

Cucumber Recombinant Inbred Lines

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Release Announcement. A set of recombinant inbred (RIL) cucumber lines (*Cucumis sativus* L.) is being released by U. S. Department of Agriculture, Agricultural Research Service as genetic stock and for breeding purposes. These RIL were developed in conjunction with mapping experiments that sought to identify molecular markers linked to economically important traits (i.e., yield components) controlled by quantitative trait loci (QTL) in F₃ families derived from a GY-7 x H-19 mating (1 and 2). These F₃ families were self-pollinated to produce RIL that were assessed in two years in field tests at the University of Wisconsin Experiment Station, Hancock, WI (HES). A RIL-based map was constructed using 14 single sequence repeats (SSR), 24 sequence characterized amplified regions (SCAR), 27 amplified fragment length polymorphisms (AFLP), 62 random amplified polymorphic DNA (RAPD), 1 single nucleotide polymorphism (SNP), and 3 economically important morphological [*F* (gynoecy), *de* (determinate habit), *ll* (little leaf)] markers (3). This map consists of seven linkage groups spanning 706 cM with mean marker interval of 5.6 cM. The RIL described herein can be used in conjunction this map to identify additional qualitative (e.g., disease resistance) and quantitative (e.g., fruit yield and quantity components) traits and for use in the development of inbred backcross lines for extensive genetic analyses (e.g., fine mapping).

Description of inbred lines used to create RIL. The monoecious, indeterminate, little leaf (40 cm²) line H-19 (University of Arkansas-Fayetteville, 1993) was crossed with the gynoecious, determinate cucumber experimental line GY7 (tested as experimental line G421; University of Wisconsin-Madison, 1997) possessing standard-sized leaves (80 cm²). H-19 plants normally have 5 to 15 primary lateral branches depending on the environment, and possess a sequential fruiting habit (i.e., several fruit enlarge on a branch). In contrast, GY7 has relatively few branches (1 to 3), and exhibits strong crown set and sequential fruit inhibition.

Development of RIL. An F₁ plant resulting from an GY7 x H-19 mating was self-pollinated to produce 250 F₂ progeny which were then self-pollinated by single seed descent to obtain 168 F₂S₆ recombinant inbred lines (RILs). The sex expression of plants exhibiting the gynoecious character during the formation of RILs was modified by treatment with silver thiosulfate to allow for self-pollination.

Evaluation and description of RIL. Recombinant inbred lines, parents and F₁ were evaluated in one locations (HES) in 1999 and 2000. RILs were arranged in randomized complete block design with three replications per location. Each replication had 12 plants and consisted of single rows with plants spaced 13 cm apart in rows to include edge borders positioned on 1.5 m centers corresponding to a plant density of ~51,000 plants/ha. Data were collected on plant habit, days to anthesis, sex expression, leaf type, number of lateral branches originating from the mainstem, and fruit number and fruit length/diameter ratio. Considerable variation in the traits examined among RIL was observed in plant habit (determinate and indeterminate), earliness (45 to 57 days to anthesis), sex type (gynoecious and monoecious), lateral branches (1 to 9), fruit number (1 to 7 fruit per plant), and L:D (2.8 to 3.1). Multiple branching lines were identified that produced commercially acceptable fruit (Figure 1). Complete descriptions of RILs are detailed by Fazio (3).

Availability

Breeder's seed, produced under screen isolation, will be provided to U.S. hybrid-seed producers and cucumber breeders by J.E. Staub, ARS/USDA, Dept. of Horticulture, Univ. of Wisconsin, Madison, WI 53706. The development of mapping information from these RIL was partially supported by grant No. IS-2708-96 from the U.S.-Israel Binational Agricultural Research and Development (BARD) Fund.



Figure 1. Gynoecious multiple lateral determinate cucumber germplasm.

Literature Cited

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2. Serquen, F. C., J. Bacher, and J. E. Staub. 1997b. Mapping and QTL analysis of a narrow cross in cucumber (*Cucumis sativus* L.) using random amplified polymorphic DNA markers. *Mol. Breeding* 3:257-268.
3. Fazio, G. 2001. Comparative study of marker-assisted and phenotypic selection and genetic analysis of yield components in cucumber. Ph.D. Diss., University of Wisconsin, Madison. (Diss. Abstr. 3033308.)