Cucumber (Cucumis sativus L.; 2n = 2x = 14) is produced worldwide and is consumed as a fresh (fresh or slicing types) or as a processed vegetable [processing or pickling types] and as a cooked vegetable (e.g., China)] product in several market classes (Staub et al., 2008). The European Long market-type cucumber is grown for the fresh market in protected-culture environments (primarily glasshouse and plastic “hoop houses”). Harvestable fruit are 32 to 40 cm in length, smooth, dark green, fine-spined, and seedless (parthenocarpic, non-pollinated fruit set). Plants are gynoeocious and develop multiple lateral branches that are pruned continuously, where single stems of plants are trained on trellis systems.

Cucumber has an extremely narrow genetic base with 3% to 8% polymorphisms among elite and exotic germplasm and 12% between botanical varieties [C. sativus var. sativus L. and var. hardwickii (R.) Alef.] (Dijkhuizen et al., 1996; Horejsi and Staub, 1999; Meglic and Staub, 1996). The European Long market class has the narrowest genetic diversity [genetic distance (GD) = 0.00 to 0.24] among the major commercial cucumber market classes (e.g., Mediterranean types; GD = 0.09 to 0.55; Dijkhuizen et al., 1996; Horejsi and Staub, 1999). This is in large part the result of the initial use of relatively few PIs in germplasm development and the extensive use of the germplasm “Corona” in modern (since 1950) breeding (Staub et al., 2008; Kees Hertogh and Gerhard Reuling, personal communication, 2002). To our knowledge the last intensive, long-term public breeding effort for this market type ended in the 1950s (Andeweg, 1956).

European Long Greenhouse cucumber breeding and genetics have been hampered by not only its lack significant genetic diversity, but also by the lack of appropriate genetic stocks for rapid genetic mapping of economically important traits and the inability to carry on strategic assessments of epistatic interactions. The inbred backcross breeding method (Wehrhahn and Allard, 1965) has been useful for broadening the genetic base of cucumber and providing novel populations for genetic analysis of complex traits in cucumber (Owens et al., 1985a, 1985b). Given the narrow germplasm base and the lack of ongoing public breeding efforts, a series of 116 European Long Greenhouse market-type IBL were developed (according to Wehrhahn and Allard, 1965) and released in Jan. 2011 by the Agricultural Research Service, U.S. Department of Agriculture. The IBL were developed by crossing an elite long cucumber European Long Greenhouse line and PI 432858 (China; long-fruited, Northern China) to produce BC1 and PI 432858 (China; long-fruited, Northern China) to produce BC1 (recurrent parent) to produce BC1 (parental lines using NTsys Version 2.01 computer software (Exeter Software, Setauket, NY).

Line NZ1 is an elite, gynoeocious, multi-pistillate, parthenocarpic European Long inbred line that produces moderately long (28 to 33 cm), uniform moderately dark green, white-spined [spines small (≈1 to 2 mm) and thin], ribbed fruit that are set sequentially (Table 1; Delannay, 2009). It possesses a multiple lateral branching habit (zero to two branches per plant in the first three main stems) under Wisconsin greenhouse-growing conditions. In contrast, fruit of the monoeocious, occasionally multipistillate, access BI PI 432858 are long (37 to 39 cm), non-ribbed, uniform green, and bear comparably course light black spines. Parthenocarpic tendency and sequential fruit setting capacity of this accession varies with the environment (Madison WI, greenhouse spring and winter evaluation 2007 and 2008; Delannay, 2009), where several genes are involved in conferring parthenocarpy (de Ponti and Garretsen, 1976; Sun et al., 2006a, 2006b). It develops comparatively few lateral branches (two to four branches per plant) (Delannay, 2009). This PI is a component of a “test array” of the NPGS “Cucumber Core Collection” based on its genetic diversity (Staub et al., 2002).

A random F1 from a cross between NZ1 and PI 432858 (donor parent) was crossed to a cloned (meristem-propagated) NZ1 plant (parent parent) to produce BC2 (Delannay, 2009; Delannay and Staub, 2010). At BC2, 30 of 288 individuals were selected (selection intensity = 11%) as possessing the highest heterozygosity based on molecular marker profiles [19 mapped, simple sequence repeat (SSR) and sequence characterized amplified region (SCAR) markers]. Approximately 13 plants from each of the 30 BC2 families (384 plants) were marker-genotyped, and 120 BC2 individuals were then self-pollinated for three generations by single seed descent to generate 116 BC2S2 IBL. (four of the 120 IBL did not produce sufficient seed amounts for phenotypic evaluation; Tankesley et al., 1996, Wehrhahn and Allard, 1965).

