**Table 1** Sequence of SSR and Indel primers for the genetic linkage map of the numerous spines gene in cucumber

**Table 2** Validity of the SSRns-127 marker tightly linked to the numerous spines gene was tested using an F2 population with 60 plants derived from the cross of Coolgreen×NCG-127

**Table 3** Annotation of genes located in the *ns* genetic mapping region

**Figure 1.** Phenotype pictures of the parental lines and F1. a: P1 (NCG-122 fruit with numerous spines); b: P2 (NCG-121 fruit with few spines); c: F1 (fruit with few spines).

**Figure 2.** Molecular marker linkage and chromosomal mapping of the numerous spines gene in cucumber. a: chromosome 2 of cucumber; b: SSR linkage of the numerous spines gene for preliminary mapping; c: linkage of molecular markers to the *ns* gene for second mapping; d: physical map of partial molecular markers; e: predicted genes among the flanking markers. (The number on the bars shows number of recombinant plants between *ns* and flanking markers.)

**Table 1**

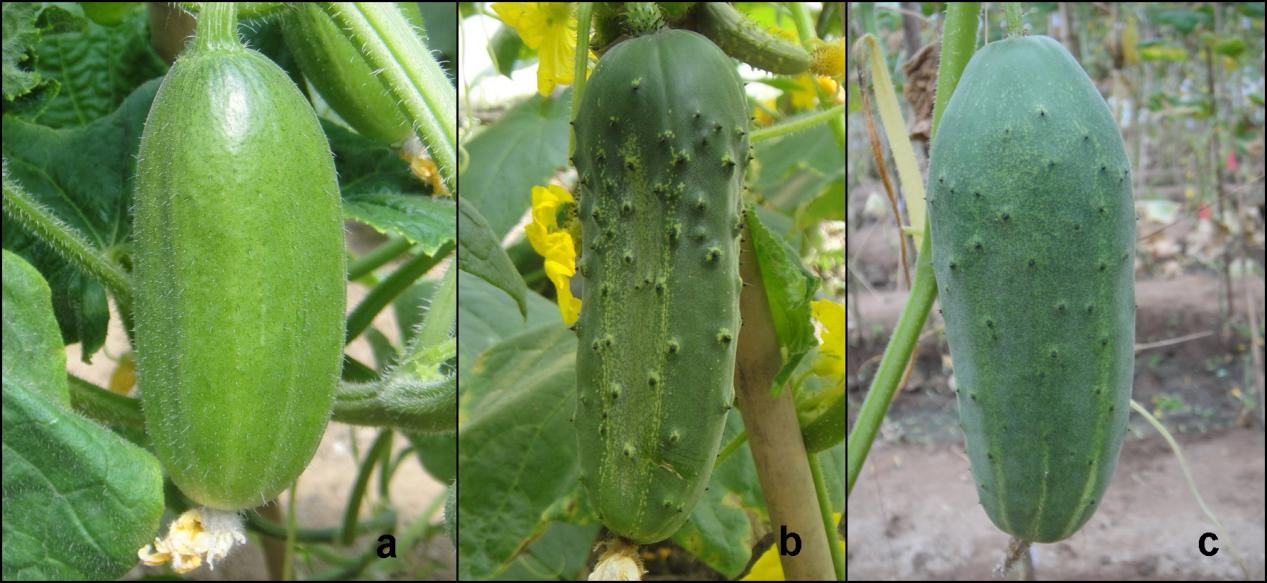
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Primer name | Forward primer | Reverse primer | Motif | Fragment size |
| SSR04869 | CCAACACCACCCTTCGTTTA | CGGAACCGTTCGTCTTCTT | (TC)27 | 202 |
| SSR22338 | GGTGGATGAAGAGGGGAAAT | TACTCCTTCCTTCGCCCTTT | (AGA)16 | 159 |
| SSRns-10 | TGAATGCATCTCTGTTGTGGA | GGCCATCCTCAAGTTCTCAA | (TCAC)5(CT)10 | 197 |
| SSRns-36 | TGATCACTTGCTTGGTGTTACC | GGCGTTTAGGCCCATAATTT | (AT)10 | 152 |
| Indelns-4 | AGAAAAGACGTTTGTTGGAG | ACCCTTATCGAGTCTTCAAA | Insertion (ACATG) | 223/228 |
| SSRns-40 | GCCATATTAAGAAAAACCAATTCAC | GCTCTGCTTGATTTCTTCTGC | (AAG)9 | 172 |
| SSRns-59 | AAGCAAAATGGGAATCCAAG | CCCTCCCTCCTTTGCTTAAT | (AAAG)5 | 240 |
| SSR11596 | TCACATAGGCTTGCTCCAAA | TCAAACACCGCGAAAGAGAT | (TA)18 | 150 |
| Indelns-16 | ATGACAAATGATCTGGTGGT | CAATATCCCGTTGTTGTCTT | Deletion (TTTCA) | 228/223 |
| SSR07108 | TAAGCAATTCCAGGAGAGGG | GTTCTTTGATGGGTGCCTGT | (GA)19 | 210 |
| SSRns-82 | AGATCCTAAAAGGGGATCTTGA | TCCAGAGGTTTTTCCTTTTCTC | (TA)9 | 155 |
| SSRns-123 | CGAAGGTGAAGGCAAAGAAG | TTTAGGGTTTCCAGCCGATA | (AC)9 | 198 |
| SSRns-127 | AGTGACAAAAAGACTAACTCAACAAA | TTGGGTATATAGATTGTCACTACTCCT | (TTA)7 | 206 |
| SSR04219 | GAGACATTGTGGGCATTTGA | CTCATTTTCATCCAAAGGGC | (AT)17 | 218 |
| SSR10518 | TCTAATTCGCTCCGGATGAT | TTGCAGCGAACAATCCTGTA | (ATTA)5(A)30 | 211 |
| SSR15172 | GGTGTGGGTTATTTTGGCAC | GAAGAAATCAAAGAGGGGGC | (CTCTTT)7 | 168 |
| SSR13818 | TTGTTAGTTCATTTGAGGTGTCAAG | TCCATATTAACTCTCTCAGGCTAACA | (TA)32 | 189 |

