

Repair of Character Genetic and Improvement of Potential Results Waxy Corn Local South Sulawesi With Technology Molecular Marker as a Selection Aid

Junyah Leli Isnaini¹, Muhammad Yusuf², Rahma Yassin³, Andi Faisal⁴

^{1,2,3}Cultivation of Plantation Crops Agricultural Polytechnic Pangkep State Makassar, Indonesia

⁴Andi Faisal BPTP. Sudiang, SULSEL Agriculture Department Makassar, Indonesia

Abstract: *The riset aims to repair of character genetic and potential results family waxy corn local South Sulawesi resulting from back crossing with his parents of molecular markers as a selection aid (the year 1), in Maros Regency. The crossing technique used is repeated selection, namely making a cross between the selected family (recombination). the number of cross-tests of 5 selected families and 2 comparison lines (superior pulut strain) with 2 replications. Each replication consisted of 10 test cross lines and comparative lines with a distance of 20 cm x 50 cm, the total number of plants in this riset was 140 plants. Each row represents 5 plant samples, so a total sample of 70 plants. The results showed that of the 5 selected families crossed with their parents, in general they could improve their character genotypic and potential yield. The selected waxy corn local has superior character (phenotype appearance and potential yield is better than the parent and its comparison).*

Keywords: character genetic, potential results, waxy corn local

1. Introduction

In some areas in South Sulawesi, waxy corn is one of the main foodstuffs of the community, so it has potential in the development of food crops. One type of maize used as foodstuff and potentially developed is waxy corn. Waxy Corn is one of the highly prospective business commodities developed because it has many benefits. Production of seeds can be consumed in the form of boiled, baked, made cakes can also be made maize marning. Waxy corn is used as maize on the cob because it tastes good and tasty. This is due to the amylopectin content in waxy corn almost 100%. In waxy corn there is a wx recessive gene in the homozygous state (wxwx) that affects the chemical composition of starch, causing a tasty and tasty flavor [1].

The endosperm content of waxy corn is almost all amylopectin According to Alexander and Creech (1977) in [1], Ordinary corn consists of a mixture 72% amylopectin and 28% amylose (Jugenheimer, 1985 in [1]). Marning maize made from local waxy corn is generally consumed as a snack. While biomass can be used for horse and cattle feed, the biomass of maize is used for animal feed and manure, and the stem is used as firewood (Warisno, 1998 in [2]).

The planting of waxy corn in South Sulawesi is usually done in rainfed rice fields or on dry land. However, the existence of local waxy corn South Sulawesi started to shift with the existence of the national superior corn pulp. The shift is due to farmers' reluctance to plant because the corn is low production of only 1-2, t / ha, high plant growth and susceptible to pests in storage. In fact, South Sulawesi waxy corn has several advantages: the early age, the taste of pulen,

sweet, and high adaptability compared to other waxy corn (national superior or from other regions).

Until now, waxy corn breeding has not received much attention, especially in increasing the yield potential, where as the demand for waxy corn continues to increase, especially for industry marning corn. For the manufacture of marning corn kernels required larger size for better quality than using small seeds. For that it needs genes waxy corn into white corn larger seeds, higher productivity, and has a value biological high. Therefore, there is a need for various efforts in improving the nature and production of plants to be equivalent to the national waxy corn and resistant to pests during storage. To achieve these targets there is need to improve the character of plant genetic characteristics that can increase production, long-lasting hold also able to provide quality seeds for the development of these plants.

The formation of local superior waxy corn can be obtained by combining genes from various sources or elders. To obtain the superior gene from local waxy corn, it is necessary to purify the variety. Purification of these varieties begins with the formation of the basic population to make the family selected. Selected families are reselected by repeated selection techniques (recombination), in this way will be obtained population better than the initial population.

Back-cross selection procedures are used to improve existing strains but need to add other characters such as agronomic characters and resistance to pests and diseases. The line that is to be fixed is the recurrent parent, the characters are retained, except the characters that are to be introjected from the donor parent. Line A (repeating parent) is crossed with donor X line, then F1 or F2 is crossed again with line A.