The full set of 116 IBL was evaluated for plant phenotype in Wisconsin replicated

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Table 1. Combined three-location (Madison, WI; Haelen and Bergschenhoek, The Netherlands) trait means and SEs of parents (NZ1 and PI 432858) and their derived cucumber (Cucumis sativus (BC2S3) as evaluated in 2007 through 2009.

| Trait | Mean SD Minimum Maximum Mean SD Minimum Maximum Mean SD Minimum Maximum |
|-------|--------------------------------------------------|
| Percent gynoecious | 100.00 0.00 100.00 100.00 0.00 0.00 0.00 0.00 78.57 38.75 0.00 100.00 41.45 46.67 0.00 100.00 |
| Lateral branch number | 2.50 1.46 0.00 5.00 3.20 1.30 1.00 4.00 8.85 1.80 0.00 13.00 8.70 2.01 0.00 13.00 |
| Harvest group | 2.44 1.82 0.00 5.00 3.67 1.53 2.00 5.00 3.21 1.74 0.00 8.00 3.68 2.04 1.00 8.00 |
| Fruit yield | 2.00 1.46 0.00 10.00 5.98 1.30 0.00 10.00 6.94 1.92 0.00 18.00 5.92 1.57 0.00 18.00 |
| Sunburst coloration | 0.11 0.32 0.00 1.00 0.67 0.58 0.00 1.00 0.26 0.44 0.00 1.00 0.16 0.37 0.00 1.00 |
| Ribbed fruit | 0.47 0.51 0.00 1.00 0.47 0.51 0.00 1.00 0.79 0.41 0.00 1.00 0.75 0.43 0.00 1.00 |
| Spine fruit | 0.37 0.11 0.00 0.00 0.37 0.11 0.00 0.00 0.56 0.50 0.00 1.00 0.56 0.50 0.00 1.00 |
| Genetic distance | 0.37 0.11 0.12 0.62 0.37 0.11 0.12 0.62 0.77 0.49 0.09 1.00 0.49 0.16 0.00 1.00 |

Description

Analysis of variance and multivariate analyses (principal component analysis) of phenotypic and genotypic data led to a characterization of IBL and allowed for comparative analyses (Delannay, 2009; Delannay and Staub, 2010). Test locations performed similarly for the cumulative two-harvest yield, fruit length, and the occurrence of ribbed and spiny fruit, and no significant location-by-line interaction was detected for cumulative two-harvest yield.

Principal components (PC) 1 to 3 accounted for 88% of the observed phenotypic variation among IBL (PC1 = 49%, PC2 = 22%, and PC3 = 17%; Delannay, 2009; Delannay and Staub, 2010). Although all traits evaluated contributed equally to the ordination of IBL by PC1, spines on fruit were mainly responsible for IBL ordination in PC2, and fruit length largely determined IBL ordination in PC3. Of the subset of 38 IBL evaluated across all locations, the morphology of IBL 4, 10, 16, 33, 36, 41, 43, 44, 46, 49, 50, 51, 56, 68, 72, 78, 80, and 83 showed differences in cumulative two-harvest yield, sex expression, and occurrence of spines on fruit and fruit length. For instance, IBL 99 typically develops the longest fruits (35.1 cm) and IBL 51 the shortest fruits (25.2 cm), and IBL 46 generally yields the highest fruit number (43.3 fruits/plant). These and selected IBL from the central cluster should be considered a test array for initial evaluation of potential use based on morphology alone. If useful variation is found in a production target environment, then other IBL (i.e., remaining 78 IBL) could be evaluated for their horticultural potential. Their potential is supported by the transgressive segregation observed for lateral branching, days to flower, and sunburst pattern on the fruit blossom end (Table 1). These traits are controlled by relatively few genes (three to five depending on population), which are in some cases epistatic (lateral branching and days to anthesis) (Fazio et al., 2003). The alignment of complimentary greenhouse conditions in summer and spring of 2007 and 2008, respectively (Delannay, 2009; Delannay and Staub, 2010). The morphological characteristics of a subset of 38 of the 116 (33%) IBL (randomly chosen) were evaluated in Madison, WI, and in Haelen and Bergschenhoek, The Netherlands, under commercial greenhouse-growing conditions in 2008 (July to October) and 2009 (January to April) (Delannay, 2009; Delannay and Staub, 2010). Parents, F1 progeny, and IBL were replicated and mature plants were evaluated for days to anthesis, sex expression, number of lateral branches, yield over two harvests, fruit length, fruit weight, and exterior fruit quality [a full description of IBL can be found in Delannay (2009)].
alleles may provide a partial explanation for the observed transgressive segregation (Robbins et al., 2008).

