Genetic analysis on frequency distribution using measures of skewness and kurtosis in F_2, F_3segregating populations ofsix rice crosses (*Oryza sativa* L.)

Abstract

This study analyzed the genetic basis of skewness and kurtosis segregating generations of six rice crosses. Skewness and kurtosis values were calculated for ten biometrical traits across the populations. The traits examined included plant height, number of productive tillers, panicle length, grain yield, and grain dimensions. Results showed diverse patterns of skewness and kurtosis across traits, crosses, and generations. Platykurtic distributions were predominant for most traits, suggesting flatter distributions with lighter tails compared to normal. Skewness varied between positive and negative across traits and crosses. Some traits like grain length-to-breadth ratio tended to show positive skewness more frequently. Plant height often exhibited negative skewness. The diversity in distribution characteristics indicates significant genetic variability in the populations. Traits showing platykurtic distributions with negative skewness, such as plant height in several crosses, suggest duplicate epistasis and polygenic control. Positively skewed platykurtic distributions for traits like grain dimensions in some crosses indicate complementary epistasis requiring intense selection. The findings provide insights into the genetic control of key rice traits and have implications for breeding strategies. The complex distribution patterns revealed offer a rich basis for selective breeding, depending on specific trait objectives.

Key words: Skewness, Kurtosis, Segregating generations and Rice

1.0 Introduction

Rice genetics and breeding have seen significant advancements in recent decades. Understanding the genetic architecture of complex traits in rice is crucial for crop improvement. Traits such as yield, grain quality, and stress tolerance are typically controlled by multiple genes and are influenced by environmental factors. The study of segregating populations, particularly in early generations like F2 and F3, provides valuable insights into the genetic basis of these traits. Analysis of trait distributions in these populations can reveal important information about gene actions, interactions, and the number of genes controlling a trait.

Skewness and Kurtosis are statistical measures that provide insights into the asymmetry and flatness, tail heaviness of a frequency distribution of segregating populations in rice, these measures help to understand the nature of the data distribution and make informed decisions about analyzing different plant populations. In case of skewness, if skewness value of zero indicates a perfectly symmetrical distribution, positive skewness suggests that the distribution is skewed to the right, indicating that there may be more plants with lower values and negative skewness suggests that the distribution is skewed to the left, indicating that there may be more plants with higher values. In case of kurtosis, if kurtosis value of zero is considered normal or mesokurtic. Values higher than zero indicate heavier tails, while values lower than zero indicate lighter tails, Positive kurtosis indicates a distribution with heavy tails and a sharp peak (leptokurtic), suggesting that extreme values are more likely and negative kurtosis indicates a distribution with light tails and a flatter peak (platykurtic), suggesting that extreme values are less likely.In this context, measures of distribution such as skewness and kurtosis offer powerful tools for genetic analysis. Skewness provides information about the asymmetry of trait distribution, while kurtosis indicates the peakedness or flatness of the distribution relative to a normal distribution. These parameters can suggest the presence of major genes, the nature of gene action (additive, dominance, or epistasis), and the relative number of genes controlling a trait.The present study aims to investigate the genetic basis of skewness and kurtosis in F2 and F3 segregating populations derived from six rice crosses. By examining these distribution properties for ten important biometrical traits, we seek to gain insights into the genetic control of these traits. This information will be valuable for designing effective breeding strategies, predicting breeding progress, and ultimately contributing to the development of improved rice varieties to meet future global food demands.

2.0. Materials and Methods

The present study on measures of distribution was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Chidambaram during *Kharif* season of 2021 and *Kharif* season of 2022. The seeds from the F_1population of six crosses involving five parents namely ADT 43, ADT 45, ASD 16, ASD 12 and TKM 6 were raised as F_2 population and seeds collected from the F_2 plants were forwarded as F_3 population. The F2 and F3 generations were derived from the following crosses *viz.*,Cross 1 (ADT 43 X TKM 6)**,** Cross 2 (ADT 43 X ASD 12),Cross 3 (ADT 45 X TKM 6)**,** Cross 4 (ADT 45 X ASD 12),Cross 5 (ASD 16 X TKM 6) and Cross 6 (ASD 16 X ASD 12).

2.1. Karl Pearson's measures of skewness

Skewness refers to the symmetry of distribution., we mean the asymmetry of the distribution to compare the Skewness of different distribution we prefer to use a dimensionless number. If we have more mass to the right of the highest ordinate of the frequency curve, the curve is said to be positively skewed and it's negatively skewed of more mass is to the left of the highest ordinate. A measure of skewness is obtained as making use of the second and third moments about the mean. β1 as a measure of skewness does not talk about the direction of skewness, *i.e.*, positive or negative. Because μ3 being the sum of cubes of the deviations from mean may be positive or negative but μ_3 is always positive. Also, μ2 being the variance always positive. Hence, β_1 would be always positive.This drawback is removed if we calculate Karl Pearson's Gamma coefficient $\gamma_1$which is the square root of β_1. The interpretation method of skewness is presented in Table 1.

Karl Pearson defined the following β and γ coefficients of skewness, based upon the second and third central moments:

$$\gamma_1 = \pm\sqrt{\beta_1}$$

$$= \sqrt{\frac{\mu_3^2}{\mu_2^3}}$$

whereas,

μ_2 = Second order central moment of distribution

μ_3 = Third order central moment of distribution

$$\mu_2 = \frac{\sum(x-\bar{x})^2}{N}$$

$$\mu_3 = \frac{\sum(x-\bar{x})^3}{N}$$

Table 1. Interpretation of Skewness and Kurtosis based on obtained values

Measures of Skewness		**Measures of Kurtosis**	
γ_1 value	**Type of skewness**	**$\gamma_2$value**	**Type of kurtosis**
γ_1 is positive	Positively skewed	γ_2 is positive	Leptokurtic
γ_1 is negative	Negatively skewed	γ_2 is negative	Platykurtic
γ_1 is zero	Symmetrical distribution	γ_2 is zero	Mesokurtic

2.2. Karl Pearson's measures of kurtosis

Kurtosis refers to the degree of fatness or peakness in the region about the mode of a frequency curve. For calculating the kurtosis, the second and fourth central moments of variable are used. The method of interpretation of kurtosis is presented in Table 1.

The measure of kurtosis is the value of the co-efficient β_2, it is defined as

$$\beta_2 = \sqrt{\frac{\mu_4}{\mu_2}}$$

whereas,

$$\mu_2 = \frac{\sum(x-\bar{x})^2}{N}$$

$$\mu_4 = \frac{\sum(x-\bar{x})^4}{N}$$

μ_2 = Second order central moment of distribution

μ_4 = Fourth order central moment of distribution

The deviation of the β_2 is used as a measure of kurtosis, γ_2 is designed as

$\gamma_2 = \beta_2 - 3$

3.0. Results and Discussion

The study of distribution properties such as co-efficient of skewness (third degree statistic) and kurtosis (fourth degree statistic) provided insight into the nature of gene action (Fisher *et al.*,1932) and number of genes controlling the traits (Robson, 1956), respectively. The parameter 'd' and 'h' in the genetic expectations of skewness ($-3/2\ d^2h$) represented additive gene effects and dominance gene effects, respectively. Skewness and kurtosis were more powerful than first order and second order statistics which revealed interaction genetic effects (Choo and Reinbergs, 1982).

The skewed distribution of a trait in general suggesting that the trait was under the control of non-additive gene action, especially the epistasis and influenced by environmental variables (Pooni *et al.*, 1977 and Roy, 2000). Maximizing the genetic gain in respect of these biometrical traits with positively skewed distribution required more intense selection from the existing variability (Roy, 2000 and Thirugnanakumar*et al.*, 2011). Skewness was a measure of the asymmetry of the probability distribution of a real-valued random variable about its mean. In a frequency distribution, if the peak is at left and the right tail was longer called as positively skewed and if the peak is towards the right and the left tail is longer, then it was said to be negatively skewed. Positive skewness was associated with complementary gene interactions while negative skewness was associated with duplicate (additive x additive) gene interactions. The genes controlling the trait with skewed distribution tend to be predominantly dominant irrespective of whether they had increasing or decreasing effect on the trait. Genetic gain in respect of all the mentioned traits showing negatively skewed distribution was rapid under mild selection from the existing variability.

