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|  |  | **INBRED LINE DEVELOPMENT** |  |  |
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|  | *An inbred line is a homozygous breeding line developed and maintained by self-pollination*. When developing inbred lines in a hybrid breeding program in a cross-pollinated species such as corn, breeders normally start by self-pollinating heterozygous plants. The heterozygous plants may have been selected by the breeder from (a) a natural population of a cross-pollinated species, or a cross-pollinated population improved through a recurrent selection procedure, or (b) the second generation (F2) progeny from a cross between homozygous parent lines. In breeding hybrid corn the inbred lines were originally developed by selfing selected heterozygous plants from fields with uncontrolled pollination (also referred to as *open-pollination*) as in (a) above. In a mature hybrid corn breeding program, inbred lines of corn are more generally developed from the hybrid progeny created by crossing two elite inbred lines as in (b). The latter is identical to the hybridization procedure described for self-pollinated crops in Chapter 9. In (a), the original heterozygous *selfed plant* is normally referred to as the S0 plant, and the progeny obtained from selfing this plant as the S1 (*first-generation selfed*) progeny. The *second-generation selfed progeny are* called the S2, and so on. If the heterozygous plant originates from a cross between homozygous inbred lines, the F1, F2, etc., designation would be used as in self-fertilized species. |  |
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|  | The purpose of inbreeding is to reduce the offspring of a heterozygous plant into an array of dissimilar, homozygous, inbred lines. Striking differences are observed between lines with successive generations of inbreeding; within lines, plants become more alike and the individual inbred lines become more distinguishable from each other. With successive generations of inbreeding, homozygosity and uniformity are increased within the progeny lines. The *variance within lines is reduced while the variance between lines is increased*. In a cross-pollinated crop like corn, five to seven generations of self-fertilization and pedigree selection are necessary to obtain inbred lines that are uniform in plant and seed characteristics and that will remain uniform under continued self-fertilization. This procedure is identical to the pedigree-selection procedure utilized in the breeding of self-pollinated crops, where a cross between selected parents is followed with several generations of self-pollination and selection to generate uniform, true-breeding progeny lines (Fig. 9.2). During inbreeding, many undesirable recessive alleles at heterozygous loci will be replaced by dominant alleles and the recessive alleles eliminated from the progeny; at other loci, recessive genes will become homozygous contributing to an overall loss of vigor in the inbred. Greatest vigor is lost during the early generations of inbreeding, the loss in vigor declining as the inbred lines gradually approach homozygosity. After no further loss of vigor is experienced, the genotype of the inbred may be maintained by self-pollination, unless mutations or outcrossing occur. |  |
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|  | Selection during the early generations of inbred line development is based largely on visual observations of the inbred plants for characteristics that will affect the suitability of the inbred to be utilized in commercial hybrid production. Are the plants strong and vigorous? Do they stand without lodging? Do they produce seeds in sufficient abundance and quality to assure maintenance of the inbred line? Are the plants free from insects and disease? How do they yield? |  |
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|  | During the period of inbreeding and selection, it is desirable to subject the partially inbred lines to adversities, such as high plant density, unfavorable high or low temperatures, drought, lodging, disease, or insect pests, as appropriate for the particular species being inbred and the |  |
| environments. It is also important in inbred line development to find new inbred lines that will contribute to greater productivity when crossed with other inbred lines. | | | |  |
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|  | ***Combining Inbreds into Single Crosses*** |  |
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|  | The utility of the inbred line is determined by its genetic contribution to the hybrid progeny when crossed with another inbred line, not in its production potential per se. However, it needs sufficient production potential so that it can be economically maintained and utilized as a parent line in the production of hybrid seed. Vigor and productiveness that were lost during inbreeding are recovered in the hybrid when the inbred lines are crossed. From experience it has been learned that some inbred lines will combine with a large number of other inbreds to produce high-yielding hybrid progenies; other inbred lines will combine satisfactorily with few or no inbred lines. The ability of the inbred line to transmit desirable performance to the hybrid progeny is referred to as *combining ability*. |  |
