Sindh Univ. Res. Jour. (Sci. Ser.) Vol. 48(3) 541-546 (2016)

SINDH UNIVERSITY RESEARCH JOURNAL (SCIENCE SERIES)

Covariance Structure among Yield-Components and Morphological Traits for Oilseed Genotypes

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Received 28th October 2015 and Revised 13th March 2016

Abstract: Factor-Analysis was conducted using estimation methods: Principal-Components-Factor-Analysis (PCFA) and Maximum-Likelihood-Factor-Analysis (MLFA) to investigate the covariance-structure which may exists among physical/morphological and yield component traits and to replace the system of traits into two or three factors that can represent and explain maximum of variation present in original system of traits for Brassica-Napus, Helianthus-Annuus and Arachis-Hypogaea. Factor-Analysis on multi-trait of Brassica-Napus data showed that first four factors extracted 85.45% and 72.3% of total variation present in the original system of traits using PCFA and MLFA respectively. Both methods produced approximately same loadings for traits for factor-1 and factor-4, while factor-2 and factor-3 were observed slightly different. Traits such as: days-to-maturity, plant-height, branches/plant and silique/plant all have high positive loadings for factor-1 in both methods and so this factor might be labeled as biological-yield whereas factor-2 appeared as contrast in days-to-flowering with seeds-weight in PCFA but days-to-flowering has only dominating loading for factor-2 using MLFA so it can be labeled as flowering-time factor. Similarly, factor-4 turned out as oil-yield factor in both methods. The estimated residual matrices ($R - \tilde{L}\tilde{L} - \tilde{\Psi}$), showed that MLFA estimates of loadings($\tilde{L}$) and specific-variances($\tilde{\Psi}_i$) did better job in reproducing R as compared to PCFA estimates. So comparison based on residual-matrices, possible factors extracted and interpreted using MLFA can be considered more reliable. In context of Helianthus-Annuus multi-trait data, both methods showed that first four factors extracted 87.4% and 73.5% of total variability respectively and produced same loading pattern for first three factors while loading pattern for fourth factor was turned out different. Days-to-flowering-initiation, days-to-flowering-completion and days-to-maturity all have high positive loadings for factor-1 in both methods so it might be labeled as flowering-duration factor whereas in second factor: head-diameter and %oil-contents both have high loading and it might be regarded as yield factor in both methods. In comparison of methods w.r.t. specific-variances and estimated residual-matrices, PCFA was found to be more appropriate as compared to MLFA. Similarly, factor analysis using Arachis-Hypogaea data revealed that PCFA extracted three factors and captured 83.4% while MLFA extracted four factors with 80.3% of total variation in multi-trait system. Moreover, shelling% and SMK% showed high positive loadings for factor-1 in both methods so it might be labeled as Arachis-Hypogaea-yield factor. Also in factor-2, germination% and days-to-maturity, both showed high loading in PCFA and only days-to-maturity showed high loading in factor-2 using MLFA and it might be regarded possibly as time-to-biological-yield factor in both estimation methods.

Keywords: Principal-Components-Factor-Analysis; Maximum-Likelihood-Factor; covariance-structure; loadings; specific-variances.

1. INTRODUCTION

Oilseed breeder interested in covariance or correlation structure among physical/morphological and yield component traits and in present study covariance structure among system of traits of oilseed genotypes for selected crops was analyzed and interpreted. In literature a series of statistical techniques exists which can be used in modeling crops yield but factor analysis is most commonly and effectively used towards a clear understanding about covariance structure which exists among system physical and yield component traits. Factor Analysis used by Walton (1972) to reduce a larger system of traits into two or three variables called factors that capture the maximum variability and detect the covariance structure present among traits for their classification. Thurstone (1931) used factor analysis as a tool for data reduction and covariance structure detection. Similarly, factor analysis used by Mohamed (1999) in order to identify growth and plant traits of wheat. Also Leilah *et al.* (2005) used factor analysis to elaborate correlation structure present in soybean traits. Similar analysis was also conducted by Naser and Leilah (1993) to explain covariance structure among various yield and other physical traits of sugar beet and sesame crops data respectively. Bello and Olaoye (2009) discussed that breeding for high yield of maize requires information on the nature, magnitude of variation in the available materials, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters. Arshad *et al.* (2010) analyzed 37 sunflower genotypes with 8 agronomic characters under field conditions in order to estimate genetic parameters, correlation coefficient, path analysis and principal components analysis. ANOVA, mean yield and its components revealed significant differences among all the genotypes for all the traits indicating the diverse nature of hybrids.

