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THESIS

MODIFIED S_1-FULL SIB SELECTION FOR HIGH YIELD INBREDS AND HYBRIDS OF MAIZE (*Zea mays* L.)

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Six commercial single crosses were used for the improvement of composite and inbred lines. Modified S_1-full sib selection was applied to improve the three sister line composite. Lines were visually selected under low-competition environment in honeycomb arrangement with equilateral triangular lattice side 0.866m. Testcross as well as diallel cross were applied to identify high combining lines. All yield trails were conducted in randomized completed block design with 4 replications, 1 row plot of 5m long and 0.75 x 0.25m plant spacing. Standard cultural practices were regulated and irrigation was applied as needed.

Statistically, there was no clear advantage of yield between composite and inbred lines in early generation testcrosses. Besides, the inter-family diallel sets of both groups of lines gave similar results. However, the top-2 crosses of overall trials came from composite crosses even though it was not significant. In addition, composite lines were superior to S_3 lines in yield, earliness and plant height. Modified S_1-full sib selection is a flexible breeding method but its merit for the construction of early generation parental lines of hybrids must be thoroughly investigated even though the positive results were observed.

Student's signature　　Thesis Advisor's signature　　03 / 05 / 06

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Nguyen Phuong

April 2006

TABLE OF CONTENTS

LIST OF TABLES

LIST OF TABLES (Continued)

LIST OF FIGURES

MODIFIED S_1-FULL SIB SELECTION FOR HIGH YIELD INBREDS AND HYBRIDS OF MAIZE (*Zea mays* L.)

INTRODUCTION

The ultimate goal of most maize (*Zea mays* L.) breeding programs is the production of improved hybrids with high yield and quality for commercial use. To obtain good parental lines for hybrid seed production, breeders can use various methods. The pure-line method of maize breeding has been the basic breeding method used in developing lines and hybrids since the suggestion of Shull in 1909. Modifications of the pure-line method of breeding have been made during the past 80 years as information, techniques, and equipments became available. However, modification of the pure-line method will continue (Hallauer, 1989). Modern maize breeding methods are primarily a twentieth century phenomenon. The most often used plant breeding method for inbred line development in maize is the pedigree method. It emphasizes knowing the materials with complementary traits for breeding starts and keeping record that show family relationship. Moreover, all methods use the pedigree method for final development of the inbreds and the pedigree method is still the most popular breeding method for improvement of inbred (Troyer, 2001). The combination of self-pollination and evaluation of inbreds in hybrids is the basic breeding method in maize breeding. Jenkin and Brunson (1932) suggested the cross of lines under development with a common tester to evaluate the relative combining ability of inbred lines. Testcrossing with appropriate testers has been adopted extensively and has become the standard approach. The stage of testing varies among breeders and depends on the traits under consideration and the effectiveness of visual selection. Two basis systems are used: late testing and early testing. In late testing, hybrid evaluation is delayed until advanced generations of selfing (e.g. S_5 or S_6). In early testing, evaluation of hybrid performance is conducted in early generations of inbreeding (S_1 to S_3). Jenkin (1935) and Sprague (1964) proposed testing at early inbreeding stages to identify lines with above average combining ability, assuming that combining ability will be similar in subsequent generations. Inbreeding depression is observed primarily in S_1 and S_2 generations, where lines can be eliminated before making testcross.

Even though, development of single cross hybrid of maize is the ultimate goal of most of maize breeding programs. However, finding stable high yield inbred lines to ensure the high level of economic return for commercial hybrid seed production is the main obstacle of small and new emerge single cross development program. Combined line selection and testing for combining ability is time and space consuming processes. Instead of five or six generations of selfing usually practice in the development of inbred lines, composite-sibbing lines from individual of S_1 progenies have been proposed (Kinman, 1952). The method fixed the composite-sibbed lines since the first selfing and therefore improvement in the combining ability or other characteristics of composite-sibbing lines can not be made after several generations of mass sibbing unless effective selection is practiced. In other way, line selection from cross between closely related parents has been proved to be an effective method for inbred line development (Rasmusson and Phillips, 1977; Troyer, 1999). Selection for high and low yield lines effectively separated lines into high and low combining ability group but yield of lines within group can not be used as criterion for combining ability of lines (Lamkey and Hallauer, 1986). In addition, for effective differentiation of lines, Fasoula and Fasoula (1997) proposed line selection under nil-competition environment in honeycomb designs. In order to improve yield and combining ability of population, Landi and Frascaroli (1993) applied full-sib selection in F_2 population of single cross. The method proved to be very effective for several cycles of selection. However, the previous study of Genter (1976) which applied the same method suggested that using S_1 instead of S_0 to form full-sibs was more effective to identify high yielding full-sibs as well as improvement of population per se. This finding was well agreed with suggestion of Lonnquist (1950) that testing for combining ability after one generation of selfing was desirable when the composite-sib breeding method was used.

The above finding suggested that alternate selfing and full sibbing among few closely related lines under nil-competition environment should lead to uniform, high yield and high combining composite lines as high level of homozygosity is approached and provide a chance for continuous improvement of composite lines in the successive cycles.

The present study therefore aim to formulate the effective breeding method for the development of composite lines and evaluate its merit as compare to the conventional line selection with early generation testing for combining ability. The modified S_1-full sib selection within related lines is proposed.

Objectives

The objectives of this study were:

1. To develop high yield composite lines.
2. To determine the potential inbred lines based on combining ability.
3. To compare the composite lines and inbred lines of the same germplasm.

LITERATURE REVIEW

Genetic Improvement

The importance of genetic diversity of inbred lines used in hybrid breeding program is generally accepted. Genetic different between varieties have probably arisen through geographical isolation accompanied by a combination of genetic drift and selection in different environment. Therefore the degree of geographical separation and degree of ancestral relationship in so far as it is known can be used as an indication of genetic diversity (Moll et.al., 1962)

There are numbers of options available for genetic improvement of maize breeding such as selection, hybridization or cross breeding. The purpose of a selective breeding program is to change the average performance of a population in a defined direction. During selection, individuals or families are chosen on the basis of commercially important traits to change the population mean in the next generation. If the desired phenotype of an organism is controlled by additive genetic variance and expressed high level of heritability (h^2), the character will respond well to selection. The change produced by selection is the change of population mean. Response to selection is the difference of mean phenotypic value between the offspring of the selected parents and mean of the parental generation before selection (Falconer, 1989).

There are several approaches for selection including mass selection, family selection and within family selection (Falconer, 1989). Each has its own merit depending on the nature of the characters to be selected and the resources available for the selection program. Mass selection or individual selection involves the selection of individuals on the basis of their value of commercially important traits. Individual or mass selection can be efficiently applied when traits are mainly influenced by additive genetic variance (high h^2 value). When the character selected has a low heritability (less than 0.2) family mean is taken into account and the whole family is considered as a single unit for selection. Within family selection has an advantage of environmental variance common to all family members and thus would eliminate large non-genetic component of variation (Tave, 1995).

Population Selection

Selection within population is directed toward the improvement of the population itself and is done by increasing the frequency of favorable genes within the population. This is a dynamic process since gene frequency is gradually changed; the phenotypic mean which correlates to gene frequency is also changed. This change indicates the gain from selection which differs among population and selection methods. However, the most precise evaluation of gain from selection is obtained when the check population, the improved population represented each cycle, and some commercial hybrids or varieties used as check are represented in yield trial replicated over environment. Moreover, expected gain from selection is also used for comparing selection methods because each method require different time and labor cost to complete one cycle of selection. The best method must require less time and labor cost but gain more progress from selection (Allard, 1960)

Determining the appropriate number of lines to retain during line development is crucial from the standpoint of allocating resources. Within each generation, genetic means of lines increased with increasing selection intensities. Retaining fewer families but evaluating a large number of plants per family resulted in more genetic gain of line per se as compared to saving a large number of smaller families. Identifying the superior lines early in the program and discarding those that are inferior could save resources. The subject of optimum selection intensity is important from the standpoint of genetic gain, fixation of loci, and expenditure of resources in breeding programs Shebeski (1967); Sneep (1977); Yonezawa and Yamagata (1978).

Recurrent selection is commonly used to improve population of maize (*Zea mays* L.). The populations improved by recurrent selection are used directly as open-pollinated cultivars, non-inbred progenitors of non-conventional hybrids and as source of germplasm to derive inbred lines. In the modified, ear-to-row selections were used with the selection intensities of 50 to 60% for among family selection and 6 to 18% for within-family selections (Vasal *et al*., 1997)

Modified ear-to-row and modified S_1 selection methods involve selection at two levels: among family selection and within family selection. The genetic gain per cycle of a method is equal to the sum of the gains due to among family selection and within family selection (Empig *et al, 1972;* Utz, 1984; Hallauer and Miranda, 1988; Dhillon and Khehra, 1989).

Smith (1983) concluded that recurrent selection was effective for increasing grain yield and improving other agronomic characters in population crosses. However, effects of drift due to small population size were evident in the population per se. He wrote on his conclusion if the heritability of seed yield was sufficient high, faster progress might be made using phenotypic recurrent selection, particularly if it could be applied annually.

Inbred lines development and evaluation

The pure line method of maize breeding has been the basic breeding method used in developing lines and hybrids since the suggestion of Shull in 1909.

Modifications of the pure line method of breeding have been made during the past 80 years as information techniques, and equipment became available. Heterosis is the basis of the modern cultivars utilized in maize. The primary aim of maize breeders is to develop populations and inbred lines that can be crossed to form superior hybrids (Hallauer, 1989).

The main difference between inbreds and a population is in genotypic frequencies. Gene frequencies remain constant, but genotypic frequencies change under inbreeding because inbreeding decreases the frequency of heterozygotes and consequently increase the frequency of homozygous geneotypes (Hallauer and Miranda, 1988).

Since the final product desired from recent maize breeding program is single cross hybrids, evaluation of inbred lines performance *per se* and their combining ability with tester or other inbred are important. Good performance *per se* of inbred lines, i.e., high yields, are required in orders to produce single cross seed efficiently and economically. Furthermore, a high combining ability of inbred lines is required to produce a good hybrid.

Breeders assume favorable correlation between plant, ear, and grain traits of the parental lines and performance in hybrid combination. Several studies have shown that correlation of an inbred trait with the same trait in the hybrid is relatively high, except for yield. Although many value of inbred traits, including yield, with hybrid yield have been positive and significant, in most instances they have been too low to be of predictive value (Hallauer et al., 1988). However, Sprague (1964), observed that correlation of inbreds with the mean of all their hybrids progeny is higher than correlation of inbreds with their specific single cross hybrids. These results show that inbred yields predicted general combining ability more accurately than they predicted specific combining ability. Lamkey and Hallauer (1986) observed that selection for high-yielding inbreds would tend to select lines that are above average for hybrid yields.

Today, with many elite sh_2 inbreds and hybrids available, pedigree breeding is the main method used to develop inbreds. Single, three-way, or double crosses of elite commercial inbreds may be the parental material. Parents are chosen with the specific breeding objective in mind. Crossing elite inbreds is best and the parents should complement one another (Tracy, 1997).

Hallauer and Miranda (1981) indicated that most of the inbred lines used commercially have been developed by pedigree breeding. This method is very effective when the strengths and weaknesses of lines for specific traits are known. Inbreds derived by pedigree breeding can be introgressed into the appropriate FR (Full-sib Recurrent) or RRS (Reciprocal Recurrent Selection) in breeding population.

Pedigree selection was and is the most commonly used selection method of line development. Pedigree selection became common after Shull (1906 and 1909) outline the principle of inbreeding and hybridization. Progenies are developed from source populations by some form of inbreeding, with selfing the most commonly used. Pedigree selection is extensively used in recycling of lines that have known strengths and weakness for specific traits. Pedigree developed by recycling of lines can became quite complex, but parentage control permits develop of lines to meet specific requirement (Hallauer and Miranda, 1988).

