

Research Article

Genetic architecture of yield traits and popping quality in popcorn (*Zea mays* var. *everta*) inbred lines

N. V. Soni^{1*} and S. M. Khanorkar²

¹Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand-388 110, Gujarat, India

²Main Maize Research Station, Anand Agricultural University, Godhra - 389 001, Gujarat, India.

*Email: soni1211@gmail.com

(Received: 21 Jan 2014; Accepted: 24 Jan 2014)

Abstract

Genetic architecture of yield, its attributing traits and popping quality traits were studied using diallel cross method involving ten inbred lines of popcorn through Hayman's diallel approach. The estimated value of average degree of dominance revealed that non-additive genetic effect was more pronounced in the inheritance of all the traits. The proportions of dominant and recessive genes were not in symmetry as per estimates of $H_2/4H_1$. The traits plant height, ear height and grain moisture content satisfied the general assumptions of additive-dominance model of diallel set. The graphical analysis and value of $(H_1/D)^{1/2}$ revealed over dominance type of gene action for these traits. The narrow scattering of parental arrays in Vr, Wr graphs indicate less diversity of parents for plant height. Based on the results, population improvement method was suggested for exploiting heterosis. The parents, I-07-42-1-2, I-07-42-6-3, I-07-63-18-3 and I-07-35-7-3 were identified as good parents for hybridization.

Key words: Popcorn, Diallel, Gene action, Hybridization, Non-additive.

Introduction:

The maize (*Zea mays* L.) is now used as diversified value added consumptions as specialty corn and contributed 9% to food market in India (Biology of *Zea mays*, Ministry of Science and Technology, New Delhi, India). Popcorn is one of them and popularized as high fibre, healthy and nutritious snack throughout the world. In India, the varieties viz., Amber popcorn, VL popcorn and Jawahar popcorn are under commercial cultivation. These popcorn cultivars are composite varieties, low yielder with low popping quality (Agridaksh, 2013). Hence, good quality popcorn with desirable popping is still imported from Argentina, Brazil and other countries. Estimate from governmental sectors and TPMGTA (The Popcorn Maize Growers' and Traders' Association) pointed out that around 25,000 tonnes of popcorn maize were imported in 2012-13 mostly from Argentina and the U.S. which is 50% of the demand around 50,000 tonnes of popcorn per annum in India (Department of Agriculture & Cooperation, Government of India, New Delhi and TPMGTA 2013). Therefore, there is an urgent need to improve popcorn inbred lines for developing hybrids with higher grain yield and better popping quality.

Further strengthening and improvement of popcorn through genetic approaches determines the study of gene action. Moreover formulation of comprehensive breeding strategies is to be done based on understanding the nature of gene action involved for a specific trait to be improved.

Dominance gene action is desirable for developing hybrids and additive gene action implies that standard selection protocols would be effective for improving the character. Among the different methods available to assess the nature of gene action the diallel cross method as suggested by Hayman (1954) was effectively used. The method was used to study gene action and genetic parameters in normal maize by Kumar and Gupta (2003); Kumar *et al.* (2005); Ali *et al.* (2007); Zare *et al.* (2011); Kumar *et al.* (2012). With this objective, the present study was envisaged after careful selection of popcorn inbred parents for understanding gene action and genetic effects for quantitative and qualitative traits governing grain yield and popping quality.

Material and method

Ten inbred parental lines, I-07-44-3-2 (P₁), I-07-44-4-3 (P₂), I-07-44-7-1 (P₃), I-07-43-7-3 (P₄), I-07-42-1-2 (P₅), I-07-42-6-3 (P₆), I-07-35-7-3 (P₇), I-07-63-1-2 (P₈), I-07-63-18-3 (P₉) and I-07-63-36-1 (P₁₀) developed at Main Maize Research Station, Anand Agricultural University, Godhra, were used to get all possible 45 cross combinations without reciprocals in *kharif*, 2011. The resultant F₁s along with their parents were grown in Randomized Complete Block Design (RCBD) with three replications in *rabi*, 2011-12 at Agronomy Farm, Anand Agricultural University, Anand (latitude/longitude 22°-35' North latitude and 72°-55' East longitude, elevation 45.1m a.s.l., yearly rainfall 877.6 mm, average yearly temperature 24°C). This location has Inceptisol soils of sandy

loam texture having pH of 7.2. The plot sizes were in two rows of 4.0 m with 0.60 m between rows and 0.20 m between plants. All the cultural practices were followed to raise a normal maize crop.

