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by Entis Halimi

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GENETIC IMPROVEMENT OF CORN (*Zea mays* L.) VARIETIES FOR HIGH-QUALITY PROTEIN CONTENT

E. S. Halimi
Department of Agroecotechnology Faculty of Agriculture University of Sriwijaya
Kampus Unsri Indralaya, OI 30662, South Sumatera, Indonesia.

Abstract

Corn is an important food crop. Any research to develop corn with high protein content is very important, since the researh has a great potential to solve the world's need for a cheap source of protein. The objective of this research were to improve genetic quality, to estimate the role of genetic factor, and to innitate breeding program in Corn for high quality protein content in Indonesia. Research utilized "Top-cross" procedure to cross intoduced germplasm of high quality-protein content of HQPSSS and HQPSCB accessions to national corn varieties of "Arjuna", "Bisma", and "Kalingga" . This research resulted six newly-crossed-corn populations, namely "Toray populations" consisted of Toray-1 to Toray-6. These populatios showed good-hard kernel characteristic with estimated potetial protein content of more than 10 %. Genetic analysis suggested that additive gene action played an important role on the trait, and proven heritable, with estimate of heritability value and its standard error of 0.41 and 0.01, respectively.

Keywords: Genetic, improvement, corn, protein,

Introduction

The role of high quality protein corn in Indonesia is very important. Dorosh et al., (1987) reported that corn was a staple food for more 18 millions people and grown by more 10 millions farm-households in Indonesia. Besides as animal feed, corn is used in many modern food industry and suplement for baby food (Prastowo, 1997; Pradilla *et al*., 1975 Timmer, 1987; Sudaryanto et al., 1997). Corn seems to remain important in the human nutrition.

Research indicated that most existing corn varieties in Indonesia have low-quality protein characteristic with total protein content far below 10%. Mudjisihono et al., (1991) reported protein content of several national corn varieties in Indonesia, such as Arjuna, Kalingga, and Bima were 9.0 %, 9.5%, aand 9.4%, respectively. The quality was considered low, because of low content of lysine and tryptophane which were only about 8.1 and 1.8 g per 100 g protein (Glover and Merizt, 1987). Any research to improve corn variety with high-quality protein content is, therefore, very important. The research has a great a potential for solving the world's need for a cheap source of high-quality protein, particularly in Indonesia, where corn is used for human consumption.

Researcher in the world, have shown their intention to develop high-quality protein corn, since problem in protein need occurred all over the world (Altschul, 1975; Anderson, 1975, and Pradilla, 1975). Most researcher, however, incorporated a higher lysine content of apaque-2 gene into their adapted varieties or hybrid. Simply converting normal corn into opaque-2 type, however, resulted in undesirable characteristics. Researchers reported that introgression of opaque-2 gene into normal corn resulted vulnerable kernel, because of softer and chalkier texture. The total yield also generally reduced about 10%, owing to low density of grain and loosely packed stracht granule (Carangal, 1975).

The HPSSS and HQPSS accession contain mutant opaque-2 gene. Unlike other high-quality protein accession thar contain regular opaque-2 gene, the HQPSSS and HQPSCB produce hard kernel and have more desirable characters. The nutritional value was also superior, with total protein and lysine content in bulk seed sample were about 11.73% and 43 g per 100 g protein, respectively (Zehr and Hammaker, 1995). For that reason, this research incorporated the HQPSSS

and HQPSCB accession 1) to improve genetic quality of several Indonesian corn varieties for high quality protein content, 2) to innitate breeding program in Corn for high quality protein content in Indonesia, and 3) to estimate the role of genetic factor in developing corn with high-quality protein content.

Material and Methods

Genetic material of this research consisted of US elite germplasm sources for high-quality protein content of HQPSSS and HQPSCB populations (Zehr and Hammaker, 1995) and national corn variety in Indonesia of Arjuna, Bisma, and Kalingga populations. Seeds of HQPSSS and HQPSCB were introduced to Indonesia by E.S. Halimi in 1996 through letter of authorization from Ministry of Agriculture RI No:UP.220.226.

