

## Development of New STMS markers for sugarcane

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|                                            |                                |
|--------------------------------------------|--------------------------------|
| Primer Name                                | : NKS 3                        |
| Forward Sequence                           | : <b>cggtgttcctcttcaacaacg</b> |
| Reverse Sequence                           | : <b>tgttcgctatatatgggttca</b> |
| Gene Bank accession No. of source sequence | : <b>AF062734</b>              |
| Type of sequence                           | : cDNA                         |

Source Sequence:

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1  cacgacggcgggcggaacgcgttcccgtggagcaatgcgatgctgcagtggcagcgcacg
61  ggattccacttccagccgcagaagaactggatgaacgacccaatggcccggtgtactac
121 aagggctggtaccacctgttctaccaatacaaccggacggcgccatctggggcaacaag
181 atcgcgtggggccacgcgctctccgcgacctcatccacggcgccacctcccgtggcc
241 atggtgcccgaccagtggtagcaccaacggcgtgtggacgggctccgccaccacgctc
301 cccgacggccgcctcgccatgctctacacgggtccaccaacgcctcggtgcaggtgcag
361 tgcttcgctgcccgcgcgacgacgcgacccgctgctcaccaactggaccaagtacgag
421 ggcaaccgggtgctgtacctgcgcgccccgggatcgggcccagggaacttccgggacccccacc
481 acggcgtgggttcgacctcggaactccacctggcgcatcgctcatcggtccaaggacgac
541 gccgagggcgaccacgcgcggcatcgccgtggtgtaccgcaccagggaacttcgtgcacttc
601 gagctcctcccggacctgctccaccgcgtcgcggggacggggatgtgggagtgcacgac
661 ttctaccccgtcgccaccgcggcaaggtctccgggaacggcgctcgacatgtccgacgcc
721 ctcggaagaacggcgccgtcgctcggggacgtggtgcacgtcatgaaggccggcatggac
781 gacgaccgacatgactactgcgcgtcgggaggtatgacgcggccgccaacgcgtggacg
841 ccgctcgacgcccaggaaggacgtcggcaccggcctgcggtacgactggggcaagttctac
901 gcgtccaagacgtttctacgacccggccaagcgccgcgcgctgctctggggatgggtcggc
961 gagaccgactcggagcgcgctgacgtctccaagggaatgggcatcgctgcaggggtatcccc
1021 cggacggtgctgctggacaccaagacgggcagcaacctgctgcagtggcccgtggaggaa
1081 gtggagacgctgcgcaccaactccacggacytcagcggcatcaccatcgactacgggtcc
1141 gcgttcccgtcaacctccgccgcgccacgcagctggacatcgaggcggagttcgagctg
1201 gaccgcccgcgcgtcatgtccctcaacgaggccgacgtgggctacaactgcagcaccagc
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1261 ggcgggcgccgcccgcggcgcgctgggccccttcggcctgctcgctcctcgccgacaag  
 1321 cacctgcacgagcagacggccgtctacttctacgtggccaagggcctggacgggtccctc  
 1381 accacgcacttctgccaggacgaggtcccggtcggtccagcgccaacgacatcgtaagcgc  
 1441 gtcgtcggcagcgccgttcccgtgctggaggacgagaccacactctcgyttcggtgctc  
 1501 gtcgaccactccatcgctcgagagyttcgcgcgagggtggaaggtaacggccacctcgcg  
 1561 gtctacccccaccaaggccatttacgccaacgcggcggtgttcctcttcaacaacgcccacc  
 1621 gccgcgcgcgtcaccgccaagaagctcgctcggtccacgagatggactcgctcctacaaccac  
 1681 gactacatgggtcacggacatctgatgtgtgtgtgtgtgtgatccgctcggtccatccaacc  
 1741 caccgctgcacccaatttttttgaacccatatatagcgaagcatcttcttgtacctatcaa  
 1801 ttcccatc

Repeat Motif : (tgc)5

Total number and names of the germplasm lines tested: 48 (link table)

No. of PCR products amplified : 2

The size range of the PCR product : 191 & 198

The general PCR protocol used : 200 µM of each dNTPs, 6pmol each of the forward and reverse primer, 0.5 units of Taq DNA polymerase

The PCR cycling condition: Pre-denaturation: 94<sup>0</sup>C (5 min),  
 25 cycles of Denaturation: 94<sup>0</sup> C (50 sec),  
 Annealing : 58<sup>0</sup> C (50 sec),  
 Extension : 72<sup>0</sup> C (50 sec) and  
 Final extension : 72<sup>0</sup> C (7 min).

Reference: Unpublished