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Full Length Research Article

Assessment of genetic diversity for some essential nutrients and breeding for high yield Maize (*Zea mays* L)

Naveed Ahmad[1], Sheeza Nazir[1], Muhammad Awais[1*] and Shoukat Sajad[2]

[1]Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.
College of Horticulture, Anhui Agricultural University, Hefei, PR China Hefei, 230036, PR China.
[*]Corresponding author: awaisbhuttah@gmail.com

Abstract

To assess the genetic diversity in nutrients and yield contributing traits under the normal environmental conditions an experiment was conducted in the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Analysis of variance indicated significant diversity among the genotypes for all traits except manganese and magnesium. Variability for different traits was ranging as following; 116.5-216 cm for plant height, 10-20.5 cm for cob length, 0.5-4 for bad husk, 44.5-55 for days to 50% tasselling, 48-58.5 for days to 50% silking, 0.5-4 for anthesis silking interval, 1.23-1.985 for ear per plant, 208-379.5 for grains per ear, 7.5-34.5 for grains per row, 5.5-17.5 for row per ear, 3.37-4.545 cm for cob diameter, 21.1-47.25 g for hundred grains weight, 6.013-43.626 ppm for iron, 19.64-38.29 ppm for zinc, 0.9635-3.95 ppm for copper, 1.275-2.675 ppm for manganese, 2.0847-3.54 for magnesium, 1.05-4.9 ppm for potassium, 51.892-79.967 ppm for calcium and 0.315-1.5879 ppm for sodium. This quality and yield based variation provided a valuable source for developing high yielding and nutrient rich maize germplasm to eradicate the issues of food security and malnutrition.

Key Words: Maize, genetic diversity, essential nutrients, yield
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INTRODUCTION

Maize (*Zea mays* L.) belongs to family Poaceae and has diploid chromosome number 2n = 20. It is the third most important staple cereal crop after wheat and rice and used animal feed. Maize is monoecious, tall, annual grass with broad leaves. (Sleper and Poehlman, 2006). China and Brazil are largest producers of maize following USA which is producing 0.366 million metric tons (FAO, 2020). Maize is cultivated in tropical, sub-tropical, temperate, and hilly zones of Asia, America, Africa and Europe (Anonymous 2012).

Maize feed around one billion people in developing countries (Ndukwe *et al*., 2015). It is highly rich in nutrition and used as raw material in poultry, animal feed and food industry (Khan *et al*., 2011). Maize oil contains very low amount of unsaturated fatty acids which can be used for human consumption (Khan *et al.*, 2011).

Microelement deficiency in human beings is an important issue (Goudia *et al.*, 2015). Approximately 1/3rd population of the world is suffering from micronutrients deficiency like iron (Fe) and zinc (Zn) ultimately a main disease source in third world countries (Kanwal *et al.*, 2010). Microelement deficiency is a major issue worldwide, however, third world countries are being affected severely as they depend upon staple food only which is naturally deficient in microelements. Micronutrient plays vital role in human nervous system, cellular signalling, and reproductive health (Comertpay *et al.*, 2016). Since, micronutrients could not be produced by human bodies therefore they must be provided through the food. Insufficient micronutrients will result in poor health (Bouis, 2002; Welch and Graham, 2002). Most importantly Fe^{2+} and Zn^{2+} in the cereal grain are important source for feed and food (Mason and D Croz-Mason, 2002). It was reported that notable amount of genetic diversity is present in the maize grain which can be used for enhancement of micronutrients (Graham *et al.*, 1999; Bänziger and long, 2000; Welch and graham, 2002).

The development of effective breeding technique to enhance the micronutrients concentration in maize grain mainly based on the presence of genetic diversity in species (Menkir, 2008). Many new strategies for increasing micronutrients concentration in the maize seed were being developed. Among these, bio-fortification seems to be very important, sustainable and cost-effective method particularly for enhancement of zinc, iron, potassium, calcium, manganese and copper (Welch and Graham, 2002; Cakmak, 2008).

Diversity regarding yield components and nutrient enrichment have great significance in plant breeding programs. Keeping in view a study was conducted to observe diversity of the different maize genotypes for essential nutrients and yield components. The assessment of genetic diversity of maize for high yield and essential nutrient traits would be used in future breeding programs.

MATERIALS AND METHODS

Germplasm was collected from Plant Genetic Recourses Institute, National Agriculture Research Center, Islamabad, Pakistan and sown in the research area of the Department of plant Breeding and Genetics, University of Agriculture, Faisalabad. In total 40 maize accessions were used for experiment. The seed of all varieties were sown in complete randomized block design (RCBD) with row-to-row distance 75 cm and plant to plant to distance 15 cm. Five plants were tagged randomly for each variety to study traits like plant height (cm), cob length (cm), bad husk, days to 50 % silking, days to 50% tasselling, anthesis-silking interval (ASI), ears per plant, grains per row, grains per ear, row per ear, cob diameter(cm), 100 grain weight (g), mineral contents. For micronutrient digestion wet-ashing method was used (Pinta and DeWele, 1975). The samples of maize accessions for microelements were dried in sunlight and then grinded. These samples were then analysed following standardized methods of (Van Soest *et al.* 1991). Potassium (K^+), calcium (Ca^{2+}) and sodium (Na^+) estimation were done by flame photometer (1385/1382) from (Esico) using their respective methods (Banerjee, 2020).

Some parameters were recorded manually with the help of measuring tape and meter rod, while microelement contents were measured by standard methods (Van Soest *et al*. 1991). Analysis of variance was used for checking diversity among indigenous maize using the procedure of Steel *et al*. (1997).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) showed highly significant variation among the 40 maize genotypes for plant height (Fig. 1). The genotypes mean showed that highest plant height was produced by genotype 14882 (216 cm) followed by 14894 (215 cm) and lowest plant height was observed in 14858 (116.5 cm). Salami *et al.* 2013 also studied variation for plant height in maize crop.

Cob length also showed notable variations as maximum cob length produced by the genotype 14906 (20.5 cm), medium by 14889 (15 cm) and minimum by 14920 (9 cm) as shown in Fig. 2. Another researcher Turi *et al*. (2007) also reported highly notable variation for cob length in maize genotypes.

Bad husk also significantly differed among genotypes as revealed by ANOVA. Rosales *et al*. (2015) studies were different from our findings because of climate difference. Bar graph showed that maximum bad husk produced by genotype 14913 (4g) and minimum by 14934 (0.5g) respectively (Fig. 3).