Duvick (1999) stated that although the inbred-hybrid yield correlations were positive and indicated a tendency for high yielding inbreds to produce high yielding hybrids. The low value of the correlation indicated that it was not high enough to warrant selecting inbred on the basis of their yield per se; performance in crosses was and still is essential for evaluating the worth of an inbred for yield in hybrids.

Roles of Plant Densities

Donald and Hamblin (1976) distinguished three simple ecosystems in which genotypes are grown by plant breeders: spaced plants, plants within a mixed community of genotypes, and plants in a dense monoculture, a crop. They suggested further that it might be useful in plant breeding practice to divide ecosystems into three major categories: (1) isolation environments, where widely spaced plants exclude plant-to-plant interference, (2) competition environments, composed of interactions between genetically dissimilar genotypes, and (3) crop environments, composed of interactions between genetically identical genotypes.

According to Yan and Wallace (1995), the crop yield potential of a genotype consists of two components: potential yield per plant, measured in the isolation environment, and tolerance to density. This is shown by their equation $Y_{max} = (1/4) a^2b^{-1}$, where the crop yield potential of a given genotype (Y_{max}) is expressed as the product of the square of the single plant yield potential in the absence of competition (a^2), multiplied by the genotype's tolerance to plant density (b^{-1}).

Duvick (1997) focused attention to the importance of potential yield per plant of maize hybrid in low stress environments, as a means of improving the crop yield potential. In addition, he arrived at this conclusion after studying the response to plant density of maize hybrids during past 70 years and after finding out that, the potential yield per plant (1 plant/m^2) of maize hybrids remained unchanged.

At high plant densities, yield per unit area was maximal on account of superior exploitation of the available resources, but the yield differentiation among cultivars was reduced to almost zero. This implies that even if breeders were in a position to mimic the conditions of dense monoculture for every individual genotype during the early segregating generations, the reduced differentiation in dense stand would impair response to selection. Fasoula (1995), and Fasoula and Fasoula (1997) proposed selection under isolation environment in honeycomb designs to avoid plant-to-plant competition, minimize soil heterogeneity, promote highest expression of genetic potential, enhance differentiation among lines and thus facilitate line selection.

On the contrary, higher plant densities provide greater stress on the progenies and thus selected progenies were able to withstand stress said by Troyer and Rosenbrook (1983) and Russell (1991). In addition, they suggested that selection should be conducted under higher plant densities than normal growing condition to enhance grain yields in maize. The inconclusive of selection under plant densities have been an issue of discussion (Krisda and Tanapong, 2002).

Tollenaar (1991) demonstrated that the higher tolerance of the new maize hybrids to plant density stress is associated with the general improvement in tolerance to the different stresses that contribute to uniform growth. Apparently, improving tolerance to environmental stresses constitutes a safe way to ensure tolerance to increasing plant density as well. Increased plant densities were not only indispensable for attaining maximal yields, but as pointed out by Fery and Janick (1970); they also facilitate mechanical harvest through early and concentrated yield.

Fasoula and Fasoula, 1997 concluded about the effect of competitive ability on the productivity of both the crop and the competition environments may be condensed as follows: Yield per unit area in dense stands is maximized under one condition: when the interference among the plants exclusive use of the limited resources is reduced to zero. The inverse relationship found between yields of cultivars grown in pure and mixed culture results from the negative relationship between yielding and competitive ability. This has at least four implications: (1) It prevents yield maximization in the competition environment; (2) it renders the competition environment unfit for selection; (3) it limits the use of heterozygous and heterogeneous population as potential cultivars; and (4) it establishes that evolution via interplant competition by natural selection favors competitive ability at the expense of yielding ability.

Apparently, the maximization of phenotypic differentiation through increased plant spacing in honeycomb design erases the disturbing effects of density and competition that prove to be larger than the disturbing effects of soil heterogeneity.

On the grounds that desirable selection designs are those allocating entries under comparable growing condition by effectively sampling for environment variation. Fasoula (1973 and 1993) developed the honeycomb selection designs over the last three decades. The novel designs were termed honeycomb designs because of the hexagonal arrangement of plot in the field. Plots that best fit honeycomb designs are hill plots ranging from single plots to multiple plots. Although systemic in nature, honeycomb designs accomplish effective sampling for soil heterogeneity by means of large number of moving replicates.

Fasoula (1995) wrote on his conclusion honeycomb designs by combining the advantage of systematic arrangement with the Fisherian principles of replication, randomization and local control, enhance the chances for success in plant breeding. For the honeycomb design, selection of plant and evaluation of better performance of genotype (high yield and other agronomic traits) are mostly done moving circle selection. Because this moving circles selection have some advantages. Moving circle selection applied to both unreplicated and replicated material and increases reliability as a result of at least four advantages: (1) The sum of distances separating the central plant from the others plants within the circle is minimal compared to the same number of plants in grids of other shapes. (2) Regardless of the way in which moving-circle selection is performed, either by hand or by a computer. (3) Plants are selected at all levels of soil fertility. (4) Selection pressure is adjusted by the size of the moving circle, allowing the best balance between representative sample and soil heterogeneity control.

The honeycomb breeding adopted the following principles: (1) evaluation in the absence of interplant competition; (2) enhancement of gene fixation; (3) increased sampling of selection sites to cover the target area of adaptation; (4) utilization of the honeycomb designs; (5) development of criteria that predict crop yield based on evaluation of single plants in the absence of competition; (6) adoption of non-stop selection (Fasoula and Fasoula, 1997).

MATERIALS AND METHODS

Materials

Six single cross hybrids namely: Monsanto 919, Monsanto 949, Pacific 984, Pioneer A33, Pioneer 3012 and Syngenta NK 48 and an inbred KRi 208 were chosen to start this study.

Sources of germplasms were:

Monsanto 919 released by Monsanto Company
Monsanto 949 released by Monsanto Company
Syngenta NK 48 released by Syngenta Company
Pacific 984 released by Pacific Seed Company
Pioneer A33 released by Pioneer Company
Pioneer 3012 released by Pioneer Company
Suwan 4452 released by Suwan Farm (National Corn and Sorghum Research Center, Kasetsart University, Thailand)

And inbred KRi 208 developed from Pioneer 3012/3013 by Department of Agronomy, Kasetsart University.

All experiments were conducted from September 2004 to March 2006 at National Corn and Sorghum Research Center, Suwan Farm, in Nakhon Ratchasima province ($14^0$30'N, $101^0$30'E, and 356m asl.), Thailand under standard cultural practices. Basal fertilizers were applied at planting time at the rate of 75 kg ha^{-1} of N and 100 kg ha^{-1} of P_2O_5. Top-dressing was done at the 6 to 8 leaf stages with rate of 75 kg N ha^{-1}. Pre-emergence herbicides (Atrazine and Alachlor) were used by mixing at the rate 1.5 and 1 kg a.i. per ha, respectively. Thinning was done at 14 days after sowing. Irrigation was applied when necessary.

Data observation

- Field weight: the weight of ears harvested from every plant within plot. It is measured in kilogram plot $^{-1}$.

- Grain moisture content: five random ears of each plot were shelled and bulk-sample grains were measured by using Dole moisture tester.

- Shelling ratio: five random ears of each plot were weighed and shelled. Shelling percentage was calculated with the formula:

Shelling ratio = (weight of sample grains) (weight of sample ears)$^{-1}$.

- Grain yield: grain yield was measured based upon field weight plot^{-1} (FW), grain moisture content (MC) at harvest, and shelling ratio (SR). This was calculated in ton ha^{-1} and adjusted to 15% standard moisture content with the formula:

$$\text{Grain yield} = \frac{\text{FW x (100-MC)}}{\text{100- 15}} \text{ x SR x } \frac{10{,}000}{\text{Plot size}} \text{ x } \frac{1}{1000}$$

- Length of ear: average of length of ears is measured in centimeter

- Diameter of ear: average of diameter of ears is measured in centimeter

- Row number: the total number of row per ear

- Grain types: color and type

- Days to anthesis and silking: days to anthesis defined as numbers of days from planting to 50 percent of plants in the plot is shedding of the pollens. Days to silking defined as numbers of days from planting to 50 percent of plants in the plot is displaying visible silk.

- Root lodging: root lodging was defined as the percentage of plants leaning more than 30 degrees from the vertical position in each plot. The rating score employed was 1 to 5 where 1 = very good, 5 = poor.

- Plant and ear height: plant height was measured after anthesis, from the ground level to the collar of the flag leaf. Ear height was measured from the ground level to the highest ear-bearing node of 10 competitive plants.

- Leaf disease resistance: rating resistance to Southern rust (*Puccinia polysora* Undrew), leaf blight (*Bipolaris maydis* (Nisik) Shoem), and sorghum downy mildew will be done. The rating score employed were 1 to 5 where 1 = highly resistant, 5 = highly susceptible.

- Plant uniformity: plant uniformity was defined as the percentage of irregular plant height by visual observation in each plot.

Statistical procedure

All trials statistical analysis were conducted in adjacent areas using randomized complete block design with 4 replications, 1 row-plot of 5 m long and 0.75 x 0.25 m plant spacing. Five original hybrids and Suwan 4452 were used as common checks. Pacific 984 was excluded because it was dropped out from the market and there was no seed available.

Analyses of variance were computed by using the SAS system for windows release 6.12 (copyright @ 1989-1996 SAS Institute Inc.). Means were compared using Duncan's multiple range tests.

Methods

Season one

Six single cross hybrids; Monsanto 949, Monsanto 919, Pioneer A33, Pioneer 3012, Pacific 984, and Syngenta NK48 were planted in normal spacing (0.75 x 0.25m) and selfed to obtain S_1 ears. Nine S_1 ears within each family were randomly grouped in to 3 ear sets, 3 sets per family and therefore resulted in 18 sets of 3 S_1 and 54 individual S_1 lines. The resulting 18 S_1 sets were set 1-3 (Pacific 984), set 4-6 (Monsanto 949), set 7-9 (Pioneer A33), set 10-12 (Syngenta NK 48), set 13-15 (Pioneer 3012) and set 16-18 (Monsanto 919).

Season two

Eighteen S_1 sets and 54 S_2 lines were separately ear-row in honeycomb arrangement (HC) with equilateral triangular lattice of side 0.866m (Fig. 1):

(2.1) Three best S_1 plants within each set were intercrossed plant to plant (full sibbing) to form 18 intra-set diallel crosses and will be refered to as F_1 intra-sets.

(2.2) While, three selected S_1 plants of the best line of each S_1 set by visual selection were selfed to obtain 18 S_2 lines.

Season three

Consequently, 18 F_1 intra-sets from (2.1) and 18 S_2 lines from (2.2) were ear-row in HC and then:

(3.1) Three best F_1 plants per set were selfed to obtain 18 S_1 sets for the successive cycle of F_1 intra-sets.

(3.2) The best 3 F_1 plants of each F_1 intra-set were intracrossed in all possible combinations to form 18 F_2 composite lines and they will be refered as F_2 composite sibbed lines cycle 1 (C1#).

(3.3) The best C1# by visual selection, one from each original family were inter crossed (using bulk pollens from each C1#) to form 15 inter-family diallel crosses of 6 C1#.

(3.4) Three best plants from each C1# were also testcrossed (bulk pollens) to KRi 208 to obtain 18 C1# testcrosses.

(3.5) Three best S_2 plants from (2.2) were testcrossed (bulk pollens) to KRi 208 to obtain 18 S_2 testcrosses.

(3.6) The best S_2 lines by visual selection, one from each original family were intercrossed (using bulk pollens from each line) to obtain 15 inter-family diallel crosses of 6 S_2.

(3.7) At the same time, three best S_2 plants from (2.2) were further selfed to obtain 18 S_3 lines.

Season four

(4.1) Yield trial of 18 C1# from (3.2) was planted in normal density (0.75 x 0.25m).

