

A Review on Genetic Analysis of Rice (*Oryza Sativa L.*) Crop of yield contributing Traits

Abstract

Rice gives primary source of energy inside the international population. In any crop breeding programme, presence of genetic variability is vital for broadening the gene pool. For choosing a genotype having excessive applicable traits, excessive magnitude of variability should be present in the population. The heritability estimates at the side of amount of genetic variability provide us an idea about genetic gain due to choice. specific direct developments (number of panicle/plant, filled grains/plant and test weight) and indirect tendencies (tiller number/plant, plant peak) determine the yield component of rice. Present overview draw a clear photo of ways variability affects the selection method and also how yield is related to distinct direct and indirect developments. Genotypes shows high variability and suitable characters can be used in similarly breeding programme. A glimpse of molecular advances in rice breeding also has been integrated inside the gift overview.

Keywords: Additive, gene action, Staple food; variability; desirable traits; selection; heritability; Rice Marker Assisted selection

Introduction:

[1] Rice (*Oryza sativa L.*) crop presents meals for majority of the arena's populace, offering nearly 21% of strength [2] Rice is one of the maximum important food grain and economically viable crop which rank 2nd (2nd) next to wheat with 770.3 million tons produced. For the expression of a particular person, distinct gene moves are worried. In rice crop, di allele evaluation offers important records on gene action by way of using distinct yield and its contributing traits. In some specific scenarios, traditional breeding is likewise helpful to apprehend the type of gene movement worried within the expression of a trait. In rice crop besides breeding techniques, addition of herbal components peptides, nano particles. [3] with biological activities may also boom gene expression. Grain yield is enormously prompted by diverse biotic (bacteria, viruses, fungi) and abiotic (water logging, salinity)

stresses. Beneath complicated environmental situation in any crop breeding programmes, direct selection for yield is blunders susceptible and creates confusion. consequently, correct choice manner depends at the genetic variability present inside the populace and additionally the affiliation amongst different morpho agronomic developments with yield. Estimation of correlation coefficient offers an concept approximately dating of the extraordinary developments with grain yield. affiliation analysis helps plant breeders to find superior genotypes by specializing in perfect tendencies. So the prevailing paper gives an overview of the concept of genetic diversity and additionally describes how the yield issue is decided through distinct direct and indirect results. [4] amino acids natural extracts and vital oils.

GENETIC VARIABILITY IN RICE

Any breeding programme especially depends at the quantity of genetic variability present in the population. The phenotypic observable variant of an man or woman is the end result of genetic variability and variability due to environment. For any crop development programme, estimation of genetic variability is the important thing requirement. as a way to discover the genetic and non-genetic components of a populace, partitioning of overall phenotypic variability is critical for any successful breeding programme. A take a look at became carried out to assess thirtyfive (35) rice genotypes for genetic variability, genetic develop and heritability for yield and its associated traits. For developments like-days to panicle initiation, plant peak, days to 50 % flowering, variety of panicle/plant, panicle length (cm), range of spikelets/panicle a extensive range of variant changed into found. [5] big difference changed into located amongst numerous genotypes in a look at with rice crop via taking into account of 13 (13) characters to estimate the nature and importance of variability, genetic strengthen and heritability. comparable large genetic variability was additionally discovered for all of the characters in a study with rice crop. Slight genotypic and phenotypic coefficient of variance become observed in trends like range of grains/panicle, productive tillers/plant and seed yield/plant. [6] In a latest examine variety analysis became carried out with forty (40) wild rice germplasm traces for twelve (12) quantitative characters the usage of D^2 analysis. Seven (7) clusters were made based on the overall performance of genotypes wherein cluster I own most (32) quantity of genotypes followed via cluster-IV and different clusters. [7] To examine the character association and genetic variability, observations have been recorded for 49 rice cultivars. direction analysis changed into completed with individual association to discover the effect of yield with its associated traits. significant variations among genotypes were discovered after thinking about all the developments. For traits like wide variety of

grains/panicle, grain yield and check weight, PCV and GCV became determined slight to excessive [8]. Estimation of correlation changed into additionally executed alongside with genetic variability and heritability for one hundred rice germplasms by the usage of alpha lattice design having three replications. ANOVA examine revealed that tremendous variations have been observed for all of the tendencies studied.[9]