Genotypic relationships between all IBL were characterized by multivariate analysis (44 markers) and genetic affinities were estimated (Delannay and Staub, 2010). Lines 28, 30, and 31 were determined to be genetically identical by marker analyses (GD = 0.00), and IBL 36 and 66 were the most distant from other IBL (GD = 0.77). A majority of the IBL evaluated were dissimilar to PI 432858 (GD = 0.60 to 0.90). However, IBL 4, 28, 42, 55, 69, 79, 96, 117, and 125 were least similar to PI 432858 (GD = 0.90).

General morphological and molecular genetic diversity are not necessarily equivalent among the IBL (Table 1; Delannay, 2009). For instance, although IBL 5 and 116 share common morphological characteristics, they do not possess substantial genetic similarities (GD = 0.39). However, IBL 28, 30, and 31 were genetically identical (GD = 0.00) and possess similar morphological characteristics.

Potential Use of Inbred Backcross Lines

This is the first public release of European Long cucumber lines in 50 years and genetically characterized IBL can be used directly for plant improvement and genetic analysis. These IBL form a family of related lines that are homozygous but heterogeneous (Delannay, 2009). Because of this population structure, the genetic and morphological differences between European Long cucumber IBL described here can assist in the development of genetically diverse germplasm through phenotypic and marker-assisted selection strategies (Staub et al., 2008). For instance, early generation progeny resulting from a cross between IBL 5 and 116 will likely result in the recovery of diverse gynoecious, early-flowering, high-yielding progeny through marker-assisted and phenotypic selection (Fan et al., 2006; Fazio et al., 2003). Likewise, the gynoecious IBL 116 displays a relatively large number (approximately four fruit/plant) of spineless, relatively smooth, uniformly green fruit but shares little genetic similarity with commercial parental line NZ1 (GD = 0.46; Delannay, 2009). Its inclusion in narrow-based breeding efforts would likely enhance genetic diversity in current breeding programs.

Lateral branching is desired in certain production systems (e.g., hoop house in Spain and Turkey and “Energy-Saving greenhouse” in China; Staub et al., 2008) and, therefore, can be an important trait for plant improvement. The gynoecious IBL 5 exhibits high yield (approximately four fruit/plant), multiple lateral branching (≥13 branches), and early flowering (≤12 d to anthesis) traits and could be intermated with monocline lines such as IBL 20 (one lateral branch) or 127 (approximately three lateral branches) to develop genetically diverse gynoecious, high-yielding, multiple lateral parthenocarpic germplasm with multiple lateral branches (Delannay, 2009).

Broad- and narrow-based genetic maps exist for cucumber (Fazio et al., 2003; Ren et al., 2009). However, published, highly saturated maps originating from European Long market types are not publicly available and, therefore, a mating between divergent lines of this market class would be useful for map construction and subsequent cucumber improvement (Fan et al., 2006). The genotypically different IBL described here [more specifically by Delannay (2009) and Delannay and Staub (2010)] could be used to create such a genetic map. Using specific IBL in conjunction with bulk segregant analysis (Michelmore et al., 1991), single-gene traits could be positioned on the map [e.g., sex expression (F, m), multipistilate character (mp), spine color (B), fruit color (u), spine number (n), spine size (s), parthenocarpy (Pc)] (Xie and Wehner, 2001), because variation for such traits was visually observed IBL but unpublished. Moreover, comparative analysis between specific IBL could allow for genetic trait analysis of epistasis in economically important traits (e.g., parthenocarpy, lateral branch number; Robbins et al., 2008), and a recombinant inbred line-based map constructed using divergent parents could be used to map quantitative trait loci (Fazio et al., 2003). Such a map could be constructed using IBL 5 (gynoecious, parthenocarpic, multipistillate, multiple lateral branching, high yield, early flowering, and large, dark-colored fruit) and IBL 20 [monoeocious, non-parthenocarpic (Wisconsin growing conditions), few multipistillate nodes, unilateral branching, low yield, late flowering, and comparatively short, light-colored fruit].

Availability

Seed of European Long Greenhouse IBL 116 is available from a hand-pollinated greenhouse increase and may be obtained by addressing requests to P.W. Simon, Vegetable Crops Research, U.S. Department of Agriculture, Agricultural Research Service, Department of Horticulture, University of Wisconsin, Madison WI 53706. Homozygous but heterogeneous IBL 4, 10, 16, 33, 36, 41, 43, 44, 46, 50, 51, 56, 68, 72, 78, 80, 82, 83, 89, 90, 91, 95, 99, 103, 104, 116, 121, and 130 are being released as a test array, which circumscribes the phenotypic variation observed in IBL. The remaining IBL being released (88) differ in their molecular marker profiles and morphological characteristics (Delannay, 2009) and can be used directly in genetic experiments to assign single-gene traits to genetic maps and for investigations into epistatic interactions.

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