(4.2) Yield trial of 15 C1# inter-family diallel crosses from (3.3) was planted in normal density (0.75 x 0.25m).

(4.3) Yield trial of 18 C1# testcrosses from (3.4) was planted in normal density (0.75 x 0.25m).

(4.4) Yield trial of 18 S_2 testcrosses from (3.5) was planted in normal density (0.75 x 0.25m).

(4.5) Yield trial of 15 S_2 inter-family diallel crosses from (3.6) was planted in normal density (0.75 x 0.25m).

(4.6) Yield trial of 18 selected S_3 lines from (3.7) was planted in normal density (0.75 x 0.25m).

(4.7) Three best S_3 lines from (3.7) were selfed to obtain 18 S_4 lines.

(4.8) Repeating cycle of intra-set diallel of 18 S_1 sets for successive cycle of F_1 intra-sets.

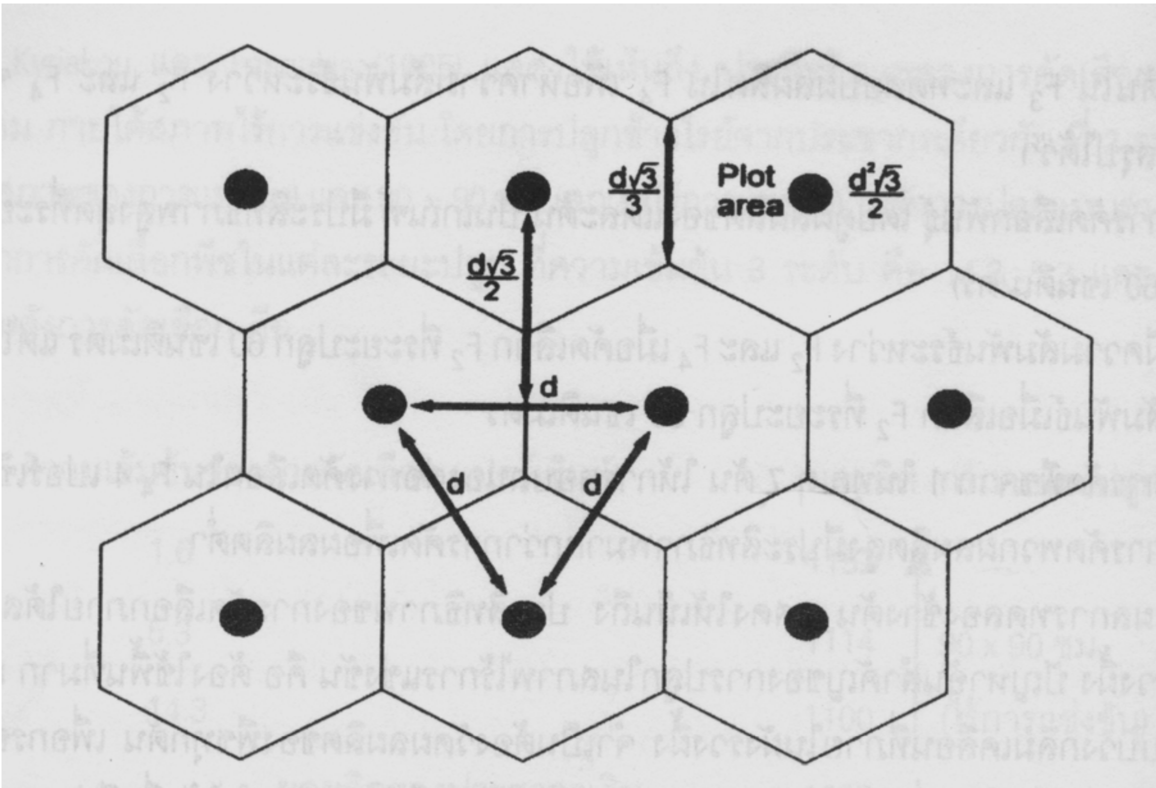

Figure 1 Honeycomb arrangement

Source: Fasoulas and Fasoula, 1995

In the figure 1, the position of hill plots is represented by the black dots. If d is the interplot distance, the distance between two rows is the height of the triangle which is equal to 0.866d. Two-thirds of the height [i.e., 0.866d x 2/3 = 0.577d] is the side of each hexagon and $0.866d^2$ is the plot area that each hexagon occupies.

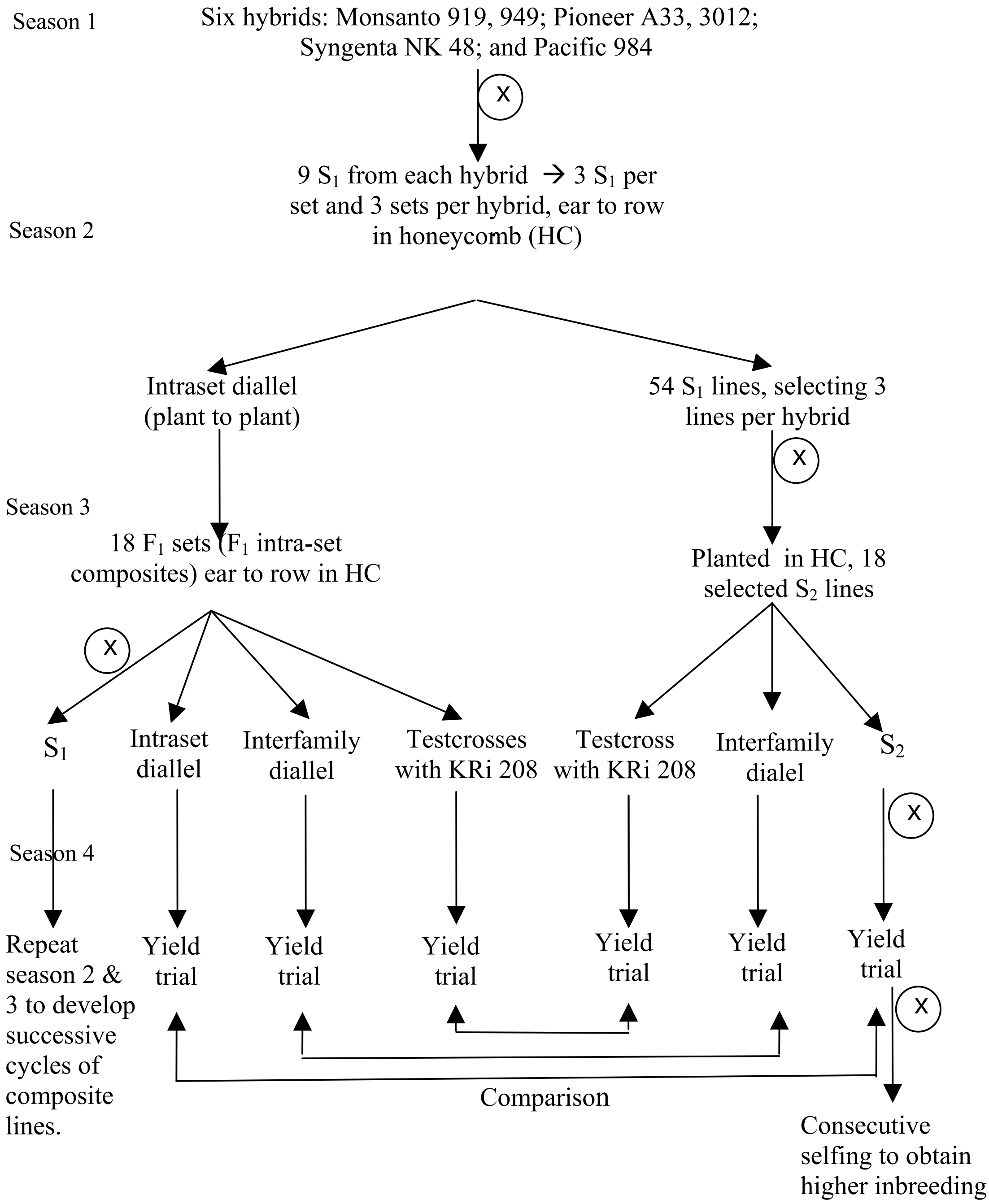

Figure 2 The breeding scheme of present study

RESULTS AND DISCUSSION

1. S_3 line yield trial

Mean grain yield and other agronomic traits of selected S_3 lines and KRi208 were presented in Table 1 and 2. The overall mean grain yield ranged from 2.00 ton ha^{-1} of line 403-6 to 4.21 ton ha^{-1} of line 401-6 while grain yield of inbred, KRi 208 was 3.01 ton ha^{-1}. However, the KRi 208 had higher level of homozygosity by line selection over 15 cycles. Among the top 10 S_3 lines, there were 9 selected S_3 lines gave higher yield than inbred KRi 208 but statistically only line 401-6 showed significant difference over it. Another line 406-3 (Pio.3012) gave yield lower than inbred KRi 208. Among the top 10 selected S_3 lines, there were three lines from Monsanto 949; other three lines from Pacific 984; Pioneer A33, Monsanto 919, Syngenta NK 48 and Pioneer 3012 had one line each.

Most of selected lines from each source were varied considerably on their yielding ability. However, lines from Monsanto 949 and Pacific 984 gave relatively high yield than lines from other sources (Table 1).

Agronomic traits, days to anthesis and silking of selected S_3 lines and the inbred KRi 208 were 2 days more or less different compared to overall all mean. Although significant difference in statistics was observed, it should has no impact on practical point of view. Moisture content at harvest time ranged from 19.8% of line 403-6 (mon.919) to 25.6% of line 402-6 (Mon.949), while 25.5% was observed for inbred KRi 208. In the top 10 yielded S_3 lines, statistics showed non-significant difference of moisture content compared to inbred check (except line 403-5) but the top line, 401-6 (Pacific 984) had fairy low moisture content of only 21.9%.

Uniformity of each composite and S_2 lines was varied considerably. Naturally, their uniformity should be improved in the successive selection cycles especially if selection pressure for uniformity was applied. However, most of them showed desirable grain type, root lodging and disease resistance (Table 2). Besides, there was no clear evident for advantage or disadvantage of other agronomic traits among selected lines but line 403-5 demonstrated a superior shelling percentage over other lines.

Table 1 Grain yields at 15 percent moisture and other agronomic traits of S_3 lines and KRi 208 conducted at Suwan Farm, Thailand in November, 2005 (dry season).