Kurtosis was a measure of the “peakness” of the probability distribution of a real valued random variable. A normal distribution had kurtosis exactly 0, called mesokurtic. A distribution with kurtosis (< 0) was called platykurtic. A distribution with kurtosis (> 0) was called leptokurtic. The traits with leptokurtic and platykurtic distribution were controlled by fewer and large number of genes, respectively. Kurtosis was negative or close to zero in the absence of gene interaction and it was positive in the presence of gene interactions (Pooni *et al.,* 1977; Choo and Reinbergs, 1982; Kotch *et al.,* 1992). Studies on the amount of gene interaction were undoubtedly needed so as to increase the efficiency of our selection and breeding programmes. Selection intensity could be higher under complementary than under duplicate relationship. Probably, progress in improving population performance may be greater under complementary interaction than under duplicate gene interaction (Choo and Reinbergs, 1982). The inferences on the relative number of genes and nature of genetic control of different traits in F_2 and F_3 generation of two rice crosses are discussed below,

Platykurtic and negatively skewed distribution was observed for plant height, number of productive tillers per plant, total number of tillers, panicle length, number of grains per panicle, and grain yield per plant in both F_2 and F_3 generation and thousand grain weight, grain length traits in F_2 generation in ADT 43 X TKM 6. The traits plant height, panicle length, grain length in F_2 and F_3 generation and trait grain breath in F_3 generation. The traits plant height, panicle length, grain length in both F_2 and F_3 generation and grain breath in F_3 generation of ADT 43 X ASD 12. The traits plant height, number of productive tillers, total number of tillers in both F_2 and F_3 generation, grain length in F_2 and panicle length in F_3 generation in ADT 45 X TKM 6. The traits number of productive tillers, total number of tillers, grain breath, grain yield per plant in F_2 and F_3 generation then thousand grain weight in F_2 and grain length in F_3 generation in ADT 45 X ASD 12. The traits number of productive tillers, total number of tillers, grain breath, grain length in F_2 and F_3 generation then thousand grain weight, grain yield per plant in F_2 and plant height in F_3 generation in ASD 16 X TKM 6. The traits panicle length, number grains per panicle, thousand grain weight, grain breath in both F_2 and F_3 generation and number of productive tillers, grain yield per plant in F_3 generation in ASD 16 X ASD 12 which suggested the involvement of more segregating genes with majority of them having increased effects and duplicate type of epistasis. Hence, a greater number of genes segregates for these traits and the selection was not be more effective in other words, it indicated a slow selection response. Similar observations were reported by Karim *et al.* (2014) and Nikhitha*et al.* (2020). The trait plant height of majority of crosses exerted a significant negatively skewed platykurtic distribution signifying the prevalence of dominance and dominance-based duplicate epistasis, specifying that more than one gene controls the trait.

Platykurtic and positively skewed distribution suggested the involvement of relatively large number of segregating genes with majority of them had a decreasing effects and dominance based complementary type of interaction in the inheritance of grain length in F_2 generation and grain length, grain breath, grain L/B ratio and thousand grain weight in F_3 generation of ADT 43 X TKM 6. The traits number of productive tillers, total number of tillers, number of grains per panicle, grain yield per plant in both F_2 and F_3 generation and grain breath, grain L/B ratio in F_2 generation of ADT 43 X ASD 12. The traits number of grains per panicle, thousand grain weight, grain breath in both F_2 and F_3 generation then panicle length in F_2 and grain length, grain yield per plant in F3 generation of ADT 45 X TKM 6. The traits number of grains per panicle, panicle length in both F_2 and F_3 generation and trait panicle length in F_2 generation of ADT 45 X ASD 12. The traits panicle length, plant height in F_2 generation and traits panicle length, number of grains per panicle, thousand grain weight, grain yield per plant in F_3 generation of ASD 16 X TKM 6. The traits plant height, grain L/B ratio in both F_2 and F_3 generation then traits grain length, grain yield per plant in F_2 generation of ASD 16 X ASD 12. The Maximization of genetic gain in respect of the traits with positively skewed distribution required intense selection from the existing variability (Shamini and Selvi, 2022).

Leptokurtic and positively skewed distribution was noticed for grain L/B ratio in F_2 generation of ADT 43 X TKM 6. The traits thousand grain weight in F_2 and grain L/B ratio in F_3 generation of ADT 43 X ASD 12. The trait grain L/B ratio in F_3 generation of ADT 45 X TKM 6. The trait grain L/B ratio in F_2 and F_3 generation of ASD 16 X TKM 6. The traits number of productive tillers, total number of tillers in F_2 and traits total number of tillers, grain length in F_3 generation of ASD 16 X ASD 12 which is in agreement with outcomes of Sheshaiah *et al.* (2018), Priyanka *et al.* (2019) and Nikhitha *et al.* (2020) for number of productive tillers per plant. The mentioned traits indicated that involvement of fewer segregating genes with majority of these had a decreasing effects and complementary type of interaction in the inheritance of these traits.

Leptokurtic and negatively skewed distribution reported for the trait thousand grain weight in F_3 generation of ADT 43 X ASD 12. The trait grain L/B ratio in F_2 generation of ADT 45 X TKM 6. The traits grain length, grain L/B ratio in F_2 generation and traits thousand grain weight, grain L/B ratio in F_3 generation of ADT 45 X ASD 12. The trait number of grains per panicle in F_2 generation of ASD 16 X TKM 6. To achieve maximum genetic gain in respect to this traits, intense selection would be required. The method of using skewness and kurtosis for detecting additive epistasis is very simple and could be used for crop improvement.

In case of skewness on both generations, traits showed a mix of positive and negative skewness across the crosses.There was no consistent pattern of skewness for most traits across all crosses. Some traits, like grain L/B ratio, tended to show positive skewness more often than others.Plant height often showed negative skewness, indicating a tendency towards shorter plants.In case of kurtosis on both generations, Platykurtic distributions were predominant for most traits in both generations.This suggests that many traits had flatter distributions with lighter tails compared to a normal distribution.Leptokurtic distributions were less common but occurred occasionally, especially for traits like grain L/B ratio and thousand grain weight. The cross-specific observations reveal that, while there were variations between crosses, no single cross consistently produced dramatically different distribution characteristics compared to the others. Each cross had its own unique combination of skewness and kurtosis values for different traits.The diversity in skewness and kurtosis values across traits, crosses, and generations indicates significant variability in the genetic populations.This variability suggests potential for selection and improvement in breeding programs.

The generation-specific trends of skewness and kurtosis shows that, there were no dramatic shifts in distribution characteristics from F_2 to F_3 for most traits.Some traits showed slight changes in skewness or kurtosis between generations, but these changes were not consistent across all crosses.Trait-specific observations of important traits shows that,number of tillers (both productive and total) frequently showed negative skewness.Grain yield per plant showed mixed skewness across crosses and generations.Grain L/B ratio often stood out with positive skewness and leptokurtic distributions in several crosses.The skewness and kurtosis values of F_2 generation, F_3 generation are presented in Table 2 and Table 3, respectively. The figures 1 to 6 shows the frequency distribution patten of ten observed biometrical traits of six rice crosses in F_2 generation and figure 7 to 12 shows the frequency distribution patten of observed ten biometrical traits of six rice crosses in F_3 generation. Similar studies for frequency distribution using skewness and kurtosis analysis were done by Thirugnanakumar*et al.*(2011), Kiran*et al.* (2013), Ajay*et al.* (2016), Hosagoudar and Shashidhar (2018), Choudhary*et al.* (2018), Nirubana*et al.* (2019), Priyanka*et al.* (2019), Khandappagol*et al.* (2019), Nikhitha*et al.* (2020), Fathima*et al.*(2021), Shamini and Selvi (2022).