Yol *et al.* (2010) evaluated characters association by conducting *Path analysis* and *Factor analysis* on 345 sesame hybrids originating from twenty nine sesame

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producing countries. It was observed that plant height, number of branches, number of capsules/plant and 1000-seed_weight had positive significant effect on seed yield while days to first flowering and 50% flowering had showed negative effect on seed yield. Factor analysis reduced the covariance structure of nine traits into three factors and these three factors captured about 70% of variation. According to factor analysis; plant height, number of branches and number of capsules/plant can be considered as important characters of sesame. Both analyses suggested that sesame breeding for higher seed yield could be based on these characters as selection criteria. Lin *et al*. (2011) analyzed 52 rice cultivars to access the genetic differences among cultivars using factor analysis. A high variability in different functional properties in rice flour was observed. Factor analysis indicated that 4- factors containing: amylose content, gel textural, gelatinization and protein content explained 80% of the total variation present in the rice data. A larger role of amylose with respect to protein and lipid in determining the rice flour quality was also observed using correlation analysis.

Vahid *et al.* (2011) classified bread wheat cultivars and find existing relations among yield parameters for grain in drought environment. In the factor analysis, they observed that there exists 3-hidden factors and these factors contributed about 88% variability of the total variation present in the data. These factors were identified as yield potential, harvest index and phenological factors.

Objectives of study are:

1. To elaborate the covariance structure present among yield related and other morphological traits of oilseed genotypes in term of few but unobservable random quantities (called factors).

2. Comparison between estimation methods: Principal-Component-Factor-Analysis (PCFA) and Maximum-Likelihood-Factor-Analysis (MLFA) used for estimation of parameters of factor model in factor analysis.

2. MATERIALS AND METHODS

Multi-traits (morphological and yield component traits) data for three oilseed crops: *Brassica Napus, Helianthus Annuus* and *Arachis Hypogaea* was analyzed and interpreted using multivariate statistical technique; *Factor Analysis*. Details of traits included in analysis for each oilseed crop were listed in first columns of each Table given in section-3. Factor Analysis (FA) is used to investigate the covariance structure which may exists among physical and yield component traits and one step ahead it identifies the categories of similar traits/characters with the objective to determine how many categories are sufficient to capture the bulk of the information present in the original set/system of traits.

Factor analysis can be considered as a forward step of Principal Component Analysis (PCA) and in methodology if the observable matrix say "$\boldsymbol{Z}$" of random traits say "$\boldsymbol{p}$" components which has mean vector "$\boldsymbol{\mu}$" with variance-covariance matrix "$\sum$" then factor model postulates that Z is linearly dependent on a few but unobservable random quantities/variables say: $\boldsymbol{F_1, F_2, F_3, \ldots, F_m}$ which are called common factors along with $\boldsymbol{\mathcal{E}_1, \mathcal{E}_2, \mathcal{E}_3, \ldots, \mathcal{E}_p}$ as additional sources of variations known as specific-factors or specific-errors. Then factor model can be written as:

$$\boldsymbol{Z_{(P\,X1)} - \mu_{(P\,X1)} = L_{(P\,Xm)} F_{(m\,X1)} + \mathcal{E}_{(m\,X1)}}$$

