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EXPLORING TRANSGRESSIVE SEGREGATION FOR YIELD AND COMPONENT TRAITS IN EARLY GENERATIONS OF MUNGBEAN (*VIGNA RADIATA* L. WILCZEK)

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ABSTRACT

Transgressive segregation, a key mechanism utilized by plant breeders, plays a vital role in enhancing crop traits by exploiting genetic diversity within breeding populations. Four crosses *viz*. HUM 1 x ML 818, HUM 1 x RMG 975, IPM 205-02 x RMG 975, and LGG 4604 x ML 818 along with their parents, which were evaluated in a randomized block design with three replications during the Kharif season of 2022 at the Institutional Farm of Sri Karan Narendra College of Agriculture, Jobner, Jaipur. In this study, transgressive segregants exhibiting desirable traits were observed across eight key characteristics in the F2 generation of four mungbean crosses. The highest percentage of transgressive segregants was observed for plant height (23.33%) in the HUM 1 x ML 818 cross, followed by seed yield per plant (20.00%) in the HUM 1 x RMG 975 cross. Across all crosses, the highest proportion of transgressive segregants was consistently recorded for seed yield per plant (92), followed by plant height (84), pods per plant (83), pod length (81), seeds per pod (76), 100-seed weight (67), clusters per plant (67), and pods per cluster (55). Moreover, the study explored the simultaneous transgression of seed yield per plant with other yield-contributing traits, indicating complex genetic interactions underlying mungbean productivity. Promising transgressive segregants were identified in each cross, displaying substantial improvements in seed yield per plant and other agronomic traits, highlighting their potential for crop improvement. The findings underscore the importance of continued research in transgressive breeding to unlock novel genetic combinations and develop high-performing mungbean varieties capable of addressing agricultural sustainability and food security challenges.

Keywords **:** Transgressive segregation, mungbean, crop improvement, genetic diversity, trait expression and yield-contributing traits

Introduction

Mungbean (*Vigna radiata* L.) stands as a significant pulse crop not only in India but also across tropical and subtropical regions worldwide. Its high protein content, easy digestibility, and complementary nutritional profile when combined with cereals make it a valuable dietary component. Mungbean is rich in essential elements such as iron, calcium, zinc, vitamin A, folate, and notably, antioxidant vitamin C, especially prominent in mungbean sprouts.

The complexity of mungbean yield arises from its multifaceted nature, comprising interconnected components. Its journey from its origins in the Indian subcontinent to global cultivation and consumption underscores its importance in providing nutrition, economic sustenance, and environmental advantages to farmers and consumers alike (Zhou et al., 2020).

Rajasthan emerges as a leading producer and cultivator of mungbean, boasting favorable agro-climatic conditions conducive to its growth. In the state, particularly in districts like Nagaur, Ajmer, Jaipur, Jodhpur, Churu, and Bikaner, mungbean finds a thriving cultivation environment, owing to the warm and dry climate prevalent in these regions. Rajasthan leads the group in terms of both production and area dedicated to growing mungbean. In Rajasthan, the total

area planted with mungbean for 2022 was 2.33 million hectares, producing 1.17 million tonnes with a productivity of 504 kg/ha (Anonymous, 2022). Despite these conducive conditions, mungbean's average productivity remains below its potential due to various factors. Cultivation on marginal and degraded lands, dependence on rain-fed conditions, suboptimal fertilizer usage, susceptibility to pest and disease infestations, dearth of high-yielding and compatible varieties, absence of definitive types, and inadequate knowledge about improved agricultural practices collectively contribute to this productivity gap.

In the pursuit of enhancing mungbean productivity, the production of transgressive segregants for yield and its contributing characters assumes paramount importance in breeding programs. Transgressive segregants, characterized by performance outside the range of either parent, hold significant potential, particularly those surpassing the better parent in superiority. Consequently, breeders are keen on maximizing the frequency of transgressive segregants within segregating populations, as it provides a broader scope for selective breeding aimed at improving productivity.

Hence, this study focuses on investigating four F_2 populations to identify transgressive segregants for seed yield and its associated traits, aiming to contribute towards the enhancement of mungbean productivity through targeted breeding efforts.