4.0. Conclusion

In culmination, the platykurtic with negative skewness suggested duplicate epistasis, large number of segregating genes, and slow selection response for traits like plant height, number of productive tillers per plant, total number of tillers, grain yield per plant in ADT 43 X TKM 6, ADT 45 X TKM 6, ADT 45 X ASD 12, ASD 16 X TKM 6 and for number of grains per panicle, panicle length in ADT 43 X TKM 6, ASD 16 X ASD 12 crosses, indicated the polygenic control and duplicate epistasis. The platykurtic with positive skewness suggested complementary epistasis, more segregating genes with decreasing effects, and need for intense selection for traits like grain length, grain breath, grain yield per plant also showed platykurtic and positive skewness for ADT 43 X ASD 12, ADT 45 X TKM 6, ASD 16 X TKM 6, suggesting need for intense selection. The Leptokurtic suggested that, the fewer segregating genes with complementary epistasis for traits like grain L/B ratio in crosses. Traits like grain L/B ratio showed variable skewness and kurtosis across generations and crosses, indicating complex genetic control.

This analysis reveals complex distribution patterns across traits, crosses, and generations. The predominance of platykurtic distributions and the mix of positive and negative skewness values indicate diverse genetic expressions in these rice populations. This variability provides a rich basis for further selective breeding, depending on the desired traits and breeding objectives.

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Table 2. Skewness and Kurtosis values for six rice crosses in F_2 generation

F_2	Cross 1		Cross 2		Cross 3		Cross 4		Cross 5		Cross 6	
Traits	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**
PH	-0.49	-0.54	-0.17	-0.58	-0.06	-1.31	0.02	-1.30	0.10	-1.02	0.40	-0.22
NPT	-0.30	-0.46	0.14	-0.87	-0.12	-0.98	-0.12	-0.98	-0.49	-0.18	0.56	0.03
TNT	-0.27	-0.49	0.09	-0.87	-0.10	-1.03	-0.46	-0.69	-0.54	-0.15	0.70	0.38
PL	-0.33	-1.05	-0.13	-1.03	0.01	-0.53	0.26	-0.84	0.2	-0.49	-0.03	-0.60
NGP	-0.16	-0.78	0.12	-1.19	0.11	-0.76	0.35	-0.65	-3.49	2.57	-0.15	-0.28
TGW	-0.10	-0.20	0.68	0.55	0.26	-0.59	-0.16	-0.38	-0.07	-0.17	-0.26	-0.43
GL	-0.003	-0.53	-0.02	-0.58	-2.47	2.88	-1.59	1.64	-0.05	-0.41	0.18	-0.17
GB	0.01	-0.44	0.03	-0.41	0.017	-0.15	-0.23	-0.13	-0.15	-0.55	-0.01	-0.58
L/B R	0.84	0.76	0.51	-0.004	-2.78	0.19	-1.97	5.64	1.01	1.16	0.21	-0.93
GYP	-0.18	-0.51	0.30	-0.50	0.20	-0.33	-0.29	-0.60	-0.40	-0.20	0.46	-0.01

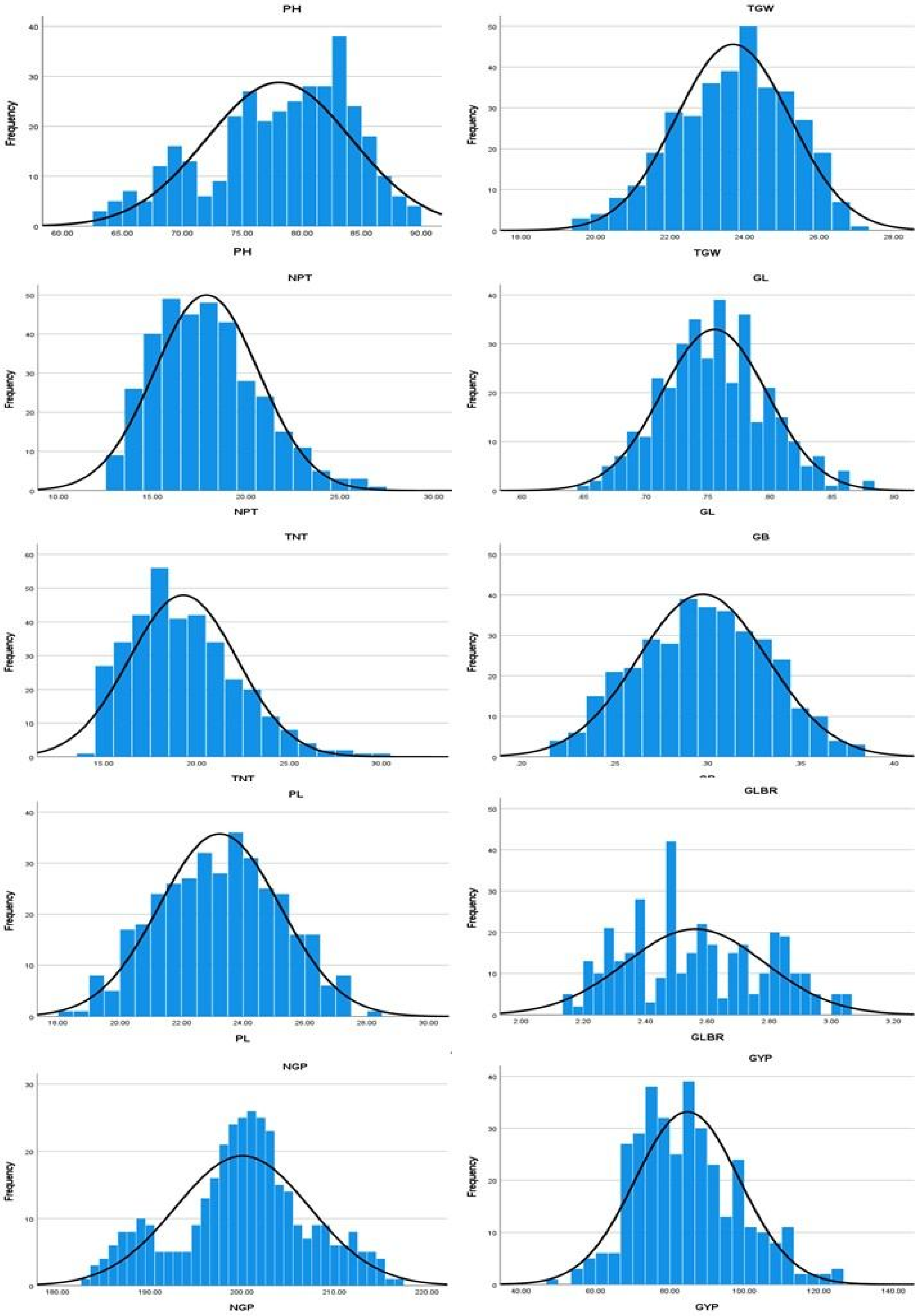
Where, SKW – skewness, KRT – Kurtosis, PH – Plant Height, NPT – Number of Productive Tillers, TNT – Total Number of Tillers, PL – Panicle Length, NGP – Number of Grains per Panicle, TGW – Thousand Grain Weight, GL – Grain Length, GB – Grain Breath, L/B R – Length/Breath ratio and GYP – Grain Yield per Plant.