The traits, days to 50% tasseling (DFT), days to 50% silking (DFS), days to maturity (DM), plant height (cm) (PH), ear height (cm) (EH), seed index (g) (SI), grain yield per plant (g) (GY), dry fodder yield per plant (g) (DFY), popping expansion (cc/g) (PE), grain moisture content (%) (GMC), protein content (%) (PC), starch content (%) (SC) and oil content (%) (OC) in seed were studied. The data were recorded on yield and quality traits on five randomly selected plants. Popping expansion was measured in sample of 30.0 g of seeds that were popped in an automatic Popcorn Maker developed by Skyline according to Vieira *et al.* (2011). Seed index was measured by taking 100-seeds weight. A statistical procedure as developed by Hayman (1954) was followed for genetic component analysis.

Results and discussion

Analysis of variance indicated significant differences among the parents, hybrids and parents v/s hybrids for all the traits under study. It indicated that experimental material had sufficient genetic variability for these characters. The estimates of genetic components and heritability (h^2) in narrow sense are furnished in Table 1. Both additive (D) and non-additive (H_1) components showed significant estimates for days to 50% tasseling, days to 50% silking, plant height, ear height, popping expansion, grain moisture content, protein content, starch content in seed, whereas only dominant component was significant for days to maturity, seed index, grain yield, dry fodder yield and oil content in seed. Higher magnitude of non-additive component (H_1) indicate greater role of non-additive gene action for inheritance of traits viz., days to 50% tasseling, days to 50% silking, plant height, ear height, popping expansion, grain moisture content, protein content, starch content in seed. Similar finding were also reported earlier by Kumar *et al.* (2012) for grain yield and Ali *et al.* (2007) for days to 50% silking, days to maturity, plant height and ear height; Muhammad *et al.* (2010) for days to 50% tasseling, days to 50% silking, plant height, ear height and grain yield per plant and Zare *et al.* (2011) for plant height and grain yield.

Positive estimates of F for all the traits except days to maturity and grain yield indicated the overall excess of dominant genes for the traits having positive estimates. The estimates of H_2 component was smaller than H_1 for all the traits reflecting asymmetrical distribution of positive and negative alleles at all the loci in the parents and the same was attested by the ratio of $H_2/4H_1$, which were not

in closer to the theoretical value of 0.25. Kumar *et al.* (2005) and Muhammad *et al.* (2010) obtained similar results for days to 50% tasseling and days to 50% silking, plant height and grain yield.

The values of average degree of dominance as estimated by $(H_1/D)^{1/2}$ in various components were above unity for all the traits which indicated existence of over dominance, which can be utilized for developing hybrid varieties for improving these traits. These results are in agreement with reports cited for days to 50% tasseling and days to 50% silking (Kumar *et al.*, 2005), plant height (Prakash *et al.*, 2004; Kumar *et al.*, 2005; Irshad-Ul-Haq *et al.*, 2010; Zare *et al.*, 2011) and grain yield (Prakash *et al.*, 2004; Ali *et al.*, 2007; Irshad-Ul-Haq *et al.*, 2010; Khodarahmpour 2011). However, the finding of Singh and Roy (2007) revealed additive gene action involved in the inheritance of plant height, thereby differing with the present results. The difference might be due to variation in the genetic material and environmental condition.

The ratios of dominant and recessive genes (KD/KR) revealed higher proportion of dominant alleles in the parents for days to 50% tasseling, days to 50% silking, plant height, ear height, seed index, dry fodder yield, popping expansion, grain moisture content, protein content, starch content and oil content. This was also confirmed by the positive estimates of F for these variables, whereas for days to maturity an excessive of recessive alleles was indicated. The distribution of dominant and recessive genes was highly symmetrical in case of grain yield per plant having KD/KR value of 0.93.