The coefficient l_{ij}'s are called loadings of $\boldsymbol{i^{th}}$ trait on $\boldsymbol{j^{th}}$ factor and matrix "*L*" in model is known as matrix of loadings. The "*p*" deviations: $\boldsymbol{Z_1-\mu_1, Z_2-\mu_2, Z_3-\mu_3, \ldots Z_p-\mu_p}$ are expressed in term of "$p+m$" random but unobservable variables $\boldsymbol{F_1, F_2, F_3, \ldots, F_m}$ and $\boldsymbol{\mathcal{E}_1, \mathcal{E}_2, \mathcal{E}_3, \ldots, \mathcal{E}_p}$. In the presence of so many unobservable random quantities it is hopeless to verify the above factors model without making some additional assumption which can be viewed from Johnson and Wichern (2007). The proportion of variance of the $\boldsymbol{i^{th}}$ trait contributed by the "$\boldsymbol{m}$" common factors is called the $\boldsymbol{i^{th}}$ communality denoted by $\boldsymbol{h_{ii}}$. Also the part of $\boldsymbol{var(z_i)=\sigma_{ii}}$ due to the specific-factor is called specific-variance. Mathematically it can be written as:

$$\boldsymbol{\sigma_{ii} = (l_{i1}^2 + l_{i2}^2 + \cdots l_{im}^2) + \Psi_i \quad \text{For } i=1, 2, \ldots p}$$

$$\boldsymbol{Var(z_i) = communality + specific\ variance}$$

$$\boldsymbol{communality = h_{i1}^2 = l_{i1}^2 + l_{i2}^2 + \cdots l_{im}^2}$$

$$\boldsymbol{\sum = LL' + \Psi \text{ (in matrix form)}}$$

The $\boldsymbol{i^{th}}$ communality is the sum of squares of loadings of the $\boldsymbol{i^{th}}$ trait on "$\boldsymbol{m}$" common factors. If we have with "$\boldsymbol{p}$" correlated traits say Z_1, Z_2, Z_3, . . ., Z_p then factor analysis represents the original set of traits into smaller number of factors that can capture maximum of variability among original traits. If variance-covariance matrix "$\sum$" of original traits deviated significantly then in such situation factor model would be meaningful then the initial step is to estimate factor loadings l_{ij}'s and specific-variances. In literature two most popular estimation methods such as: Principal Component Factor Analysis (PCFA) and Maximum Likelihood Factor Analysis (MLFA) methods can be used for estimation of model parameters. The solution obtained from either method needed to rotate (here varimax rotation was used) if needed in order to obtain more simplified interpretation of factors.

3. RESULTS AND DISCUSSIONS

In order to analyze the covariance structure that might exists among traits; factor analysis is conducted on correlation matrices of traits using *Principal-Components-Factor-Analysis* (*PCFA*) and *Maximum-Likelihood-Factor-Analysis* (*MLFA*). In the first step all the traits were tested and found to be approximately normally distributed and then factor analysis was conducted on *Brassica Napus* data that consists of "$\boldsymbol{P = 9}$**"** traits each measured on "$\boldsymbol{n = 80}$**"** observation (genotypes) out of which four **(**$\boldsymbol{m = 4}$**)** factors were extracted using estimation methods: *PCFA* and *MLFA* and resultant factors loadings, communalities, specific factors, factors variances and their %variation were displayed in **(Table-3.1)**. It can be seen in **(Table-3.1)** that first four factors extracted 85.45% and 72.3% enough variation of total variation present in the original multi-traits data using *PCFA* and *MLFA* respectively. In this case both methods produced approximately same loadings in both estimation methods for different traits in factor-1 and factor-4 while factor-2 and factor-3 were observed slightly different in both estimation methods. Traits such as: days to maturity (*DM*), plant height (*PH*), branched per plant (*B/P*) and silique per plant (*S/P*) all showed high positive loadings for factor-1 in both estimation methods and so this factor might be labeled as biological-yield factor whereas the second factor appeared to be a contrast in days to flowering (*DF*) with seeds weight (*SW*) in *PCFA* but days to flowering (*DF*) has only dominating loading for factor-2 using *MLFA* so it can be labeled as flowering-time factor. Similarly, factor-4 turned out as oil-yield factor using both estimation methods. The four factor solution, using *PCFA*, captured much of the total standardized variation with reasonably small values for specific-variances ($\widetilde{\Psi}_i$), while four factor solution, using *MLFA*, accounted less standardized variation of total variability as compared to *PCFA* but estimated specific-variances ($\widehat{\Psi}_i$) in case of *MLFA* was observed to be larger in some cases (for example in silique length (*SL*) and in seeds weight (*SW*)) and this suggested that some traits require specific attributes while for others traits not require.

