to determine sensitivity or tolerance of strawberry genotypes to *Phytophthora cactorum, Verticillium dahliae, Colletotrichum acutatum, Sphaerotheca macularis, and Tetranychus urticae.* On an annual basis, we characterize sensitivity and tolerance/resistance of a wide range of strawberry genotypes to specific plant pathogens and pests. In conducting genetic screens for tolerance/sensitivity soilborne plant pathogens, it is essential that the experimental site be free of soilborne pathogens: this can only be accomplished with a highly effective soil fumigant such as MBCP. Typically, our genetic screens involve about 50 cultivars and advanced selections for which yield and fruit quality have been well-documented. Replicate plots of infected and non-infected control plants enable comparisons of growth and vigor or other plant attribute. This type of information is useful to growers in selecting the most appropriate cultivars for the particular disease situations in their fields, and is useful for the breeders in selecting disease-resistant selections and cultivars.

Aeroponic Culture by Root Spray of Nutrient Solution for Setting Plants Production of Strawberry through Runner-cutting

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Aeroponics was attempted to produce the nursery plants of strawberry from cuttings of runner plant by spraying with an atomized nutrient solution on the root zone. The cutting benches were built in two stairs and two Styrofoam containers in a stair. The Styrofoam boards with holes of 4 cm diameter were placed on top of the containers. The runner plants of strawberry were separated from the mother plants and stored at 1±1°C. After 3 days of storage, the unrooted runner plants were put into the holes of the Styrofoam boards in a 38%-shading plastic house of southern exposure. For the early 10 days, the cutting benches were covered with polyethylene film and white nonwoven fabric to keep relative humidity in the shade and underground water sprayed. Thereafter the Yamazaki's nutrient solution was sprayed for 2 minutes at 30 minutes interval. The survival ratio of runner plants was higher at the shady low-stair of the north bench of low illuminance. Roots emerged in 3 days after cutting and the new daughter plants were well-rooted and established for field transplanting. After 85 days, the fresh weight of daughter plants was much greater as 7.4 g or more and the average diameter of crown was about 7.7 mm from the plants grown at the north bench. The chlorophyll content of new third leaves was more than 37 as SPAD value (Konica Minolta) without relation of the bench position. The daughter plants grown using aeroponics were planted and cultured by drip-irrigation of Yamazaki's solution in a greenhouse. Approximately 98% of the daughter plants survived after transplanting. Aeroponic roots were not susceptible to wilting and leaf loss, or loss due to transplant shock.

Molecular Map of *Fragaria virginiana*, Progenitor of Cultivated Strawberry

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Recent efforts to genetically map octoploid strawberry species included attempts to associate the resulting linkage groups (28 expected) with the seven linkage groups identified in diploid strawberry maps. Here we present one such genetic map, created from a mapping population derived from a cross between two *Fragaria virginiana* clones. Other genetic maps have been generated from octoploids *Fragaria chiloensis* and the cultivated strawberry, *Fragaria ×ananassa*. In each case, simple sequence repeat (SSR) molecular markers used in efforts to create genetic maps of both diploid and octoploid species were also used to assemble octoploid linkage groups into seven homeologous groups, ie seven sets of four linkage groups that are thought to each have been evolutionarily derived from one of the seven diploid linkage groups. This was possible, partly because many of the SSR markers were present in two or more octoploid linkage groups. Since many of these markers were derived from expressed genes, it can be assumed that several of the traits important in the cultivated strawberry could be affected by more than one locus in some populations. Strawberry breeders attempting to manipulate such traits can expect that some breeding populations will segregate at one locus and others will segregate at multiple loci. Other breeding populations may be examples of the classic allelism test in which a cross of two parents with a desired trait results in a population of no progeny with the desired trait. Because the octoploid homeologous groups are fairly easy to determine, the diploid linkage groups and genomic sequence should be useful as a source of markers to test when attempting to discover markers associated with traits of interest.

Strawberry Yield of North American Varieties in Nonfumigated Fields in South Brazil

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The goal of this work was evaluated the yield and quality of strawberry varieties in nonfumigated fields looking for the most promising to produce in the southern Brazil region. The cultivars studied were Camarosa, Diamante, Aromas, Ventana, Albion, Camino Real, Earlibrite, Festival and Sabrosa. The experiment was carried out at Embrapa Temperate Climate, Pelotas, RS, Brazil, where the plants were cultivated under low tunnels system in double rows and nonfumigated soil. The plantlets were imported from Chili and Argentine nurseries being planted in July 2009. Weekly, from September until December, strawberries were harvested in each plot and were evaluated regarding to fresh weight fruit, number of fruit, yield, diameter and misshape. The experimental designer was randomized blocks with four repetitions being the experimental unit composed for 12 plants. All cultivars had the same behavior regarding the production cycle with the peak production in November. Cultivars Florida Festival and Camarosa had the highest yield and highest number of fruit per plant, while the other cultivars showed the highest fresh weight of fruits.

Preliminary Genetic Analysis of Multiple Traits in the University of Florida Strawberry Program

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Improving strawberry yield, quality traits and resistance to pests and diseases requires estimation of genetic parameters of the traits of interest to determine the best breeding strategies and to predict genetic gains. A field research trial to estimate genetic parameters for several morphological and physiological traits was established at the Gulf Coast Research and Education Center (GCREC) in Balm, FL, in Oct. 2009. Seven control pollinated families, corresponding to the crossing of one wild selection and 10 advanced selections from the University of Florida, representing a total of 633 genotypes, were tested in a randomized complete block design with four clonal replications. Narrow sense heritability (h^2) and broad-sense heritability (H^2) were calculated for each trait and clonal genotypic (and phenotypic) correlations were estimated among all pairs of traits.Narrow-sense heritabilites (h^2 = 0.22–0.45) and broad-sense heritabilites (H^2 = 0.22–0.58) were low to moderate for the majority of traits mainly due to the presence of substantial additive variance, indicating the potential for making gains in future cycles of breeding. Other traits such as soluble solids, titratable acidity and proportion of misshapen fruit, showed no additive variance suggesting that improvement of these traits should be made by selecting superior individuals from clonal trials. Genotypic correlations were low for most pairs of traits ($r_g < 0.25$), low to moderate for a few (r_g = 0.32–0.45) and high (r_g = 0.78) for early marketable weight and total marketable weight. The phenotypic correlation between early marketable weight and total marketable weight was also high (r_p = 0.66) suggesting that early yield is a good predictor of total yield. A low negative genotypic correlation (r_g = –0.17) was observed between the total number of flowers and the total number of runners but a moderate negative correlation (r_g = –0.40) was found between the latter trait and open canopy architecture. Genotypic correlations between diseases and other traits tended to be low but the correlation between botrytis and early marketable weight (r_g = 0.41) was moderate and decreased for the whole season (r_g = 0.29). These genetic parameters are preliminary but provide valuable information for the breeding program at the University of Florida. More precise estimates are under way from trials, planted in 2010, testing larger populations replicated across locations.