S_3 lines	Source of germplasms	Grain Yield (ton/ha)	Days to Anthesis (days)	Days to Silking (days)	Moisture Content (%)	Plant Height (cm)	Ear Height (cm)	Shelling (%)
401-6	Pacific 984	4.21 a	68.7 a-d	69.0 bcd	21.9 a-d	131.5	54.2 bc	76.6 a-d
402-6	Mon.949	3.77 ab	68.3 a-e	67.3 edf	25.6 a	140.2	60.3 abc	73.6 bcd
404-4	Pio.A33	3.71 ab	67.7 b-f	67.3 edf	23.7 abc	140.3	63.5 abc	73.9 bcd
402-8	Mon.949	3.63 ab	66.7 ef	67.0 ef	24.9 ab	134.3	60.7 abc	75.6 bcd
401-9	Pacific 984	3.40 ab	70.0 a	68.8 b-e	23.4 a-d	131.3	54.3 bc	79.1 ab
402-7	Mon.949	3.38 ab	66.3 f	66.3 f	23.9 abc	138.0	52.3 c	75.7 bcd
405-4	Syn. NK48	3.36 ab	67.0 def	67.7 c-f	22.8 a-d	134.7	60.5 abc	71.8 cd
403-5	Mon.919	3.21 abc	68.0 b-f	68.0 b-f	20.2 cd	126.0	52.3 c	82.2 a
401-7	Pacific 984	3.08 a-d	70.0 a	69.0 bcd	22.0 a-d	131.5	58.7 abc	78.0 ab
406-3	Pio.3012	2.89 b-d	70.0 a	68.8 b-e	24.5 ab	151.5	68.2 ab	74.6 bcd
404-2	Pio.A33	2.87 b-d	67.3 c-f	67.7 c-f	20.2 cd	138.8	65.0 abc	78.7 ab
406-1	Pio.3012	2.82 b-d	67.3 c-f	69.3 bc	24.4 ab	143.3	61.8 abc	77.8 ab
403-4	Mon.919	2.80 b-d	68.7 a-d	68.3 b-e	21.1 b-d	131.8	61.5 abc	76.1 bcd
404-6	Pio.A33	2.16 cd	68.0 b-f	68.0 b-f	24.1 ab	137.0	61.5 abc	73.2 bcd
406-2	Pio.3012	2.05 d	69.3 ab	71.0 a	23.5 a-d	150.8	70.5 a	70.8 d
405-6	Syn. NK48	2.02 d	69.3 ab	69.3 bc	23.3 a-d	143.5	51.0 c	71.8 cd
403-6	Mon.919	2.00 d	68.0 b-f	68.3 b-e	19.8 d	121.7	37.5 d	76.9 abc
KRi 208	Pio.3012/3013	3.01 bcd	69.0 abc	69.7 ab	25.5 a	120.3	50.2 c	73.5 bcd
	Mean	3.02	68.31	68.37	23.04	135.9	58.0	75.54
	F-value	**	**	**	**	ns	**	**
	CV(%)	19.57	1.34	1.35	8.49	10.56	13.46	3.97

- ns: non significant, * : significant, ** : highly significant
- Means within a column followed by the same letter are not significantly different at $P \leq 0.05$ according to Duncan's multiple range tests.

Table 2 Agronomic traits of S_3 lines and KRi 208 conducted at Suwan Farm, Thailand in November, 2005 (dry season).

S_3 lines	Source of germplasms	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Disease resistance (1-5)[1/]	Root lodging (1-5)[1/]	Plant uniform (%)	Grain type
401-6	Pacific 984	14.5 ab	3.5 bc	12.7	1	1	>95	OY-F
402-6	Mon.949	14.1 a-d	3.8 ab	13.7	1	1	90	OY^SF
404-4	Pio.A33	14.3 abc	3.9 a	14.9	1	1	95	OY^SD
402-8	Mon.949	12.9 b-e	3.6 abc	13.7	1	1	90	OY^F
401-9	Pacific 984	13.8 a-e	3.5 bc	14.7	1.5	1	80	OY^F
402-7	Mon.949	14.2 a-d	3.6 abc	13.9	1	1	90	O^F
405-4	Syn. NK48	15.0 a	3.9 a	13.2	1	1	>95	OY^F
403-5	Mon.919	12.5 ef	3.0 e	13.1	1	1	>95	O^F
401-7	Pacific 984	14.0 a-e	3.5 bc	13.6	1	1	90	O^F
406-3	Pio.3012	13.9 a-e	3.8 ab	13.6	1	1	>95	OY^SF
404-2	Pio.A33	12.8 b-e	3.7 abc	13.5	1	1	>95	Y^SD
406-1	Pio.3012	12.7 de	3.4 cd	12.7	1	1	>95	O^SF
403-4	Mon.919	13.6 a-e	3.4 cd	13.2	1	1	>95	OY^F
404-6	Pio.A33	11.1 g	3.8 ab	13.5	1	1	95	Y^SD
406-2	Pio.3012	12.9 b-e	3.4 cd	14.1	1	1	>95	O^F
405-6	Syn. NK48	12.7 de	3.8 ab	12.5	1	1	85	O^SF
403-6	Mon.919	12.5 ef	3.1 de	11.7	1	1	>95	OY^SF
KRi 208	Pio.3012/3013	13.1 b-e	3.6 abc	13.1	1	1	>95	O^F
	Mean	13.4	3.6	13.4	-	-	-	-
	F-value	**	**	ns	-	-	-	-
	CV(%)	6.07	4.93	8.37	-	-	-	-

[1/] 1 = good, 5 = bad.

- ns: non significant, * : significant, ** : highly significant
- O: orange, Y : yellow, F : flint, D : dent, S ; semi

2. F_2 Composite sibbed line of cycle 1 (C1#) yield trail

Mean grain yield and other agronomic traits of 16 C1# are presented in Table 3 and 4. Set 6 (Mon.949) and set 9 (Pio.A33) were deleted because of poor seed set of female lines. Significant mean grain yield between lines were observed and ranged from 3.60 ton ha^{-1} of set 15 (Pio.3012) to 6.13 ton ha^{-1} of set 4 (Mon.949). The top-6 C1# gave higher yield than the overall mean but only set 4 (Mon.949) gave an outstanding yield over other sets.

Among the top-10 C1#, two of each were from Mon.949 (set 4 and 5), Syn. NK48 (set 10 and 11), Pac.984 (set 2 and 3) and Pio.A33 (set 7 and 8), while Mon.919 (set 18) and Pio.3012 (set 14) contributed one of each. In general, C1# of Monsanto gave higher vigor in yielding ability following by Syngenta, Pacific and Pioneer, respectively.

For agronomic traits, the range between days to anthesis and silking of each C1# were from 0 to less than 2 days except C1#-set 18 (Mon.919) which gave wider range of 3 days. Moisture content and shelling percentage have an effect on grain yield. This yield trial gave moisture content ranged from 20.6 % of set 12 (Syn. NK48) to 25.6 % of set 5 (Mon.949). In the top-10, C1#-set 18 gave lowest moisture content, while set 5 and set 4 were the highest, respectively. About shelling percentage, there were three sets: set 8, set 14 and set 18 gave shelling percentage over 80 %. Besides, all C1# were relatively uniform in plant height as well as other agronomic characters. Generally, set 18 not only gave high yield (5.26 ton ha^{-1}) but also showed outstanding features of earliness, low moisture content and high shelling percentage but rather poor in synchronization of male and female flowers.

In comparison S_3 with C1# lines, the C1# lines were consistently superior in the characteristics used as measures of vigor; grain yield, earliness of anthesis and silking, plant and ear height. They were earlier, taller and higher yield regardless of germplasm sources. Moreover, better distribution of germplasm sources of top-10 C1# was evident. All six germplasm sources presented in the top-10 C1# while in the top-10 S_3 lines leaned toward Monsanto 949 and Pacific 984. The results indicated that C1# was more stable by outcrossing. On the other hand, inbred lines of each germplasm source should had different level of inbreeding depression and thus selection for performance per se by visual selection was biased toward the less inbreeding depression germplasm. In this case, Pioneer 3012 was lost from the top-10 S_3 lines.

The present results were well agreed with report presented by Kinman (1952) of which selective mass sibbing within individual S_1 progenies was used. In Kinman's words, the population is closed at the time of first sibbing, it should not be expected that improvement in the combining ability or other characteristics of composite-sibbed lines will be made even after several generations of mass sibbing unless effective selection is practiced. Unlike Kinman's method, the modified S_1-full sib selection within three sister line composite employed in the present study provided a more flexible approach. Selection for S_1 performance per se alternate with diallel crossed of individual of 3 selected S_1 lines (full sibbing) should improve general combining ability (GCA) as well as specific combining ability (SCA) of S_1 lines from successive cycles. In the meantime, the new emerged S_1 sets as well as F_1 sets of each cycle can be fixed by mass sibbing method and used in early generation hybrid combinations while the successive cycles will move slowly toward higher level of homozygosity and hence more uniform, high yield lines and hybrids in later stage.

Table 3 Grain yields at 15 percent moisture and other agronomic traits of composite sibbed lines of cycle 1 conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Composite lines	Source of germplasms	Grain Yield (ton/ha)	Days to Anthesis (days)	Days to Silking (days)	Moisture Content (%)	Plant Height (cm)	Ear Height (cm)	Shelling (%)
Set 4	Mon.949	6.13 a	67.3 abc	67.3 bc	25.5 a	168.7	82	77.2
Set 5	Mon.949	5.53 ab	65.0 d	67.0 bc	25.6 a	165.6	71.2	79.2
Set 18	Mon.919	5.26 abc	63.0 e	66.0 c	21.4 cd	157.4	63.9	80.8
Set 10	Syn. NK48	4.91 bc	66.0 cd	66.7 bc	21.9 bcd	173.3	80.3	79.6
Set 11	Syn. NK48	4.87 bcd	66.0 cd	67.0 bc	22.9 bcd	161.2	67.7	72.9
Set 2	Pacific 984	4.81 bcd	68.3 ab	67.7 bc	23.8 abc	171.8	75.2	79.4
Set 8	Pio.A33	4.66 bcd	66.7 a-d	67.0 bc	22.8 bcd	165.8	80.8	80.2
Set 14	Pio.3012	4.64 bcd	68.0 abc	67.7 bc	22.0 bcd	158.1	69.2	80.2
Set 3	Pacific 984	4.63 bcd	68.7 a	68.3 ab	23.8 abc	159.3	65.5	79.7
Set 7	Pio.A33	4.58 bcd	66.3 bcd	67.0 bc	22.6 bcd	150.3	67.7	79.5
Set 17	Mon.919	4.48 bcd	66.3 bcd	66.7 bc	21.7 bcd	158.8	63.7	79.4
Set 12	Syn. NK48	4.46 bcd	67.3 abc	66.7 bc	20.6 d	157.2	66.8	77.6
Set 1	Pacific 984	4.09 cd	68.7 a	68.7 ab	22.4 bcd	163.2	69.5	80.0
Set 16	Mon.919	4.09 cd	67.7 abc	66.7 bc	22.2 bcd	165.2	73.5	77.4
Set 13	Pio.3012	3.97 cd	68.7 a	70 a	24.1 ab	164.7	77.7	78.2
Set 15	Pio.3012	3.60 d	68.0 abc	67.7 bc	21.3 cd	158.3	71.3	79.4
	Mean	4.69	67	67.4	22.8	162.4	71.6	78.8
	F-value	*	**	*	**	ns	ns	ns
	CV(%)	14.08	1.73	1.58	5.82	7.11	15.45	3.29

- ns: non-significant, * : significant, ** : highly significant
- Means within a column followed by the same letter are not significantly different at P≤0.05 according to Duncan's multiple range tests.

Table 4 Agronomic traits of composite sibbed lines of cycle 1 conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Composi_te lines	Source of germplasms	Ear length (cm)	Ear diameter (cm)	Number of rows per ear (row)	Disease resistance (1-5)[1/]	Root lodging (1-5)	Plant uniform (%)	Grain type
set 4	Mon.949	15.1 b-e	4.1 ab	15.5 a	1	1	>95	OY^F
set 5	Mon.949	14.8 cde	4.0 abc	15.5 a	1	1	95	OY^SF
set 18	Mon.919	18.0 a	3.9 abc	14.8 abc	1	1	>95	OY^SF
set 10	Syn. NK48	15.5 bcd	4.1 ab	13.1fg	1	1	>95	OY^SF
set 11	Syn. NK48	13.4 e	4.0 abc	13.3 efg	1	1	>95	OY^F
set 2	Pacific 984	18.0 a	4.1 ab	13.9 c-f	1	1	>95	OY^F
set 8	Pio.A33	14.3 de	4.3 a	15.1 ab	1	1	95	Y^SF
set 14	Pio.3012	14.5 cde	3.6 c	14.3 b-e	1.5	1	90	OY^F
set 3	Pacific 984	17.1 ab	4.0 abc	13.9 c-f	1	1	90	OY^F
set 7	Pio.A33	16.0 bcd	4.2 ab	14.7 a-d	1.5	1	90	Y^SF
set 17	Mon.919	16.7 abc	3.8 bc	13.3 efg	1	1	>95	Y^SF
set 12	Syn. NK48	14.1 de	3.9 abc	13.6 ef	1	1	95	OY^F
set 1	Pacific 984	14.3 de	3.8 bc	13.7 edf	1	1	>95	OY^F
set 16	Mon.919	14.1 de	3.8 bc	12.5 g	1	1	>95	Y^SF
set 13	Pio.3012	16.6 abc	3.6 c	14.3 b-e	1.5	1	95	OY^SF
set 15	Pio.3012	15.3 b-e	3.7 bc	14.7 a-d	2	1	90	OY^F
	Mean	15.5	3.9	14.1	-	-	-	-
	F-value	**	*	**	-	-	-	-
	CV(%)	6.83	5.84	3.83	-	-	-	-

[1/] 1 = good, 5 = bad.