Days to 50% tasselling also depicted significant difference among all genotypes. Maximum days to 50% tasselling produced by the genotype 14861 (55) medium by 14934 (51.5) and minimum by 14904 (44.5) as shown in Fig. 4. Results of Golam *et al.* (2011) were not in accordance with our study. Similarly, days to 50% silking also differed among genotypes. LSD test results those maximum days to 50% silking produced by the genotype 14931 (58.5), medium by 14937 (55), and minimum by genotype 14906 (48) as shown in Fig. 5. Hussain *et al.* (2010) also studies significant difference for days to 50% silking in maize germplasm which is in accordance with our experiment.

Analysis of variance results indicated that the genotypes performance was significantly dissimilar for anthesis silking interval. Mean comparison showed that maximum days of anthesis silking interval were taken by the genotype 18867 (4) followed by 18866 (3) and lowest anthesis silking interval was taken by the genotype 14919 (0.5) as shown in Fig. 6. Ngugi *et al.* (2013) studies are different from our results because of stress environment used in that study.

Number of ears per plant of maize accessions under the field condition was found to be notably different from each other. As shown in the Fig. 7 that highest number of ears per plant was measured in genotype 14855 (1.985), medium in 14882 (1.765) and lowest in genotype 14936 (1.23). Similar results were reported by Qamar *et al*. (2007).

Analysis of variance showed that grain per ear of all 40 maize genotypes were notably different from one another. Mean comparison test concluded that maximum number of grains per ear was produced by the genotype 14855 (479.5) followed by 14933 (1.97) and minimum number of grains per ear was produced by 14870 (208) as illustrated in Fig. 8. Opposite results were obtained by Abuzar *et al.* (2011).

Grains per row showed variation among the maize genotypes. Comparison of mean for maize accessions showed that highest grains per row were observed in the genotype 14855 (34.5) followed by 18856 (13) and lowest grains per row were found in the genotype 14897 (7.5) as shown in Fig. 9. Vafa *et al.* (2014) also studied variation in grains per row in stress environment and these results are different from our study.

The number of rows per ear in maize accessions indicated variation among genotypes. Mean comparison for cob length in forty maize accessions was assessed by LSD test. Highest number of rows per ear was produced by the genotype 14866, 14860 and 14922 (17.5) followed by 14863 (15) and lowest number of grains per ear was produced by 14915 (5.5) as shown in Fig. 10.

Similar findings were reported by Tahir *et al*. (2008).

Cob diameter also revealed significant diversity among the 40 maize genotypes. The value (3.14) was recorded for coefficient of variance. Results of mean comparison are shown in the bar graph which revealed that maximum cob diameter was measured in genotype 14895 (4.545 cm) followed by 14915 (4.3 cm) and lowest diameter of cob was observed in 14902 (3.3 7 cm) as shown in Fig. 11. Similar extent of variation in cob diameter was reported by Alaei *et al* (2012).

Results of analysis of variance showed that the performance of genotypes was different for hundred grain weight. The genotype means indicated that highest 100 kernel weight was produced by genotype 14897 (47.25 g) followed by 14919 (41.05 g) and lowest hundred grain weights was observed in 14866 (21.1g) as shown in Fig. 12. Contrary results were reported by Aghdam *et al*. (2014) who studied grain weight by applying different levels of urea.

Highest concentration of iron ($Fe^{2+)}$ was produced by genotype 14856 (43.626 ppm) followed by 14927 (43.434 ppm) and lowest iron content was observed in 14861 (6.013 ppm) as illustrated in Fig. 13 Contrary results were reported by (Oikeh *et al* 2003).

The variation among genotypes was considerably different for Zinc (Zn^+) contents. Highest Zn^+ concentration was produced by the genotype 14923 (38.29 ppm) followed by 14913 (37.865 ppm) and lowest zinc content was produced by 14902 (19.649 ppm) as shown in Fig. 14. Our results are in accordance with (Harvest plus, 2006).

Analysis of variance for copper (Cu) concentration indicated that the variation among the maize genotypes was significant. Highest average copper concentration was measured in genotype 14931 (3.95 ppm) followed by 14919 (3.75 ppm) and lowest copper concentration was observed in genotype 14893 (0.9635 ppm) as shown in Fig. 15. Ziarati *et al*. (2015) found that considerable difference was present for copper concentration in maize genotypes.

ANOVA results showed that the performance of genotypes was not different for average concentration of manganese (Mn^{2+}). The highest Mn concentration was shown by genotype 14915 (2.675 ppm) followed by 14913 (2.65 ppm) and minimum manganese content was shown by genotype 14893 (1.275 ppm) as indicated by Fig. 16. But other studies showed that significant differences were present for manganese content in maize accessions which may be due to pH, soil composition or due to deficiency of organic matter (Manasek, 2013).

Likewise non-significant differences were observed for magnesium (Mg^{2+}) contents. Highest concentration of Mg^{2+} was produced by the genotype 14863 (3.5404 ppm) followed by 14906 (3.5313 ppm) and lowest zinc concentration was produced by 14861 (2.0847 ppm) as shown in Fig 17. Some other studies showed extensively different results (Drinic *et al*. 2015).

Highly considerable diversity among the maize genotypes was identified for potassium (K^+) contents. The genotypes mean indicated that highest K^+ concentration was produced by genotype 14897 (4.9 ppm) followed by 14901 (4.85 ppm) and lowest K content was observed in 14913 (1.05 ppm) as shown in Fig. 18.

Highly significant results were observed in calcium (Ca^+) concentration among all genotypes. Highest Ca^+ concentration was identified by the genotype 14907 (79.967 ppm) followed by 14857 (78.041 ppm) and lowest Ca^+ concentration was identified by the genotype 14924 (51.892 ppm) as shown in Fig. 19. Contrary results were reported by (Ikramullah, 2010) due to different locations, their soil composition

Sodium (Na^+) concentration showed significant variation between genotypes. Coefficient of variance value was 18.81. Genotype 14867 (1.5879 ppm) showed highest concentration of Na^+ followed by 14902 (1.1758 ppm) and lowest Na^+ concentration was produced by 14897 (0.315 ppm) as shown in Fig.20. Ikramullah (2010) also studied those maize accessions have different concentrations of Na^+ in grains and these studies are different from our experiment results which may be due to genetic factor or environmental factors which included irrigation methods or soil composition.

Conclusion:

It was concluded that notable genetic difference was shown by plant height, cob length, bad husk, days to 50% tasselling, days to 50% silking, anthesis silking interval, ear per plant, grain per ear, grain per row, row per ear, cob diameter, 100 grain weight, grains per cob, iron, zinc, copper, manganese, magnesium, potassium calcium, sodium. Maize germplasm showed significant genetic difference under normal condition which can be used for biofortification and yield traits improvement.

