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Identification of promising transgressive segregants for grain zinc, iron and productivity traits in segregating generations of finger millet (*Eleusine coracana* L.)

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Abstract

Finger millet (*Eleusine coracana* L.), an ancient cereal crop, is valued for its resilience, nutritional richness and adaptability to marginal environments. Despite being a staple food in many regions, it has received limited attention in modern breeding programs. The present study aimed to assess the extent of transgressive segregation for yield and nutritional traits in F_2 and F_3 populations derived from the crosses GPU-28 × GE-1746 and GPU-28 × GE-6635. A total of 310 and 181 F_2 plants were selected from the respective crosses and evaluated for six quantitative traits along with grain Fe and Zn contents. Transgressive segregants were identified as individuals performing beyond parental limits. Results revealed varying frequencies of transgressive segregants across traits and crosses. Cross GPU-28 × GE-6635 exhibited a higher frequency of desirable transgressive segregants for productive tillers, finger number, finger length, grain yield and Fe content, while GPU-28 × GE-1746 showed superiority for Zn content. Superior F_3 plants outperforming parents and checks were identified for grain yield, Fe and Zn. Notably, some plants combined high yield with elevated micronutrient content, indicating complementary gene action and potential for biofortification. These findings highlight the utility of transgressive segregation in enhancing yield and nutritional quality in finger millet improvement programs.

Keywords: Biofortification, complementary gene action, finger millet, transgressive segregants

Introduction

Finger millet (*Eleusine coracana* L. Gaertn.), commonly known as ragi**,** is one of the oldest cultivated cereals and is widely recognized for its resilience under harsh growing conditions. Believed to have originated in East Africa, it later spread to India, where it became an important staple food, particularly in the southern states (Dida *et al*., 2008) [3]. Today, India is the leading producer of finger millet, contributing over half of the global acreage and production. Unlike many other cereals, ragi thrives in marginal soils with minimal inputs, showing remarkable tolerance to drought and adaptability to diverse agro-climates (Hittalmani *et al*., 2017) [5]. Its long shelf life and resistance to storage pests have earned it the reputation of being a “poor man’s crop” or even a “famine food,” ensuring food security in vulnerable communities (Gopalan *et al*., 1976) [4].

Nutritionally, finger millet is often described as a Nutri-cereal because it offers higher levels of calcium, iron, zinc and dietary fiber compared to major cereals like rice and wheat (Chethan & Malleshi, 2007; Saleh *et al*., 2013) [2, 9]. The grain is gluten-free and has a low glycemic index, making it suitable for people with celiac disease, diabetes and cardiovascular disorders. In addition, its rich profile of polyphenols and antioxidants provides further health-promoting benefits. Despite these advantages, ragi has received relatively little attention in terms of modern crop improvement compared with other cereals. With increasing concerns about hidden hunger and micronutrient malnutrition, finger millet has emerged as a promising target for biofortification programs, especially to enhance grain iron and zinc content while maintaining good yield potential (Kumar *et al*., 2016) [6].

Transgressive segregation refers to phenomenon through which we get variation in F_2 or later generation outside the range of both parents. Production of transgressive segregants for yield and its component traits and for nutrients content plays a vital role in breeding programme. Although transgressive segregants includes lines which fall outside the range of performance of either parents, but only those being superior to better parents in desirable direction are of practical value. Therefore, a breeder is more concerned with obtaining higher frequency of transgressive segregants in segregation population. There is no much published information available on this aspect in finger millet, hence report on other crops and traits are also reviewed herewith.

Transgressive segregation produces progeny phenotypes that exceed the parental phenotypes. Unlike heterosis, extreme phenotypes caused by transgressive segregation are heritably stable. Maximum genetic variation in F_2 population provides the first opportunity for selection of individual plants, any one of which may end up into a new cultivar. F_2 plants that surpassed the parental limits were observed in both the crosses for all the traits. Production of transgressive segregants for yield and its component traits and for nutrients content plays a vital role in breeding programme (Bharathi *et al*., 2019) [1]. The frequency of transgressive segregants was estimated for all the traits in F_2 population of both crosses, number of plants scoring lower than the lower scoring parent and higher than the higher scoring parent were counted and designated as transgressive segregants.