Materials and Methods

The experiment was conducted at the Research Farm of Sri Karan Narendra College of Agriculture, Jobner, Jaipur (Rajasthan), situated at an elevation of 450 meters above mean sea level, with coordinates of latitude 26°5' N and longitude 75°28' E, falling within agro-climatic zone III A (Semi-arid eastern plain zone) in Rajasthan.

The experimental material comprised F2 populations resulting from four crosses, namely, HUM 1 x ML 818, HUM 1 x RMG 975, IPM 205-02 x RMG 975, and LGG 4604 x ML 818, along with five parental lines, namely, HUM 1, IPM 205-02, LGG 4604, ML 818, and RMG 975, obtained from the Department of Plant Breeding and Genetics, SKN College of Agriculture, Jobner (Rajasthan). The experimental layout followed a Randomized Block Design (RBD) with three replications during the Kharif season of 2022. The F2 seeds were harvested from selfed F1 populations. Each F2 population was represented by five rows, with a single row of parents involved in each cross replicated within each block. The row length was maintained at 3.0 meters, with

inter-row spacing of 30 cm and intra-row spacing of 10 cm. As basal fertilization, urea and single superphosphate were applied to supply 20 kg N and 40 kg P2O5 per hectare, respectively. Thinning was carried out after 15 days of sowing to retain a single seedling per hill. Standard irrigation, weeding, and plant protection measures were implemented as per recommended practices to ensure optimal crop growth and health. Observations were recorded on various morphological traits including plant height, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight, and seed yield per plant. Forty best-selected plants were observed in each selected F2 population, while ten randomly selected plants from each parent were observed in each plot for all traits. Statistical analysis was conducted as per the procedures outlined by Panse and Sukhatme (1995). Transgressive segregants were identified based on the threshold value (T.V.), calculated using the mean (P(+)) and standard deviation (σP(+)) of the increasing parent. Individuals exceeding this threshold limit were deemed as transgressive segregants resulting from transgressive segregation.

The threshold value (T.V.) was determined using the formula:

$$T.V. = P(+) + 1.96 \times \sigma P(+)$$

Where, P(+) and б P(+) are the mean and standard deviation of increasing parent, respectively.

Transgressive segregants were individuals whose trait values surpassed this calculated threshold value, signifying their deviation from the expected trait expression based on parental performance.

Results and Discussion

Transgressive segregation stands out as a pivotal mechanism wielded by plant breeders to enhance crop traits. Such segregants emerge in F_2 or later generations due to segregation and recombination, where favorable genes from the parental lines involved accumulate. Diverse parents exhibiting superior combining abilities are more likely to yield transgressive segregants.

In the present study, transgressive segregants in the desirable direction were observed across all eight characters in the F_2 generation of the four crosses under examination (Table 1). This observation aligns with previous research findings by Shivani *et al.* (2011), Karkute *et al.* (2016), and Reddy *et al.* (2021).

In addition to identifying the frequency of transgressive segregants, this study examined the intensities of character expressions achieved by transgressants across the four crosses, providing

insights into the extended limits and intensities of desired character expression achieved through transgressive breeding (Table 2). Desirable transgressive segregants were observed in each of the four crosses for all eight characters in the F_2 generations. The highest proportions of individuals transgressing beyond the increasing parent were recorded for pod length (11.67% to 25%), seed yield per plant (14.17% to 23.30%), pods per cluster (7.50% to 15%), pods per plant (15.00% to 20.83%), plant height (13.33% to 17.50%), clusters per plant (13.33% to 15.83%), seeds per pod (15% to 17.50%), and 100-seed weight (12.50% to 15%) across the overall crosses.

Notably, the highest percentage of transgressive segregants varied across the four crosses. In Cross I, the highest proportion was observed for plant height (23.33%), followed by seed yield per plant (19.17%). Conversely, in Cross II, the highest proportion was observed for seed yield per plant (20.00%), followed by plant height (17.50%). Similarly, in Cross III, the highest proportions were recorded for seed yield per plant (23.33%) and pods per plant (20.83%). In Cross IV, the highest proportions were observed for pod length (25.00%) followed by seeds per pod (17.50%).These findings are consistent with similar reports by Shivani et al. (2011), Karkute *et al.* (2016), and Reddy et al. (2021), affirming the efficacy and reproducibility of transgressive segregants in crop improvement.