References

Abuzar, M.R., G.U. Sadozai, M.S. Baloch, A.A. Baloch, I.H. Shah, T. Javaid and N. Hussain. (2011). Effect of plant population densities on yield of maize. *J. Anim. Plant. Sci.* 21(4): 692-695.

Aghdam, S.M., Y. Farhood, K. Bijan, S. Edris. (2014). Effects of different urea levels on yield and yield components of corn 704. *Int. J. Adv. Bio. Biom. Res*. 2(2): 300-305.

Alaei, Y. (2012). Correlation analysis of corn genotypes morphological traits. *Int. Res. J. Appl. Basic Sci.* 3(12): 2355-2357.

Anonymous, (2012). FAOSTAT. http://faostat.fao.org

Bänziger, M., J. Long. (2000). The potential for increasing the iron and zinc density of maize through plant breeding. Food and Nutrition Bulletin. 20: 397-400.

Bak, K., G. Renata, B. Anna. (2016). Accumulation of nitrogen, phosphorus and potassium in mature maize under variable rates. Fragm. *Agron*. 33(1): 7–19.

Banerjee, P. and B. Prasad. (2020). Determination of concentration of total sodium and potassium in surface and ground water using a flame photometer. *Appl Water Sci* 10:113.

Bukhash, H. A., M. A. Alias, A. Riaz, M. Ishaque and U. M. Asmat. (2009). Response of maize hybrids to varying potassium application in Pakistan. *Pak. J. Agri. Sci*. 46(3): 179-184.

Bouis, H. (2002). Plant breeding: a new tool for gating micronutrient malnutrition. *J. Nutr*. 132: 491-494.

Cakmak, I. (2008). Enrichment of cereal grains with zinc: agronomic or genetic biofortification. *Plant Soil*. 302: 1–17.

Comertpay, G., F.S. Baloch, B. Kilian, A.C. Ulger, H. Ozkan. 2016. Genetic variation for bio fortifying the maize grain. Turk. JAF. Sci. Tech. 4(8): 684-691.content in kernels of maize. *J. Maize Sci*. 12: 13–15.

Drinic, S.M., V. Dragicevic, M. Filipovic, M. S. Ovic, Z. Camdzija, D. Simic and D. Kovacevic. (2015). Variability of microelements and antioxidants in maize hybrids and their patental inbred lines. Proceedings. 50th Croatian and 10th Int. Symp.on Agri. Opatija. Croatia. 3: 247-251.

FAO, US department of Agriculture. (2020). USDA-grain: world markets and trade-2020

Graham, R.D., D. Senadhira, S. Beeb, C. Iglesias, I. Monasterio. (1999). Breeding for micronutrient density in edible portions of staple food crops. Conventional approaches. *Field Crops Res*. 60: 57-80.

Golam, F., F. Nurul., F.Z. Mohamad., A.M. Nazia., M.M. Rahman., M. Motior Rahman and A. K. Mihdzar. (2011). Grain yield and associated traits of maize (Zea mays L.) genotypes in Malaysian tropical environment. *African J. Agri. Research*. 6(28): 6147-6154.

Goudia, B.D. and C.T. Hash. (2015). Breeding for high grain Fe and Zn levels in cereals. *Int. J. Innovation and Applied Studies* 12: 342-354.

Harvest Plus. (2006). Biofortified maize (available at www.harvestplus.org).

Hussain, N., Qamar-uz-Zaman, A.N. Muhammad. (2010). Response of maize varieties under agro ecological conditions of dera ismail khan. *J. Agric. Res.* 48(1): 59-63.

Ikramullah., A. Muhammad and F. Arifa. (2010). Chamical and nutritional properties of some maize (Zea mays L.) verities grown in NWFP, Pakistan. *Pak. J. Nutri*. 9(11): 1113-1117.

Kanwal, S., A.M. Rahmatullah, A. Rashid. (2010). Zinc partitioning in maize grain after soil fertilization with zinc sulfate. *Int. J. Agri. Biol*. 12: 299–302.

Khan, S., Ahmad, S.Q. F. Ahmad and M. Ghaffar. (2011). Genetic diversity analysis for yield and other parameters in maize (Zea mays L.) Genotypes. *Asian J. Agri. Sci*. 3(5): 385-388.

Manasek, J., L. Tomáš, P. Karel, H. Jaroslav, V. Monika, S. Petr, F. Radek. (2013). Effect of nitrogen and potassium fertilization on micronutrient content in grain maize (Zea mays L.). Acta Universitatis Agriculturae et Silviculturae Mendelianae Brunensis.1: 123-128.

Mason, S. C., N. E. D Croz-Mason. (2002): Agronomic practices influence maize grain quality. *J. Crop Product*. 5: 75-91.

Menkir, A. (2008). Genetic variation for grain mineral content in tropical-adapted maize inbred lines. *Food Chemist*. 110: 454-464.

Ndukwe, O. K., H.O. Edeoga and G. Omosun. (2015). Variatal differences in some nutritional composition of ten maize (Zea mays L.). *Int. J. Acad. Res. Ref*. 3: 1-11.

Ngugi, kahiu., C. Jerono, M. Cecillia and C. George. (2013). Anthesis to silking interval usefulness in developing drought tolerant maize. *Journal of Renewable Agriculture*. 1(5): 84-90.

Oikeh, S.O., A. Menkir, B.M. Dixon, R.M. Welch and R.P. Glahn. (2003). Genotypic differences in concentration and bioavailability of kernel-iron in tropical maize varieties grown under field conditions. *J. Plutr*. 26: 2307-2309.

Pinta, M. and G. DeWele. (1975). Etalons vegetaux pour Ianalyse foliare. Le controle de Ialimentation des plantes cultivees. Kozma, P.: 159-172.

Qamar, M., Z. A. Gurmani, H.N. Malik and S.K. Tanveer. (2007). Evaluation of maize hybrids/synthetics under double cropping zone of northern areas of Pakistan. Sarhad *J. Agrie*. 23(4): 1009-1012.

Rafiq, M.A., A. Asghar, A.M. Muhammad and H. Mumtaz. (2010). Effect of fertilizer levels and plant densities on yield and protein contents of autumn planted maize. *Pak. J. Agri. Sci*. 47(3): 201-208.

Rosales, M. D. C. F., J. H.G. Arahon, G.M. Abel Gil-Muñoz, A.L. Pedro, P.I. Filemon and V.G.C. Felix. (2015). Variability in cornhusk traits of landraces from the state of puebla, mexico. *Agro. J*. 107(3): 1119-1127.

