# Genetic Diversity of Melon (*Cucumis melo* L.) Estimated by SSR Markers

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**Introduction:** SSRs are excellent markers, being PCR markers, co-dominant and highly polymorphic. In addition, SSR markers are known to be most useful anchor markers for map merging, and their usefulness in melon has been demonstrated (1, 2, 4, 5). Here we report the polymorphism detected by a set of 48 SSRs in a collection of 102 melon (*Cucumis melo* L.) genotypes. The information presented is valuable for the selection of SSRs for future applications.

**Material and Methods**: *Plant material.*: A collection of melon genotypes was obtained from the following seed companies (7-10 genotypes from each company): Rijk Zwaan, The Netherlands; De Ruiter Seeds, The Netherlands; Semillas Fito, Spain; Syngenta Seeds, France; Sakata Seed Corporation, Japan; Enza Zaden, The Netherlands; Hazera, Israel; Seminis Inc, USA; Nunhems Zaden, The Netherlands and Zeraim Gedera, Israel. DNA was extracted from a bulk of roots of 8-10 plants for each genotype, using the mini-procedure described by Fulton et al. (3). In addition, four parental lines of mapping populations from the Newe Ya'ar collection were included: PI414723; 'Dulce'; 'Vedrantais'; PI161375 (2, 5). Altogether, 102 genotypes belonging to different market types (e.g. Cantaloup, Charentais, Honey Dew, Ananas, Galia, Inodorus, and Oriental Melon) were scored.

*SSR markers*. Forty-eight SSR markers developed in our laboratory were chosen for this study. All of these markers were previously found to be polymorphic between the parental lines of at least one of the mapping populations mentioned above. Twenty-eight of the markers have already been published (1, 2, 4).

PCR amplification and polyacrylamide gel electrophoresis were performed as described by Danin-Poleg et al. (1).

*Gene diversity*. Allele frequencies, allele number and gene diversity were calculated. Gene diversity was calculated as:
Gene Diversity = $1 - \Sigma P^2_{ij}$ , where $P_{ij}$ is the frequency of the jth allele for ith SSR locus summed across all alleles for the locus, as described by Danin-Poleg et al. (1).

**Results and Discussion**: All 48 SSR markers amplified clear DNA fragments in all 102 genotypes (for illustration see Fig. 1). A total of 212 alleles were scored (Table 1). The highest number of alleles was detected using the marker CMATN89 (13 alleles) and the lowest number was found to be 2 alleles detected by each of 6 SSRs (CMAGN55, CMTAAN87, CMCAN90, CMGAN92, CMTGGN99, CMGA15). The selected SSR markers generated an average of 4.3 alleles per locus, and gene diversity varied between 0.04 and 0.82 (Table 1). The high level of polymorphism detected indicates that these SSR markers provide a useful tool for estimating genetic variation in melon**.**

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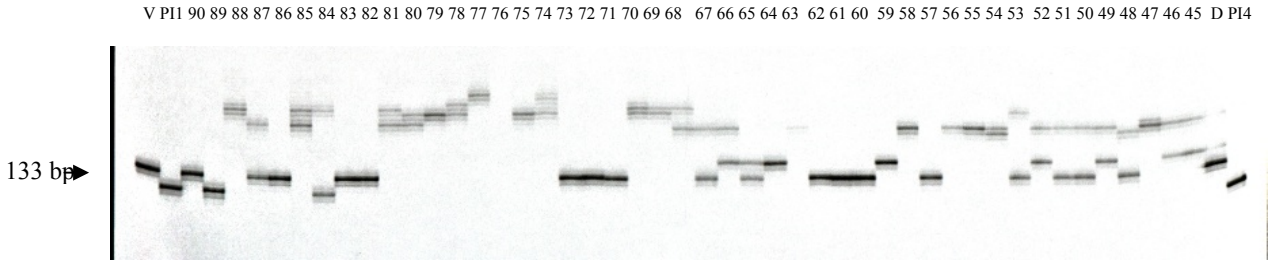


Figure 1. A group of melon genotypes scored using the marker CMATN89 on polyacrylamide gel. V – 'Vedrantais', PI1 – PI161375, D – 'Dulce', PI4 – PI414723, 45-90 melon genotypes from the collection. The arrow indicates the size of the allele of 'Dulce'.

Table1. The number of alleles and the gene diversity detected by 48 SSR markers in a collection of 102 melon genotypes.

| Marker name | Number of alleles | Gene Diversity | Marker name | Number of alleles | Gene Diversity |
|---|---|---|---|---|---|
| CMGAN3** | 3 | 0.27 | CMTCN62** | 3 | 0.5 |
| CMCTN4** | 3 | 0.54 | CMTCN65** | 4 | 0.45 |
| CMCTN7** | 3 | 0.44 | CMTCN66** | 7 | 0.65 |
| CMTCN14** | 3 | 0.61 | CMCTN71** | 7 | 0.63 |
| CMATN22** | 3 | 0.55 | CMAGN73** | 7 | 0.43 |
| CMGAN24** | 3 | 0.08 | CMAGN75** | 7 | 0.6 |
| CMGAN25** | 3 | 0.53 | CMAGN79** | 10 | 0.81 |
| CMTCN30** | 4 | 0.72 | CMGAN80** | 4 | 0.53 |
| CMTCN34 | 6 | 0.66 | CMGTN84 | 3 | 0.55 |
| CMAG36* | 8 | 0.7 | CMCTN85 | 5 | 0.53 |
| CMGAN37 | 4 | 0.57 | CMCTN86 | 6 | 0.56 |
| CMTCN40 | 4 | 0.33 | CMTAAN87 | 2 | 0.05 |
| CMTCN41** | 4 | 0.42 | CMATN89 | 13 | 0.82 |
| CMCTTTN44 | 4 | 0.42 | CMCAN90 | 2 | 0.13 |
| CMAGN46 | 4 | 0.54 | CMTTCN91 | 3 | 0.59 |
| CMGAN48 | 4 | 0.05 | CMGAN92** | 2 | 0.04 |
| CMAGN52** | 6 | 0.6 | CMTGGN99 | 2 | 0.39 |
| CMCTN53** | 4 | 0.13 | CMATN101 | 5 | 0.08 |
| CMAGN55 | 2 | 0.3 | CMGA104* | 6 | 0.68 |
| CMTCN56** | 4 | 0.55 | CMGA15* | 2 | 0.04 |
| CMCTN57 | 3 | 0.15 | CMCT44* | 3 | 0.04 |
| CMCTN58 | 3 | 0.11 | CMGT108* | 4 | 0.47 |
| CMGAN59 | 7 | 0.35 | CMTA134a* | 5 | 0.66 |
| CMAGN61** | 3 | 0.51 | CMGA120 | 5 | 0.43 |

* Primers published by Danin-Poleg et al. (1, 2).

** Primers published by Gonzalo et al. (5).