# Effect of different locations on yield and yield trial of potato (Solanum tuberosum L.)

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### ABSTRACT

Statistical Analysis of 12 varieties of potato to study the effect of five different locations on its yield was conducted during 2005-2006. The analysis was conducted on 12 varies of potato *viz.*, Gulmarg Special(GS),Gulmarg Special-1(GS1), Gulmarg Special-2(GS2), Gulmarg Special-3(GS3), Gulmarg Special-4(GS4), Gulmarg Special-5(GS5), Kufri Jyoti(k.Jyoti), PP48(PP48), KufriBadsha(K.Badsha), PP250(PP2500), L.Hirpura (L. Hirpura), Kufri Giriraj (K.Giriraj) replicated thrice with a Randomized Block Design (RBD). Among locations Larnoo and amongst genotypes GS-3 was found best in terms of yield. The interaction effect GS\*Gulmarg recorded 9qt/ha higher yield.

Key words : Analysis of variance, Differences of means, Contrast comparison

## **INTRODUCTION**

The potato (Solanum tuberosum) is a starchy, tuberous crop from the perennial of the Solanaceae family. It is extensively grown in Kashmir, Himachal Pradesh etc. It is an allopolyploid with a chromosome number of 48. It is propagated by stem tubers as well as by seed. It is the richest source of carbohydrate. The predominant form of this carbohydrate is starch. Yield data of potato needs to be analyzed statistically so that relevant information regarding relative performance of different varieties at different locations can be obtained. The analysis of variance model is typically concerned with comparison of k treatments for which the mean responses are  $\mu = (\mu_1, \mu_2, \dots, \mu_n)^T$  (Box and Tiao, 1973). Henderson (1953) was the landmark paper dealing with methods for the estimation of variance components using unbalanced data. Harville (1977) deals with the ML and REML estimation of variance components from a non Bayesian view point. The distribution of µ is multivariate t distribution discovered independently by Cornish (1954) and by Dunnet and Sobel (1954). In practice, we are most often concerned with questions as "How different are the effects of the treatments?" Such questions must be answered in terms of comparison among the us. Taking all these views in consideration the present investigation was carried out to see the effect of locations on the yield and yield trial of Potato.

## MATERIALS AND METHODS

To investigate the effect of locations on yield of potato an experiment was conducted at five different research stations of SKUAST (K) namely Shalimar, Tangmarg, Gurez, Larnoo and Gulmarg during the year 2005-2006. The design of experiment was Randomized Block Design with three replications. Twelve genotypes of potato *viz.*, Gulmarg-Special (GS), (GS-1), (GS-2), (GS-3), (GS-4), (GS-5), Kufri Jyoti(k.Jyoti), PP-48, Kufri-Badsha,PP2500, L.Hirpura Kufri Giriraj were tried at five research stations of SKUAST-K Shalimar. This experiment was carried out to find the best genotype and the best location among the given genotypes and locations. The seed rate comprises of 20-25qt/ha, with a spacing of 20cms plant to plant and 60cms row to row.

All recommended cultural operations were done in time and plant protection measures were adopted as and when required. The data of yield, Tuber weight, Average Tuber No. of each genotype at different locations was collected and analyzed statistically using R and S-plus software's. Three fundamental books written by Becker *et al.* (1988), Chambers and Hastie (1992) and Venables and Ripley (2004) are of immense use for understanding these softwares. Khan and Mir (2005) discussed in detail the application of R- software in agricultural data analyses. One of the important feature of R- software is that it is an Open Source and freely available on website http:// cran-project.org.

# **RESULTS AND DISCUSSION**

The graphical results pertaining to analysis of variance is presented in Table 1. Plots in Fig. (a) are known as box plots. Box plots are one of the comprehensive presentations of a data. It shows centre as well as spread of a distribution. Thus, variability can also be depicted along with point of centrality. A line in the box is placed at the median value. The width of the box is equal to interquartile range IQR, which is the difference between the third and first quartiles. Thus, width of the box shows the variability present within the

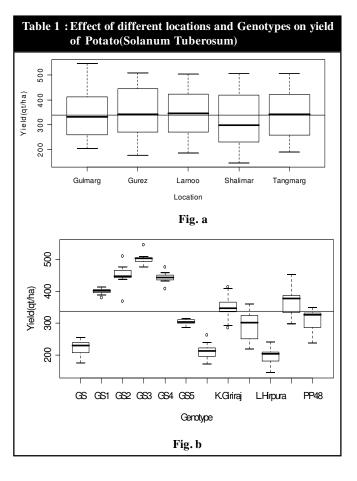
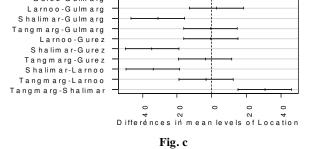


Table 2 : 95% concentration   comparing			long with erent location	
Multiple comparisons of means				
Location	diff	lwr	upr	padj
Gurez-Gulmarg	3.23	-12.25	18.72	0.97
Larnoo-Gulmarg	2.69	-12.79	18.18	0.98
Shalimar-Gulmarg	-31.15	-46.64	-15.66	0.00
Tangmarg-Gulmarg	-0.55	-16.0	14.93	0.99
Larnoo-Gurez	0.54	-16.03	14.95	0.99
Shalimar-Gurez	-34.38	-49.88	-18.89	0.00
Tangmarg-Gurez	-3.79	-19.28	11.69	0.96
Shalimar-Larnoo	-33.84	-49.34	-18.35	0.00
Tangmarg-Larnoo	-3.25	-18.74	12.23	0.97
95% family-wise confidence level				
Gurez-Gulmarg Larnoo-Gulmarg				