The estimated residual matrix: $R - \tilde{L}\tilde{L} - \widetilde{\Psi}$ for four-factor solutions using both *PCFA* and *MLFA*, which are listed in **(Table-3.4)**, showed that *MLFA*(regular cases) estimates of factor loadings: $\hat{L}$ and specific-factor/variances: $\widehat{\Psi}_i$ did better job in reproducing R as compared to *PCFA*(Italic cases) estimates of factor loadings $\tilde{L}$ and specific-factor/variances $\widetilde{\Psi}_i$ because of having small values in the residual matrix obtained from *MLFA*. So residual matrices based comparison the possible factors extracted and interpreted using *MLFA* as estimation methods can be considered more reliable.

In context approximating correlation structure among nine *Helianthus Annuus* traits each measured on sixty five observations/genotypes, both *PCFA* and *MLFA* factor loadings estimation procedure were analyzed and resultant factors loadings, communalities, specific-variance and %variation explained by each extracted factor were displayed in **(Table-3.2)**. In **(Table-3.2)**, it can be observed that first four factors extracted 87.4% and 73.5% of total variability present in the whole system of traits using *PCFA* and *MLFA* respectively. In **(Table-3.2)**, both methods produced approximately same loadings pattern for first three factors while loadings pattern for fourth factor turned out different. It can be seen that days to flowering initiation (*DFI*), days to flowering completion (*DFC*) and days to maturity (*DM*) all showed high positive loadings for factor-1 in both estimation methods and so this factor might be labeled as flowering-duration factor while in second factor: head diameter (*HD*) and oil content (*OC*) both have high loadings and it might be regarded as yield-factor in both estimation methods. Moreover, 100-seeds-weight has high loadings for factor-3 in both methods and this factor might be labeled as yield-weight factor.

In context of comparison between *PCFA* and *MLFA* w. r. t. specific-variances and estimated residual matrices using *Helianthus Annuus* multi-traits data, it was observed that measures such as: estimated specific-variance and %variance (explained by extracted factors) were found to be more appropriate and reliable due to *PCFA* as compared to *MLFA*. Also on the other hand residual matrix listed in **(Table-3.5)** showed very small off diagonal entries which were evidence of good approximation of correlation structure through extracted factors but approximation made is more appropriate and reliable using *MLFA* because of having small entries in the residual matrix as compared to entries in residual matrix provided by *PCFA*.

Similarly, factor analysis was also conducted for *Arachis Hypogaea* genotypes' multi-traits data which consists of "*P*=6" traits each measured on 56 genotypes (taken as observations) and summary results obtained by using both *PCFA* and *MLFA* estimation methods were displayed in **(Table-3.3)**. Residual matrix given in **(Table-3.6)** was also computed in order to test the effectiveness of each method in approximating the correlation matrices/covariance-structure in term of few extracted factors.

In (**Table-3.3)**, it can be seen that *PCFA* extracted first three factors and captured 83.4% of total variability present in original system of traits while *MLFA* extracted four factors and explained 80.3% of total variability present in the system of traits and it means

that *PCFA* worked more efficiently as compared to *MLFA*. Moreover, a wide variation among factors' loadings was observed in both estimation methods but with reference to percent variation accounted, estimated communalities and specific-factor/variance, principal component solution of factor analysis can be suggested more appropriate. It can also be seen that shelling (%) and SMK (%) both showed high positive loadings for factor-1 in both *PCFA* and *MLFA* estimation methods and so this factor might be labeled as *Arachis Hypogaea*-yield factor.