Table 3. Skewness and Kurtosis values for six rice crosses in F_3 generation

F_3	Cross 1		Cross 2		Cross 3		Cross 4		Cross 5		Cross 6	
Traits	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**	**SKW**	**KRT**
PH	-0.53	-0.27	-0.27	-0.96	-0.11	-1.30	-0.08	-1.25	-0.09	-1.22	0.17	-0.75
NPT	-0.08	-0.41	0.13	-0.97	-0.42	-0.66	-0.65	-0.55	-0.19	-0.27	-0.19	-0.27
TNT	-0.24	-0.34	0.11	-1.07	-0.67	-0.47	-0.73	-0.32	-0.32	-0.29	0.52	0.46
PL	-0.40	-0.90	-0.30	-0.81	-0.41	-0.26	0.43	-0.75	0.61	-0.19	-0.20	-0.89
NGP	-0.35	-0.61	0.20	-1.14	0.41	-0.89	0.48	-0.61	0.09	-1.43	-0.08	-0.58
TGW	0.14	-0.77	-0.18	0.23	0.27	-0.41	-0.56	1.01	0.12	-0.51	-0.08	-0.41
GL	0.16	-0.46	-0.07	-0.50	0.20	-0.43	-0.09	-0.58	-0.23	-0.16	0.55	0.45
GB	0.32	-0.53	-0.03	-0.40	0.15	-0.63	-0.11	-0.65	-0.33	-0.31	-0.13	-0.70
L/B R	0.43	-0.06	0.56	0.01	0.30	0.51	-4.55	3.48	1.08	1.20	0.25	-0.99
GYP	-0.13	-0.66	0.31	-0.61	0.44	-0.11	-0.36	-0.89	0.22	-1.05	-0.04	-0.53

Where, SKW – skewness, KRT – Kurtosis, PH – Plant Height, NPT – Number of Productive Tillers, TNT – Total Number of Tillers, PL – Panicle Length, NGP – Number of Grains per Panicle, TGW – Thousand Grain Weight, GL – Grain Length, GB – Grain Breath, L/B R – Length/Breath ratio and GYP – Grain Yield per Plant.

Fig. 1. Frequency distribution of F_2 generation in cross ADT 43 X TKM 6 for ten



biometrical traits

Fig. 2. Frequency distribution of F_2 generation in cross ADT 43 X ASD 12 for ten biometrical traits

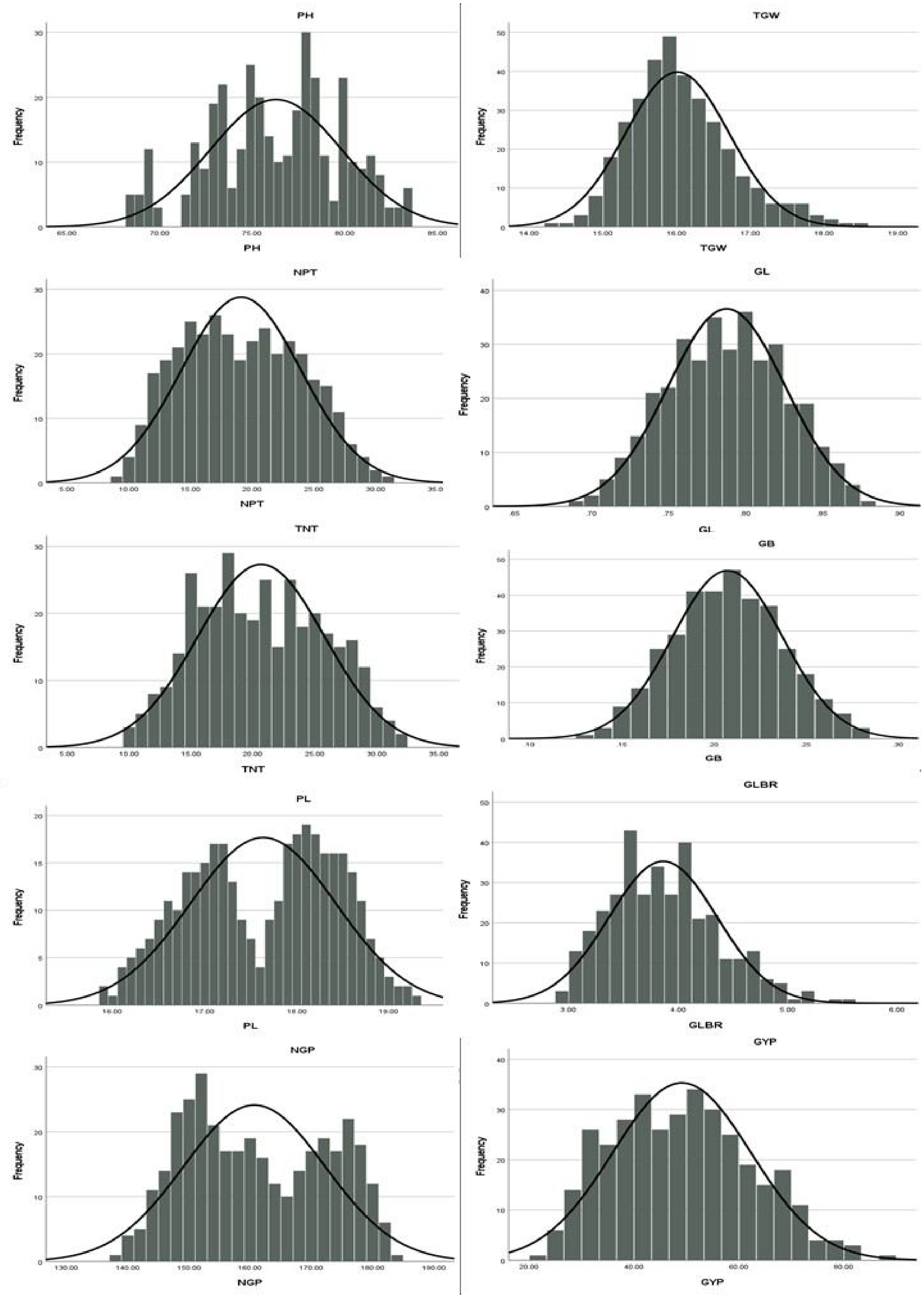


Fig. 3. Frequency distribution of F_2 generation of cross ADT 45 X TKM 6 for ten biometrical traits