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|  | **GENERAL COMBINING ABILITY.** *General combining ability (gca) of an inbred line is the average contribution that the inbred makes to hybrid performance in a series of hybrid combinations in comparison to the contribution of other inbred lines to hybrid performance in the same series of hybrid combinations*. It is not possible from visual observation to predict the contribution of an inbred line to hybrid performance. The gca of an inbred line is evaluated by crossing it with other inbred lines and comparing the overall performance of the single-cross progenies. General combining ability evaluates the *additive* portion of the genetic effects. If inbred lines A, B, C, D, and E are crossed in all possible combinations (diallel mating) and the single-cross hybrids are grown in a yield trial, the inbred whose single crosses have the highest average yield would have the greatest gca. If that inbred is A, the implication is that A will contribute to high yield in a wider array of crosses than inbred lines B, C, D, or E. With large numbers of inbred lines, it is not always feasible to make all possible diallel matings and grow the hybrid progenies in performance trials. The number of possible single-cross combinations that can be made from n inbred lines is equal to n(n- 1)/2. With 10 inbreds, the possible number of single-cross combinations is 45; with 100 inbreds, the possible number of single-cross combinations is 4950, an impossible number to produce or grow in a performance trial. These burdensome numbers made it clear to the early breeders of hybrid corn that a simple and efficient system of screening inbred lines for combining ability was needed before pairing the inbred lines in single-cross yield trials. |  |
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|  | From testcross experiments (often called topcrosses in corn), it was demonstrated that yields of corn inbred lines pollinated with a mixture of pollen, such as from an open-pollinated cultivar or from a double-cross or single-cross hybrid, were highly correlated with the average performance of the inbred line in a wide array of single-cross combinations. This led to the use of *testcrosses* for preliminary screening for gca of large numbers of newly developed inbred lines. As new inbred lines were generated, they were first pollinated with a heterogeneous genotype proven to be an efficient tester, and the testcross progeny evaluated in yield trials. Only inbred lines with superior gca were retained for testing in single-cross combinations. |  |
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|  | **SPECIFIC COMBINING ABILITY**. *Specific combining ability (sca) is the contribution of an inbred line to hybrid performance in a cross with a specified inbred line, in relation to its contributions in crosses with an array of specified inbred lines*. Specific combining ability   |  |  |  | | --- | --- | --- | |  | evaluates nonadditive gene action and is utilized to identify the inbred x inbred cross combination with superior performance. The inbred lines identified as having superior gca are crossed in all possible pairs (*diallel crossing*) to create single crosses, which are then evaluated in yield trials for sca. For example, if all possible single crosses among inbreds A, B, C, D, and E are made, and the combination A × E produces the highest single-cross yield performance, the A × E cross combination would have superior sca. Whether two particular inbreds combine to produce a high-yielding single cross depends upon the extent that the favorable genes for yield from the two parent inbreds complement each other. Experience has shown that inbreds derived from unrelated populations will combine to produce high-yielding single crosses more frequently than inbreds derived from related parent material. |  | |  | | | |  | | |  |  |  |  |  |  | | --- | --- | --- | --- | --- | |  |  | | |  | |  | | | |  | **BROAD- VS. NARROW-BASED TESTERS**.  In early hybrid corn breeding programs, testers with a broad genetic base, such as open-pollinated cultivars, were used to evaluate gca of corn inbred lines. As the hybrid breeding programs in particular species, such as corn, became more advanced, changes were made in the way in which the breeder goes about the task of screening inbred lines for combining ability and fitting the lines into hybrid combinations. The gca of new corn inbreds is now evaluated more frequently by crossing with narrow-base testers, such as elite inbreds, related inbred lines, or single crosses of related lines, making it unnecessary to conduct preliminary screening tests with heterogeneous testers. This change has evolved because in mature hybrid breeding programs, inbred line development is directed more toward replacement of a specific inbred line in an already established hybrid, rather than toward the development of a group of new inbred lines to be used in the production of completely new hybrids. If an inbred line is sought to replace an inbred in an established single-cross hybrid, the opposite inbred would be the logical tester to use. The testing procedures should be designed so that they will identify whether the new inbred line corrects the weakness of the inbred line being replaced. Growing the testcross progenies at multiple locations is essential to evaluate genstype × environment interactions and to identify inbred lines with stable progeny performance in a broad array of environments. |  | |  | | | |  | | |  |  |  |  | | --- | --- | --- | |  |  |  | |  | |  |