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DIVERSITY OF HEMIPTERA FAUNA OF DADAR NAGAR HAVELI WILDLIFE SANCTUARY AREA, DADAR NAGAR HAVELI, INDIA

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ABSTRACT

Dadar & Nagar Haveli, is well known Union Territory of India, comprising two widely separated areas, Dadar and Nagar Haveli respectively. Total area of Dadra & Nagar Haveli is 491km2. Overall 30 species had been reported first time from Sanctuary area Silvasa and Dadra and Nagar Haveli respectively. All these species are reported first time from this area.

Key words : *Daman and Diu, Fudam Bird Sanctuary, Hemiptera, Mangrove.*

INTRODUCTION

The area of Dadra &Nagar Haveli spread between Gujarat in North and Maharashtra in South. It was liberated from Portuguese Rulers by people of this area on 2nd August 1954. The people of the Union territory established free Administration of Dadra & Nagar Haveli, which was finally merged in to Union of India in the year 1961. Forest area of this Union territory has moist deciduous forest.

In the 'Fauna of British India', a detailed account on Hemiptera of Indian region is dealt by Distant (1902a & b, 1904, 1906). Later on publication on Hemiptera of central India were published by Chandra (2008, 2009), Chandra et al. (2010, 2012) and Chandra and Kushwaha (2013, 2014 a & b). Earlier study of some parts DNH has been done by Chandra et al.2017.

Dadra & Nagar Haveli Wildlife Sanctuary area is commonly known as Satimalia Deer park situated in capital Dadra & Nagar Haveli, Silvasa District. This is first ever study of this protected area.

Present paper deals with the study of 37 species under 11 families of order Hemiptera reported first time from Wildlife sanctuary area of DNH, in which 6 species were recorded first time from Fudam Bird Sanctuary, Diu and 5 species from Dadra and Nagar Haveli.

Abbreviation used: VH-Very high; H-High; L-

Low; R-Rare; VR-Very Rare; FRH-Forest Rest House; DNH- Dadra and Nagar Haveli.

MATERIALS AND METHODS

The tour party of Zoological Survey of India, Headquarters, Kolkata, made an effort for exploration of faunal diversity of Daman and Diu& Dadra & Nagar Haveli. Team of ZSI collected about 254 bugs specimens from various localities by hand picking, net trap and light tarp methods, collected specimens were shorted out and bugs were pinned and drayed and handed over to identification lab for their identification, pinned bugs were identified with the help of literature available in ZSI library and Fauna of British India. Morphology of bugs were studied by Leica microscope M205-A.

S. No.	Suborder / Superfamily / Family / Species	Status In DNH	Date of observation	Area
	Suborder: Auchenorrhyncha			
	Infraorder: Cicadomorpha			
	Superfamily: Cercopoidea			
	Family: Cercopidae			
1	*Callitettix versicolor* (Fabricius)	L	19.i.2018	DNH Guest house
	Suborder: Heteropterodea			
	Infraorder: Cimicomorpha			
	Superfamily: Reduvioidea			
	Family: Reduviidae			
2	*Tribelocephala indica* (Walker)	R	20.i.2018	Khanvel
3	*Ectrychotes dispar* Reuter	R	24.i.2018	Deer park
4	*Polididus armatissimus* Stal	H	23.i.2018	Near Lion safari
5	*Onchocephalus schioedtei* Reuter	L	22.i.2018	Near butterfly Park
6	*Ectomocoris cordiger* Stal	L	22.i.2018	
7	*Rhynocoris marginatus* (Fabricius)	R	20.i.2018	Nature Park
	Infraorder: Pentatomorpha Superfamily: Lygaeoidea			
	Family: Lygaeidae			
8	*Elasmolomus sordidus* (Fabricius)	L	24.i.2018	Near Lion safari
9	*Metochus uniguttattus* (Thunberg)	VH	22.i.2018	Khanvel
10	*Spilostethus hospes* (Fabricius)	VR	23.i.2018	Deer Park
	Superfamily: Pyrrhocoroidea			
	Family: Phyrrhocoridae			