**Table 2**

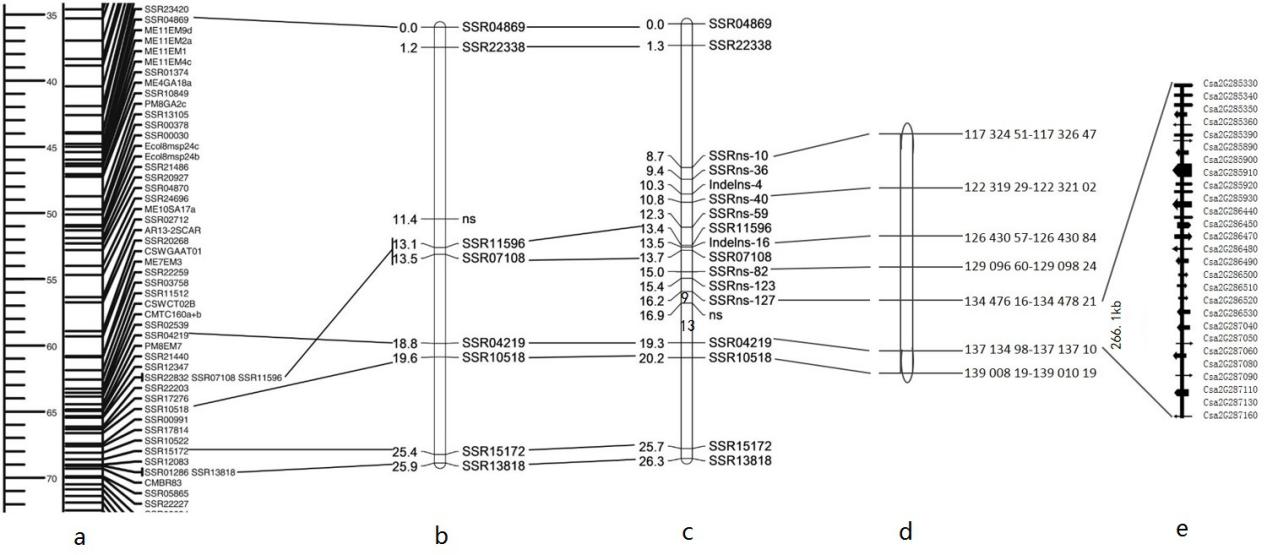
|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Material code | Fruit spines Phenotype | SSRns-127 | Material code | Phenotype | SSRns-127 | Material code | Phenotype | SSRns-127 |
| Coolgreen | numerous | b | F2-19 | few | h | F2-40 | few | h |
| NCG127 | few | a | F2-20 | few | h | F2-41 | few | a |
| F1 | few | h | F2-21 | numerous | b | F2-42 | few | a |
| F2-1 | few | h | F2-22 | few | h | F2-43 | few | h |
| F2-2 | few | a | F2-23 | few | h | F2-44 | numerous | b |
| F2-3 | few | h | F2-24 | numerous | b | F2-45 | few | h |
| F2-4 | few | a | F2-25 | few | a | F2-46 | numerous | b |
| F2-5 | few | h | F2-26 | few | a | F2-47 | few | h |
| F2-6 | few | b | F2-27 | few | h | F2-48 | numerous | b |
| F2-7 | few | a | F2-28 | few | h | F2-49 | few | a |
| F2-8 | numerous | b | F2-29 | few | a | F2-50 | few | h |
| F2-9 | few | h | F2-30 | few | h | F2-51 | few | h |
| F2-10 | few | h | F2-31 | few | h | F2-52 | few | h |
| F2-11 | few | a | F2-32 | few | h | F2-53 | few | h |
| F2-12 | few | h | F2-33 | few | h | F2-54 | numerous | h |
| F2-13 | numerous | b | F2-34 | few | h | F2-55 | numerous | b |
| F2-14 | few | a | F2-35 | few | a | F2-56 | few | a |
| F2-15 | numerous | b | F2-36 | few | a | F2-57 | few | a |
| F2-16 | numerous | b | F2-37 | few | a | F2-58 | few | h |
| F2-17 | numerous | h | F2-38 | few | h | F2-59 | few | a |
| F2-18 | few | a | F2-39 | few | h | F2-60 | numerous | b |