From some back crossing with line A it will be obtained by line A 'which has the same character as line A, but contains the desired gene derived from strain X. in return crossing must be clear the desired character so that it can be followed during the selection process. F1 plants contain 50% of gene lines A, crosslinking 1 (BC1) 75%, BC2 increases to 87.5%, BC3 increases 93.8%, and BC4 increases to 96.9%. However, in the back cross process it must be followed by the ability to combine so as not to change from the partner's line in making hybrids [9].

2. Methods

2.1 Location and Area

The Location was research Maros District, where this area Altitude place is located 5 meters above sea level. The geographical position of the study site coordinates 400 45'-500 07 'South Latitude and 1090 205' - 1290 12 'East Longitude.

2.2 Materials and Devices

Materials used are: seed waxy corn, chicken manure, urea, TSP, and KCl , water, plastic, paper bag, and labels. The tools used were; machetes, scales, meter, hoe, scissors, tugal, and stationery.

2.3 Research Methods

2.3.1 The design of experiments

This research is using a randomized block design, 7 treatments. The number of cross-test of 5 selected families and 2 comparison line with 2 replications, so consists of 10 experiment plots. The 5 families are: a) wx C1, b) wx C4, c) wx C5, d) wx C7, e) wx C10. The comparison line are: 1) GA Samsp A1, 2) GA Samsp 7 B.

2.3.2 Population and Sample

In the research is consists of 20 plots (20 cm x 40 cm). Each plots was 2 lines and each line there are with 10 plant, so total experimental 140 unit plants. Each line represented 5 sample plants, so the total sample of 70 plants.

2.3.3 Model Statistics

Statistical model for the experiment is randomized block design are as follows:

$$Y_i = \mu + \alpha_i + \beta_j + \epsilon_{ij}$$

Where:

Y_i = the observations of each variable

μ = common middle value,

α_i = effect of entry / potential varieties,

β_j = effect of block,

ϵ_{ij} = error effect

2.3.4. Parameter Observation

The observations were observed in this research are as follows:

- 1) Plant height,
- 2) The height of cob location,
- 3) Age of male flowering,
- 4) Age of female flowering,

- 5) Level of husk cover, The level of husk cover scoring is done by criteria as following:
 - score 1.husk cover closes well, so some cobs can be tied
 - together at the end of cob
 - score 2.husk cover closes tight only to tip of cob just
 - score 3.husk cover closes somewhat loose tip of cob
 - score 4.husk cover closes the cob less well, tip of the ear looks
 - score 5.husk cover closes the cob very bad, some seeds appear not protected of cob.,
- 6) weight wet cob, Another section of your paper,
- 7) moisture of the seed,
- 8) seed yields potential

3. Results and Discussion

The variance results for all parameters generally show no significant difference between all test crosses, however, the test cross has a superior appearance than the parent and the comparative lines. There are two families that are significantly higher in wet cob weight parameters compared to the parent and the comparison lines. The sample chosen is a plant that has a superior appearance (the appearance of the phenotype is better and seed yield potential is higher than the parent and its comparison). The average plant height, cob height, female flowering age, male flowering age can be seen in Table 1 and Table 2 below.

Table 1: The Average Plant height, and height of cob location family Superior

<i>Family Superior</i>	<i>Plant Height (cm)</i>	<i>Height of Cob Lokation (cm)</i>
wx C1p2b5	138,0	69,0
wx C 4p2b6	138,5	69,1
wx C5p2b4	140,8	70,9
wx C7p1b4	140,6	71,2
wx C10p2b2	140,4	70,4
GA Samsp A1p2b3	150,6	76,0
GA Samsp 7Bp1b4	155,8	77,9

Table 2: The Average Age flowering female and Age Flowering male family superior

<i>Family Superior</i>	<i>Age flowering female (day)</i>	<i>Age flowering male (day)</i>
wx C 1p2b5	47,5	35,2
wx C 4p2b6	47,5	39,2
wx C5p2b4	42,0	36,0
wx C7p1b4	46,4	42,5
wx C10p2b2	47,5	42,0
GA Samsp A1p2b3	48,1	43,7
GA Samsp 7Bp1b4	48,5	45,7

Table 1 show the results of plant height and the location of the cob family superiors shorter than their comparison galur . The height of the plant and the height location cob have a relationship with the homeness. Plants height tend to fall more easily than short plants. Firmness is very important in obtaining stable results. Strapping plants can withstand drought. Plants height l will disturb at harvest time, fruit, or seeds easily rot so that the quality of seed yield will be low [3]. Table 2 shows the age flowering male and flowering

females of family superior faster than their comparison line. In the table the average flowering age range of male superior family superior is 35,2-42,5 days and the female flowering age is 42,0-47,5 days, while the comparison liner, male flowering age 43,7-45,7 days and age flowering female 48.1-48.6 hst. The faster the flowering age, the harvest age is faster [4]. The average level husk cover, wet cob weight, moisture of the seed, and seed yield 5 family superior can be seen in the Table 3 and Table 4 below.