Sleper, A.D and J. M. Poehlman. (2006). Breeding field crops. Blackwell Publishing. 5: 277-296.

Salami, S., M. Salaheddin, A.N. Kaivan, R.A. Anvar. (2013). Growth and yield response of Maize (Zea mays L.cv. SC704) to different rates of potassium and boron. *Intl J Agri Crop Sci*. 5: 236-240.

Steel, R. G. D., J. H. Torrie and D. A. Dickey. (1997). Principles and procedures of statistics: A biometrical approach. 3rd ed. Mc Graw-Hill Inc. Book Co., New York.

Turi, N. A., S. Salim Shah, A. Sajid, H. Rahman, A. Tahir and S. Muhammad. (2007). Genetic variability for yield parameters in maize (Zea mays L.) genotypes. *J. Agri. and Bio. Sci*. 2: 4-5.

Tahir, M., T. Asif., A. Asghar, A. Muhammad and A. Wasaya. (2008). Comparative yield performance of different maize (Zea mays L.) hybrids under local conditions of Faisalabad-Pakistan. *Pak. j. life soc. sci*. 6(2): 118-120

Vafa, P., N. Rahim, M. Meysam and J. Taiebeh. (2014). Evaluation of qualitative and quantitative traits of maize (cv.604) under drought stress and plant density. *J. Stress Physio & Bioche*. 10 (2): 144-154.

Van Soest, P. V., J. B. Robertson and B. A. Lewis. (1991). Methods for dietary fiber, neutral detergent fiber, and nonstarch polysaccharides in relation to animal nutrition. Journal of dairy science, 74(10), pp.3583-3597.Welch., RM, R.D. Graham 2002. Breeding crops for enhanced micronutrient content. *Plant and soil*. 245: 205-214.

White, P.J., M.R. Broadley. (2009). Biofortification of crops with seven mineral elements often lacking in human diets iron, zinc, copper, calcium, magnesium, selenium and iodine. *New Phytol*. 182: 49-84.

Ziarati, P and A. Akram. (2015). Chemical composition profile of canned and frozen sweet corn (Zea mays L.) in iran. Oriantal. *J. Cheme*. 31(2): 1065-1070.