The most important parameter, which, directly represents the heritable portion of general variance and is estimated on the basis of additive variance is heritability in narrow sense [$h^2(NS)$ %]. In present study, estimates were observed to be low to moderate for traits viz., days to 50% tasseling, days to 50% silking, days to maturity, seed index, grain yield, dry fodder yield which could be attributed to more prevalence of non-additive gene action in these traits. These results were corroborated with Zara *et al.* (2011) and Khodarahmpour (2011) for grain yield and Irshad-Ul-Haq *et al.*, (2010) for days to 50% tasseling and days to 50% silking. But the trend was reverse in case of plant height and ear height, which permits direct selection for genetic improvement due to high narrow sense heritability. Kumar and Gupta (2003) obtained higher estimates of $h^2(NS)$ % for plant height and ear height. With respect to quality traits, the values of heritability were low for popping expansion, grain moisture content, protein content, starch content and oil content. Khodarahmpour (2011) also obtained low heritability for protein and starch content in normal maize seeds. The h^2/H_2 values were less than unity

for ear height, seed index, grain yield, popping expansion including nutritional quality traits viz., grain moisture content, protein, starch and oil content in seed implied to be governed by one gene. Days to maturity, plant height and dry fodder yield were assumed to be governed by two genes or groups of genes. Whereas, the value of h^2/H_2 indicated three dominant gene blocks were influencing the traits days to 50% tasseling and days to 50% silking. Hayman (1954) pointed out that the estimates of h^2/H_2 might indicate lower values in the event of h^2 effects of all the genes being unequal in size and in the event of uncorrelated gene distribution. The value of h^2/H_2 might be depressed by complementary gene action (Hayman 1954).

Graphical analysis is a good estimator of the prepotency of parents and thus provides a basis for choosing parental combinations for selective improvements of the character concerned (Sanjeev kumar *et al.*, 2007). In the present study, regression coefficient (b) of three traits viz., plant height, ear height and grain moisture content was significantly deviated from zero and showed non-significant deviation from unity suggesting the absence of epistasis gene action indicating additive-dominance model was satisfactory in these cases (Table 1). Thus, these three traits fulfilled the general conditions of diallel analysis. These respective values of these traits were darkened in the Table 1. This reflects that these characters had a strong relationship between V_r and W_r of parental material and thus V_r, W_r was effective for genetical studies of parental material with respect to these traits. For the remaining characters additive-dominance model was not satisfactory, hence V_r, W_r graphs were not plotted (Hayman, 1954). V_r, W_r graphs showed that regression line intersected W_r -axis below the point of origin for plant height, ear height and grain moisture content suggesting the role of overdominance for these traits (Fig. 1-3). These results were also supported by the estimates of $(H_1/D)^{1/2}$ for these three traits.

The array points indicated that parent I-07-42-6-3 (P_6) was situated nearest to the point of origin and thus possessed most of the dominant alleles for plant height. Whereas, I-07-44-3-2 (P_1), I-07-44-7-1 (P_3) and I-07-35-7-3 (P_7) were far away from the point of origin, indicating that they possessed most of the recessive alleles for same trait. In case of ear height, I-07-42-6-3 (P_6) and I-07-43-7-3 (P_4) possessed most of the dominant alleles. Whereas, I-07-35-7-3 (P_7), I-07-63-1-2 (P_8), I-07-63-36-1 (P_{10}) and I-07-44-3-2 (P_1) possessed most of the recessive alleles. For grain moisture content, parents, I-07-44-3-2 (P_1) possessed most of the dominant alleles. The parents namely, I-07-42-6-3 (P_6) and I-07-63-18-3 (P_9) possessed most of the recessive alleles. In general, wide scattering of parental points along the regression line in V_r, W_r

graphs were observed for ear height and grain moisture content. This suggested sufficient diversity among the parents for these traits. On the other side, plant height exhibited narrow scattering of the parental arrays indicating less diversity among the parents for the trait.

As regards to remaining traits, for which the graphs were not plotted, the values of (V_r+W_r) are presented in Table 2. The lowest value corroborates with the presence of more number of dominant genes while the highest value to that of more recessive genes. Higher proportion of dominant genes were implied in parent, I-07-42-6-3 (P_6) for days to 50% tasseling; I-07-42-1-2 (P_5) for days to 50% silking and grain yield; I-07-35-7-3 (P_7) for popping expansion and starch content in seed and parent, I-07-63-18-3 (P_9) for seed index, protein and oil content in seed. Parental lines having equal proportions of dominant and recessive genes viz., I-07-44-3-2 (P_1) for days to 50% silking, seed index, popping expansion and starch content and I-07-43-7-3 (P_4) for days to 50% tasseling, seed index, grain moisture content and starch content. These parents may be exploited for getting improved populations/heterotic hybrids for these traits.