Materials and Methods

The F_2 populations derived from the crosses GPU 28 × GE 1746 and GPU 28 × GE 6635 were sown over a large area during the summer of 2021. Selection was carried out based on phenotypic superiority, resulting in the identification of 310 single plants from GPU 28 × GE 1746 and 181 single plants from GPU 28 × GE 6635. These plants were harvested individually to collect seeds. Observations were recorded on six quantitative traits of the selected F_2 plants and their grain Fe and Zn contents were estimated using the Atomic Absorption Spectroscopy (AAS) method. The number of plants scoring lower than lower scoring parent and higher than higher scoring parent for plant height, productive tillers per plant, finger number per main ear, finger length, grain yield per plant in F_2 population were counted and designated as transgressive segregants. Superior F_3 plants among F_3 progenies in each cross which shows the outperformance to parents and checks for traits grain yield, grain Fe and Zn content were regarded as desirable transgressive segregants in F_3 generations. The Salient features of finger millet varieties used as parents in the crosses and checks are presented in Table 1.

Results and Discussion

The frequencies of transgressive segregants were found to be different for all the traits and across the two crosses. Higher frequency of desirable transgressive segregants for productive tillers per plant, finger number per main ear, finger length, grain yield per plant and grain Fe content in cross GPU-28 × GE-6635 whereas grain Zn content in cross GPU-28 × GE-1746 were recorded. This indicates that the parent GE 6635 contributed positive alleles for grain iron content whereas the parent GE1746 contributed complementary alleles for high grain zinc content in the recipient parent (GPU 28) background. Hence, there is a lot of scope to bring in beneficial alleles into a single genotype through rigorous selection in later generations for grain yield and grain Fe and Zn content. The frequencies of transgressive segregants for Fe and Zn from both crosses are presented in Table 2.

Transgressive segregants with lower value than lowest parent was in high frequency for productive tillers per plant and grain yield per plant in cross GPU-28 ×
GE-1746. In GPU-28 × GE-6635 cross, plant height, finger number main per ear, finger length, grain Fe and Zn content recorded higher frequency of lowest value transgressive segregants. Occurrence of such transgressions is possibly due to accumulation of complementary alleles from both the parents at multiple loci in certain F_2 population (Tanksley, 1993) [10] and unmasking of recessive deleterious alleles due to inbreeding (Rick and Smith 1953) [8].

The frequencies of segregants that surpassed the higher scoring parent were found to be very low for finger number per main ear and grain Fe content in F_2 population of both crosses (Table 3). However, the realization of transgressive segregants for all other traits under study suggests that, it is possible to identify and develop pure lines that outperform the parental limits. Comparable performance was noticed between F_2 populations of two crosses for most of the parameters studied and reported above may be attributable to the involvement of common female parent in two crosses (connected crosses).

The F3 plants which outperformed the checks and parents with respect to grain yield, grain Fe and Zn content were identified in F3 progenies in both crosses. Among the F_3 progenies 49 and 32 superior F_3 plants for grain yield, four and nine superior F_3 plants for grain Fe content and 77 and 56 superior F_3 plants for grain Zn content were identified in cross GPU-28 × GE 1746 and GPU-28× GE 6635 respectively, among them top ten plants were represented below in respective tables. P refers to the progeny row and the number given in the parenthesis refers to the plant number in the progeny row.

Among superior F_3 plants identified for grain yield in cross GPU-28 × GE 1746, the plant P131(2) also has higher amount of grain Fe and Zn content. Plants such as P72(1), P71(4), P91(1) and P55(3) have higher grain Zn content compared to best check variety (Fig. 1). For grain Fe content, superior F_3 plants are P107(5), P131(2), P10(2) and P121(2) in cross GPU-28 × GE 1746. Among them P131(2) also has high grain yield and Zn content. Plants P107(5) and P121(2) have high grain Zn content compared to best check *i.e.* KMR 301. Superior F_3 plants identified based on grain Zn content in cross GPU-28 × GE 1746, the F_3 plants such as P107(5), P131(2), P87(1), P145(5) and P121(2) also have high grain Fe content. And plants P131(2), P142(1) and P71(4) have high grain yield compared to best check i.e. KMR 301.