Random seeds of each populations were germinated in the petridish. Germinated seeds, then, were grown in the field of three crossing blocks in 1:2 ratio. To anticipates variation in anthesis, the seeds were planted in a multiple planting scheme in every two days in 10 days period. Standard practices for liming, organic and anorganic fertilization, weeds and pest control were applied according to the recommendation to promote maximum growth and development. Improvement of corn genotype for high-quality protein was made by using "Top Cross Procedure" as outlined by Fehr (1987). The procedurs was done by making artificial pollination between plants of introduced population (HQPSSS and HQPSCB) as male parent and plants of national variety populations (Arjuna, Bisma, Kalingga) as female parents. The artificial crosses were employed during anthesis by transferring pollen grains of male sources to the silk of respected female sources. To avoid undesirable crosses the ears of female sources were individually enclosed with "Silking-bag" (Abdurahman, 2002).

At harvesting, identity of crosses was tagging in each corn ear to indicated halfsib family and visual observation was made on the hardness and characteristic of the kernel. Furthermore, determination of protein content in each crossed populations was done according to the "Integral System Procedures" as outlined by Villegas (1975) as follows: 1) the analysis was done by using a composite sample of F1 seeds. 2) to make an appropriate assesment , the endosperm was removed and protein content was analyzed based on the embryo, 3) the analysis was done by using "Standard Micro-Kjeldahl Procedure" and percent of protein was calculated by factor 6.25 x % N, and 4) protein analysis of parental population was done on the remnant seeds as control.

Genetic analysis to estimate heritability (h^2) was made based on the protein content data, by using method of "Regression of Offspring on Mid-parent" (Falconer, 1989; Wricke and Weber, 1986) based on linear additive model of $Y=bo+b1\ X$; in which Y= Persent of protein content of crossed progeny; bo=intecept, b1=slope; while X= Average persent of protein content of respected female and male parents (mid-parent). The heritability values (h^2) was estimated as $h^2 \approx 2\ b1$ and its standard error, SE (h^2) was estimated as $SE(h^2) \approx 2\ SE\ (b1)$. Statistical calculations were performed using Statististical Analysis System (SAS, 1988) at $\alpha = 0.05$.

Result and Discussion

In order to make genetic improvement of national corn variety of Indonesian , this research create six newly corn genoty derived from the cross of Arjuna, Bisma, and Kalingga plants by US introduced populations of HQPSSS and HQPSCB. As shown on Table 1, hereafter, these crossed populations were called as "Toray" population" (Toray-1, Toray-2, Toray-3, Toray-4, Toray-5, Toray-6) as appreciation to the Indonesian Toray Science Foundation (ITSF) for providing grant to this research.

Unlike reported by many researchers that development of high-quality protein corn generally end up with undesirable characters of vulnerable kernel, softer and chalkier texture (Carangal, 1975), physical observation showed that Toray populations have normal-hard kernel as seen in many corn varieties grown in Indonesia. Hard kernel characteristic is very important in corn breeding, especially in Indonesia, where pest and disease are predominatly found all the year arround.

Result from protein analysis (Table 1), showed that protein content of crossed populations (Toray-1, Toray-2, Toray-3, Toray-4, Toray-5, Toray-6) were more than 10%, significantly higher than protein content of national varieties (Arjuna, Bisma, Kalingga) with protein content about 9%. Although, this protein content was calculated as total protein, the values was appropriate and closely represent the quality of protein (Villegas, 1975). As mentioned earlier, the samples for the protein analysis of this research, were composite material randomly choses from the F1 seeds without endosperm. In addition, Copeland (1976) and Kozlowski (1972) explained that great majority of corn protein, especially lysine adn tryptophan, were metabolically inactive deposited in the aleurone layer of embryo, not in the endosperm. In addition, Seka and Cross (1995) stated that chemical analysis on the F1 seeds should not include endosperm, since it's endosperm contained 3n=3x set of chromosomes, in which 2n=2x set derived form female sources and 1n=1x set derived from male sources. While it's embryo contained 2n=2x set chromosomes, in which each 1n=1x set derived from male and female sources. This research succesfully improves genetic quality of variety Arjuna, Bisma, and Kalingga that lead to the innitiation of corn breeding program for high quality protein content in Indonesia.