The present study revealed that the pattern of inheritance was largely governed by non-additive gene action for all the traits. Maize is a highly cross pollinated crop and non-additive type of gene action involved hybrid breeding will reward in this crop. The distribution of dominant and recessive genes was highly symmetrical in case of grain yield per plant. Coefficient of regression (b) was observed to be significantly deviated from zero and non-significantly with unity for plant height, ear height and grain moisture content, which indicated that these traits fulfill the general assumptions of additive-dominance model of diallel set. The graphical analysis and value of $(H_1/D)^{1/2}$ exhibited over dominance for plant height, ear height and grain moisture content. The inbred lines, I-07-42-1-2, I-07-42-6-3 and I-07-63-18-3 for grain yield and its associated traits and I-07-35-7-3 inbred line for quality traits are identified to be promising on account of possessing desirable dominant genes for grain yield and popping qualities. Parental lines, I-07-44-3-2 and I-07-43-7-3 having equal proportions of dominant and recessive genes may be exploited for getting improved populations/heterotic hybrids for grain yield and popping quality traits.

References

- Agridaksh, 2013. Division of Computer Applications, IASRI, PUSA, New Delhi. http://agridaksh.iasri.res.in/jsp/locationSelectio_n_action.jsp. (Accessed January 22, 2013).



- Ali, G., Rather, A.C., Ishfaq, A., Dar, S.A., Wani, S.A. and Khan, M.N. 2007. Gene action for grain yield and its attributes in maize (*Zea mays* L.). *International J. Agric. Sci.*, **3**(2): 767-788.
- Hayman, B. L. 1954. The theory and analysis of diallel cross. *Genetics*, **39**: 789-809.
- Irshad-Ul-Haq, M., Ajmal, S.U., Munir, M. and Gulfaraz, M. 2010. Gene action studies of different quantitative traits in maize. *Pak. J. Bot.*, **42**(2): 1021-1030.
- Khodarahmpour, Z. 2011. Genetic control of different traits in maize inbred lines (*Zea mays* L.) using graphical analysis. *African J. Agric. Res.*, **6**(7):1661-1666.
- Kumar, P. and Gupta, S. C. 2003. Genetic analysis in maize (*Zea mays* L.). *J. Res. Birsa Agric. University*, **15**(1): 107-110.
- Kumar, R., Singh, M., Narwal, M. S. and Sharma, S. 2005. Gene effects for grain yield and its attributes in maize (*Zea mays* L.). *National J. Plant Improv.*, **7**(2): 105-107.
- Kumar, S.T., Reddy, M.D., Naik, S.V., Parveen, I. S. and Subbaiah, P.V. 2012. Gene action for yield and morpho-physiological traits in maize (*Zea mays* L.) inbred lines. *J. Agric. Sci.*, **4**(5): 13-16.
- Muhammad, I.H., Ajmal, S.U., Munir, M. and Gulfaraz, M. 2010. Gene action studies of different quantitative traits in maize. *Pak. J. Bot.*, **42**(2): 1021-1030.
- Prakash, S. and Ganguli, D.K. 2004. Combining ability for various yield component characters in maize (*Zea mays* L.). *J. Res. Birsa Agric. Univ.*, **16**(1): 55-60.
- Sanjeevkumar, Singh, H.B. and Sharma, J.K. 2007. Gene action for grain yield, its components and quality traits in hill rice (*Oryza sativa*) varieties. *Indian J. Genet.*, **67**(3): 275-277.
- Singh, P.K. and Roy, A.K. 2007. Diallel analysis of inbred lines in maize (*Zea mays* L.). *Intl. J. Agric. Sci.*, **3**(1): 213-216.
- Vieira, R.A., Scapim, C.A., Tessmann, D.J. and Hata, F.T. 2011. Diallel analysis of yield, popping expansion, and southern rust resistance in popcorn lines. *Revista Ciência Agronômica*, **42**(3): 774-780.
- Zare, M., Choukan, R., Bihanta, M. R., Majidi Heravan, E. and Kamelmanesh, M. M. 2011. Gene action for some agronomic traits in maize (*Zea mays* L.). *Crop Breed. J.*, **1**(2): 133-141.