Table 3: Level of husk cover and Wet cob Weight. family Superior

Family Superior	Level husk cover	Weight Wet cob (kg)
wx C 1p2b5	1	2,8++
wx C 4p2b6	1	2,4+
wx C5p2b4	1	2,5 +
wx C7p1b4	1	2,,9++
wx C10p2b2	1	2,7++
GA Samsp A1p2b3	1	1,5
GA Samsp 7Bp1b4	1	2,0

Information: ++ = real higher than 2 waxy corn comparison at 50% LSD Level

+ = real higher than GA Samsp A1p2b3

Table 4: The Average Moisture of the seed and seed yield family Superior

Family Superior	Moisture of the seed (%)	Yield Potential (t/ha)
wx C 1p2b5	20,5	3,5
wx C 4p2b6	21,9	2,6
wx C5p2b4	23,4	2,8
wx C7p1b4	23,0	3,9
wx C10p2b2	22,0	3,4
GA Samsp A1p2b3	23,7	2,9
GA Samsp 7Bp1b4	20,1	2,8

Table 3 shows the husk cover and the weight of wet cobs. In the table, it can be seen that the husk cover family group is the same as the average husk cover of the his comparison (level 1; husk cover closes well, so some cobs can be tied together at the end of cob). But the weight wet cob of the cross-tested in the family wx C1p2b5, wx C7p1b4, and wx C10p2b2 was significantly higher than the waxy corn the two his comparison. The cob that closes tight can reduce the intensity of water that seeps into the cob so that it can prevent mold growth. The cob which closes well and tightly can protect cob and seeds from Sitophilus zeamais Motsh pests [5]. Differences in weight of wet cobs affect the high and low yield of seeds. high weights wet cob tend to give high seed yields. The difference in weight wet cob maybe because differences number of rows of seeds, the length and diameter of the cob, and the moisture content of the seeds at harvest [6]. genotype 3 Waxy corn showed the highest seed yield potential compared to other genotypes and his comparison lines genotypes which were 3.9 t/ha.. This is influenced by genetic traits and the ability to interact with different growth environments. According to Takdir et al. (1998), that maize seed yield is influenced by the interaction between genotypes and the environment, the presence of genotype interactions with the environment caused by the ability of different genotypes in utilizing environmental conditions [10].

Table 4 shows the moisture of the seed and seed yields potential. While the yields of each family selected average higher (ranging from 2.6 to 3.9 t / ha) of the comparison line who only ranges 2.8-2.9 t / ha. The ability of a variety to produce a faster harvest time is not the same, depending on the genetic and environmental characteristics. The superior family of the test cross is due to the gene contribution of the crossed variety which has superior characteristics united to form a different character from its parent.

Differences in phenotypic characters that appearance and can be seen due to the differences in genes that regulate the characters of these varieties. The diverse genes of each variety are visualized on diverse characters. This is according to what Yatim (2001) in [7], that each gene has its own work to grow and regulate the various types of characters in the body. Different phenotypic expressions that are displayed differently are the genetic variations of each of the corn origins. Different genotypes will respond differently when planted in the same environment, and the otherwise.

The superior appearance by the family is the result of recombination of local waxy corn from 10 development areas that local waxy corn in South Sulawesi. Production waxy corn superior resulting from recombination (back cross), the seed yield of waxy corn that result selection 1 (S1) recrossed with the parents. 5 families superior are capable of resulted a higher character phenotype and the average seed yield potential,. this is probably because they have superior genes inherited by their parents. Genes each lokal waxy corn is able to work together in various characters. According to Haris and Askari (2008) in [7], if there are differences between two individuals in the same environment and can be measured, this difference comes from the variation of the genotypes of the two plants. The characters observed and have a narrow variability value are quantitative characters that are controlled by many genes (polygen). Quantitative properties that are controlled by many genes are defined as the end result of a growth process related to physiological properties. This situation illustrates that the properties of plant height, stem diameter, leaf area, leaf number, ear diameter, ear length, number of cob lines, weight per ear and weight of 100 seeds did not show an opportunity for effective and efficient improvement efforts through selection does not provide flexibility in the selection of desired genotypes [8].