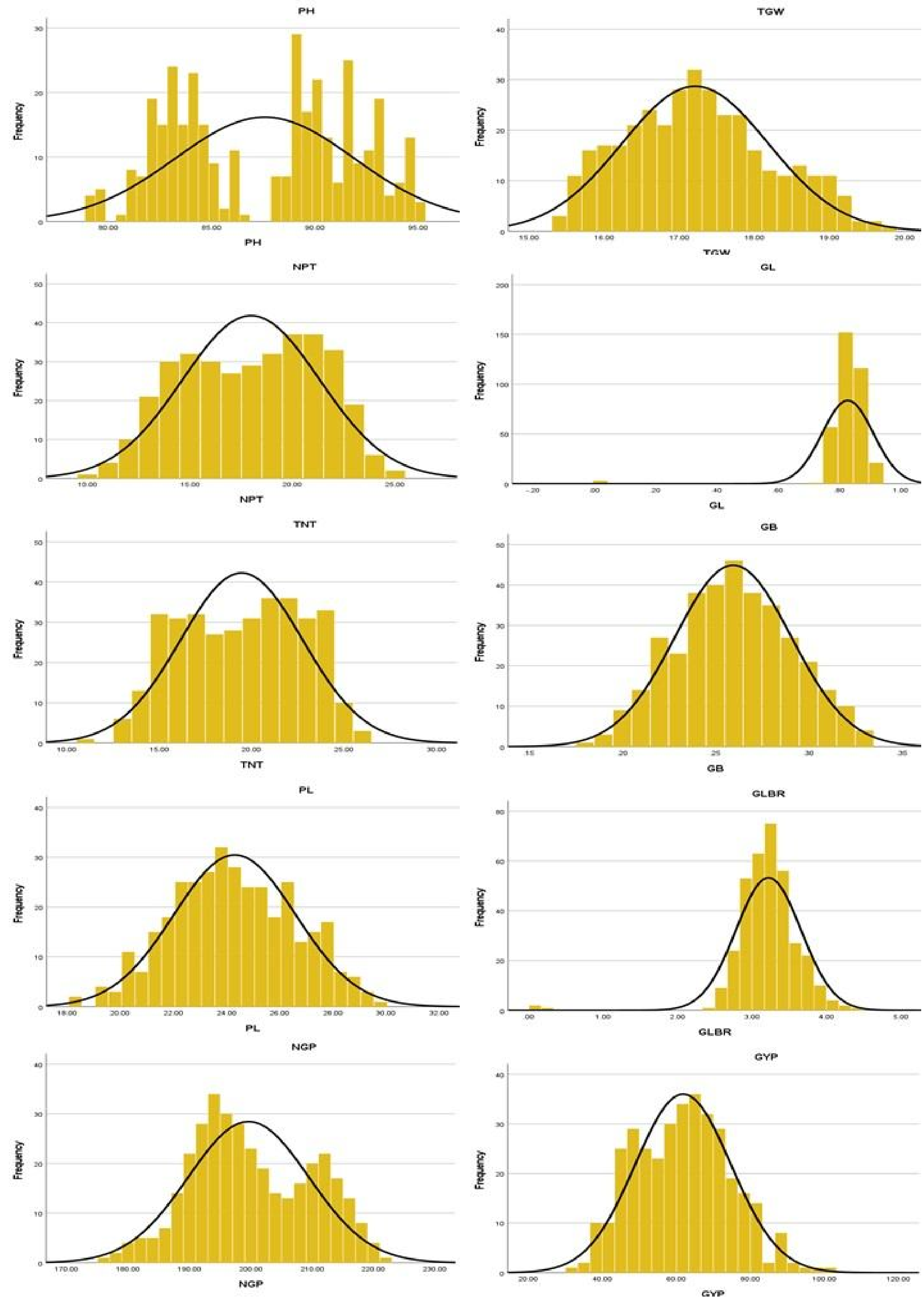


Fig. 4. Frequency distribution of F_2 generation of cross ADT 45 X ASD 12 for ten biometrical traits

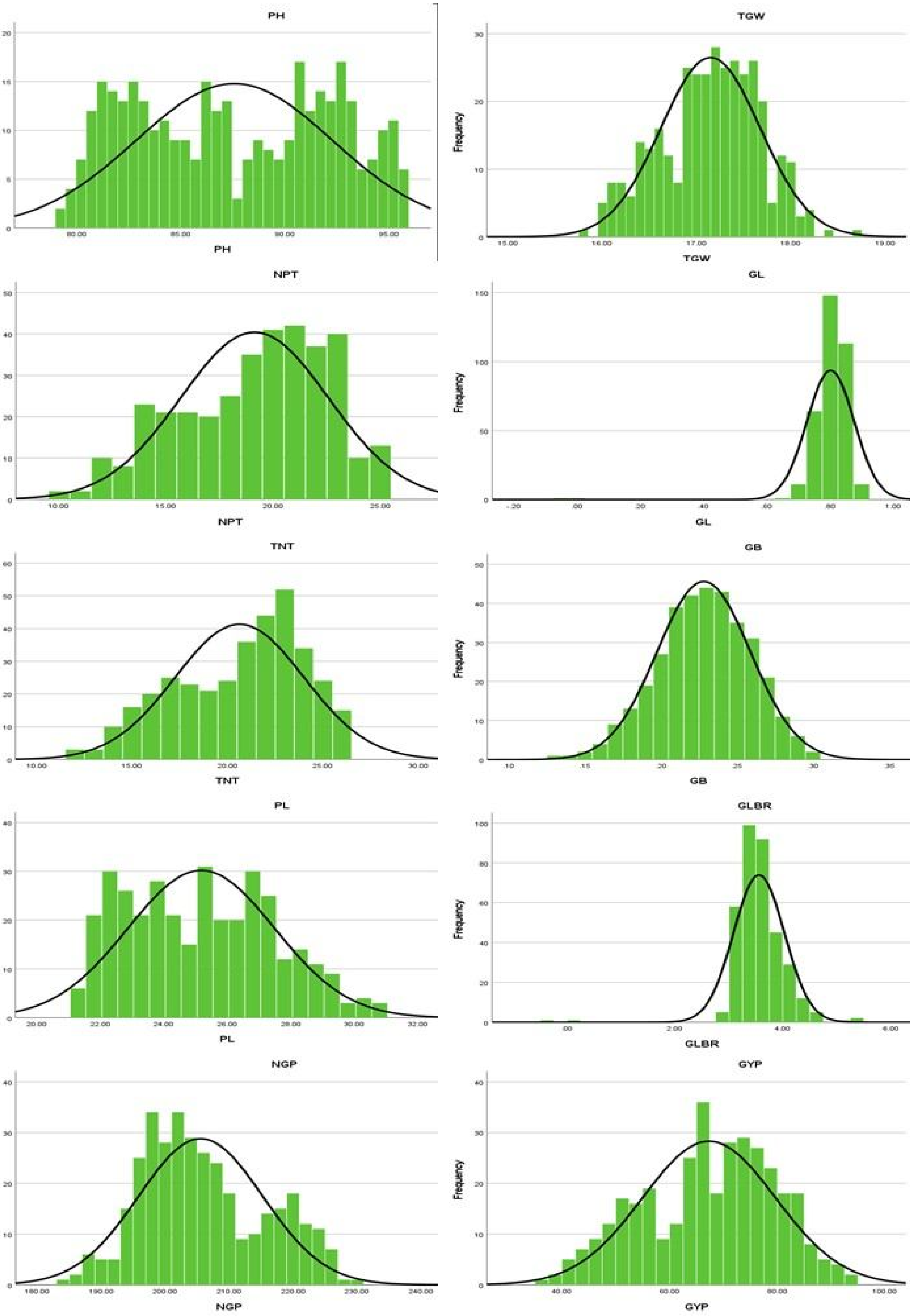


Fig. 5. Frequency distribution of F_2 generation of cross ASD 16 X TKM 6 for ten biometrical traits