The observed variations in the proportion of transgressive segregants among crosses underscore the importance of genetic diversity and combinatorial effects of parental traits in shaping the outcome of transgressive segregation. Such insights are valuable for breeding programs aiming to exploit the full genetic potential of crop plants. Overall, the presence of desirable transgressive segregants across multiple traits in each cross highlights the potential of transgressive breeding as an effective strategy for enhancing crop performance and achieving desired trait expression beyond the limits set by parental lines. Further evaluation and selection of promising segregants can lead to the development of superior crop varieties with enhanced yield and other desirable agronomic traits.

In the total of four crosses investigated (Table 3), seed yield per plant exhibited the highest proportion of transgressive segregants (92), indicating its significance in transgressive breeding. This was followed by plant height (84), pods per plant (83), pod length (81), seeds per pod (76), 100-seed weight (67), clusters per plant (67), and pods per cluster (55). These

findings are consistent with previous studies by Kant and Singh (1998) in lentil and Dole and Reddy (2011) as well as Sabale and Girase (2014) in mungbean, highlighting the wide applicability of transgressive breeding across different crop species.

Furthermore, the investigation delved into the intensities of character expression achieved by the transgressants in each cross, shedding light on the extended limits and intensities of desired character expression facilitated by transgressive breeding. In the present investigation, the highest yielding transgressants produced 9.05, 8.60, 9.10 and 8.90 g seed yield per plant in HUM 1x ML818, HUM 1x RMG 975 and IPM 205-02 x RMG 975 and LGG 460x ML818 respectively, as against 6.63, 6.63, 5.92 and 6.39 seed in yield per plant produced by their respective increasing parents. Cross 1 (HUM 1x ML818), cross 2 (HUM 1x RMG 975), cross 3 (IPM 205-02 x RMG 975) and cross 4 (LGG 460 x ML 818) produced the pods per plant were 31, 35, 30 and 25 respectively as against 17.00, 17.00, 14.23 and 14.53 per plant, produced by their respective increasing parents. These intensities for the pod length were 8.90 (HUM 1x ML 818), 9.50 (HUM 1 x RMG 975), 9.70 (IPM 205-02 x RMG 975) and 9.57 (LGG 460 x ML 818) higher than those of their respective increasing parents.

It is evident from the data that transgressive breeding can effectively extend the limits of character expression, particularly when the desired intensity of a character is not readily available in the parental lines. This method, although exerting greater selection pressure, results in the highest character recovery compared to other breeding approaches. Hence, it emerges as a valuable tool for isolating rare genotypes and achieving desired trait expression in crop improvement programs.

Moreover, in each of the four crosses examined, seed yield per plant of the increasing parent was simultaneously transgressed with one or several other characters, such as clusters per plant, pods per cluster, pods per plant, pod length, and seeds per pod. This indicates the existence of complex genetic interactions underlying these traits, with the potential for simultaneous improvement through transgressive breeding.

The identification of important and rare transgressive segregants, albeit low in frequency, underscores the potential of transgressive breeding to uncover novel genetic combinations with desirable agronomic traits. Such findings highlight the importance of continued exploration and evaluation of

transgressive segregants in breeding programs to harness their full potential for crop improvement

Observations on eight characters, including seed yield per plant, were meticulously recorded on 120 plants in each of the four crosses (Table 3). In Cross HUM 1x ML818, HUM 1x RMG 975, IPM 205-02 x RMG 975, and LGG 460 x ML818, a total of 23, 24, 28, and 17 individuals, respectively, exhibited transgression for seed yield per plant and its combination with other five characters. This phenomenon of simultaneous transgressive segregants has also been documented in previous studies by Dhole and Reddy (2011), Karkute *et al.* (2016), Marwiyah *et al.* (2020), Singh *et al.* (2020), Reddy *et al.* (2021) and Reddy *et al.* (2022) and Chauhan *et al.* (2018) Shivakumar *et al.* (2013), Deokar *et al.* (2020) and Sundaram *et al.* (2023) involving mungbean, urdbean, and chickpea, underlining its widespread occurrence and relevance in legume breeding. Out of total number of transgressive segregants for seed yield per plant in these crosses, 92 individuals transgressed beyond the increasing parent in the F_2 generation