Table 3.1 Analysis of *Brassica Napus* traits using *Principal Component Factor Analysis* (PCFA) and *Maximum Likelihood Factor Analysis* (MLFA)

Traits	Principal Component Factor Analysis						Maximum Likelihood Factor Analysis					
	Estimated Varimax Rotated Factor Loading				$\tilde{h}_{ii}^2$	$\tilde{\Psi}_i$	Estimated Varimax Rotated Factor Loadings				$\hat{h}_{ii}^2$	$\hat{\Psi}_i$
	F_1	F_2	F_3	F_4			F_1	F_2	F_3	F_4		
Days to Flowering (DF)	0.018	0.835*	-0.248	0.064	0.763	0.237	0.002	0.966*	-0.199	-0.111	0.986	0.014
Days to Maturity (DM)	0.774*	0.204	-0.213	-0.293	0.773	0.227	0.692*	0.224	-0.253	0.204	0.634	0.366
Plant Height (PH)	0.947*	-0.001	-0.037	0.107	0.910	0.090	0.921*	0.025	-0.043	-0.097	0.859	0.141
Branches / Plant (B/P)	0.958*	-0.013	-0.088	0.078	0.932	0.068	0.962*	0.008	-0.114	-0.081	0.945	0.055
Silique Length (SL)	0.175	-0.018	-0.85*	0.187	0.789	0.211	0.193	0.030	-0.452	-0.087	0.250	0.750
Seeds per Silique (S/S)	0.014	0.241	-0.77*	-0.372	0.796	0.204	-0.021	0.203	-0.94*	0.242	0.977	0.023
Silique / Plant (S/P)	0.951*	0.020	-0.018	0.107	0.916	0.084	0.946*	0.007	-0.059	-0.101	0.908	0.092
Seeds Weight (SW)	-0.067	-0.85*	-0.066	0.077	0.731	0.269	-0.064	-0.470	0.023	-0.089	0.233	0.767
Oil Contents (OC %)	-0.069	-0.007	-0.017	-0.95*	0.909	0.091	-0.069	0.037	-0.051	0.839*	0.713	0.287
Variance	3.359	1.514	1.444	1.202	7.519		3.192	1.249	1.206	0.858	6.505	
%Variance	0.373	0.168	0.160	0.134	0.835		0.355	0.139	0.134	0.095	0.723	

Table 3.2 Analysis of *Helianthus Annuus* traits using *Principal Component Factor Analysis* (PCFA) and *Maximum Likelihood Factor Analysis* (MLFA)

Traits	Principal Component Factor Analysis						Maximum Likelihood Factor Analysis					
	Estimated Varimax Rotated Factor Loadings				$\tilde{h}_{ii}^2$	$\tilde{\Psi}_i$	Estimated Varimax Rotated Factor Loadings				$\hat{h}_{ii}^2$	$\hat{\Psi}_i$
	F_1	F_2	F_3	F_4			F_1	F_2	F_3	F_4		
Days to Flowering Initiation (DFI)	0.856*	-0.172	-0.037	0.093	0.773	0.227	0.734*	-0.160	-0.008	-0.138	0.583	0.417
Days to Flowering Completion (DFC)	0.920*	-0.072	0.049	0.160	0.879	0.121	0.977*	-0.089	0.039	-0.020	0.963	0.037
Days to Maturity	0.874*	0.040	0.059	0.190	0.805	0.195	0.801*	0.004	0.046	-0.168	0.672	0.328
Plant Height (PH)	0.309	-0.229	-0.036	0.92*	0.996	0.004	0.416	-0.315	-0.049	-0.470	0.496	0.504
Head Diameter (HD)	0.017	-0.91*	-0.084	0.113	0.841	0.159	0.024	-0.95*	-0.063	-0.014	0.904	0.096
100Seeds Weight(100SW)	-0.039	-0.02	-0.99*	0.028	0.995	0.005	-0.039	-0.023	-0.99*	-0.023	1.000	0.000
Oil Content (OC)	0.129	-0.89*	0.058	0.126	0.829	0.171	0.136	-0.69*	0.030	-0.166	0.526	0.474
Variance	2.456	1.704	1.011	0.946	6.117		2.328	1.512	1.008	0.297	2.328	
%Variance	0.351	0.243	0.144	0.135	0.874		0.333	0.216	0.144	0.042	0.735	