Table 1: Salient features of finger millet varieties used as parents in the crosses and checks

Parents and Checks	Pedigree	Year of release	Duration (days)	Average yield (q/ha)	Salient features
KMR 301	MR 1×GE1409	2009	120-125 (Long)	30-35	Open ears with curved fingers, high grain weight, bold grains, suitable for *kharif* and rabi
GPU 66	PR 202 × GPU 28	2018	113-115 (Medium)	35-40	Compact ears with tip incurved fingers, resistant to finger and neck blast disease, suitable for Summer and *kharif*
GPU48	GPU 26 × L 5	2005	95-100 (Short)	28-30	Purple pigmentation on all parts of plant and resistant to finger and neck blast disease, suitable for Summer, *Kharif* and Late *kharif*
GPU 28	Indaf 5 × (Indaf 9× IE 1012)	1998	110-115 (Medium)	35-40	Medium tall plant, semi compact ears with tip incurved fingers and resistant to finger and neck blast disease
GE 1746	Germplasm accession Collected from Almora				High grain Fe content (50.01ppm)
GE 6635	Germplasm accession Collected from Malawi				High grain Zn content (27.33ppm)

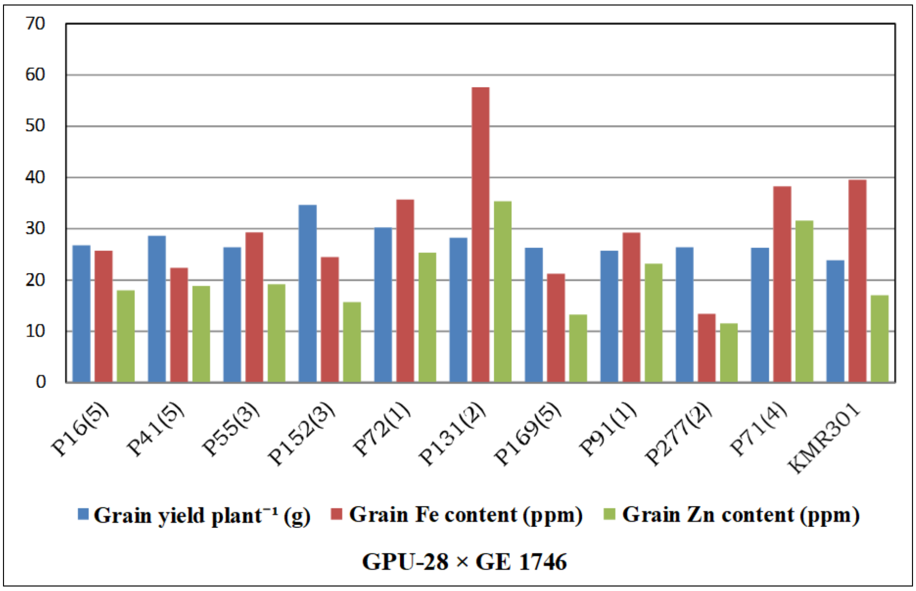
Table 2: Frequency of transgressive segregants for grain yield and its component traits along with grain Fe and Zn content in F_2 population of two crosses

Characters	Less than the lower scoring parent				Higher than the higher scoring parent			
	C1		C2		C1		C2	
	No. of plants	Frequency	No. of plants	Frequency	No. of plants	Frequency	No. of plants	Frequency
Plant height (cm)	103	0.33	147	0.81	88	0.28	18	0.09
Productive tillers per plant	74	0.23	34	0.18	178	0.57	117	0.64
Finger number per main ear	79	0.25	140	0.77	18	0.05	33	0.18
Finger length (cm)	118	0.37	74	0.40	75	0.24	107	0.59
Grain yield per plant (g)	88	0.28	44	0.24	162	0.51	127	0.70
Grain Fe content (ppm)	53	0.16	88	0.48	17	0.05	31	0.17
Grain Zn content (ppm)	65	0.20	90	0.49	74	0.23	3	0.016