Table 4 elucidates that in the majority of cases where the seed yield per plant of the increasing parent was transgressed, simultaneous transgression occurred for one or more other yield-contributing characters such as clusters per plant, pods per cluster, pods per plant, pod length, and seeds per pod. This interdependence among yield-related traits suggests a complex genetic architecture underlying seed yield per plant in mungbean. Similar observations have been reported by Karkute *et al.* (2016), Marwiyah *et al.* (2020), Reddy *et al.* (2021) and Reddy *et al.* (2022) in mungbean, Chauhan *et al.* (2018) in urdbean and Shivakumar *et al.* (2013) and Sundaram *et al.* (2023) in chickpea across various legume crops, indicating a common genetic linkage or dependency among these traits. The identification of such genetic linkages implies that selection for transgressive segregants exhibiting favorable traits such as clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, and 100-seed weight could potentially lead to an increase in seed yield per plant in mungbean. This underscores the importance of considering multiple yield-contributing traits in breeding programs to achieve holistic improvements in crop productivity and quality.

. Based on the analysis of transgressive segregants for seed yield per plant (Table 5), several promising individuals were identified across the four crosses studied. In the cross HUM 1x ML 818, plant no. 117 exhibited particularly noteworthy performance, demonstrating a 30.46% increase in seed yield per plant compared to the increasing parent. Furthermore, this plant displayed higher expression levels for clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, and 100-seed weight, indicating its potential for improved overall yield and quality traits.

Similarly, in the cross HUM 1x RMG 975, transgressive segregants plant no. 29 and 91 showed significant promise, achieving 19.15% and 23.68% higher seed yield per plant, respectively, compared to the increasing parent. These plants also exhibited enhanced expression for various yield-contributing traits, suggesting their potential for comprehensive yield improvement

In cross IPM 205-02 x RMG 975, transgressive segregants No. 115 and 96 emerged as the most profitable, displaying 18.24% and 19.93% higher seed yield per plant, respectively, than their increasing parent. These individuals also exhibited superior performance in terms of clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, and 100-seed weight, highlighting their potential for enhancing multiple yield-related traits.

In the case of cross LGG 460 x ML 818, transgressive segregant plant no. 112 stood out as the most promising, yielding 14.24% more seed yield per plant compared to the increasing parent. Additionally, this plant displayed improved expression for various yield-related traits, indicating its potential for contributing to overall crop productivity and quality. Girase and Deshmukh (2002) also observed the simultaneous transgressive segregation for seed yield and its attributes in chickpea.

The simultaneous occurrence of transgressive segregation for seed yield and its associated traits underscores the complex genetic interactions underlying yield determination in mungbean. The identification of such promising transgressive segregants warrants further evaluation to assess their consistency and stability across multiple generations. If proven consistent, these individuals hold significant value for crop improvement efforts, either through variety release or integration into future breeding programs to harness their genetic potential for enhancing mungbean productivity and quality.

The findings of this study are consistent with previous research highlighting the occurrence of simultaneous transgressive segregation and the potential of transgressive breeding to unlock novel genetic combinations for crop improvement across various legume crops. Continued research in this direction is crucial for developing high-performing

mungbean varieties capable of meeting the evolving challenges of agricultural sustainability and food security.

Conclusion

In conclusion, transgressive segregation emerges as a pivotal mechanism in crop breeding, offering opportunities to enhance multiple agronomic traits beyond the limits set by parental lines. The present study demonstrates the widespread occurrence of transgressive segregants across various yield-contributing traits in mungbean, with notable variations observed among different crosses. Through meticulous analysis, promising transgressive segregants were identified, exhibiting significant improvements in seed yield per plant and other key agronomic traits. These findings underscore the potential of transgressive breeding as an effective strategy for achieving holistic improvements in crop productivity and quality. Further evaluation and selection of promising segregants hold promise for the development of superior mungbean varieties capable of addressing the challenges of agricultural sustainability and food security. Continued research in this direction is essential for unlocking the full genetic potential of crop plants and advancing crop breeding efforts to meet the demands of an ever-changing agricultural landscape.