Fig. 1 Vr, Wr graph for Plant height (cm)

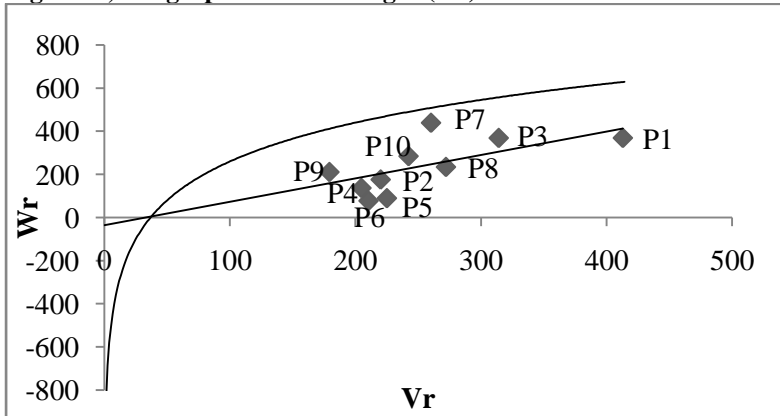


Fig. 2 Vr, Wr graph for Ear height (cm)

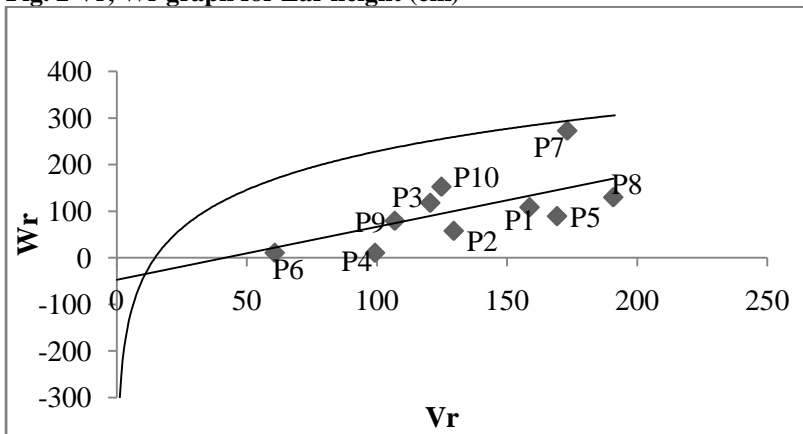


Fig. 3 Vr, Wr graph for Grain moisture content (%)

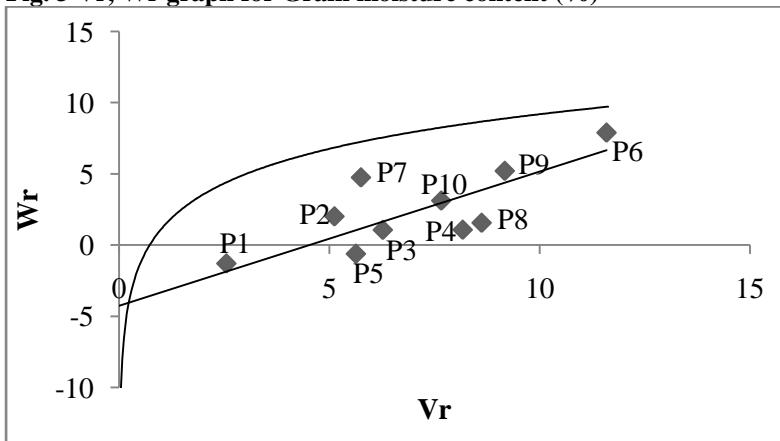




Table 1. Estimates of genetic components of variation for yield, its associated traits and quality traits in popcorn