C1- GPU-28 × GE-1746, C2- GPU-28 × GE-6635

Table 3: Frequency of desirable transgressive segregants realized for grain yield and its component traits along with grain Fe and Zn content in F_2 population derived from two crosses

Traits	Number of plants	Frequency
Plant height (cm)	106	0.21
Productive tillers per plant	295	0.60
Finger number per main ear	51	0.10
Finger length (cm)	182	0.37
Grain yield per plant (g)	289	0.58
Grain Fe content (ppm)	48	0.09
Grain Zn content (ppm)	77	0.15



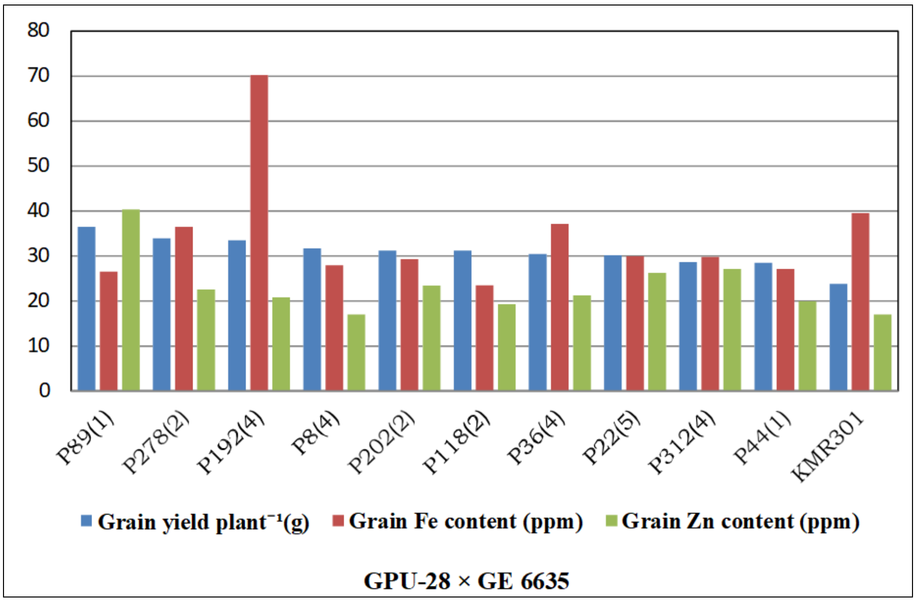


Fig 1: Graphs depicting superior F_3 plants identified based on grain yield compared to best check in cross GPU-28 × GE 1746 and GPU-28 × GE 6635

Conclusion

Progenies of the cross GPU-28 × GE 6635 recovered higher frequency of desirable transgressive segregants for grain Fe content, whereas cross GPU-28 × GE1746 recovered higher frequency of transgressive segregants for Zn content. This indicates that the parent GE 6635 contributed positive alleles for grain iron content whereas the parent GE1746 contributed complementary alleles for high grain zinc content in the recipient parent (GPU-28) background even though donor parents selected for vice-versa. The superior F_3 plants identified based on grain yield, grain Fe and Zn content from both crosses are suggested to be forward for further evaluation. As it was observed that cross GPU-28 × GE 6635 performed well for grain yield and its attributing traits and also for grain Fe and Zn content in both generations, it should be evaluated in later generations, which may contribute in developing a high yielding variety with appreciable amount of grain Fe and Zn content.

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Competing Interests

The authors declare that they have no competing interests.

Authors Contribution

Sangappa Arjun Teli conceived and designed the study, performed the experiments, and drafted the manuscript. S. R. Spoorthi and V. Prashantha assisted in data collection, analysis, and interpretation. H. S. Saritha and K. M. Shirisha contributed to field trials and laboratory work. Premakumar and Bharat provided technical support and guidance during the research. Jayarame Gowda supervised the study, provided critical suggestions, and reviewed the manuscript. All authors read and approved the final manuscript.

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