Table 1. Threshold value (TV), Normal deviation value (ND), frequency, percentage and range in the values of transgressive segregants for six characters in four crosses of Mungbean

Character	N.D.	Threshold value	Desirable transgressive segregants		Range in value of T.S.
			Frequency	T.S. %	
Cross I : HUM 1 x ML 818					
Plant height (cm)	47.63	57.54	28	23.33	53 to 61
Clusters per plant	2.37	5.49	19	15.83	6 to 8
Pods per cluster	-3.12	4.45	18	15.00	5 to 5
Pods per plant	15.69	19.21	20	16.67	20 to 31
Pod length (cm)	-16.64	8.67	17	14.17	8.76to 8.9
Seeds per pod	-0.57	14.57	18	15.00	15 to 18
100-seed weight (g)	-33.56	3.44	18	15.00	3.46to 3.59
Seed yield per plant (g)	0.55	6.83	23	19.17	6.85 to 9.05
Cross 2 : HUM 1 x RMG 975					
Plant height (cm)	43.84	57.54	21	17.50	58 to 67
Clusters per plant	1.09	5.49	16	13.33	6 to 9
Pods per cluster	0.17	4.45	15	12.50	5 to 6
Pods per plant	16.25	19.21	18	15.00	21 to 35
Pod length (cm)	-6.94	8.67	20	16.67	8.76 to 9.5
Seeds per pod	7.41	15.75	18	15.00	16 to 18
100-seed weight (g)	-22.22	3.47	17	14.17	3.49 to 3.8
Seed yield per plant (g)	-0.17	6.83	24	20.00	6.9 to 8.6
Cross 3 : IPM 205-02 x RMG 975					
Plant height (cm)	23.76	51.47	16	13.33	52 to 54
Clusters per plant	1.65	5.71	16	13.33	6 to 8
Pods per cluster	-0.51	4.31	13	10.83	5 to 5
Pods per plant	14.19	17.50	25	20.83	18 to 30
Pod length (cm)	-15.56	8.64	14	11.67	8.70 to 9.7
Seeds per pod	4.56	15.25	19	15.83	16 to 17
100-seed weight (g)	-21.92	3.47	17	14.17	3.48 to 3.66
Seed yield per plant (g)	1.70	6.45	28	23.33	6.60 to 9.10
Cross 4: LGG 4604 x ML 818					
Plant height (cm)	46.53	51.64	19	15.83	52 to 62
Clusters per plant	2.40	5.56	16	13.33	6 to 8
Pods per cluster	0.06	4.13	9	7.50	5 to 5
Pods per plant	15.75	18.39	20	16.67	19 to 25
Pod length (cm)	-12.15	8.53	30	25.00	8.55 to 9.57

Character	N.D.	Threshold value	Desirable transgressive segregants		Range in value of T.S.
			Frequency	T.S. %	
Seeds per pod	6.29	15.33	21	17.50	16 to 17
100-seed weight (g)	-30.06	3.54	15	12.50	3.55 to 3.7
Seed yield per plant (g)	-0.37	7.19	17	14.17	7.3 to 8.9

Table 2: The extended limits achieved by transgressive segregants in respect of various characters in F_2 generation of four crosses

Characters	Highest intensity of character expression in four crosses			
	F_2			
	Cross 1	Cross 2	Cross 3	Cross 4
Plant height (cm)	61 (54.27)	67 (54.27)	54 (49.73)	62 (54.77)
Clusters per plant	8 (4.90)	9 (4.90)	8 (4.83)	8 (3.77)
Pods per cluster	5 (3.47)	6 (3.47)	5 (3.37)	5 (3.83)
Pods per plant	31 (17.00)	35 (17.00)	30 (14.23)	25 (14.53)
Pod length (cm)	8.90 (8.55)	9.50 (8.55)	9.70 (8.47)	9.57 (8.40)
Seeds per pod	18 (13.63)	18 (13.63)	17 (14.33)	17 (14.00)
100-seed weight (g)	3.59 (3.34)	3.80 (3.35)	3.66 (3.35)	3.70 (3.40)
Seed yield per plant (g)	9.05 (6.63)	8.60 (6.63)	9.10 (5.92)	8.90 (6.39)

Cross No. 1 :HUM 1 x ML 818, Cross No. 2: HUM 1 x RMG 975,
Cross No. 3 :IPM 205-02 x RMG 975 and Cross No. 4 : LGG 460 x ML 818