Components / Ratio	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Seed index (g)	Grain yield per plant (g)	Dry fodder yield (g)	Popping expansion (cc/g)	Grain moisture content (%)	Protein content (%)	Starch content (%)	Oil content (%)
D	12.72**	12.63**	3.26ns	969.77**	496.54**	4.72ns	121.11ns	521.60ns	23.82**	8.57**	0.34*	7.02**	0.08ns
H ₁	20.69**	23.34**	23.42**	1009.61**	601.73**	32.34**	2284.06**	3796.57**	84.66**	26.55**	1.65**	19.71**	0.74**
H ₂	15.24**	18.21**	20.82**	629.70**	359.60**	25.27**	1862.07**	3209.62**	60.35**	21.88**	1.18**	13.77**	0.62**
h ²	34.32**	46.23**	29.72**	787.74**	190.31**	14.72*	1444.97**	5081.84**	5.32ns	4.32*	0.07ns	9.10**	0.01ns
F	11.01**	11.03ns	-2.96ns	987.67**	584.94**	1.29ns	-40.21ns	807.39ns	19.82ns	7.30*	0.39ns	11.71**	0.15ns
E	0.69ns	1.03ns	3.31ns	11.24ns	9.03ns	0.11ns	28.62ns	26.29ns	0.12ns	0.18ns	0.02ns	0.91ns	0ns
(H ₁ / D) ^{1/2}	1.28	1.36	2.68	1.02	1.11	2.62	4.34	2.70	1.89	1.76	2.35	1.68	3.14
H ₂ / 4H ₁	0.18	0.20	0.22	0.16	0.15	0.20	0.20	0.21	0.18	0.21	0.18	0.17	0.21
KD/KR	2.03	1.95	0.71	2.99	3.30	1.11	0.93	1.80	1.57	1.64	1.77	2.99	1.92
h ² /H ₂	2.25	2.54	1.43	1.25	0.53	0.58	0.78	1.58	0.09	0.20	0.06	0.66	0.01
h ² (NS)%	50.53	43.49	7.59	93.55	90.37	13.03	4.73	14.43	26.73	30.03	20.12	37.63	11.13
b	0.4240	0.3717	0.0605	1.2051	1.2667	0.1387	-0.0029	-0.1061	0.5370	0.8399	0.2801	0.7515	0.0497
SE (b) ±	0.1734	0.1483	0.1005	0.4912	0.5079	0.1032	0.0814	0.1805	0.1344	0.2593	0.2083	0.3266	0.2528
(b - 0)/SE	2.45*	2.51*	0.60	2.45*	2.49*	1.34	-0.04	-0.59	4.00**	3.24*	1.34	2.30	0.20
(b-1)/SE	-3.32*	-4.24**	-9.35**	0.42	0.53	-8.35**	-12.32**	-6.13**	-3.44*	-0.62	-3.46*	-0.76	-3.76**

*, ** Significant at 5% and 1% levels, respectively.

Table 2. Estimates of Vr+Wr values for yield and quality traits in popcorn

Parents	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Seed index (g)	Grain yield per plant (g)	Dry fodder yield (g)	Popping expansion (cc/g)	Grain moisture content (%)	Protein content (%)	Starch content (%)	Oil content (%)
I-07-44-3-2	10.86	11.04	4.44	782.28	267.21	10.73	351.44	424.21	16.36	1.25	0.91	3.34	0.17
I-07-44-4-3	11.31	11.47	16.81	396.52	187.17	5.01	287.78	833.3	8.12	7.13	0.35	2.1	0.28
I-07-44-7-1	19.18	20.06	13.51	683.29	238.37	10.92	686.17	1286.84	11.69	7.33	0.18	2.25	0.09
I-07-43-7-3	9.61	11.49	19.22	342.07	109.8	8.25	1150.21	736.31	15.59	9.24	0.72	3.77	0.10
I-07-42-1-2	3.88	3.98	6.1	315.06	258.55	6.32	198.15	1165.39	30.77	5.01	0.24	1.86	0.15
I-07-42-6-3	3.39	4.84	10.71	288.37	71.26	18.52	928.23	1458.12	27.17	19.49	0.37	16.78	0.13
I-07-35-7-3	6.49	5.52	12.87	699.74	445.98	11.9	1403.68	1430.83	3.59	10.5	0.82	0.55	0.33
I-07-63-1-2	19.53	24.44	10.08	506.86	320.66	33.06	1218.43	1176.85	60.28	10.18	0.46	9.56	0.21
I-07-63-18-3	5.91	5.49	9.61	390.55	186.14	2.46	291	656.9	34.85	14.38	0.06	4.63	0.08
I-07-63-36-1	6.40	6.29	15.92	527.26	277.27	3.36	490.45	368.58	83.51	10.78	0.74	4.38	0.15