- ns: non-significant, * : significant, ** : highly significant
- O: orange, Y : yellow, F : flint, D : dent, S ; semi

3. S_2 testcross (S_2 x KRi 208) yield trial

Testcross evaluation has been used to determine the relative potential of corn (*Zea mays* L.) lines in hybrid breeding programs. Choice of tester is important for efficient selection among lines for their potential hybrids. Castellanos *et al.* (1998) showed that different testers identified inbred lines differently. The results reconfirmed the finding of Matzinger (1953); Hallauer and Miranda (1988). They concluded that the best tester should be inbred line or single cross if the ultimate breeding goal is single or three-way crosses, respectively.

In present study, high yield inbred, KRi 208 was used as tester to evaluate combining ability of the 18 S_2 inbred lines. Means and ranges of grain yield and agronomic traits of testcrosses between S_2 lines x KRi 208 are presented in Table 5 and 6. The average yield of S_2 testcrosses from different germplasms was statistically different and ranged from 4.73 to 8.96 ton ha^{-1}, while yield of common checks ranged from 7.32 (Monsanto 919) to 8.47 ton ha^{-1} (Pioneer A33). The results of testcrosses between S_2 lines x KRi 208 demonstrated that lines from Pioneer germplasm gave relatively poor performance. In the top-10 testcrosses, three were from Syngenta NK48 ranged from 8.08 to 8.82 ton ha^{-1}; two from Monsanto 949 and Monsanto 919 ranged from 8.00 to 8.40 ton ha^{-1}, respectively; and one each from Pacific 984, Pioneer A33 and Pioneer 3012 at 7.70, 7.89 and 8.07 ton ha^{-1}, respectively. Statistically, yield of top-10 S_2 testcrosses were not different from the checks but the top 2 gave outstanding yield over the best check.

Lamkey and Hallauer (1986) founded that inbred line performance per se can be used as criterion to differentiate combining ability between high and low yield inbreds. However, yield per se within high or low yielding groups can not be used to predict line performance in hybrid combinations. Yielding ability of line per se in Table 1 and their testcross performance in Table 5 clearly supported the above finding.

Since all 18 inbred lines came from the top-3 high yield lines of each check hybrid therefore they should be considered as high yield lines. However, their yielding ability did not represent the combining ability of lines in the testcross combinations with the inbred tester (KRi 208), line 403-4 which was excluded from the top-10 lines gave the highest yield in the testcrosses while the top line, 401-6 ranked 9^{th} in testcrosses. Besides, only two Pioneer lines, 406-1 and 404-4 were presented in the top-10 testcrosses. This is not unexpected because the tester line, KRi 208 derived from Pioneer 3012/ Pioneer 3013. Therefore, genetic background of tester played an important role in the combination with tested lines. However, 406-1/KRi 208 is essentially a backcross to sister line and ranked 6^{th} in the top-10 testcrosses indicated a strong additive effect in this hybrid combination. Since different testers gave different performance with the same group of lines (Castellanos *et al*., 1998), all high yield lines should be tested their hybrid combinations directly to their counterpart parental lines to identify the best hybrid combination.

Statistically, all top-10 testcrosses yielded as high as the top-4 checks but somewhat better than the Monsanto 949 and Monsanto 919. However, 403-4/KRi 208 gave an outstanding feature of yield and earliness even though it was taller and lower in shelling percentage than the average.

Agronomic traits of testcrosses between S_2 lines x KRi 208 are presented in Table 5 and 6. The results showed that overall average of days to anthesis and silking as well as plant height were earlier than overall average of check hybrids. Besides, the distance between days to anthesis and silking was narrower as compare to common checks. Considering the percent of grain moisture of inbreds in Table 1 and that of S_2 testcrosses in Table 5, percent of grain moisture of the later ones leaned toward early lines. Since the tester KRi 208 had grain moisture content 25.5% and moisture percentage of S_2 testcrosses were somewhat the same as S_2 lines. For other agronomic traits, all testcrosses and checks performed no clear evident for advantage or disadvantage and all of them resisted to leaf disease, root lodging, and performed high uniformity and good gain types.

Table 5 Grain yields at 15 percent moisture and other agronomic traits of testcrosses (selected S_2 x KRi 208) and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Lines X KRi208[1/]	Source of germplasms	Grain Yield (ton/ha)	Days to Anthesis (days)	Days to Silking (days)	Moisture Content (%)	Plant Height (cm)	Ear Height (cm)	Shelling (%)
403-4	Mon.919	8.96 a	61.3 h	61.7 j	22.6 def	165.8 b-f	81.7 a-f	75.9 h-k
405-5	Syn. NK48	8.82 ab	62.3 e-h	64.0 d-i	23.0 c-f	153.3 fgh	70.3 fg	77.1 f-i
402-6	Mon.949	8.40 a-d	62.0 fgh	62.7 hij	24.9 abc	161.0 d-h	80.3 a-f	75.3 k
405-4	Syn. NK48	8.14 a-e	61.7 gh	62.3 hij	23.2 c-f	158.0 d-h	79.0 b-g	77.5 efg
405-6	Syn. NK48	8.08 a-f	63.3 b-g	64.3 b-g	24.3 bcd	157.6 d-h	82.7 a-f	75.6 ijk
406-1	Pio.3012	8.07 a-f	63.0 c-h	63.7 e-i	24.1 bcd	164.2 b-f	81.7 a-f	78.3 def
402-7	Mon.949	8.00 a-f	61.3 h	62.0 ij	24.0 bcd	150.0 gh	73.7 d-g	77.0 f-i
404-4	Pio.A33	7.89 a-f	65.0 ab	65.3 c-f	23.6 b-f	159.8 d-h	76.8 b-g	75.4 jk
401-6	Pac.984	7.70 a-g	62.7 e-h	63.3 f-j	23.4 c-f	156.3 e-h	72.7 d-g	79.5 cd
403-5	Mon.919	7.66 a-g	62.0 fgh	62.7 hij	21.9 ef	162.1 c-h	89.8 a-g	81.1 bc
401-7	Pac.984	7.48 b-g	64.7 bc	66.7 abc	23.2 c-f	163.0 c-g	82.0 a-f	78.9 cde
403-6	Mon.919	7.48 b-g	61.7 gh	63.0 g-j	22.4 def	158.3 d-h	76.0 c-g	76.9 f-j
401-9	Pac.984	7.39 c-g	63.7 b-f	65.0 c-g	23.6 b-f	160.7 d-h	72.0 efg	81.2 b
402-8	Mon.949	7.02 d-g	62.0 f-h	62.3 hij	23.8 b-e	148.4 h	68.2 g	77.7 efg
404-6	Pio.A33	6.99 efg	64.0 b-e	65.0 c-g	25.5 ab	156.4 e-h	74.7 d-g	76.9 f-h
404-2	Pio.A33	6.76 fg	63.0 c-h	63.0 g-j	24.3 bcd	153.7 fgh	78.3 b-g	77.7 efg
406-3	Pio.3012	6.33 g	65.0 ab	65.7 cde	21.7 f	158.1 d-h	77.9 b-g	78.9 cde
406-2	Pio.3012	4.73 h	64.3 bcd	65.3 c-h	24.2 bcd	169.1 a-e	84.9 a-d	78.1 def
Check	Pio.A33	8.47 abc	64.7 bc	66.0 bcd	21.9 ef	182.0 a	91.9 a	79.8 bc
Check	SW 4452	8.24 a-e	66.7 a	68.7 a	25.0 abc	177.3 ab	84.2 a-e	76.3 g-k
Check	Pio.3012	8.08 a-f	66.7 a	68.0 ab	22.4 def	165.2 b-f	89.1 ab	77.2 fgh
Check	Syn. NK48	7.86 a-f	64.0 b-e	66.0 bcd	22.7 def	171.3 a-d	74.4 dfg	77.9 ef
check	Mon.949	7.57 b-g	62.7 e-h	64.3 d-g	26.7 a	178.3 ab	81.6 a-f	77.9 ef
Check	Mon.919	7.32 c-g	63.3 b-g	65.0 c-g	23.9 b-e	176.1 abc	88.1 abc	82.9 a
	Mean of testcrosses	7.55	62.9	63.8	23.5	158.7	81.9	77.7
	Mean of check hybrids	7.93	64.7	66.3	23.8	175.0	84.9	78.7
	F-value	**	**	**	**	ns	*	**
	CV(%)	11.01	1.84	1.99	5.19	5.29	9.69	1.18

- ns: non-significant, * : significant, ** : highly significant

[1/] Pedigree of KRi 208 is Pio.3012/ Pio.3013

Table 6 Agronomic traits of testcrosses (selected S_2 x KRi 208) and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Lines x KRi 208	Source of germplasms	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Disease resistance (1-5)[1/]	Root lodging (1-5)[1/]	Plant uniform (%)	Grain type
403-4	Mon.919	18.3 abc	4.4 b-f	14.8 gh	1	1	90	OY^SF
405-5	Syn. NK48	18.5 ab	4.7 a-d	15.9 c-g	1	1	>95	OY^SF
402-6	Mon.949	17.5 b-g	4.7 a-d	18.0 a	1	1	>95	OY^SF
405-4	Syn. NK48	17.1 c-h	4.7 a-d	15.9 c-g	1	1	>95	OY^SF
405-6	Syn. NK48	17.5 b-g	4.6 a-f	16.1 b-e	1	1	>95	O^F
406-1	Pio.3012	17.5 b-g	4.3 edf	15.2 e-h	1	1	>95	O^F
402-7	Mon.949	18.2 a-d	4.8 ab	17.1 ab	1	1	>95	OY^SF
404-4	Pio.A33	18.1 a-e	4.8 ab	15.3 d-h	1.5	1	>95	OY^F
401-6	Pac.984	17.5 b-g	4.6 a-f	14.4 hi	1	1	>95	OY^F
403-5	Mon.919	17.7 a-g	4.4 c-f	15.6 c-g	1	1	>95	O^F
401-7	Pac.984	18.3 abc	4.5 a-f	15.5 d-h	1	1	>95	O^F
403-6	Mon.919	17.7 a-g	4.7 a-d	16.3 b-e	1	1	>95	OY^SF
401-9	Pac.984	18.3 abc	4.4 b-f	14.9 fgh	1	1	>95	OY^F
402-8	Mon.949	16.5 gh	4.4 b-f	17.1 ab	1	1	>95	OY^F
404-6	Pio.A33	16.9 d-h	4.6 a-f	15.9 c-g	1.5	1	>95	O^F
404-2	Pio.A33	16.9 d-h	4.8 ab	15.3 d-h	2	1	95	OY^SF
406-3	Pio.3012	18.0 a-f	4.3 ef	16.0 b-f	1.5	1	90	OY^SF
406-2	Pio.3012	16.7 fgh	4.3 ef	15.9 c-g	2	1	90	O^F
Check	Pio.A33	17.5 b-g	4.8 ab	15.9 c-g	1	1	>95	OY^SD
Check	SW 4452	18.9 a	4.9 a	16.4 bcd	1	1	>95	OY^F
Check	Syn. NK48	16.8 e-h	4.3 ef	13.5 i	1	1	>95	O^F
Check	Pio.3012	16.1 h	4.5 a-f	16.1 b-e	1	1	>95	OY^F
Check	Mon.949	17.7 a-g	4.5 a-f	16.7 bc	1	1	>95	OY^SF
Check	Mon.919	17.2 c-h	3.8 g	13.3 i	1	1	>95	OY^F
	Mean of testcrosses	17.6	4.6	15.8	-	-	-	-
	Mean of check hybrids	17.4	4.5	15.3	-	-	-	-
	F-value	*	**	**	-	-	-	-
	CV(%)	4.57	5.82	4.43	-	-	-	-

- ns: non-significant, * : significant, ** : highly significant
- [1/] 1 = good, 5 = bad.; O : orange, Y : yellow, F : flint, D : dent, S : semi

4. C1# testcross (C1# x KRi 208) yield trial

Means and ranges of grain yield of testcrosses between C1# x KRi 208 are presented in Table 7. The average yield of C1# testcrosses from different germplasm sources was statistically different and ranged from 6.01 (set 13) to 8.74 ton ha^{-1} (set 4), while the common checks ranged from 7.32 (Monsanto 919) to 8.47 ton ha^{-1} (Pioneer A33). The top-10 C1# testcrosses were three of each from Monsanto 919 and Syngenta NK48, two from Monsanto 949, and one of each from Pacific 984 and Pioneer 3012, while most C1# from Pioneer were excluded from the top-10 except set 15 (Pio.3012). The results were more or less the same as results of S_2 testcrosses.