11	*Dysdercus koenigii* (Fabricius)	VH	19.i.2018	DNH Guest house
12	*Antilochus coqueberti* (Fabricius)	VH	23.i.2018	Khanvel
	Superfamily: Coreoidea			
	Family: Coreidae			
13	*Serinetha abdominalis* (Fabricius)	H	24.i.2018	Near Lion safari
14	*Cletus punctulatus* (Westwood)	L	22.i.2018	Near butterfly Park
15	*Cletus bipunctatus* (Herrich-Schäffer)	L	23.i.2018	Deer Park
	Family: Alydidae			
16	*Riptortus fuscus* (Fabricius)	H	24.i.2018	Nature Park
17	*Leptocorisa varicornis* (Fabricius)	H	22.i.2018	Deer Park
	Superfamily: Pentatomoidea			
	Family: Cydnidae			
18	*Aethus indicus* (Westwood)	VH	20.i.2018	DNH Guest house
	Family: Pentatomidae			
19	*Halys dentatus* Fabricius	H	23.i.2018	Near Lion safari
20	*Erthesina fullo* (Thunberg)	H	24.i.2018	Khanvel
21	*Eysarcoris ventralis* (Westwood)	L	23.i.2018	Deer Park
22	*Eysarcoris guttiger* (Thunberg)	H	23.i.2018	Near butterfly Park
23	*Carbula biguttata* (Fabricius)	L	22.i.2018	Khanvel
24	*Nezara viridula* (Linnaeus)	H	23.i.2018	Near Lion safari
25	*Urochela bimaculata* Dallas	L	20.i.2018	Near butterfly Park
26	*Antestiopsis cruciata* (Fabricius)	H	22.i.2018	Deer Park
27	*Placosternum obscura* Dallas	H	21.i.2018	Near Lion safari
28	*Acrosternum gramineum* (Fabricius)	H	22.i.2018	Khanvel
29	*Cordius ianus* (Fabricius)	H	23.i.2018	Deer Park
30	*Piezodorus hybnrri* (Fabricius)	L	20.ix.2018	Deer Park

RESULTS AND DISCUSSIONS

In present work, 30 new records from Dadar & Nagar Haveli Wildlife Sanctuary area belonging to 8 families of order Hemiptera were recorded for the first time present study adds our knowledge about the True bug diversity of Dadar & Nagar Haveli Wildlife Sanctuary area.

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PROTEIN CONTENT VARIES WITH SEED SIZE AND ENVIRONMENT IN MUNGBEAN (VIGNA RADIATA L.)

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ABSTRACT

Mungbean or greengram has high nutritive value with easily digestible protein , high amount of dietary fibres , antioxidant substances, vitamins and minerals. However, in a study conducted it was observed that main constituent of mungbean seeds protein varies among diverse germplasm including released varieties tested. The diverse germplasm had different seed size ranging between 2 to 6 g test weight (hundred seed weight). The significant negative correlation (-0.61*) was observed between seed size and percent protein in seed that indicated higher seed sized genotypes had less protein as compared to smaller seeds. In order to find out the reasons behind lower protein content in large seeded mungbeans, it was found that higher sucrose synthase (SS) activity play a crucial role in determining seed size, grain filling , starch content and total carbohydrates in these genotypes. The higher SS accelerates carbohydrate synthesis and competitively suppresses protein accumulation in seeds. Under elevated CO_2 , seeds preferred to accumulate more carbohydrates than the protein resulting in higher C:N ratio in seeds. In the present context, it seems difficult to combine both the traits together i.e, high protein and large seed together which is the commercial demand of present period.

Key words : *Seed protein, germplasm diversity , seed size, impact of elevated CO2 on seed quality.*

INTRODUCTION

Grain legumes are an important part of human diet in almost every parts of the world. Among these, Mungbean (Vigna radiata L.) is one of the most commonly consumed food legumes in India. Besides being a rich and less expensive source of protein, mungbean contains a large amount of carbohydrates, dietary fibres, essentials minerals, vitamins and folates (Mubarak 2005). Mungbeans

nutrition includes a very impressive amount of protein for a plant, with about 20–24 percent of their chemical structure being amino acids (protein), Mung beans is also rich in other essential amino acids, including leucine, isoleucine and valine, which can be combined with other plant sources (like whole grains or some vegetables) to make a "complete protein." Mungbeans nutrition contains a range of phytonutrients that are considered anti-microbial and anti-inflammatory, and promote a healthy balance of bacteria within the digestive tract. The folate (vitamin B9) is an important vitamin for DNA synthesis, cell and tissue growth, hormonal balance, cognitive function, and even reproduction. Mung beans also provide about 36 percent of daily magnesium needs for the average adult woman. Many adults are actually deficient in magnesium . The data released by the National Institute of Nutrition (NIN), Hyderabad, in 2017 suggests that the foods we eat today are less nutritious than what we used to consume just three decades ago. NIN has released such data after a gap of 28 years. NIN researchers have measured the values of 151 nutrients in 528 food items including pulses collected from markets across six geographical regions. All the food items and nutrients listed in the 2017 report showed a decline in quantity and quality as compared to the same food items measured in 1989. The analysis shows an alarming trend: there is a perceptible decrease in nutrition levels in all types of food and report says that those food items are 'Healthy no more'..The pulses are being depleted of their key nutrient—protein, which plays an important role in building, repairing and maintaining tissues. Protein has reduced by 10.4 per cent in masoor lentil (whole brown lentil) and 6.12 per cent in greengram moong (whole green gram). In a 2004 study published in the Journal of the American College of Nutrition, researchers with the University of Texas at Austin, analysed food composition data for 43 crops grown between 1950 and 1999. Six nutrients—protein, calcium, iron, phosphorus, riboflavin and ascorbic acid—showed a significant decline in almost all the crops including pulses. Scientists across the world have identified two reasons for this declining food nutrition. One, intensive agricultural practices have stripped the soil of micronutrients. The second reason pertains to the impact of climate change on nutritional status of food crops. Scientists say rising levels of carbon dioxide (CO2) in the environment could also be affecting plant nutrition levels (Daniel et al., 2008).