**Table 3**

|  |  |  |  |
| --- | --- | --- | --- |
| Predicted genes | Functions | Predicted genes | Functions |
| Csa2G285330 | Glycoside hydrolase family 43;  Glycosyl hydrolase family 43 five-bladed beta-propellor domain | Csa2G286490 | Protein kinase catalytic domain;  Serine/threonine-protein kinase domain;  kinase ATP binding site |
| Csa2G285340 | Transcription factor GRAS | Csa2G286500 | Zinc finger LIM-type;  Ubiquitin interacting motif |
| Csa2G285350 | Ribosomal protein L26/L24P eukaryotic/archaeal;  KOW;  Translation protein SH3-like | Csa2G286510 | Protein kinase catalytic domain;  Serine-threonine/tyrosine-protein kinase |
| Csa2G285360 | Porin eukaryotic type | Csa2G286520 | Pentatricopeptide repeat |
| Csa2G285390 | WD40 repeat; WD40 repeat-like-containing domain | Csa2G286530 | Pentatricopeptide repeat |
| Csa2G285890 | Helix-loop-helix DNA-binding domain | Csa2G287040 | Ankyrin repeat;  Ankyrin repeat-containing domain |
| Csa2G285900 | Lipase class 3 | Csa2G287050 | Proteinase inhibitor I13 potato inhibitor I |
| Csa2G285910 | RNA recognition motif domain;  Nucleotide-binding alpha-beta plait | Csa2G287060 | mRNA splicing factor thioredoxin-like U5 snRNP;  Thioredoxin fold;  Thioredoxin-like fold |
| Csa2G285920 | Peptidase M24 structural domain;  Peptidase M24A methionine aminopeptidase subfamily 1 | Csa2G287080 | Allergen V5/Tpx-1-related;  CAP domain |
| Csa2G285930 | Transcriptional factor B3;  Restriction endonuclease type II EcoRII N-terminal | Csa2G287090 | Domain of unknown function DUF547 |
| Csa2G286440 | Calcium-binding EF-hand;  EF-hand-like domain | Csa2G287110 | POX;  Homeodomain-like;Homeodomain-related |
| Csa2G286450 | Calcium-binding EF-hand;  EF-hand-like domain | Csa2G287130 | Zinc finger C2H2-type |
| Csa2G286470 | Pentatricopeptide repeat;  Tetratricopeptide-like helical | Csa2G287160 | Transcriptional factor B3;  Restriction endonuclease type II EcoRII N-terminal |
| Csa2G286480 | Multicopper oxidase type 1;  Multicopper oxidase type 2;  Multicopper oxidase type 3 |  |  |



**Figure1.**



**Figure 2.**