Table 1. Protein content of introduced populations (HQPSSS and HQPSCB) and their progenies of crossing with national varieties of Arjuna, Bisma, and Kalinggga

Cross/parent Populations	Female sources	Male Souces	Protein content (%)
1.Toray-1	Arjuna	HPQSSS	10.50 a
2.Toray-2	Bisma	HPQSSS	10.44 a
3.Toray-3	Kalingga	HPQSSS	10.53 a
4.Toray-4	Arjuna	HQPSCB	10.51 a
5.Toray-5	Bisma	HQPSCB	10.45 a
6.Toray-6	Kalingga	HQPSCB	10.54 a
7.Parent	Arjuna	-	9.00 b
8.Parent	Bisma	-	9.00 b
9.Parent	Kalingga	-	9.50 b
10.Parent	-	HQPSSS	11.73 c
11.Parent	-	HQPSCB	11.75 c

*= Values of percent protein content followed by same letter (a,b,c) indicated not different based on the LSD analysis at α=0.05

Furthermore, Figure 1 showed that values of protein content of crossed progeny (AxS, BxS, KxS, AxB, BxB, KxB) which was referred to Toray-1, Toray-2, Toray-3,Toray-4, Toray-5, Toray-6 populations, respectively, were between values of protein content and their parents. The protein content of theses crossed progenies (about 10%) were below protein content of male parent of introduced populations of HQPSSS and HQSCB (about 11 %) and higher that protein content female parent of national corn varieties , of Arjuna, Bisma, and Kalingga (about 9%). Performance of crossed progenies that were between both parents was called by Falconer (1989) and Wricke & Weber (1986) as "intermediate to the parents", and suggested as indication for strong possibility of polygenic control and important role of additive gen action on the trait. This indication was proved by the result of genetic analysis to estimate heritability (h^2) using method of "Regression of offspring on mid-parent" (Falconer, 1989; Wricke and Weber, 1986). The statistical calculation resulted value of (h^2) =0.41 with standard error of SE(h^2)=0.014. The slope

was significant at α=0.05, and by convention was meaningful since the lower onfidence of 2 SE=0.382>0 (Halimi et al., 1994). This research showed that role genetic factor was significant, the trait has proven heritable, and therefore, further cylcle of selections program may ultimately lead to development of corn varietes with high quality protein content in Indonesia.

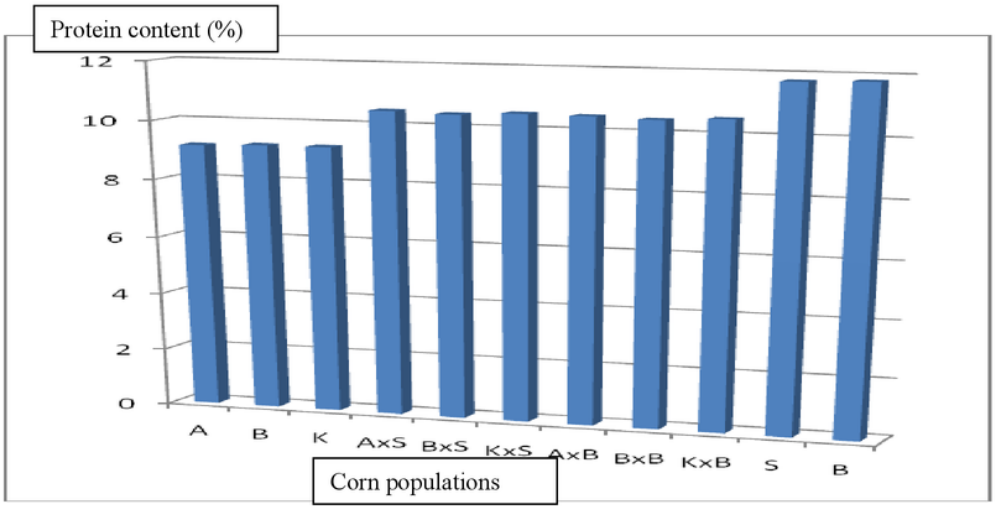

Figure 1. Protein content of female parent (A=Arjuna, B=Bisma, K=Kalingga), male parents (S=HQPSSS, B=HQPSCB) and their crossed progenies of AxS, BxS, KxS AxB, BxB, KxB (which was referred to Toray-1, Toray-2, Toray-3,Toray-4, Toray-5, Toray-6 populations, respectively).

Conclusion

This research conclude that development of corn varieties for high quality protein content has been innitiated by introducing US elite germplasm of HQPSSS and HQPSCB and crossing them to variety of Arjuna, Kalingga, dan Bisma. The resulted crossed progeny population called as "Toray populations" showed good-hard kernel characteristics with estimated potential protein content of > 10 %. The trait has proven heritable, and hence, further cycle of selection program will ultimately lead to development of corn varieties with high quality protein content in Indonesia.

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