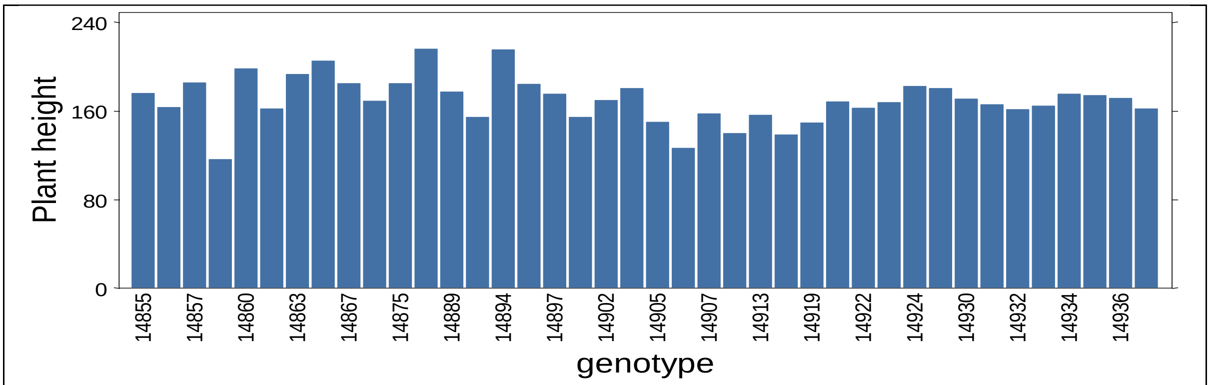

Fig. 1. Mean comparison of plant height for genotypes

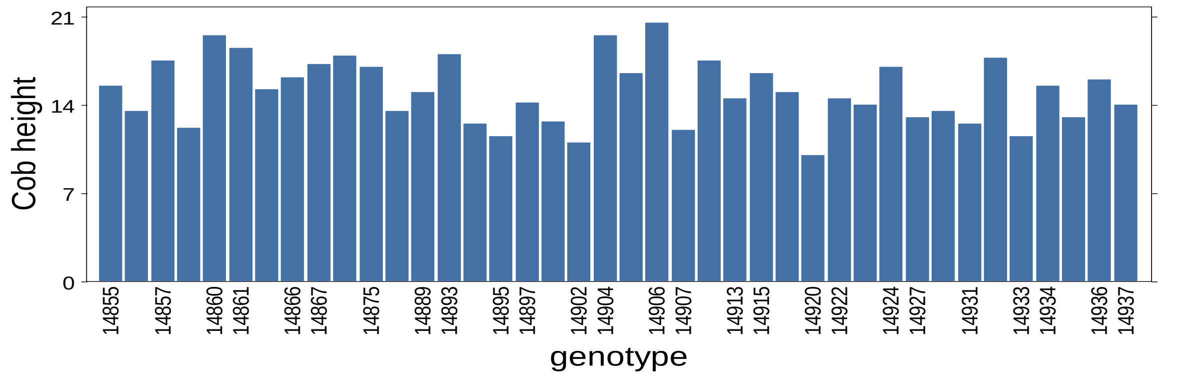

Fig. 2. Mean comparison of cob length for genotypes

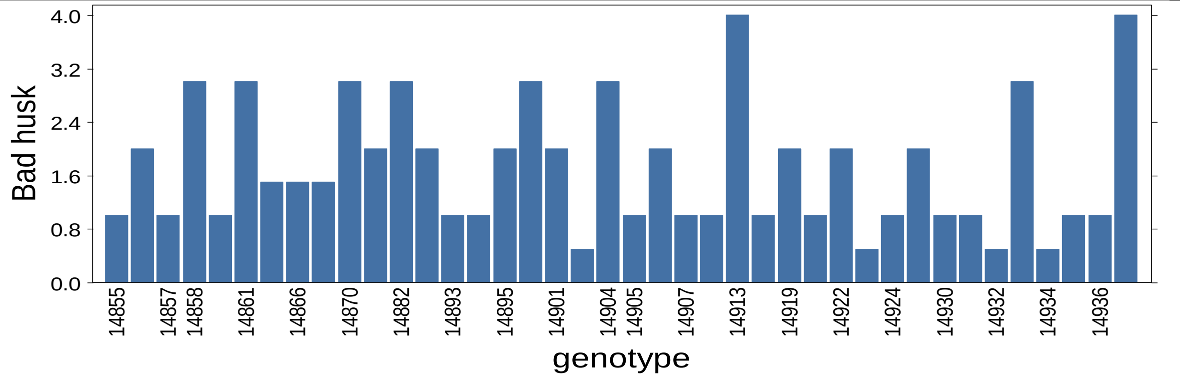

Fig. 3. Mean comparison of bad husk for genotypes

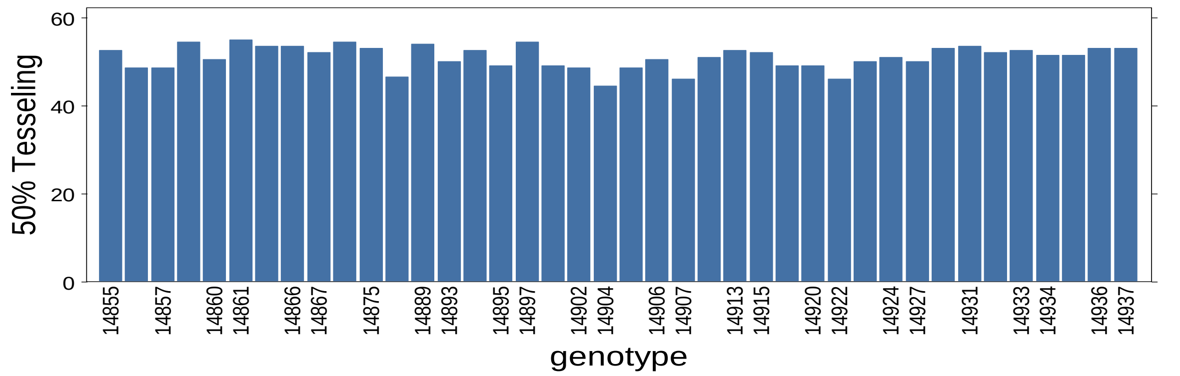

Fig. 4. Mean comparison of 50% tasselling for genotypes

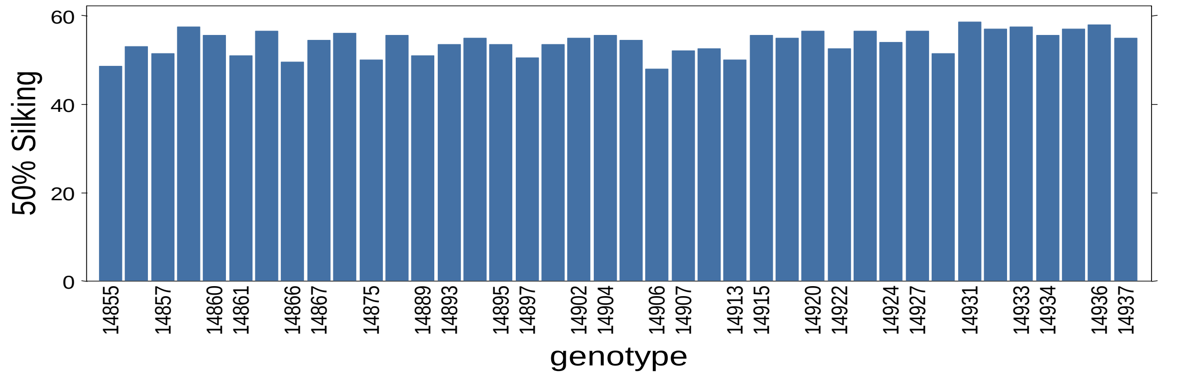

Fig. 5. Mean comparison of 50% silking for genotypes

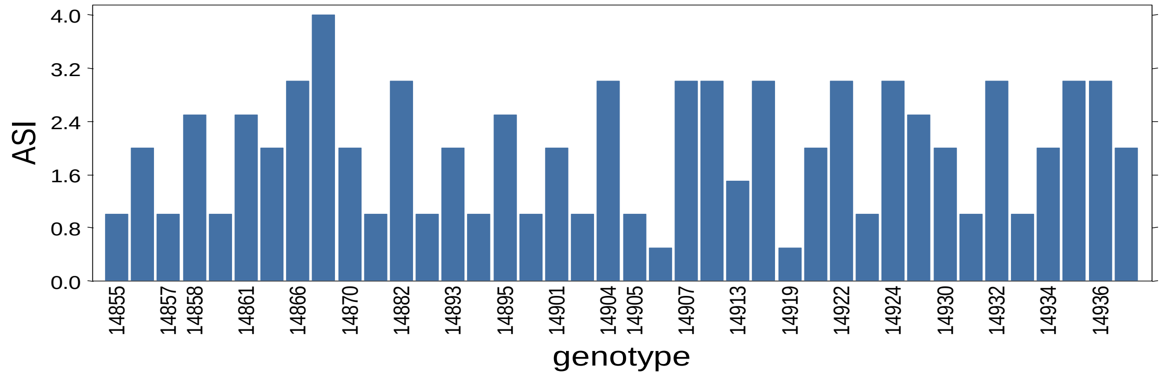