CORRELATION AND PATH COEFFICIENT ANALYSIS IN RICE

it is vital to know the feasibility of a joint choice for numerous trends rather of selecting the secondary trends for genetic advantage of essential (primary) traits [10]. For increasing the rice production, the aim of breeding programs is to use more genetic numerous population and also practice suitable choice techniques to boom yield by its element characters. Correlation evaluation helps in figuring out the relationship between yield and its component trends [11] whereas route evaluation is used to divide the influence of characters into direct and indirect effects. In course analysis (statistical device) a direction chart is used for estimation of relationships between prediction variables and reaction variables. [12] Yield is a complicated man or woman that is associated with its element tendencies (quantity of panicle/ plant, range of grains/ spike, take a look at weight and many others.) [13,14]. overall performance of rice crop depends on the relationship among yield and its related important tendencies. In such circumstance choice is ineffective if we best focus on yield trait. consequently, course analysis and correlation coefficient facilitates in segmenting the yield contributing developments into direct effect and oblique impact components [15]. course evaluation is also use as a spread criterion for improvement of rice crop [16]. A effective correlation have a look at became found in rice crop for grain yield and its associated developments. study discovered out that trait one thousand grain weight can be improved by growing the panicle duration as well as panicle range per plant [17]. some other take a look at famous a superb correlation of grain yield with related trends; trait one thousand grain weight can be stepped forward with the aid of increasing the panicle period and panicle variety according to plant. comparable correlation become observed with the effects of Kumar et al. [18], Khush [19], Bhutta *et al.* [20], Chhangte and Devi, [21]. facts about trait relationship enables plant breeders to locate suitable genotypes in various environmental conditions [22]

MODERN APPROACHES IN RICE BREEDING

Molecular breeding of rice for excessive yield, stepped forward grain nice, and excessive environmental adaptability is essential for feeding the sector's swiftly growing population

[8]. The crop yield in step with unit region have to be increased through 50 % to fulfill the protection of meals deliver by means of 2030 [23]. excessive yield is the number one goal pursued via rice breeders. tremendous rice breeding using molecular design in the model of ideal plant architecture is vital for destiny rice development programme [24]. In a few current studies with aromatic Rice indicates variation in aroma when they're grown in areas other than their normal traditional developing regions [25]. In Biriya cheera variety aroma manufacturing is because of presence of BADH2 gene which is also present within the famous scented Basmati rice [26]. For increasing the primary breeding goal this is grain yield, distinct related tendencies like- grain quantity in step with panicle, grain form, wide variety of tillers, leaf perspective and leaf length need to enhance. Gene OsbHLH079 is related to the manage of leaf attitude and grain shape in rice via brassino steroid biosynthesis and signaling pathways [27]. A study changed into conducted on grain form and grain weight to discover the effect of 7 genes GS2, GS3, GS5, GW5, GS7, SLG7, and GW8. Genetic effect changed into expected for every allelic mixture for the development of developments like grain duration, grain thickness, grain width, and thousand grain weights [28]. In rice plants, a semi-dwarfism gene, OsCYP96B4 become diagnosed which influence the content material of amino acids, γ aminobutyrate (GABA), saccharides and different secondary metabolites. Molecular observe on heterosis for unique characters like plant height, days to heading and grain yield have been additionally performed [29-32]. Parental material became two (2) subspecies of rice (*O. sativa* spp. Indica and *O. sativa* spp. Japonica) and eight QTLs were detected inside the look at [33]. CRISPR/Cas9 technique was used to perceive OsEWL4 gene that's a regulator of individual plant biomass and tiller variety. A centered mutation of rice FLW genes become used inside the technique [34]. Over expression and knockdown transformants of the OsNAR2.1 gene changed into anticipated in rice crop. With the exchange of expression level of OsNAR2.1 gene adjustments the worldwide methylation at whole genome level which in the long run modifications plant peak and grain yield [35]. any other have a look at located out that a big set of genes are expressed differentially at the shoot apical meristem and regulate traits like number of tillers in keeping with plant and panicle numbers in rice plant [36]. most of these above novel techniques are used to growth the yield ability of rice crop through expertise the molecular mechanisms.

CONCLUSION

Enhancement of yield is the top objective in any rice development programme. Genetic variability with excessive slender feel heritability should be present in a populace for

powerful choice of economically important traits. For choice of tendencies which are desired by means of farmers like big seeds, excessive yield ability and additionally for traits preferred by using plant breeders like resistance in opposition to exceptional biotic and abiotic pressure, proper dissection of nature and significance of genetic variability is vital. A have a look at on relationship among yield and its extraordinary component trends assist plant breeders to go for direct and oblique selection. specific molecular strategies are used to discover the genes liable for expression of traits. So extra emphasize should receive to characterize diverse germplasm with the aid of using different molecular tactics so they can be used in destiny breeding programme correctly.