Although yield of testcrosses from set 4 and set 5 of Monsanto 949 were not significantly different from corresponding check hybrids, but set 4 gave outstanding feature for yielding ability as well as highly uniform and early hybrid. Other C1# testcrosses tended to give lower yield than their corresponding check hybrids. However, all C1# were very heterogeneous and still have chance to be improved for their specific combining ability.

The numbers of lines from each source of germplasm involved in top-10 S_2 and C1# testcrosses in Table 5 and 7 respectively were almost the same; 4:5 (Monsanto), 3:3 (Syngenta), 2:1 (Pioneer) and 1:1 (Pacific) indicated that they responded similarity to the same tester. This because each S_2 line derived from its corresponding composite sets. Although, average yield of S_2 testcrosses was higher than that of C1# testcrosses but top testcross yields of both groups as well as the best check were more or less the same. Obviously, selection for single plant performance per se from heterogeneous lines under low-competition environment is very effective to identify high yield and high combining ability line when crossed to the same tester.

Agronomic traits are presented in Table 7 and 8. All agronomic traits of C1# testcrosses and common checks were significant difference except ear height. The overall average of plant height of C1# x KRi 208 was shorter than common checks. The result was the same with those in testcrosses of S_2 lines x KRi 208. Studies in other traits showed that the overall average between C1# testcrosses and common checks were almost the same. All of them resisted to root lodging, leaf diseases except testcrosses of set 10 x KRi 208 and set 2 x KRi 208 because these hybrids were infected by leaf blight disease.

All C1# testcrosses had narrow gap between days to anthesis and silking, less than two days difference. Grain moisture content leaned toward the earliness of C1# lines (Table 3 and Table 7).

Table 7 Grain yields at 15 percent moisture and other agronomic traits of testcrosses (C1# x KRi 208) and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Set numbers	Source of germplasms	Grain Yield (ton/ha)	Days to Anthesis (days)	Days to Silking (days)	Moisture Content (%)	Plant Height (cm)	Ear Height (cm)	Shelling (%)
set 4	Mon.949	8.74 a	62.7 fg	63.3 ghi	24.9 abc	172.5 a-d	84.4	76.1 def
set 3	Pac.984	8.31 abc	65.7 a-d	67.0 a-d	23.8 b-g	165.5 c-g	84.9	78.9 bc
set 11	Syn. NK48	7.80 a-d	64.0 c-f	65.0 d-h	22.9 b-h	163.9 d-g	78.5	74.6 fg
set 5	Mon.949	7.65 a-d	61.7 g	62.7 i	23.8 b-g	168.8 b-g	80.5	76.5 c-f
set 12	Syn. NK48	7.44 b-d	63.3 efg	64.7 e-h	22.9 b-g	160.7 efg	77.2	76.3 def
set 17	Mon.919	7.37 b-f	63.0 efg	65.0 d-h	21.1 h	161.9 d-g	81.9	76.2 def
set 10	Syn. NK48	7.34 b-f	62.7 fg	63.0 hi	22.2 fgh	160.5 fg	81.2	77.1 cde
set 15	Pio.3012	7.24 c-g	66.0 abc	67.0 a-d	24.0 b-g	159.9 g	82.3	77.2 cde
set 16	Mon.919	7.20 c-g	63.3 efg	64.7 e-h	21.7 gh	161.9 d-g	83.7	75.3 efg
set 18	Mon.919	7.20 c-g	63.7 efg	65.3 c-g	23.9 b-g	169.3 b-g	85.4	77.3 cde
set 1	Pac.984	7.15 c-g	67.0 a	68.7 a	22.6 d-g	171.0 b-f	82.5	77.5 b-e
set 2	Pac.984	6.89 d-g	67.0 a	68.0 ab	24.4 b-f	170.7 b-f	79.9	77.3 cde
set 8	Pio.A33	6.29 efg	65.7 a-d	65.3 c-g	23.8 b-g	158.9 g	82.2	78.6 bc
set 14	Pio.3012	6.25 efg	66.3 ab	67.3 abc	24.6 a-f	163.7 d-g	82.9	76.9 c-f
set 7	Pio.A33	6.15 fg	65.7 a-d	66.7 a-d	23.0 b-h	162.5 d-g	82.7	73.2 g
set 13	Pio.3012	6.01 g	65.7 a-d	67.0 a-d	24.7 a-d	163.9 d-g	84.6	75.1 efg
Check	Pio.A33	8.47 ab	64.7 b-f	66.0 b-f	21.9 gh	182.0 a	91.9	79.8 b
Check	SW 4452	8.26 abc	66.7 ab	68.7 a	25.0 ab	177.3 ab	84.2	76.3 def
Check	Pio.3012	8.08 a-d	66.7 ab	68.0 ab	22.4 e-g	165.2 d-g	89.1	77.2 cde
Check	Syn. NK48	7.86 a-d	64.0 c-f	66.0 b-f	22.7 c-g	171.3 a-e	74.4	77.9 bcd
Check	Mon.949	7.57 a-d	62.7 fg	64.3 ghi	26.7 a	178.3 ab	81.6	77.9 bcd
Check	Mon.919	7.32 b-f	63.3 efg	65.0 d-h	23.9 b-g	176.1 abc	88.1	82.9 a
	Mean of testcrosses	7.19	64.5	65.7	23.4	164.7	82.2	76.7
	Mean of check hybrids	7.93	64.7	66.3	23.8	175.0	84.9	78.7
	F-value	**	**	**	**	**	ns	**
	CV(%)	10.18	1.92	1.92	5.96	3.87	7.46	1.93

- ns: non significant, * : significant, ** : highly significant
- C1# is composite sibbed line of cycle 1

Table 8 Agronomic traits of testcrosses (C1# x KRi 208) and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Set numbers	Source of germplasms	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Disease resistance (1-5)[1/]	Root lodging (1-5)	Plant uniform (%)	Grain type
set 4	Mon.949	18.0 a-d	4.8 abc	16.8 ab	1	1	>95	O^F
set 3	Pac.984	18.0 a-d	4.9 a	16.0 b-e	1	1	95	OY^F
set 11	Syn. NK48	18.2 ab	4.8 abc	15.6 cde	1	1	95	O^F
set 5	Mon.949	17.4 b-f	4.9 a	17.3 a	1	1	>95	O^F
set 12	Syn. NK48	17.0 fgh	4.8 abc	15.7 a-d	1	1	>95	O^F
set 17	Mon.919	18.1 abc	4.5 a-f	16.3 a-d	1	1	>95	O^F
set 10	Syn. NK48	17.3 b-f	4.6 a-e	15.7 a-d	2	1	>95	O^SF
set 15	Pio.3012	17.3 b-f	4.5 a-f	15.7 a-d	1	1	>95	O^F
set 16	Mon.919	17.7 b-f	4.3 ef	15.1 e	1	1	>95	O^F
set 18	Mon.919	15.5 b-f	4.1 fg	15.7 a-d	1	1	>95	O^F
set 1	Pac.984	17.6 b-f	4.8 abc	15.2 de	1.5	1	>95	OY^F
set 2	Pac.984	18.0 a-d	4.6 a-e	15.1 e	2	1	90	O^F
set 8	Pio.A33	16.3 gh	4.7 a-d	16.7 abc	1	1	90	OY^F
set 14	Pio.3012	17.2 d-g	4.3 def	15.7 a-d	1	1	>95	O^F
set 7	Pio.A33	17.0 e-h	4.5 a-f	16.1 b-e	1	1	90	OY^F
set 13	Pio.3012	18.8 a	4.4 c-f	16.0 b-e	1	1	>95	O^F
Check	Pio.A33	17.5 b-f	4.8 abc	15.9 a-e	1	1	>95	OY^SD
check	SW 4452	18.8 a	4.9 a	16.4 abc	1	1	>95	OY^F
Check	Pio.3012	16.1 h	4.5 a-f	16.1 b-e	1	1	>95	OY^F
Check	Syn. NK48	16.8 fgh	4.3 ef	13.5 f	1	1	>95	O^F
Check	Mon.949	17.7 b-f	4.5 a-f	16.7 abc	1	1	>95	OY^SF
Check	Mon.919	17.2 b-g	3.8 g	13.3 f	1	1	>95	OY^F
	Mean of testcrosses	17.6	4.6	15.9	-	-	-	-
	Mean of check hybrids	17.4	4.5	15.3	-	-	-	-
	F-value	**	**	**	-	-	-	-
	CV(%)	3.24	5.92	4.39	-	-	-	-

- [1/] 1 = good, 5 = bad.
- ns: non-significant, * : significant, ** : highly significant
- O : orange, Y : yellow, F : flint, D : dent, S ; semi
- C1# is composite sibbed line of cycle 1

5. S_2 inter-family cross yield trail

Since different testers gave different performances with the same group of lines. Therefore, six best S_2 lines were visual selected, one from each original family and intercrossed for more thorough investigation.

Results of inter-family S_2 line crosses are presented in Table 9 and 10. Yield of inter-family crosses ranged from 4.52 (406-1 x 401-9) to 8.86 ton ha^{-1} (404-6 x 402-6) while yield of common check ranged from 7.32 (Mon.919) to 8.47 ton ha^{-1} (Pio. A33). By the overall average, interfamily crosses gave yield (6.73 ton ha^{-1}) lower than common checks (7.93 ton ha^{-1}). But the top yield S_2 cross (404-6 x 402-6) tended to give higher yield than the best check even though it was non-significant.

S_2 lines from Pioneer germplasm proved to be complemented with lines from other sources. Except only one cross (Mon.919 x Pac.984), other top-8 crosses had one of their parents from Pioneer. Syngenta 405-5 was very poor adapted line and only can be used as female parent. It is also indicated that line with high temperate background has a very limited use in tropical climate.

Agronomic traits of inter-family crosses and common checks were significantly different. Days to anthesis and silking ranged from 62.3 to 66.3 days and from 63.3 to 66.7 days, respectively. The overall average of anthesis and silking of inter-family crosses were 63.9 and 65.5 days, respectively while common checks had 64.7 and 66.3 days. They were somewhat earlier but practical not important. The data showed that the overall average of plant height of inter-family crosses (180.9 cm) was higher than that of common checks (175.0 cm). Moisture content and shelling percentage ranged from 21.8 (403-6 x 401-9) to 25.1% (404-6 x 402-6) and from 74.8 (406-1 x 402-6) to 80.6% (403-6 x 401-9), respectively.