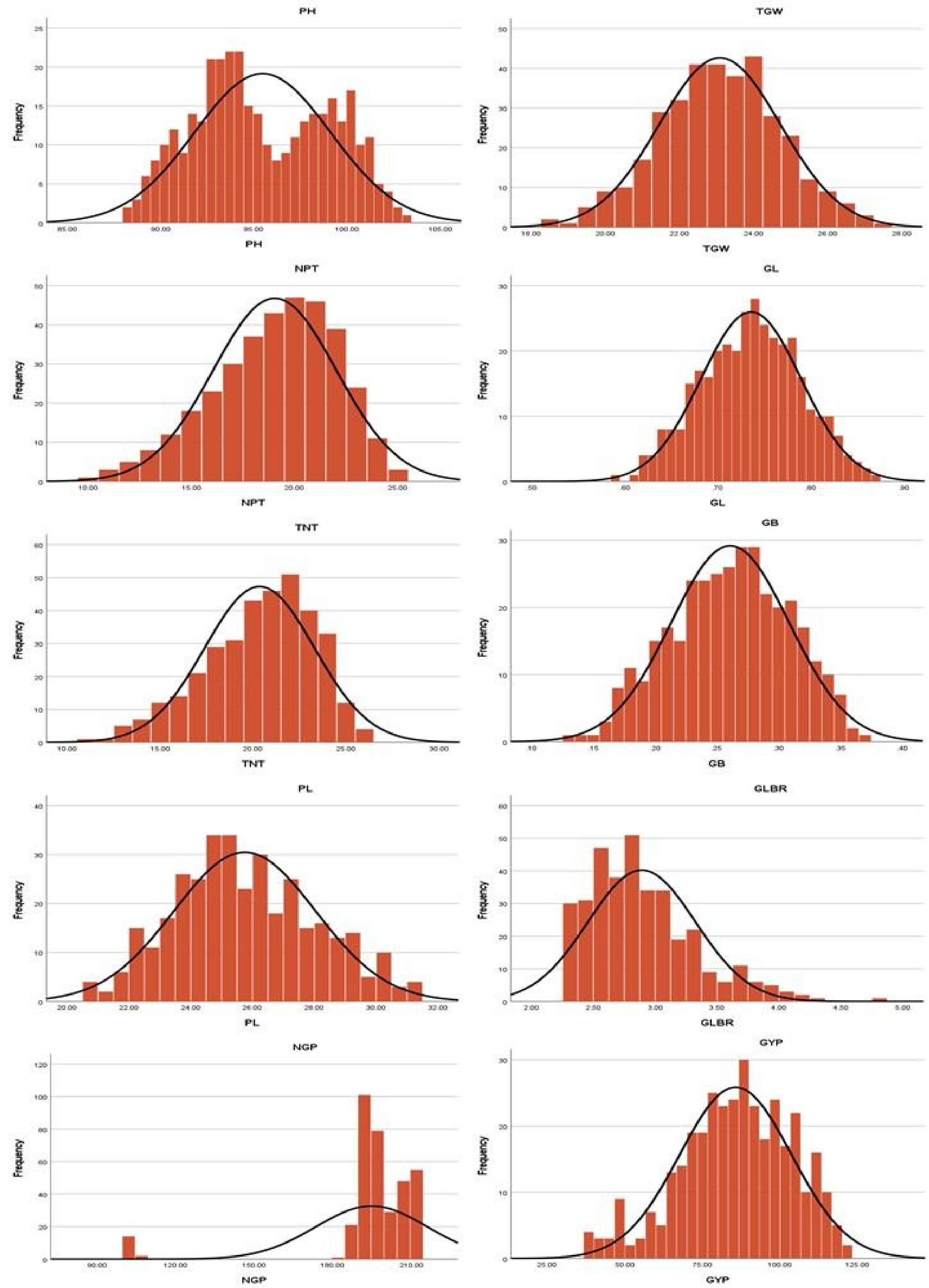
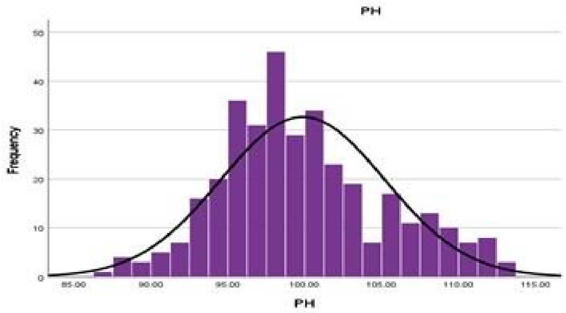


Fig. 6. Frequency distribution of F_2 generation of cross ASD 16 X ASD 12 for ten biometrical traits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Frequency
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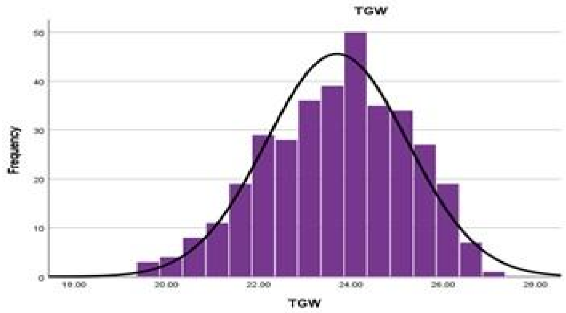
20
30
40
50
85.00
90.00
95.00
100.00
105.00
110.00
115.00
PH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Frequency
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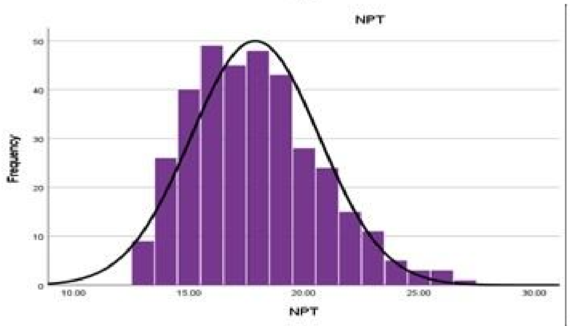
40
50
18.00
20.00
22.00
24.00
26.00
28.00
TGW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Frequency
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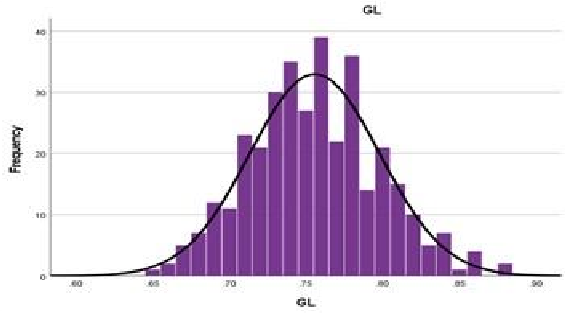
40
50
10.00
15.00
20.00
25.00
30.00
NPT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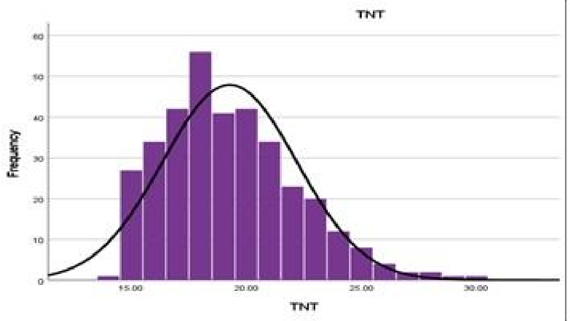
GL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15.00
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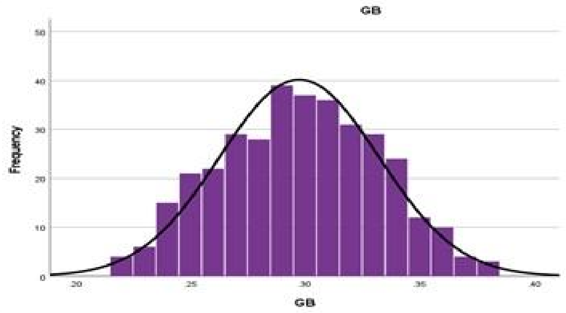
TNT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Frequency
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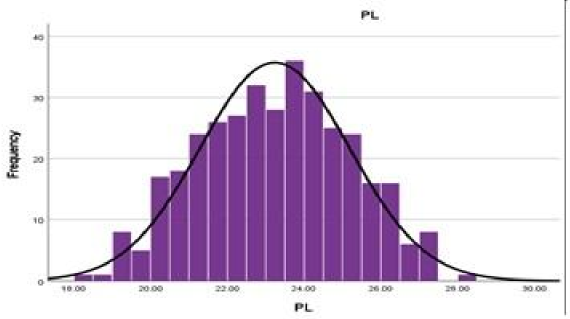
GB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Frequency
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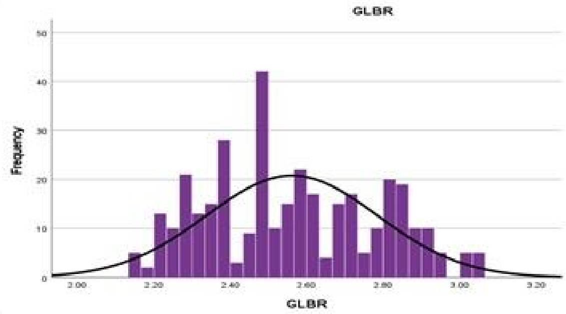
PL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2.00
2.20
2.40
2.60
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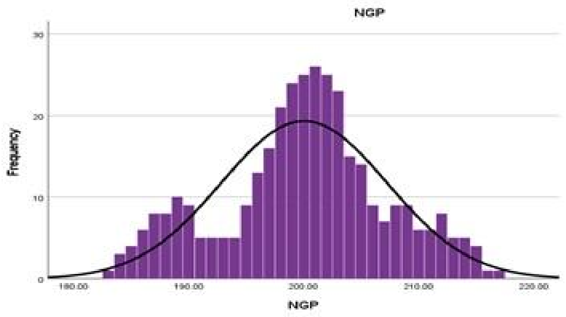
3.00
3.20
GLBR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Frequency
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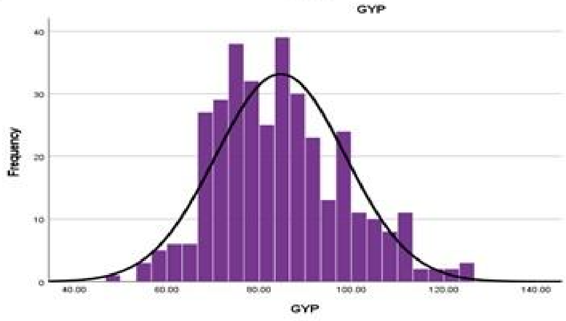
210.00
220.00
NGP