References:

- [1] Wogu MD, Omoruyi MI, Odeh HO, Guobadia JN. Microbial load in ready-to-eat rice sold in Benin City. *Journal of Microbiology and Antimicrobials*. 2011;3 (2):29-33.
- [2] Baroudy AAE, Ali A, Mohamed ES, Moghanm FS, Shokr MS, Savin I, Lasaponara R. Modeling land suitability for rice crop using remote sensing and soil quality indicators: the case study of the Nile delta. *Sustainability*. 2020;12(22):9653.
- [3] Saad AM, El-Saadony MT, El-Tahan AM, Sayed S, Moustafa MA, Taha AE, Ramadan MM. Polyphenolic extracts from pomegranate and watermelon wastes as substrate to fabricate sustainable silver nanoparticles with larvicidal effect against *Spodoptera littoralis*. *Saudi Journal of Biological Sciences*. 2021;28(10):5674-5683.
- [4] El-Sobki AE, Saad AM, El-Saadony MT, El-Tahan AM, Taha AE, Aljuaid BS, Salem RE. Fluctuation in amino acids content in *Triticum aestivum* L. cultivars as an indicator on the impact of post-emergence herbicides in controlling weeds. *Saudi journal of biological sciences*. 2021;28(11): 6332-6338.
- [5] Mall AK, Babu JDP, Babu JS. Estimation of genetic variability in rice. *Journal of Maharashtra Agricultural Universities (India)*; 2005.
- [6] Divya J, Raju CD, Rao LS, Aparna K. Genetic Variability Studies in genetically diverse rice genotypes. *Int. J. Curr. Microbiol. App. Sci*. 2018;7(4):1169-1172.
- [7] Koli GK, Upadhyay S, Rathi SR, Gupta S, Kumar K, Singh PK, Sinha B. Genetic diversity analysis for yield and yield attributing traits of wild germplasm in rice. *Journal of Pharmacognosy and Phytochemistry*. 2020;9(1):949-951.

- [8] Rao VT, Mohan YC, Bhadru D, Bharathi D, Venkanna V. Genetic Variability and Association Analysis in Rice; 2014.
- [9] Adjah, Kossi Lorimpo, et al. "Genetic variability, heritability and correlations for milling and grain appearance qualities in some accessions of rice (*Oryza sativa*L.)." *Physiology and molecular biology of plants*. 2020;26.6:1309-1317.
- [10] Ezeaku IE, Mohammed SG. Character association and path analysis in grain sorghum. *African Journal of Biotechnology*. 2006;5(14).
- [11] Akhtar N, Nazir MF, Rabnawaz A, Mahmood T, Safdar ME, Asif M, & Rehman A. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *Journal of Animal and Plant Sciences*. 2011;21(4).
- [12] PB. Samonte SO, Wilson LT, McClung AM. Path analyses of yield and yield-related traits of fifteen diverse rice genotypes. *Crop Science*. 1998;38(5): 1130-1136.
- [13] Ikeda M, Miura K, Aya K, Kitano H, Matsuoka M. Genes offering the potential for designing yield-related traits in rice. *Current opinion in plant biology*. 2013;16(2):213-220.
- [14] Zhou Y, Tao Y, Yuan Y, Zhang Y, Miao J, Zhang R, Liang G. Characterisation of a novel quantitative trait locus, GN4-1, for grain number and yield in rice (*Oryza sativa* L.). *Theoretical and applied genetics*. 2018;131(3):637-648.
- [15] Singh SK, Singh CM, Lal GM. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa*L.). *Research in Plant Biology*. 2011;1(4).
- [16] Milligan SB, Gravois KA, Bischoff KP, Martin FA. Crop effects on genetic relationships among sugarcane traits. *Crop Science*. 1990;30(4):927-931.
- [17] Karim D, Siddique MNA, Sarkar U, Hasnat Z, Sultana J. Phenotypic and genotypic correlation co-efficient of quantitative characters and character association of aromatic rice. *Journal of Bioscience and Agriculture Research*. 2014;1(1):34-46.
- [18] Kumar S, Bhuvanewari S, Devi EL, Sharma SK, Ansari MA, Singh IM, et al. Estimation of genetic variability, correlation and path analysis in short duration rice genotypes of Manipur. *Journal of Agri Search*. 2017;4(2):112-118.