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Table 3: The contrast comparison along with full coefficients         Coefficients are				
(Intercept): 338.1434				
Location: Gulmarg Gurez Larnoo Shalimar Tangmarg 5.156 8.392 9.851 -25.997 4.597				
Genotype: GS GS1 GS2 GS3 GS4 GS5 K.Badsha -112.35 62.66 113.03 164.25 105.19 -32.12 -126.65				
K.Jyoti L.Hirpura PP2500 PP48 K.Giriraj -43.57 -141.82 30.80 -30.26 10.86				
Location:Genotype: Gulmarg:GS Gurez:GS Larnoo:GS Shalimar:GS Tangmarg:GS 9.09505 -26.82077 7.14383 -39.0353 -4.16577				
Gulmarg:GS1 Gurez:GS1 Larnoo:GS1 Shalimar:GS1 Tangmarg:GS1 -7.4349444 9.1974444 -4.1571667 -20.1920000 0.5975556				
Gulmarg:GS2       Gurez:GS2       Larnoo:GS2       Shalimar:GS2       Tangmarg:GS2         4.4576111       0.4332222       4.026533       -14.822123       6.771901				
Gulmarg:GS3 Gurez:GS3 Larnoo:GS3 Shalimar:GS3 Tangmarg:GS3 3.556277 3.7921111 10.2518333 -24.5973333 6.9971111				
Gulmarg:GS4 Gurez:GS4 Larnoo:GS4 Shalimar:GS4 Tangmarg:GS4 -0.6796111 -1.7287778 -14.1885000 -24.5306667 -7.9337778				
Gulmarg:GS5 Gurez:GS5 Larnoo:GS5 Shalimar:GS5 Tangmarg:GS5 -10.2482778 -4.4107778 -1.70133 - 19.9786667 -3.6157778				
Gulmarg:K.BadshaGurez:K.BadshaLarrnoo:K.Badsha6.2677222-4.87811112.1421667				
Shalimar:K.Badsh Tangmarg:K.Badsha -11.1153333 -2.4164444				
Gulmarg:K.Giriraj Gurez:K.Giriraj Larnoo:K.Giriraj -1.6016111 -7.6374444 36.7061667				
Shalimar:K.Giriraj Tangmarg:K.Giriraj -13.0646667 14.4024444				
Gulmarg:K.Jyoti Gurez:K.Jyoti Larnoo:K.Jyoti -3.0182778 35.439333 7.2.28333				
Shalimar:K.Jyoti Tangmarg:K.Jyoti -40.7133333 1.1375556				
Gulmarg:L.HirpuraGurez:L.HirpuraLarnoo:L.Hirpura16.7290556-7.10677781.5335000				
Shalimar:L.Hirpura Tangmarg:L.Hirpura -18.7273333 7.5715556				
Gulmarg:PP2500       Gurez:PP2500       Larnoo:PP2500       Shalimar:PP2500         1.7323889       12.9298889       -2.1631667       -24.5006667				
Tangmarg:PP2500 6.0401667				
Gulmarg:PP48       Gurez:PP48       Larnoo:PP48       Shalimar:PP48         12.0015556       -12.8276111       16.7698889       -34.9773333				
Tangmarg:PP48 24.9948889				

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genotype. Whiskers, which are lines on both sides of the box which extend from the edges of the box to either side of the extreme values (*i.e.*, minimum and maximum), or to a distance of 1.5IQR from the median which ever is less. It is evident from figure (a) of Table 1 that Yield at the Larnoo location is maximum followed by Tangmarg. However minimum yield of potato was recorded at Shalimar locations. The yield of potato at Larnoo was around 350qt/ha whereas it is only around 300qt/ha at Shalimar. Similarly from Fig. b of Table 1 it can be seen that yield wise GS-3 is best genotype followed by GS-2. However, it can also be seen that L.Hirpura showed lowest yield of 200qt/ha only.

Table 2 deals with multiple comparisons which is used to determine which means are different from which. As can be seen from Table 2, that among Gurez-Gulmarg locations, Gurez is having 3.23qt/ha yield higher than Gulmarg and similar interpretation can be made for other locations as well. Also, it can be seen from the same table that the locations Shalimar-Gulmarg have p-adj less than 0.05 indicating that the two locations differ significantly from one another. Similar interpretation can be made for other locations as well. It is evident from the result of Fig. c in Table 2 that the location Shalimar differs significantly from the rest of locations, because interval corresponding Shalimar does not include zero. Similar analysis related to Genotype and Genotype within Location can be made.

From the output in Table 3 of contrast comparisons between the Genotypes, Locations and the interaction Location:Genotype, it was evident that Location Larnoo was having 9.851qt/ha higher yield than the average yield. Among the Genotypes GS3 was having 164.25qt/ha higher yield than average followed by GS2. In Genotype:Location interaction one can see that Genotype-GS is best for Location for Gulmarg producing 9qt/ha Yield higher than average. Similar interpretations can be drawn for other Location:Genotype interactions.

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Received : January, 2009; Revised : Octobter, 2009 Accepted : February, 2010