Fig. 6. Mean comparison of anthesis-silking interval for genotypes

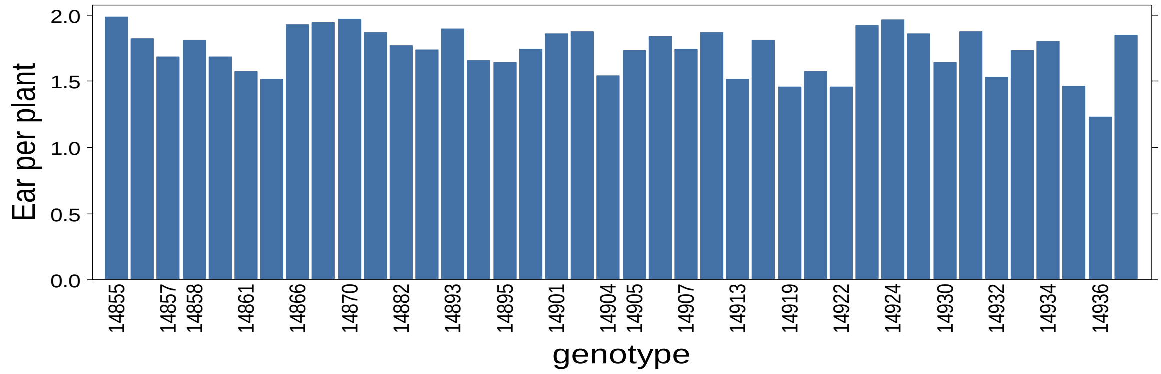

Fig. 7. Mean comparison of number of ears per plant for genotypes

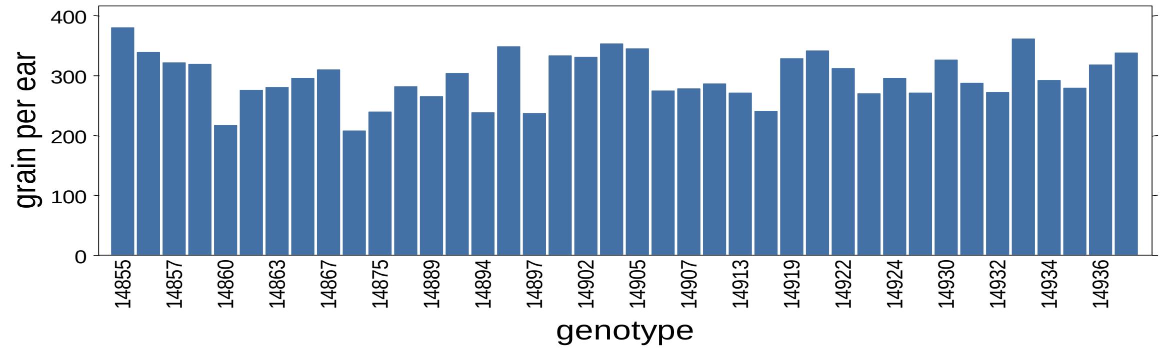

Fig. 8. Mean comparison of number of grains per ear for genotypes

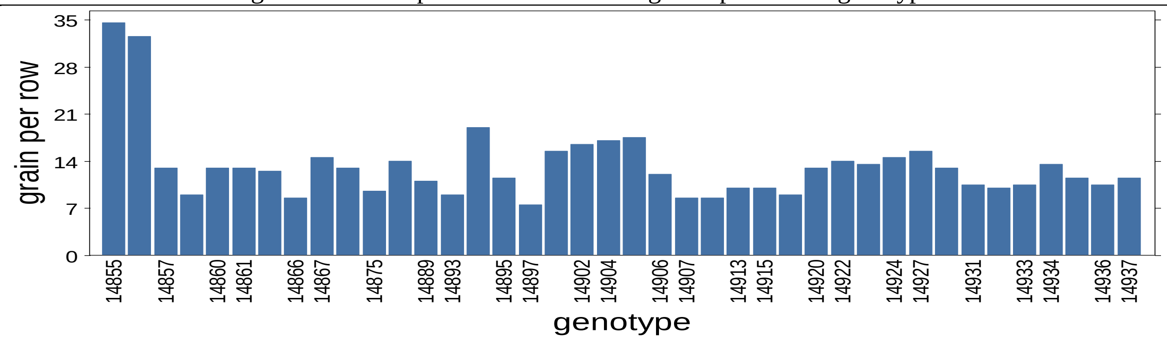

Fig. 9. Mean comparison of number of grains per row for genotypes

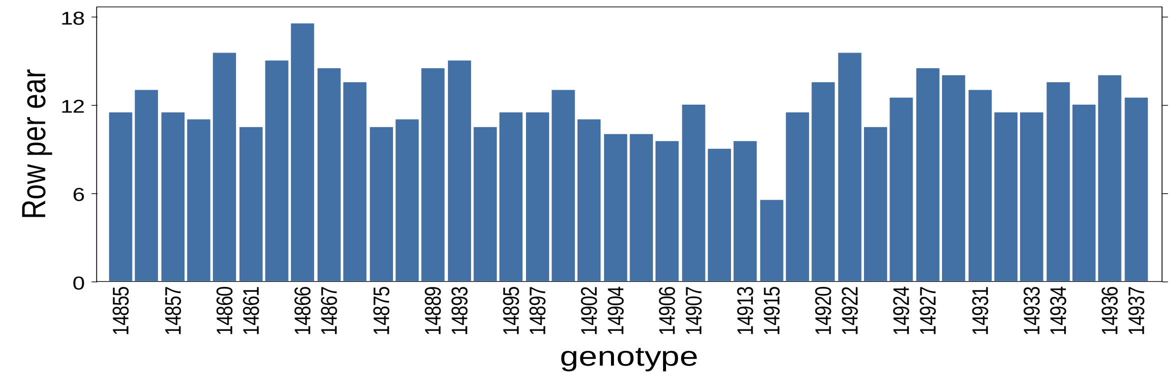

Fig. 10. Mean comparison of number of rows per ear for genotypes