4. Conclusion

The results of the above discussion concluded that;

- 1) Phenotypic appearance and seed yield potential of waxy corn local South Sulawesi selected, not significantly different from their parents except in the wet stripping weights there are waxy corn genotypes that are significantly higher than their comparison line (GA Samsp A1 dan GA Samsp 7B) ,
- 2) The genotypes waxy corn tend to show better results than their comparison line in all observed parameters,
- 3) Phenotypic all test crosses tend to be homozygous

References

- [1] Azrai, M., Mejaya, M, J., Yasin, M, HG. 2007. Special corn breeding. Hall Research and Development of Puslitbang Agriculture. Bogor.
- [2] Biba, Arsyad, M. 2013. Waxy corn. Other Maize and Cereals Research Institute. Maros. Prospect of Corn Corn Development Local to Support the Industry Products Marning (Paper Seminar National cereals). Balitsereal Maros.
- [3] Isnaini, J.L., and Yusuf, M. 2017. Formation of Basic Population for Purification waxy corn lokal South Sulawesi. Agrotan Journal. School of Agricultural Sciences (STIPER) Maros. 3 (2): 12-18, ISSN 2442-9015. September
- [4] Yatim, W. 2010. Genetics. 5th edition. Tarsito Bandung publisher.
- [5] Demissie, G.T. Tefera, and A. Tadesse. 2008. Importance of husk covering on field infestation of maize by *Sitophilus zeamays* Motsch (Coleoptera: Curculionidea) at Bako, Western Ethiopia. African Journal of Biotechnology 7(20):3777-3782. (in English)
- [6] Isnaini, J.L.1999. Evaluation of Tamnet Line Combination (Tropical Asian Maize Network) on Corn Crops. Thesis program Magister. UNHAS.
- [7] Maruapey, A. 2012. Effect of Potassium Fertilization Dosage on Growth and Production of Various Corn Origin. Journal of Agroforestry VII No.1 March
- [8] Laode Safuan, 2014. Analysis of Variability in Southeast Sulawesi Local Corn Cultivars. AGROTEKNOS journal.Vol.4, No.2, Page: 108-112, ISSN; 2087-7706, July.
- [9] Takdir, A, Sunarti, M.Sc, and Mejaya, M.J. 2007. Corn (Formation of Hybrid Corn Varieties). Hall Research and Development of Puslitbang Agriculture. Bogor.
- [10]Elkawakib S, M. Jaya, and Nurfaidah. 2012. Growth and production of various corn genotypes in various KCl fertilizer doses. Agrivigor Journal (11) 2: 179-187, ISSN 1412-2286. January- April.

Author Profile



Junyah Leli isnaini, lahir di Makassar, 1 Juni 1970. Setelah berhasil meraih gelar Sarjana Pertanian Jurusan Agronomi pada Universitas Muslim Indonesia 1994, bekerja sebagai Dosen Luar Biasa Fak. Pertanian Universitas Muhammadiyah Makassar dan Asisten Dosen di Fak. Pertanian UMI. Pada tahun 1996 melanjutkan studi ke Program Magister kajian ilmu tanaman, Universitas Hasanuddin dan berhasil meraih gelar Magister Pertanian (MP) tahun 1999. Kemudian pada tahun 2002 terangkat sebagai Dosen Yayasan di Sekolah Tinggi Ilmu Pertanian YAPIM Maros (Sekarang berubah menjadi UMMA), Berbagai kursus, training dan Seminar pernah diikuti, dan tahun 2003 terangkat sebagai Dosen Jurusan Budidaya Tanaman Perkebunan di Politeknik Pertanian Negeri Pangkep hingga sekarang dan tahun 2015 sampai sekarang diberi kepercayaan sebagai Asesor Kompetensi Bidang Pertanian oleh BNSP.