While in second factor, germination (%) and days to maturity (*DM*) both have high loadings in *PCFA* and only trait: days to maturity (*DM*) has high loading to factor-2 in *MLFA* and it might be regarded possibly as time-to-biological-yield factor in both estimation methods. Similarly, third factor's traits such as: 100-kernel-weight and 20-pod-length showed high loadings in *PCFA* solution and *MLFA* solution and can be labeled as weight-factor and length-factor respectively. As far as estimated residual matrices, given in Table 3.6, are concerned both estimation methods showed very small off diagonal entries which were evidence of good approximation of correlation structure through factors but approximation made was observed more appropriate through *MLFA* (in case of *Arachis Hypogaea*) due to small entries of residual matrix as compared to *PCFA.*

Table 3.3 Analysis of *Arachis Hypogaea* traits using *Principal Component Factor Analysis* (PCFA) and *Maximum Likelihood Factor Analysis* (MLFA)

Traits	Principal Component Factor Analysis					Maximum Likelihood Factor Analysis					
	Estimated Varimax Rotated Factor Loaings			$\tilde{h}_{ii}^2$	$\tilde{\Psi}_i$	Estimated Varimax Rotated Factor Loadings				$\hat{h}_{ii}^2$	$\hat{\Psi}_i$
	F_1	F_2	F_3			F_1	F_2	F_3	F_4		
Germination (%)	-0.317	0.733	0.432	0.824	0.176	0.343	0.455	-0.329	0.312	0.583	0.42
Days Maturity	-0.593	0.648	-0.101	0.782	0.218	0.362	0.876	-0.283	-0.095	0.963	0.04
100-K. Weight	0.219	-0.856	0.221	0.830	0.170	-0.223	-0.288	0.921	0.119	0.672	0.33
Shelling (%)	0.812	-0.293	-0.228	0.796	0.204	-0.905	-0.266	0.168	-0.138	0.496	0.50
20 Pods Length	0.013	-0.071	0.955	0.917	0.083	0.041	-0.037	0.089	0.928	0.904	0.10
SMK (%)	0.882	-0.219	0.125	0.841	0.159	-0.521	-0.408	0.218	0.093	1.000	0.00
Variance	1.936	1.829	1.225	4.991		1.391	1.296	1.119	1.008	4.815	
%Variance	0.323	0.305	0.204	0.832		0.232	0.216	0.187	0.168	0.803	

Table 3.4 Estimated Residual matrix: $R - \tilde{L}\tilde{L} - \tilde{\Psi}$for Brassica Napus traits using PCFA(Italic) and MLFA(Regular)

Traits		DF	DM	PH	B/P	SL	S/S	S/P	SW	OC
Days to Flowering (DF)	(PCFA)		*0.027*	*0.012*	*0.008*	*-0.083*	*-0.014*	*-0.014*	*0.237*	*0.017*
	(MLFA)		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Days to Maturity(DM)	(PCFA)	*0.027*		*-0.043*	*-0.061*	*-0.045*	*-0.016*	*-0.073*	*0.078*	*-0.083*
	(MLFA)	0.000		0.034	-0.005	-0.023	0.001	-0.011	0.018	0.000
Plant Height(PH)	(PCFA)	*0.012*	*-0.043*		*-0.023*	*0.005*	*0.000*	*-0.032*	*0.001*	*0.020*
	(MLFA)	0.000	0.034		-0.002	0.017	-0.001	-0.003	0.012	-0.006
Branches per Plant(B/P)	(PCFA)	*0.008*	*-0.061*	*-0.023*		*-0.010*	*0.019*	*0.006*	*-0.002*	*0.014*
	(MLFA)	0.000	-0.005	-0.002		0.004	0.000	0.002	0.017	0.003
Silique Length(SL)	(PCFA)	*-0.083*	*-0.045*	*0.005*	*-0.010*		*-0.181*	*0.004*	*-0.149*	*0.109*
	(MLFA)	0.000	-0.023	0.017	0.004		0.001	-0.011	-0.046	-0.004
Seeds per Silique(S/S)	(PCFA)	*-0.014*	*-0.016*	*0.000*	*0.019*	*-0.181*		*0.020*	*0.045*	*-0.104*
	(MLFA)	0.000	0.001	-0.001	0.000	0.001		0.000	0.000	0.000
Seeds per Pod(S/P)	(PCFA)	*-0.014*	*-0.073*	*-0.032*	*0.006*	*0.004*	*0.020*		*-0.024*	*0.019*
	(MLFA)	0.000	-0.011	-0.003	0.002	-0.011	0.000		-0.039	-0.001
Seeds Weight(SW)	(PCFA)	*0.237*	*0.078*	*0.001*	*-0.002*	*-0.149*	*0.045*	*-0.024*		*-0.036*
	(MLFA)	0.000	0.018	0.012	0.017	-0.046	0.000	-0.039		-0.009
Oil Content(OC)	(PCFA)	*0.017*	*-0.083*	*0.020*	*0.014*	*0.109*	*-0.104*	*0.019*	*-0.036*	
	(MLFA)	0.000	0.000	-0.006	0.003	-0.004	0.000	-0.001	-0.009	