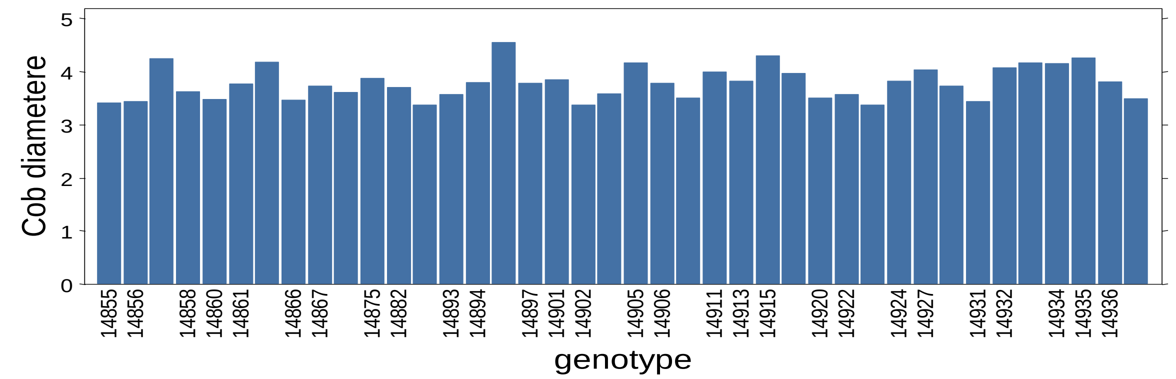

Fig. 11. Mean comparison of cob diameter for genotypes

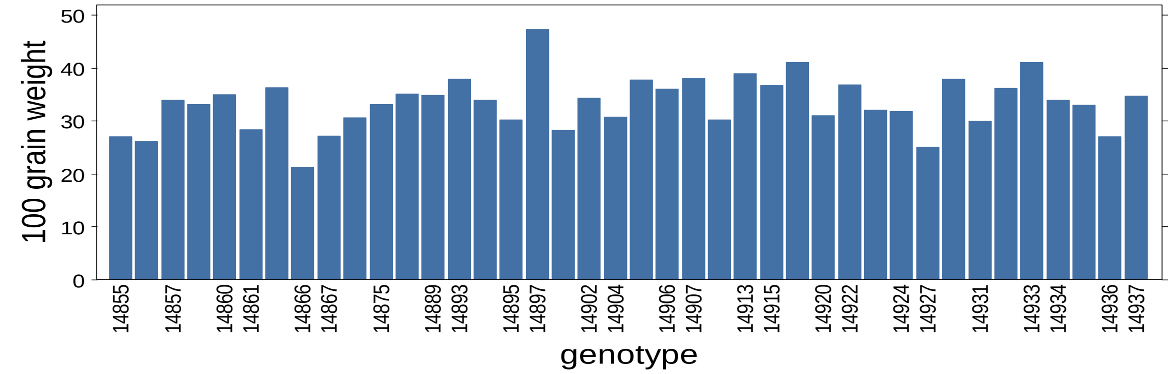

Fig. 12. Mean comparison of 100 grain weight for genotypes

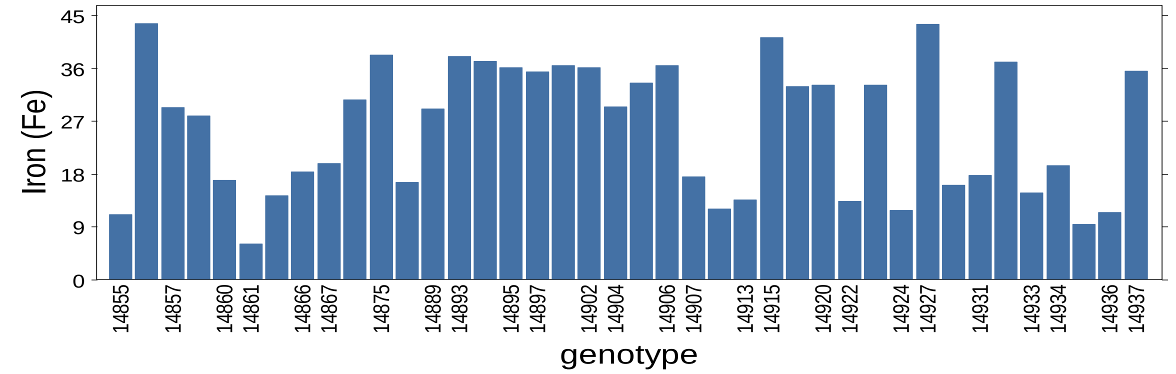

Fig. 13. Mean comparison of iron (Fe^{2+}) for genotypes

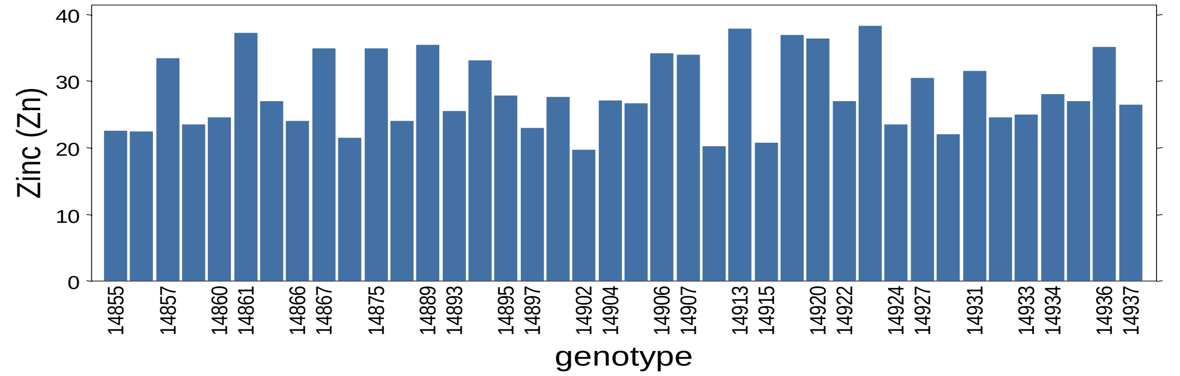

Fig. 14. Mean comparison of zinc (Zn^{2+}) for genotypes

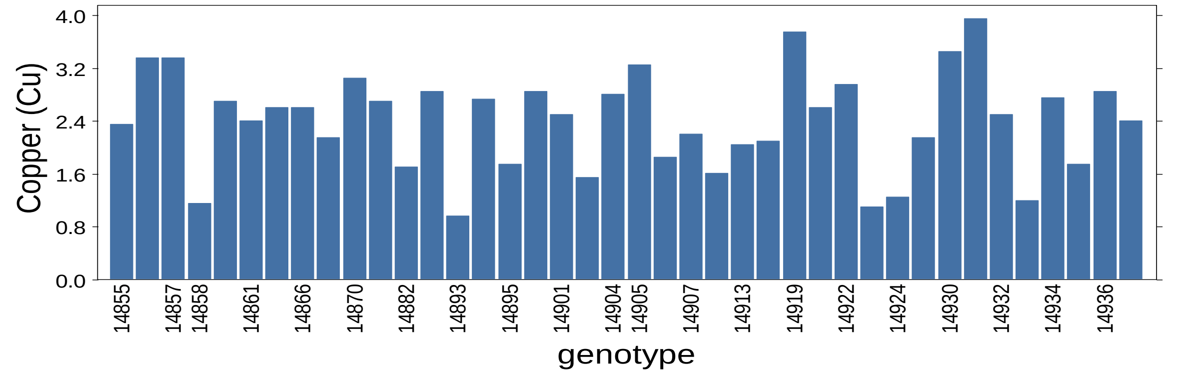

Fig. 15. Mean comparison of copper (Cu) for genotypes