GYP
Frequency
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10
20
30
40
40.00
60.00
80.00
100.00
120.00
140.00
GYP

Fig. 7. Frequency distribution of F_3 generation of cross ADT 43 X TKM 6 for ten biometrical traits

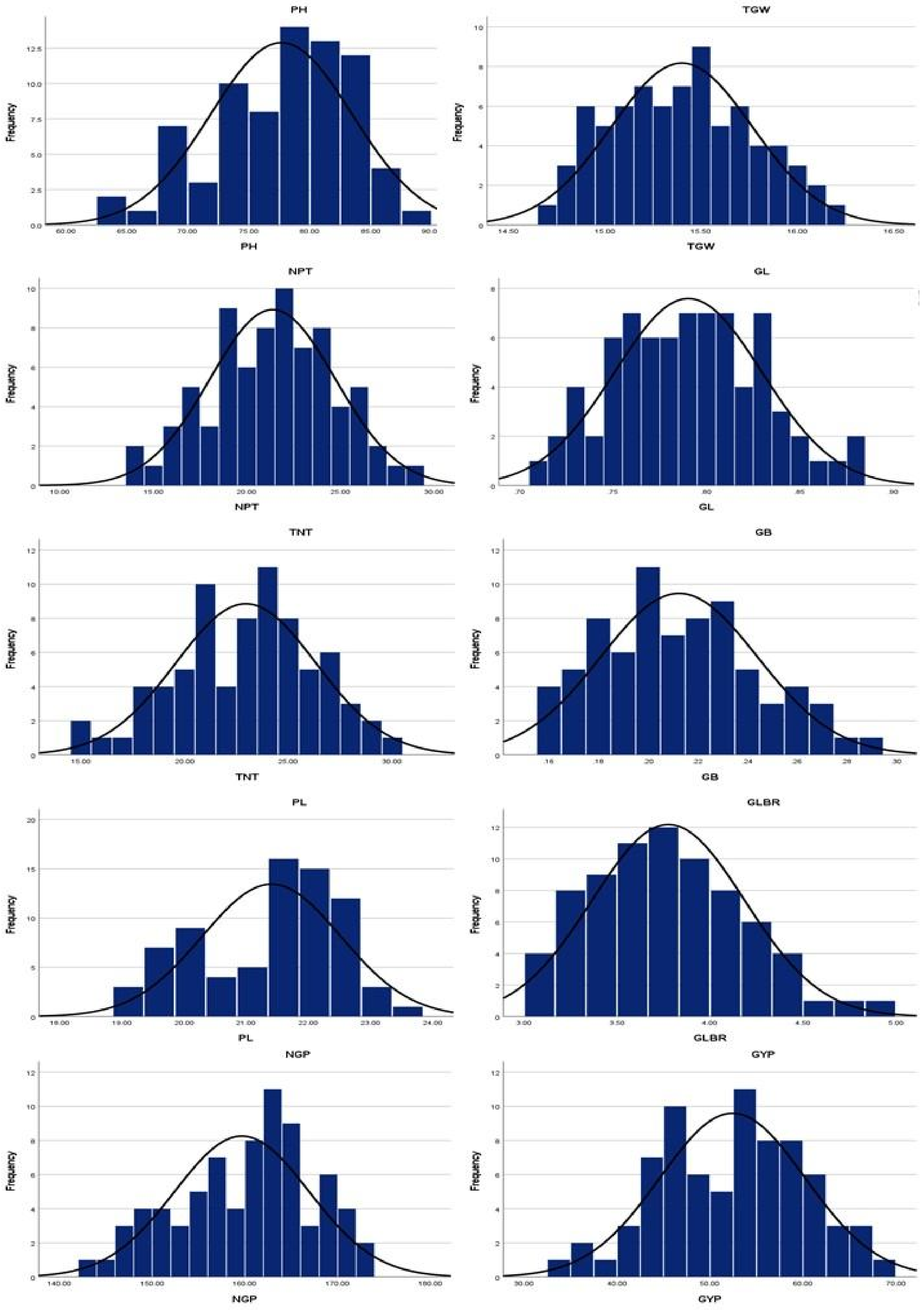

Fig. 8. Frequency distribution of F_3 generation of cross ADT 43 X ASD 12 for ten biometrical traits

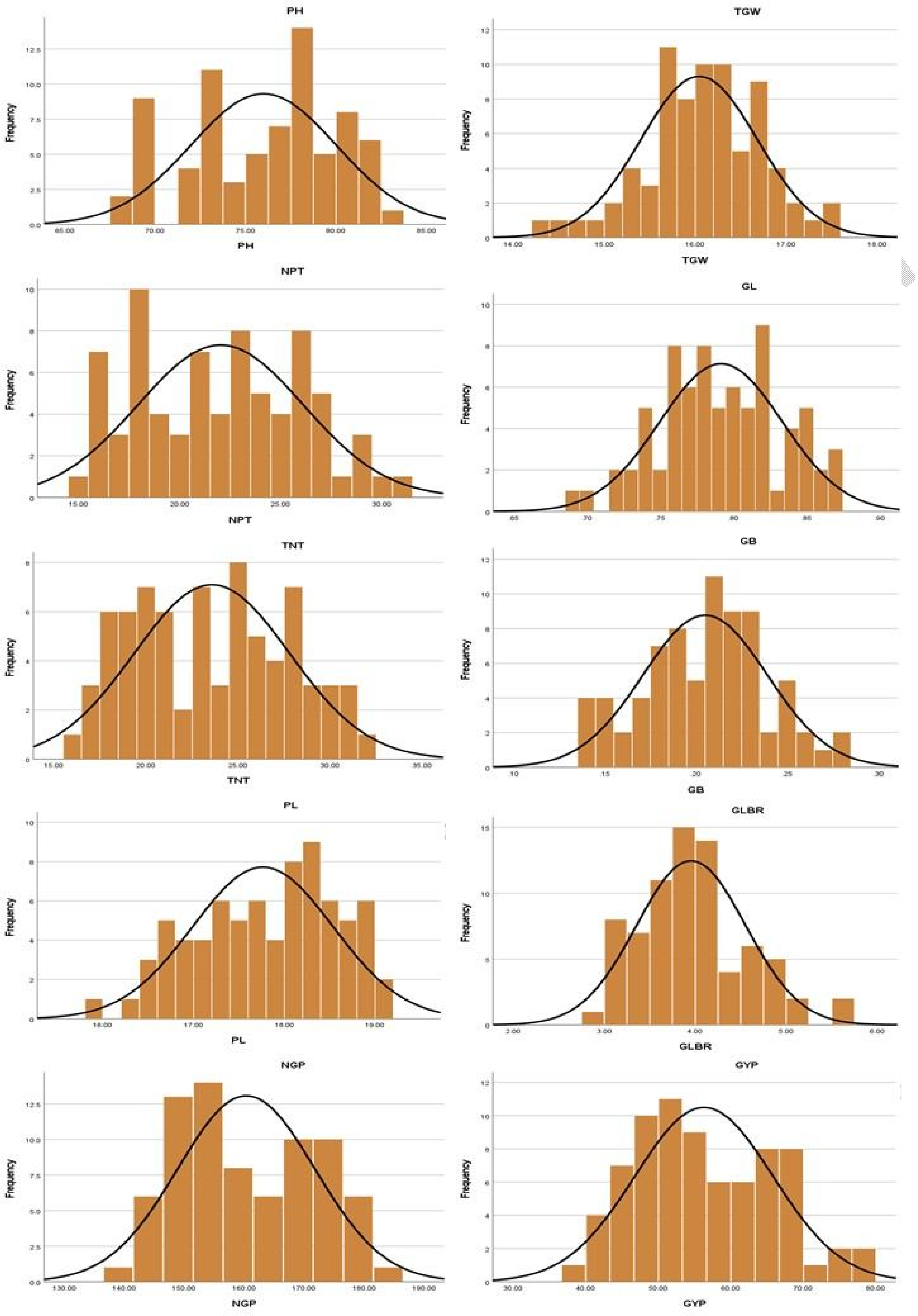

Fig. 9. Frequency distribution of F_3 generation of cross ADT 45 X TKM 6 for ten biometrical traits