In comparison between testcrosses (S_2 x KRi 208) and interfamily crosses (S_2 x S_2), as expected, the average of top-10 inter-family crosses was lower than the average of top-10 testcrosses because both parental lines of S_2 inter-family crosses were more heterogeneous than the tester line, KRi 208 in testcrosses. Moreover, 7 out of 10 S_2-inter-family crosses were involved with Pioneer 404-6 and Pioneer 406-1 and 6 out of 10 were crosses between Pioneer and Monsanto lines, while in S_2 testcrosses only two lines from Pioneer included in top-10, lines from Monsanto and Syngenta were complemented with the Kri 208. However, KRi 208 came from Pioneer 3012/ Pioneer 3013. Therefore, both sets of crosses showed the same heterotic pattern. Although most of S_2 inter-family crosses were significantly not different from the checks, 404-6/402-6 (Pioneer A33/Monsanto 949) gave outstanding features for yielding ability, earliness, plant and ear height while retained good shelling percentage. Therefore, beside the conventional testcross program, diallel cross between the top high yield lines is necessary for thoroughly used of germplasms and identification of new unique hybrid combination.

Table 9 Grain yields at 15 percent moisture and other agronomic traits of S_2 inter-family crosses and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

S_2 x S_2	Source of germplasms	Grain Yield (ton/ha)	Days to Anthesis (days)	Days to Silking (days)	Moisture Content (%)	Plant Height (cm)	Ear Height (cm)	Shelling (%)
404-6x402-6	Pio.A33 x Mon.949	8.86 a	62.3 d	63.3 g	25.1 ab	171.9 de	80.5 d-g	76.1 gh
404-6x403-6	Pio.A33 x Mon.919	7.82 abc	62.7 cd	64.3 efg	23.1 b-f	170.3 de	81.7 c-g	77.2 efg
406-1x402-6	Pio.3012 x Mon.949	7.61 bcd	66.3 a	67.3 abc	24.0 b-e	202.3 a	106.9 a	74.8 h
406-1x405-5	Pio.3012 x Syn. NK48	7.53 b-e	64.0 bcd	65.3 def	24.3 bcd	197.5 ab	96.7 ab	77.4 efg
403-6x401-9	Mon.919 x Pac.984	7.51 b-e	62.3 d	63.7 fg	21.8 efg	169.2 de	77.0 fg	80.6 b
406-1x404-6	Pio.3012 x Pio.A33	7.47 b-e	65.7 ab	66.7 bcd	23.8 b-f	194.7 abc	97.2 ab	78.2 c-f
404-6x401-9	Pio.A33 x Pac.984	7.11 cde	64.0 bcd	66.3 bcd	23.3 b-f	175.4 de	84.1 c-f	80.0 bc
406-1x403-6	Pio.3012 x Mon.919	6.59 de	63.7 bcd	65.0 d-g	22.1 def	183.5 bcd	93.3 bc	77.8 efg
405-5x402-6	Syn. NK48 x Mon.949	6.55 de	63.3 cd	65.3 def	24.6 abc	178.3 de	79.9 efg	75.0 h
401-9x402-6	Pac.984 x Mon.949	6.32 e	63.0 cd	64.3 efg	23.4 b-f	180.9 cde	77.3 efg	78.2 c-f
403-6x402-6	Mon.919 x Mon.949	4.95 f	62.7 cd	64.0 fg	21.6 fg	178.5 de	79.5 efg	76.5 e-h
405-5x401-9	Syn. NK48 x Pac.984	4.63 f	64.7 abc	66.7 bcd	23.3 b-f	166.1 e	74.8 g	78.3 cde
406-1x401-9	Pio.3012 x Pac.984	4.52 f	65.7 ab	66.0 cde	19.6 g	183.5 bcd	80.3 d-g	82.7 a
Check	Pio.A33	8.47 ab	64.7 abc	66.0 cde	21.9 ef	182.0 bcd	91.9 bcd	79.8 bcd
Check	SW 4452	8.26 abc	66.7 a	68.7 a	25.0 ab	177.3 de	84.2 c-f	76.3 fgh
Check	Pio.3012	8.08 abc	66.7 a	68.0 ab	22.4 def	165.2 e	89.1 b-e	77.2 efg
Check	Syn. NK48	7.86 abc	64.0 bcd	66.0 cde	22.7 c-e	171.3 de	74.4 g	77.9 d-g
Check	Mon.949	7.57 bcd	62.7 cd	64.3 efg	26.7 a	178.3 de	81.6 c-g	77.9 d-g
Check	Mon.919	7.32 b-e	63.3 cd	65.0 d-g	23.9 b-e	176.1 de	88.1 b-f	82.9 a
	Mean of diallel hybrids	6.73	63.9	65.5	23.1	180.9	85.3	77.9
	Mean of check hybrids	7.93	64.7	66.3	23.8	175.0	84.9	78.7
	F-value	**	**	**	**	**	**	**
	CV(%)	10.32	1.90	1.84	5.71	5.33	8.39	1.49

- ns: non-significant, * : significant, ** : highly significant

Table 10 Agronomic traits of S_2 inter-family crosses and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

S_2 x S_2	Source of germplasms	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Disease resistance (1-5)[1/]	Root lodging (1-5)	Plant uniform (%)	Grain type
404-6x402-6	Pio.A33 x Mon.949	18.5 ab	5.0 a	18.1 a	1	1	>95	OY^F
404-6x403-6	Pio.A33 x Mon.919	17.7 a-d	4.8 abc	15.6 cd	1	1	>95	Y^SD
406-1x402-6	Pio.3012 x Mon.949	18.5 ab	4.8 abc	16.4 bc	1	1	>95	OY^SF
406-1x405-5	Pio.3012 x Syn. NK48	18.3 abc	4.7 a-d	14.5 e	1	1	>95	OY^SD
403-6x401-9	Mon.919 x Pac.984	17.0 de	4.4 d-g	14.0 ef	1	1	>95	Y^F
406-1x404-6	Pio.3012 x Pio.A33	18.1 a-d	4.7 a-d	15.9 bc	1	1	>95	Y^SF
404-6x401-9	Pio.A33 x Pac.984	17.3 b-e	4.7 a-d	14.8 de	1	1	>95	Y^SF
406-1x403-6	Pio.3012 x Mon.919	17.0 de	4.3 e-h	13.5 fg	1	1	>95	OY^F
405-5x402-6	Syn. NK48 x Mon.949	18.0 a-d	4.6 a-f	16.0 bc	1	1	>95	OY^SF
401-9x402-6	Pac.984 x Mon.949	17.8 a-d	4.6 a-f	14.7 de	1	1	>95	OY^SD
403-6x402-6	Mon.919 x Mon.949	14.9 f	4.1 ghi	16.1 bc	1	1	90	Y^SD
405-5x401-9	Syn. NK48 x Pac.984	16.9 de	4.5 b-f	14.0 ef	1	1	>95	Y^SD
406-1x401-9	Pio.3012 x Pac.984	17.5 bcd	4.0 hi	12.9 g	1	1	90	Y^SF
Check	Pio.A33	17.5 bcd	4.8 abc	15.9 bc	1	1	>95	OY^SD
Check	SW 4452	18.9 a	4.9 ab	16.4 bc	1	1	>95	OY^F
Check	Pio.3012	16.1 ef	4.5 b-f	16.1 bc	1	1	>95	OY^F
Check	Syn. NK48	16.8 de	4.3 e-h	13.5 fg	1	1	>95	O^F
Check	Mon.949	17.7 a-d	4.5 b-f	16.7 b	1	1	>95	OY^SF
Check	Mon.919	17.2 cde	3.8 i	13.3 fg	1	1	>95	OY^F
	Mean of diallel hybrids	17.5	4.6	15.1	-	-	-	-
	Mean of check hybrids	17.4	4.5	15.3	-	-	-	-
	F-value	**	**	**	-	-	-	-
	CV(%)	4.44	5.08	4.04	-	-	-	-

- ns: non-significant, * : significant, ** : highly significant
- O : orange, Y : yellow, F : flint, D : dent, S : semi
- [1/] 1 = good, 5 = bad.

6. C1# inter-family cross yield trail

Top C1#, one from each of six original hybrids were intercrossed and the results are presented in Table 11 and 12. They showed highly significant different in yielding ability. Yield of C1# inter-family crosses ranged from 5.54 (set 4 x set 17) to 9.33 ton ha^{-1} (set 2 x set 4) while yield of common check ranged from 7.32 (Mon.919) to 8.47 ton ha^{-1} (Pio. A33). By the overall average, C1# inter-family crosses gave yield (7.22 ton ha^{-1}) lower than common checks (7.93 ton ha^{-1}). But the top C1# inter-family crosses gave somewhat the same yield as to common checks. Moreover, crosses between set (2 x 4) and set (4 x 7) gave respectively significant higher yield, 9.33 and 9.18 ton ha^{-1} than some of common checks.

In the top-5 C1# inter-family crosses, fourth crosses were involved with Monsanto lines. However, they showed more or less the same heterotic pattern between Pioneer and Monsanto lines in S_2 inter-family crosses.

The average yield of S_2 inter-family crosses in Table 9 and average yield of C1# inter-family crosses in Table 11 were almost the same. Surprisingly, C1# inter-family crosses gave highest yield over all other crosses and checks tested in the present studies even though they were statistically not different.

Agronomic traits of S_2 inter-family crosses and common checks were highly significant difference except plant height. Days to anthesis and silking ranged from 63.0 to 67.3 days and from 64.0 to 67.3 days, respectively. The overall average of days to anthesis and silking of C1# inter-family crosses were 65.0 and 66.2 days, respectively, while common checks had 64.7 and 66.3 days. In the other case, overall average moisture content of C1# inter-family crosses (22.0%) was lower than that of common checks (23.8%) and cross between set 2 x set 15 gave superior moisture content than any other C1# inter-family crosses including common checks. Other traits such as plant height, ear height and shelling percentage were more or less the same in overall average.