Table 3 : Number of transgressive segregants in four crosses of mungbean

S. No.	Characters	Name of cross			
		Cross 1	Cross 2	Cross 3	Cross 4
1.	Plant height (cm)	28	21	16	19
2.	Clusters per plant	19	16	16	16
3.	Pods per cluster	18	15	13	9
4.	Pods per plant	20	18	25	20
5.	Pod length (cm)	17	20	14	30
6.	Seeds per pod	18	18	19	21
7.	100-seed weight (g)	18	17	17	15
8.	Seed yield per plant (g)	23	24	28	17

Cross No. 1 :HUM 1 x ML 818, Cross No. 2: HUM 1 x RMG 975,
Cross No. 3 :IPM 205-02 x RMG 975 and Cross No. 4 : LGG 460 x ML 818

Table 4 : Rare and important transgressants

Cross No.	Frequency of transgressants (%)	Characters for which transgression was simultaneous
1	0.83	Seed yield per plant + clusters per plant + pods per cluster + pods per plant + pod length + seeds per pod
2	1.67	
3	1.67	
4	0.83	

1	0.83	Seed yield per plant + clusters per plant + pods per cluster + pods per plant + pod length
2	0.83	
3	0.83	
4	0.83	
1	1.67	Seed yield per plant + clusters per plant + pods per cluster + pods per plant
2	2.50	
3	1.67	
2	0.83	Seed yield per plant + clusters per plant + pods per cluster
3	4.17	
1	2.50	Seed yield per plant + clusters per plant
2	3.33	
3	6.67	
1	13.33	Seed yield per plant alone
2	10.84	
3	8.33	
4	12.50	

Cross No. I :HUM 1 x ML 818, Cross No. II: HUM 1 x RMG 975,
Cross No. III :IPM 205-02 x RMG 975 and Cross No. IV :LGG 4604 x ML 818

Table 5 : Promising transgressive segreagants having combinations of desirable attributes

Characters	Plant no.	Plant height	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100-seed weight	Seed yield per plant	% yield increased over increasing parent
Cross-1 (HUM 1 x ML 818)										
F₂	117	52.00	7.00*	5.00*	21.00*	8.80*	15.00*	3.53*	8.65*	30.46
Hum-1		54.27	4.90	3.47	17.00	8.55	12.23	3.34	6.63	
ML-818		47.03	4.60	3.27	15.00	8.41	13.63	3.12	6.39	
Cross-2 (HUM 1 x RMG 975)										
F₂	29	52.00	6.00*	5.00*	25.00*	9.00*	16.00*	3.30	7.90*	19.15
HUM 1		54.27	4.90	3.47	17.00	8.55	12.23	3.34	6.63	
RMG-975		49.73	4.83	2.93	14.23	7.70	13.63	3.35	5.85	
F₂	91	45.00	6.00*	5.00*	30.00*	9.50*	16.00*	3.30	8.20*	23.68
HUM 1		54.27	4.90	3.47	17.00	8.55	12.23	3.34	6.63	
RMG 975		51.27	3.57	3.70	13.33	7.18	11.03	3.31	5.50	
Cross-3 (IPM 205-02 x RMG 975)										
F₂	96	49.00	5.00*	5.00*	25.00*	9.70*	25.00*	2.96	7.10*	19.93
IPM-205-02		48.77	3.73	3.37	12.50	8.44	14.33	3.34	5.92	
RMG-975		49.73	4.83	2.93	14.23	7.70	13.63	3.35	5.85	
F₂	115	46.00	7.00*	5.00*	20.00*	8.70*	20.00*	3.26	7.00*	18.24
IPM-205-02		48.77	3.73	3.37	12.50	8.44	14.33	3.34	5.92	
RMG-975		49.73	4.83	2.93	14.23	7.70	13.63	3.35	5.85	
Cross-4 (LGG 4604 x ML 818)										
F₂	112	44.00	6.00*	5.00*	20.00*	9.37*	16.00*	3.30	7.30*	14.24
LGG-4604		47.37	4.47	2.80	12.47	8.31	14.00	3.40	5.29	
ML-818		47.03	4.60	3.27	15.00	8.41	13.63	3.12	6.39	

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