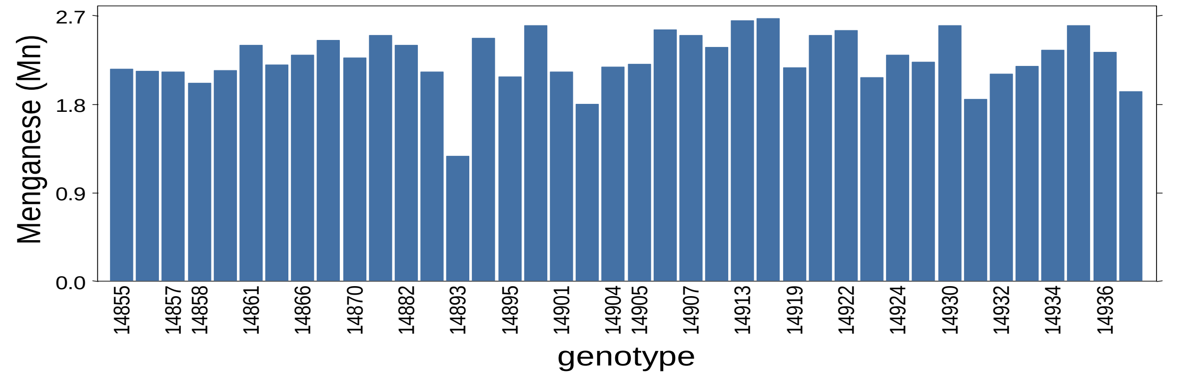

Fig. 16. Mean comparison of manganese (Mn^{2+}) for genotypes

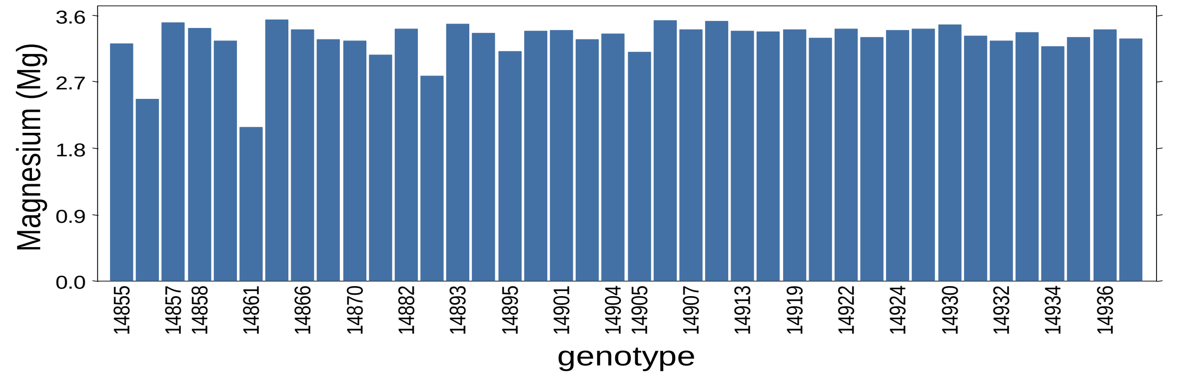

Fig. 17. Mean comparison of magnesium (Mg^{2+}) for genotypes

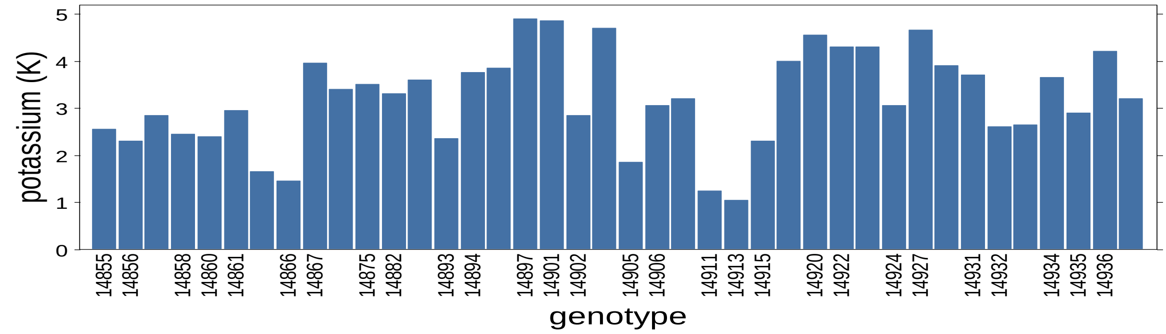

Fig. 18. Mean comparison of potassium (K^+) for genotypes

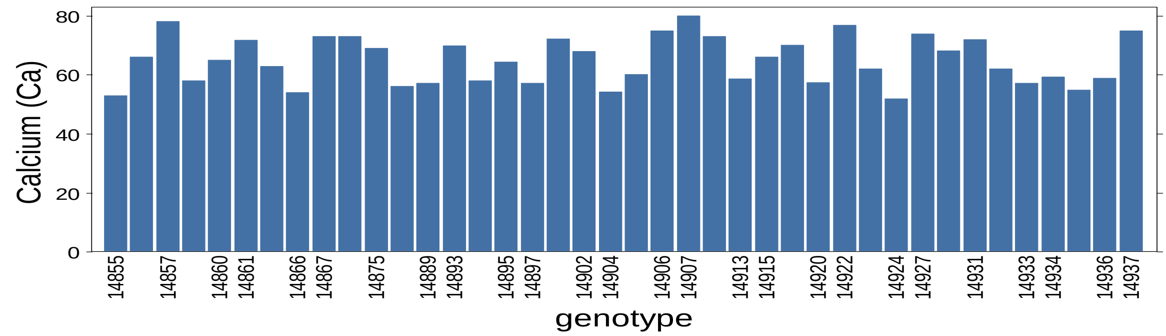

Fig. 19. Mean comparison of calcium (Ca^{2+}) for genotypes

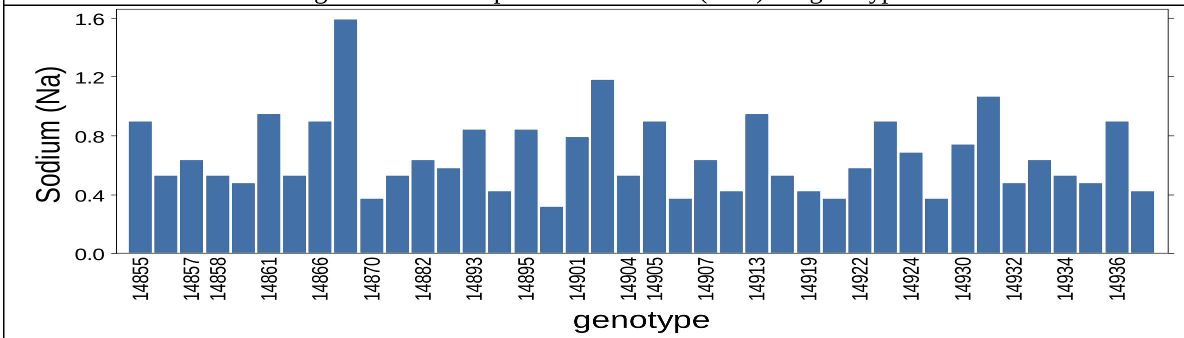

Fig. 20. Mean comparison of sodium (Na^+) for genotypes