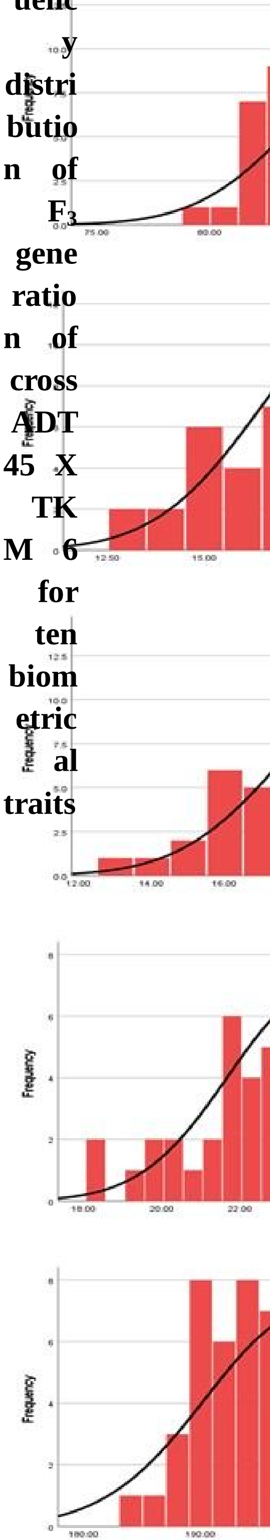

Fig. 10. Frequency distribution of F_3 generation of cross ADT 45 X ASD 12 for ten biometrical traits

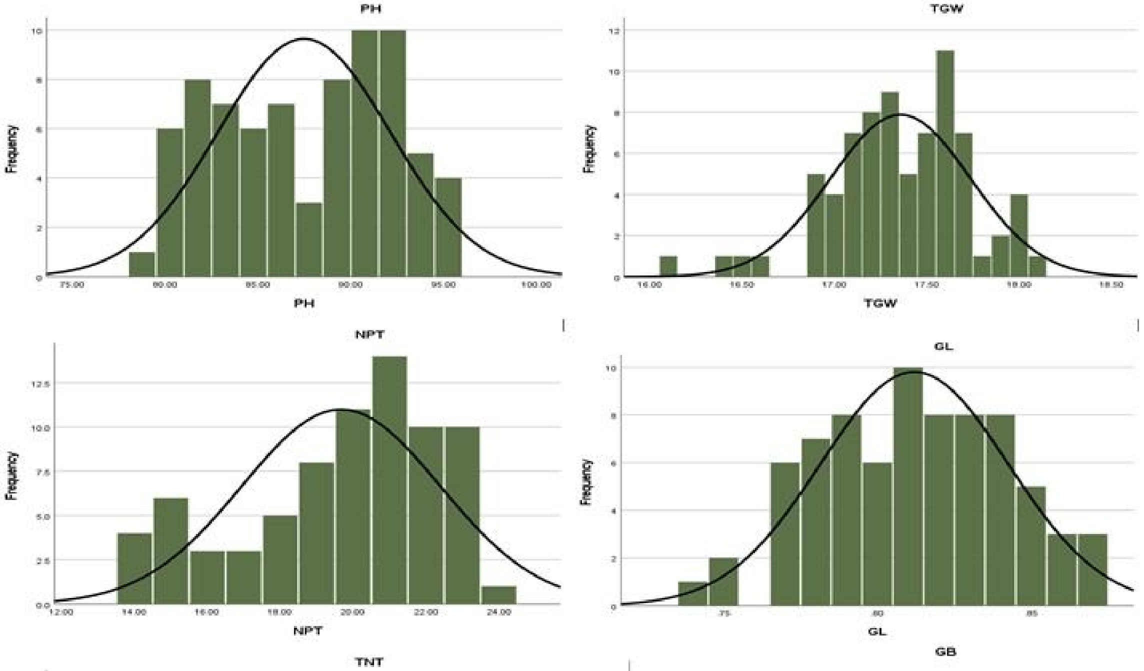

Fig. 11. Frequency distribution of F_3 generation of cross ASD 16 X TKM 6 for ten biometrical traits

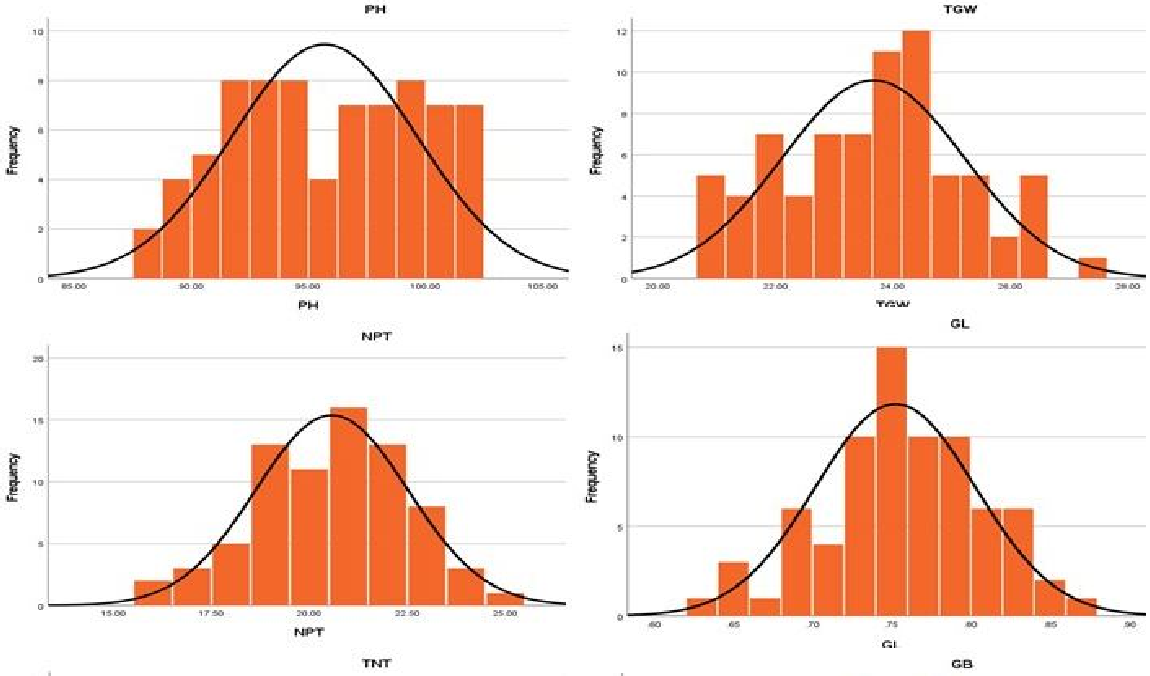

Fig. 12. Frequency distribution of F_3 generation of cross ASD 16 X ASD 12 for ten biometrical traits