Proforma for submission of success story

1. **Title of the success story**

   Computer program for DNA marker discovery

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2. **Details of beneficiary/ farmers/ group/stakeholder (Name, address, are, etc)**

Students and faculty for academic purpose

Problems/ Constraints

Conventional Random Amplification of Polymorphic DNA and Inter Simple Sequence Repeat molecular markers work on the random process, and their success depends on the availability of the priming sites on the sequences. Failure due to inappropriate primers can cause a researcher frustrated due to waste of chemicals and time. In this work, we are interested in a prior computer aided judgement of suitability of given primers by checking them on target Deoxyribonucleic acid (DNA) sequence of the organism for presence of priming sites. Use of these markers on models and less known genomes is limited and the potential to convert them to Sequence characterised amplified region (SCAR) markers offer scope. Failure due to inappropriate primers can cost as high US$ 100 (INR 7200) for a small experiment of 20 reactions. Thousands of such experiments are conducted using polymerase chain reactions (PCR) machines worldwide every year. Genome of an organism has the complete set of codes and information for genes, variation between individuals, pre-disposition to disease etc. Conventional Random Amplification of Polymorphic DNA and Inter Simple Sequence Repeat molecular markers work on the random process, and their success depends on the availability of the priming sites on the sequences. Primers are short piece of oligos similar to the bookmarks to read the complex genome books.

Interventions of the Success story (Technologies/ varieties/ breed/ package of practices/ product etc.) along with necessary details

The innovation Marker express 1.0 gives a prior computer aided judgement of suitability of given primers by checking them on target Deoxyribonucleic acid (DNA) sequence of the organism for presence of priming sites. If the primer is 10 letters long, single and random, they are easy and cheap but the success and repeatability are low. Our software is sound enough to locate the random primers at optimal distance(s) and convert them to pair of 20 letters long, specific and effective as *in silico* Sequence characterised amplified region (iSCAR) primers

The software works by following simple steps: searches for priming sites of the given primer(s) in all the target sequences, calculates priming sites of sequence(s), measures distance between priming sites, and converts best amplified primers into iSCAR primers. It requires two input text files a primer sequence file (*.txt) and a target nucleotide sequence file (*.fasta) from the user. It generates five sets of output files. We validated

software with a case study on oil palm covering 1.4 % genome where 92 % of polymorphic published primers were predicted.

3. Impact

Awarded as one of top 45 innovations of India Innovation Growth Program 2014 of DST-Lockheed Martin-Stanford Graduate Business School-IC2 Institute University of Texas at Austin-Indo-US Science and Technology Forum-TIE-FICCI.

Arunachalam V (2012) Bioinformatics software to locate priming sites of RAPD and ISSR primers. ICAR News 18(3): 6.

Premkrishnan, B.V. and Arunachalam, V. (2012) In Silico RAPD Priming Sites in Expressed Sequences and iSCAR Markers for Oil Palm. International Journal of Genomics. (formerly Comparative and Functional Genomics) Volume 2012 (2012), Article ID 913709, 5 pages http://dx.doi.org/10.1155/2012/913709

4. YouTube video link

https://www.youtube.com/watch?v=E00RtVXVTRY