Table 11 Grain yields at 15 percent moisture and other agronomic traits of C1# inter-family crosses and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Composite X composite	Source of germplasms	Grain Yield (ton/ha)	Days to Anthesis (days)	Days to Silking (days)	Moisture Content (%)	Plant Height (cm)	Ear Height (cm)	Shelling (%)
2 x 4	Pac.984 x Mon.949	9.33 a	65.0 c-h	66.3 b-e	22.9 b-e	190.1	95.3 abc	78.8 b-e
4 x 7	Mon.949 x Pio.A33	9.18 ab	63.7 g-j	64.6 def	24.4 bc	181.4	92.9 a-d	78.5 b-e
2 x 15	Pac.984 x Pio.3012	7.98 c-f	65.7 a-f	66.3 b-e	19.3 f	182.9	91.9 b-e	78.9 b-e
4 x 11	Mon.949 x Syn. NK48	7.98 c-f	63.0 ij	64.0 f	23.0 b-e	184.9	89.3 b-f	77.5 de
7 x 17	Pio.A33 x Mon.919	7.62 c-h	63.7 g-j	65.0 def	21.4 ef	177.6	95.7 ab	77.9 cde
11 x 15	Syn. NK48 x Pio.3012	7.20 d-i	65.3 b-g	66.3 b-e	22.8 c-e	187.5	100.5 a	77.6 de
2 x 17	Pac.984 x Mon.919	7.06 e-i	66.0 a-e	66.7 a-d	20.5 ef	189.5	86.3 e-g	77.3 de
7 x 15	Pio.A33 x Pio.3012	6.97 e-i	66.7 abc	68.3 ab	21.4 ef	169.7	87.1 c-g	77.8 de
4 x 15	Mon.949 x Pio.3012	6.86 f-i	64.3 e-j	65.0 def	23.1 b-e	186.5	92.4 a-e	77.8 de
15 x 17	Pio.3012 x Mon.919	6.75 ghi	63.3 i-j	65.0 def	21.0 ef	175.6	89.1 b-f	81.2 abc
7 x 11	Pio.A33 x Syn. NK48	6.47 jhi	67.3 a	68.3 ab	21.4 ef	177.7	91.6 b-e	76.4 e
2 x 11	Pac.984 x Syn. NK48	6.36 ij	66.3 a-d	68.0 abc	21.6 ef	178.7	79.8 gh	78.4 cde
11 x 17	Syn. NK48 x Mon.919	6.35 ij	63.7 g-j	64.7 def	22.4 c-f	171.1	86.5 e-g	81.8 ab
2 x 7	Pac.984 x Pio.A33	6.34 ij	67.0 ab	68.7 a	21.4 ef	158.8	100.5 a	77.9 cde
4 x 17	Mon.949 x Mon.919	5.54 j	64.3 e-j	65.3 def	22.9 b-e	178.1	87.4 b-g	78.9 b-e
Check	Pio.A33	8.47 abc	64.7 d-i	66.0 d-f	21.9 def	182.0	91.9 b-e	79.8 a-d
Check	SW 4452	8.26 a-d	66.7 abc	68.7 a	25.0 ab	177.3	84.2 efg	76.3 e
Check	Pio.3012	8.08 b-e	66.7 abc	68.0 abc	22.4 c-f	165.2	89.1 b-g	77.2 de
Check	Syn. NK48	7.86 c-g	64.0 f-j	66.0 d-f	22.7 c-f	171.3	74.4 h	77.9 cde
Check	Mon.949	7.57 c-h	62.7 j	64.3 ef	26.7 a	178.3	81.6 fgh	77.9 cde
Check	Mon.919	7.32 c-i	63.3 hij	65.0 def	23.9 bcd	176.1	88.1 b-g	82.9 a
	Mean of diallel hybrids	7.20	65.0	66.2	22.0	179.3	91.1	78.4
	Mean of check hybrids	7.93	64.7	66.3	23.8	175.0	84.9	78.7
	F-value	**	**	**	**	ns	**	*
	CV(%)	9.45	1.83	1.94	5.83	7.57	5.78	2.56

- ns: non-significant, * : significant, ** : highly significant
- C1# is composite sibbed line of cycle 1

Table 12 Agronomic traits of C1# inter-family crosses and check hybrids conducted at Suwan Farm, Thailand in November, 2005 (dry season).

Composite x composite	Source of germplasms	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Disease resistance (1-5)[1/]	Root lodging (1-5)	Plant uniform (%)	Grain type
2 x 4	Pac.984 x Mon.949	18.5 abc	4.4 def	14.3 e-h	1	1	90	Y^SD
4 x 7	Mon.949 x Pio.A33	17.7 a-f	4.7 abc	16.5 a	1	1	>95	Y^F
2 x 15	Pac.984 x Pio.3012	17.4 b-f	4.2 efg	14.7 cde	1	1	>95	O^F
4 x 11	Mon.949 x Syn. NK48	16.1 gh	4.1 fg	14.5 d-g	1	1	>95	OY^F
7 x 17	Pio.A33 x Mon.919	16.5 e-h	4.4 c-f	15.7 a-d	1	1	90	OY^SD
11 x 15	Syn. NK48 x Pio.3012	17.7 a-e	4.2 efg	14.1 e-h	1	1	80	OY^SF
2 x 17	Pac.984 x Mon.919	18.2 a-d	4.2 efg	13.3 gh	1.5	1	>95	OY^F
7 x 15	Pio.A33 x Pio.3012	16.4 e-h	4.0 gh	14.7 cde	1	1	90	OY^SF
4 x 15	Mon.949 x Pio.3012	16.5 e-h	4.3 d-g	14.5 d-g	1.5	1	95	OY^F
15 x 17	Pio.3012 x Mon.919	17.3 c-f	3.9 gh	15.2 b-e	1.5	1	95	OY^SF
7 x 11	Pio.A33 x Syn. NK48	17.8 a-e	4.6 a-d	14.4 efg	1	1	95	Y^SD
2 x 11	Pac.984 x Syn. NK48	17.7 a-f	4.3 d-g	14.3 e-h	1	1	>95	OY^F
11 x 17	Syn. NK48 x Mon.919	17.7 a-e	4.0 gh	13.1 h	1	1	>95	OY^SF
2 x 7	Pac.984 x Pio.A33	19.1 a	4.7 abc	14.4 efg	1	1	>95	Y^SF
4 x 17	Mon.949 x Mon.919	15.2 h	3.7 h	14.7 cde	1	1	95	OY^F
Check	Pio. A33	17.5 b-f	4.8 ab	15.9 abc	1	1	>95	OY^SD
Check	SW 4452	18.9 ab	4.8 a	16.4 ab	1	1	>95	OY^F
Check	Pio. 3012	16.1 fgh	4.5 b-d	16.1 ab	1	1	>95	OY^F
Check	Syn. NK48	16.8 d-f	4.3 d-g	13.5 fgh	1	1	>95	O^F
Check	Mon. 949	17.7 a-e	4.5 b-d	16.7 a	1	1	>95	OY^SF
Check	Mon. 919	17.2 c-f	3.8 h	13.3 gh	1	1	>95	OY^F
	Mean of diallel hybrids	17.3	4.2	14.6	-	-	-	-
	Mean of check hybrids	17.4	4.5	15.3	-	-	-	-
	F-value	**	**	**	-	-	-	-
	CV(%)	5.59	4.98	5.09	-	-	-	-

- ns: non-significant, * : significant, ** : highly significant
- O : orange, Y : yellow, F : flint, D : dent, S ; semi
- [1/] 1 = good, 5 = bad
- C1# is composite sibbed line of cycle 1

Remarks:

Evidences from previous studies: Genter (1976); Landi and Frascaroli (1993); Rasmusson and Phillips (1997) and Troyer (1999) showed that selection in a very narrow base populations was very effective for the improvement of the populations as well as inbred line per se. The method for composite line improvement used in the present studies is very similar to that suggested by Genter (1976) for population improvement instead only 3 S_1 lines were used to form new population of each cycle, aiming to get uniform, high yield and high combining ability composite lines for better hybrid combinations. The method is simply a modification of S_1 and full-sib selection and therefore it is refered as modified S_1-full sib selection method. Data presented in this study did not show any clear advantage of line selection over the composite line method. More advanced cycles of composite line improvement are underway to prove the merit of the method against the conventional line selection.

The composite-sibbed lines as proposed by Kinman (1952) is clearly had an advantage over line selection method when time and space are involved. Composite-sibbed lines are ready for final testing instead of five or six generations of selfing usually practice in the development of inbred lines. In the modified S_1-full sib selection, composite-sibbed lines can be derived from composite sets as used in this study or using individual S_1 and full-sib of each successive cycle. In addition, S_1 lines may be selfed for one or two additional generations in order to eliminate the undesirable alleles and several desirable sister lines may then be composited to establish the composite-sibbed lines.

CONCLUSION

Line selection combined with early generation testing for combining ability is an effective method. It gave higher average yield of top-10 S_2 testcrosses over the composite testcrosses. However, statistically, there was no clear advantage of yield between both groups of lines in early generation testcrosses of which the same tester was used. Besides, the selected S_2 and composite lines showed similar results in inter-family diallel cross sets. Visual selection under low-competition environment proved to be a very effective method to identify good combining and relatively high yield lines. However, testcross and dialel cross should be applied for thorough test of combining ability of lines.

Composite lines had clear advantages over S_3 lines in yield, earliness and plant height. The modified S_1-full sib selection for the improvement of composite lines is a flexible method of which can be applied to improve the composite as well as inbred lines. However, further investigation is required to prove its merit for the construction of early generation inbreds to form hybrids as well as for the improvement of inbred lines.

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APPENDICES

Appendix Table 1 Pedigree of composite lines

Set numbers	Pedigree	Source of germplasms
Set 1	401-1, 401-2, 401-3	Pacific 984
Set 2	401-4, 401-5, 401-6	Pacific 984
Set 3	401-7, 401-8, 401-9	Pacific 984
Set 4	402-1, 402-2, 402-3	Monsanto 949
Set 5	402-4, 402-5, 402-6	Monsanto 949
Set 7	404-1, 404-2, 404-3	Pioneer A33
Set 8	404-4, 404-5, 404-6	Pioneer A33
Set 10	405-1, 405-2, 405-3	Syngenta NK48
Set 11	405-4, 405-5, 405-6	Syngenta NK48
Set 12	405-7, 405-8, 405-9	Syngenta NK48
Set 13	406-1, 406-2, 406-3	Pioneer 3012
Set 14	406-4, 406-5, 406-6	Pioneer 3012
Set 15	406-7, 406-8, 406-9	Pioneer 3012
Set 16	403-1, 403-2, 403-3	Monsanto 919
Set 17	403-4, 403-5, 403-6	Monsanto 919
Set 18	403-7, 403-8, 403-9	Monsanto 919

Appendix Table 2 Grain yield of S_3 lines and S_1 composite lines were selected for further improvement.

lines	germplasms	Grain yield (ton/ha)
S_3 lines		
402-6	Monsanto 949	3.77 (ranked 2nd)
403-4	Monsanto 919	2.80 (ranked 13th)
402-7	Monsanto 949	3.38 (ranked 6th)
401-6	Pacific 984	4.21 (ranked 1st)
404-4	Pioneer A33	3.71 (ranked 3rd)
404-6	Pioneer A33	2.16 (ranked 14th)
Composite lines		
Set 4	Monsanto 949	6.13 (ranked 1st)
Set 5	Monsanto 949	5.53 (ranked 2nd)
Set 11	Syngenta NK48	4.87 (ranked 5th)
Set 3	Pacific 984	4.63 (ranked 9th)
Set 2	Pacific 984	4.81 (ranked 6th)
Set 7	Pioneer A33	4.58 (ranked 10th)

<u>Appendix Table 3</u> Grain yields of C1# inter-family crosses and common checks conducted at Suwan Farm, Thailand in November, 2005.

Pedigree	Set 2	Set 4	Set 7	Set 11	Set 15	Set 17
Set 2		**9.33 a**	6.34 ij	6.36 ij	7.98 c-f	7.06 e-i
Set 4			**9.18 ab**	7.98 c-f	6.86 f-i	5.54 j
Set 7				6.47 jhi	6.97 e-i	7.62 c-h
Set 11					7.20 d-i	6.35 ij
Set 15						6.75 ghi
Set 17						
Check	Pioneer A33		8.47 abc			
Check	Suwan 4452		8.26 a-d			
Check	Pioneer 3013		8.08 b-e			
Check	Syngenta NK 48		7.86 c-g			
Check	Monsanto 949		7.57 c-h			
Check	Monsanto 919		7.32 c-i			
	F-value		**			
	CV(%)		9.449			

Means within either a column or a row followed by the same letter are not significantly different at $P \leq 0.05$ according to Duncan's multiple range tests.

**: highly significant

<u>Appendix Table 4</u> Grain yields of S_2 inter-family crosses and common checks conducted at Suwan Farm, Thailand in November, 2005

Pedigree	401-9	402-6	404-6	405-5	406-1	403-6
401-9		6.32 e	7.11 cde	4.63 f	4.52 f	7.51 b-e
402-6			**8.86 a**	6.55 de	7.61 bcd	4.95 f
404-6				--	7.47 b-e	**7.82 abc**
405-5					7.53 b-e	--
406-1						6.59 de
403-6						
Check	Pioneer A33		8.47 ab			
Check	Suwan 4452		8.26 abc			
Check	Pioneer 3013		8.08 abc			
Check	Syngenta NK 48		7.86 abc			
Check	Monsanto 949		7.57 bcd			
Check	Monsanto 919		7.32 b-e			
	F-value		**			
	CV(%)		10.322			

**: highly significant

Means within either a column or a row followed by the same letter are not significantly different at P≤0.05 according to Duncan's multiple range tests.