- [19] Khush GS. Strategies for increasing the yield potential of cereals: case of rice as an example. *Plant Breeding*. 2013;132(5):433-436.
- [20] Bhutta MA, Munir SANA, Qureshi, MK, Shahzad AN., Aslam KASHIF, Manzoor H, Shabir G. Correlation and path analysis of morphological parameters contributing to yield in rice (*Oryza sativa*) under drought stress. *Pak J Bot*. 2019;51(1):73-80.
- [21] Chhangte L, Devi TR. Correlation and path analysis studies in aromatic rice germplasm of North-East region of India. *The Pharma Innovation Journal*. 2019;8(10):01-04.
- [22] Gonçalves DDL, Barelli MAA, Oliveira TCD, Santos PRJD, Silva CRD, Poletine J. P, Neves LG. Genetic correlation and path analysis of common bean collected from Caceres Mato Grosso State, Brazil. *Ciência Rural*. 2017;47(8)
- [23] Cheng S, Hu P. Development strategy of rice science and technology in China. *Chin J Rice Sci*. 2008; 22:223-226.
- [24] Yao S, Chen T, Zhang Y, Zhu Z, Zhao L, Zhao Q, Wang C. Pyramiding of translucent endosperm mutant gene *Wxm_q* and rice stripe disease resistance gene *Stv-bi* by marker-assisted selection in rice (*Oryza sativa*). *Chinese Journal of Rice Science*. 2010;24(4):341-347.
- [25] Sansenya S, Hua Y, Chumanee S. The correlation between 2-acetyl-1-pyrroline content, biological compounds and molecular characterization to the aroma intensities of Thai local rice. *Journal of Oleo Science*. 2018;67(7):893-904.
- [26] Veerabhadraswamy M, Sindhumole P, Mathew D, Shylaja MR, Joseph J, Augustine R, James, D. Molecular analysis of aroma gene (*BADH2*) in Biriyanicheera: A tropical aromatic rice genotype from Kerala, India. *Molecular Biology Reports*. 2022;1-7.
- [27] Seo H, Kim SH, Lee, BD, Lim JH, Lee SJ, An G, Paek NC. The rice basic Helix–Loop–Helix 79 (*OsbHLH079*) determines leaf angle and grain shape. *International journal of molecular sciences*. 2020;21(6):2090.
- [28] Gull S, Haider Z, Gu H, Raza Khan RA, Miao J, Wenchen T, Liang G. InDel marker based estimation of multi-gene allele contribution and genetic variations for grain size and weight in rice (*Oryza sativa* L.). *International journal of molecular sciences*. 2019;20(19):4824.

- [29] Abd El-Aty MS, Abo-Youssef MI, Galal AA, Salama AM, Salama, AA, El-Shehawi, A. M, El-Tahan AM. Genetic behavior of earliness and yield traits of some rice (*Oryza sativa* L.) genotypes. *Saudi Journal of Biological Sciences*; 2021.
- [30] Hassanin AA, Saad AM, Bardisi EA, Salama A, Sitohy MZ. Transfer of anthocyanin accumulating delila and roseal genes from the transgenic tomato micro-tom cultivar to moneymaker cultivar by conventional breeding. *Journal of Agricultural and Food Chemistry*. 2020;68(39):10741-10749.
- [31] Rao Y, Yang Y, Huang L, Pan J, Ma B, Qian Q, Zeng D. Research progress on cold stress in rice. *Mol Plant Breed*. 2013;11(3):443-450.
- [32] Saleh MM, Salem KF, Elabd AB. Definition of selection criterion using correlation and path coefficient analysis in rice (*Oryza sativa* L.) genotypes. *Bulletin of the National Research Centre*. 2020;44(1):1-6.
- [33] Yu Y, Zhu M, Cui Y, Liu Y, Li Z, Jiang N, Sui G. Genome sequence and QTL analyses using backcross recombinant inbred lines (BILs) and BILF1 lines uncover multiple heterosis-related loci. *International Journal of Molecular Sciences*. 2020;21(3):780.
- [34] Gao Q, Li G, Sun H, Xu M, Wang H, Ji J, Zhao X. Targeted mutagenesis of the rice FW 2.2-like gene family using the CRISPR/Cas9 system reveals OsFWL4 as a regulator of tiller number and plant yield in rice. *International journal of molecular sciences*. 2020;21(3):809.
- [35] Fan X, Chen J, Wu Y, Teo C, Xu G, Fan X. Genetic and global epigenetic modification, which determines the phenotype of transgenic rice?. *International Journal of Molecular Sciences*. 2020;21(5):1819.
- [36] Zhang Q, Shen L, Wang Z, Hu G, Ren D, Hu J, Qian Q. OsCAF1, a CRM domain containing protein, influences chloroplast development. *International journal of molecular sciences*. 2019;20(18):4386.