Table 3.5 Estimated Residual matrix: $R - \tilde{L}\tilde{L} - \tilde{\Psi}$ for *Helianthus A.* traits using PCFA(Italic) and MLFA(Regular)

Traits		DFI	DFC	DM	PH	HD	100SW	OC
Days to Flowering Initiation(DFI))	(PCFA)		*-0.080*	*-0.144*	*0.028*	*-0.012*	*-0.023*	*-0.038*
	(MLFA)		0.000	0.002	-0.002	0.000	0.000	0.002
Days to Flowering Completion(DFC))	(PCFA)	*-0.080*		*-0.047*	*-0.004*	*0.011*	*0.005*	*-0.007*
	(MLFA)	0.000		0.000	0.000	0.000	0.000	0.000
Days to Maturity(DM))	(PCFA)	*-0.144*	*-0.047*		*-0.024*	*0.020*	*0.015*	*0.026*
	(MLFA)	0.002	0.000		0.001	0.000	0.000	-0.004
Plant Height(PH))	(PCFA)	*0.028*	*-0.004*	*-0.024*		*-0.002*	*-0.003*	*-0.005*
	(MLFA)	-0.002	0.000	0.001		0.000	0.000	0.002
Head Diameter(HD))	(PCFA)	*-0.012*	*0.011*	*0.020*	*-0.002*		*-0.020*	*-0.158*
	(MLFA)	0.000	0.000	0.000	0.000		0.000	0.000
100 Seeds Weight(100SW))	(PCFA)	*-0.023*	*0.005*	*0.015*	*-0.003*	*-0.020*		*0.026*
	(MLFA)	0.000	0.000	0.000	0.000	0.000		0.000
Oil Contents(OC))	(PCFA)	*-0.038*	*-0.007*	*0.026*	*-0.005*	*-0.158*	*0.026*	
	(MLFA)	0.002	0.000	-0.004	0.002	0.000	0.000	

Table 3.6 Estimated Residual matrix: $R - \tilde{L}\tilde{L} - \tilde{\Psi}$ for *Arachis H.* traits using PCFA(Italic) and MLFA(Regular)

Traits		Ger%	DM	100-KW	Shelling%	20-PL	SMK%
Germination%	(PCFA)		*-0.033*	*0.127*	*0.040*	*-0.099*	*-0.026*
	(MLFA)		0.000	0.000	0.000	0.000	-0.004
Days Maturity	(PCFA)	*-0.033*		*0.102*	*0.053*	*0.019*	*0.061*
	(MLFA)	0.000		0.000	0.000	0.000	0.000
100-K. Weight (gm)	(PCFA)	*0.127*	*0.102*		*0.039*	*-0.082*	*0.037*
	(MLFA)	0.000	0.000		0.000	0.000	0.000
Shelling (%)	(PCFA)	*0.040*	*0.053*	*0.039*		*0.046*	*-0.148*
	(MLFA)	0.000	0.000	0.000		0.000	0.000
20 Pods Length(cm)	(PCFA)	*-0.099*	*0.019*	*-0.082*	*0.046*		*-0.046*
	(MLFA)	0.000	0.000	0.000	0.000		0.000
SMK (%)	(PCFA)	*-0.026*	*0.061*	*0.037*	*-0.148*	*-0.046*	
	(MLFA)	-0.004	0.000	0.000	0.000	0.000	

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