI sites are used to amplify STTM and majority backbone of pOT2 with the pBR322 origin being excluded.		
Would you like to transfer the designed STTM fi	rom pOT2 into pFGC5941 binary vector ?	
∇es		

STEP 2:

O No

If the designed sttm vector has to be transferred into another binary vector, the origin sequence must be removed from the initial DNA as the binary vector will also have an origin and the resultant DNA cannot have two origin sequences. The primers used to delete the origin segment are displayed and the user then has to select the binary vector, from a list of available vectors, to which the STTM needs to be transferred. A drop down menu is made available to do the same. In this step, the user can add their own binary vector sequence to which they can transfer the STTM. A link to add a new vector to their personal database is made available to fulfil this function.

Would you like to transfer the designed STTM from pOT2 into pFGC5941 binary vector?	
● Yes○ No	
STEP 2:	
Primers sequences for amplifying the majority backbone of pOT2-STTM are :	
* Origin-del-PacI-PF forward: TCCCTTAATTAAGTTTGCAAGCAGCAGATTACGCG * Origin-del-PacI-PR reverse: TCCCTTAATTAAGAAAGGCGGACAGGTATCCGGTAAG	
The above primers contain PacI (TTAATTAA). The PCR products are cut by PacI and inserted into the PacI site of pFGC5941 binary vector.	
Select the required vector sequence from the database : Select Click HERE to add your own vector	

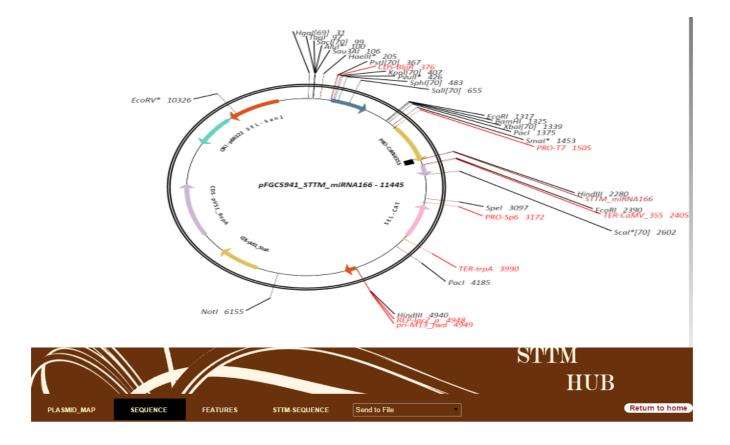
Once the user selects their desired binary vector, the vector sequence dynamically loads and is displayed. Now, enzymes to be used as cutting sites are to be selected by the user. This is the last step before the plasmid map generation.

After all the inputs are provided, a validation check takes place, which verifies for the correctness of all the input sequences and selections. If everything is valid, the STTM Hub tool generates the plasmid map for the resulting vector containing the designed STTM sequence.

Select the required vector sequence from the database : pFGC5941 ▼		
Click HERE to add your own vector		
Please review the vector sequence :		
tggcaggatatattggggtgtaaacaaattgacgcttagacaacttaataacacattgcggacgtttttaatgtactgaattaaccgaattaatt		
Select two restriction enzyme digestion sites in the vector to insert the designed STTM:		
EcoRI + HindIII +		
SUBMIT		

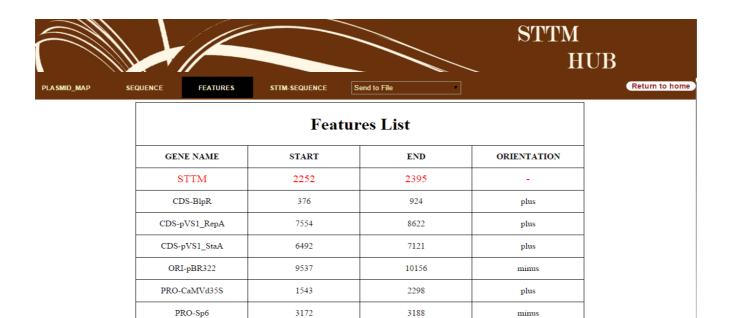
PLASMID MAP GENERATION:

The plasmid map is generated using HTML5 Canvas as the display interface and contains clean labels of all the features, enzymes and the STTM location along with their corresponding positions. Apart from the plasmid map, the resulting vector sequence is also displayed to the user highlighting the STTM sequence specially. A tabular listing of the features and their location in the vector is also displayed. The user is given an option of receiving the PDF report of the generated data through their registered email or other email address



is 233 The vector sequence after insertion of STTM:

> AGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGACATCTCCACTGACGT AAGGGATGACGCACAATCCCACCCCTACTCCAAAAATGTCAAAGATACAGTCTCAGAAGACCAAAGGGCTATTGAGA CTTTTCAACAAAGGGTAATTTCGGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCGAAAGGACAGT AGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCATTCAAGATGCCTCTGCCGACA GTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA GTGGATTGATGTGACATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGAC catttggagaggaca gcccAAGCTTTCGGACCAGGCgtaTTCATCCCCCgttgttgttgttatggtctaatttaaatatttaaatattggtctaaagaagaagaatT CGGACCAGGCgtaTTCATCCCCCGAATTCggtacgctgaaatcaccag CCGAATTCGGTACGCTGAAATCACCAGTCT ATTTCTAATTCCTAAAACCAAAATCCAGTACTAAAATCCAGATCTCCTAAAGTCCCTATAGATCTTTGTCGTGAATATA AACCAGACACGAGACGACTAAACCTGGAGCCCAGACGCCGTTCGAAGCTAGAAGTACCGCTTAGGCAGGAGGCCGTT AGGGAAAAGATGCTAAGGCAGGGTTGGTTACGTTGACTCCCCCGTAGGTTTGGTTTAAATATGATGAAGTGGACGGAA



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