Earlier studies showed that seed size and protein content in pulses is significantly negatively correlated each other. Small seeded chickpea varieties have more protein content and much tastier as compared to large seeded chickpea which are more starchy and less protein (Ankita et al., 2017). As breeders developed many short duration early maturing varieties for central India, these varieties quickly trap atmospheric CO2 as favourable conditions for high photosynthesis prevails in central India during crop season such as warmer temperature, and .higher solar radiation. In same crop season, chickpea in north India suffers from low temperature and less solar radiation during winter resulting in poor photosynthesis and ability of carbon gain is sufficiently reduced even under elevated CO2 thus giving sufficient opportunities to synthesize protein in seeds. Again the crop duration is longer enabling more diversion of protein towards seeds. Therefore, Significant genotype x environment interaction persists in pulses across the diverse climatic condition. Here taking decision is very critical, whether we need attractive commercially viable large seeded pulses having short maturing type with

less quality traits or long duration small seeded varieties with high protein and micronutrients content

The present investigation is therefore to ascertain the relationship between seed size and protein content in mungbean varities collected from diverse sources.

MATERIALS AND METHODS

Twenty eight (28) mungbean genotypes including released varieties having diverse test weight (hundrered seed weight, HSW) ranging from 2 to 6 g per hundred seeds.

Estimation of protein in seeds.

The seed protein contents in replicated samples of 28 genotypes were estimated by Kjeldahl's method based on total nitrogen content. Nitrogen content was determined by using Kel Plus distillation apparatus (modified Kjeldahl apparatus) after digestion of the samples .Accurately 1 gm of sample was weighed and put in a digestion flask. 10 gm potassium sulphate, 0.7 gm mercuric oxide and 20 ml sulphuric acid were added. The flask was heated gently at an inclined angle until frothing subsides and then boiled until the solution clears. Boiling went on for an additional half hour. On cooling, about 90 ml. Distilled water was added, re cooling was done, 25 ml. Sulphide solution was added and mixed. Small pieces of boiling chip added at prevent bumping and 80 ml. of sodium hydroxide solution while tilting the flask so that two layers were formed. The condenser unit was connected rapidly, heated, and collected distilled ammonia in 50 ml. Boric acid/indicator solution. 50 ml of distillate was collected. On completion of distillation; the receiver was removed and titrated against standard acid solution.

Calculation

Nitrogen content of sample (%)

= ml acid X Normality of standard acidwt of sample (gm)×0.014 X 100

Crude protein content (%) = Nitrogen content X 6.25

Controlled environmental studies

Potted experiments were carried out using two contrasting mungbean genotypes having contrasting test weight such as SML 668 (large seeded 5.0 g) and ML 818 (Small seeded 3.2 g). Well-watered plants with recommended doses of fertilizer NPK were raised under open bright sunlight . When potted plants started flowering they were brought to controlled environmental chamber (High point Taiwan). Different concentration of CO_2 (350, 450 and 550 ppm) were created in different chambers in same controlled environment . The temperature was kept at max/min 35/20 0C and irradiance level 500 µmol photons $m^{-2}s^{-1}$. The plants were grown till maturity and seeds harvested for analysis.

Total carbohydrates and C:N ratio

Total carbohydrates , sugars of the seeds were measured by employing method as described by Yemm and Willis (1954) and starch by Clegg 1956 while C:N ratio was the ratio of total carbohydtates over total nitrogen estimated by Kjeldahl's method.

Sucrose synthase activity

Sucrose synthase in cotyledons with embryo was estimated by the method as described by Haem et al (1993)

Statistical analysis

The mean value of three replications of seed size and protein content were analyzed for Spearman's rank correlation

RESULTS AND DISCUSSION

A significant negative correlation (-0.61**; $P<0.01$) was observed between seed size (HSW) and per cent protein content indicating negative influence of large seed size on protein content of the seeds (Table 1). Relationship between seed size and protein content in newly developed high protein lines of pigeonpea has been reported by Saxena et al (1987). The key

enzyme for sucrose synthesis in developing seeds was almost 6 times higher in genetically large seeded mungbean(Fig 1).

The sucrose synthase activity in the developing cotyledons of large seeded mungbean SML 668 with test weight of 5 g was 5.84 nmol sucrose mg-1protein h-1 having percent protein content 14.7% as compared to small seeded genotype ML 818 having sucrose synthase activity of 1.40 nmol sucrose mg-1protein h-1 with increased protein percent of 19.6 in seeds (Fig 1). Poeta et al., 2016 discussed the variation in seed protein concentration and seed size .SML 668 and ML 818 grown under high CO2 condition (about 550 ppm) under controlled growth chamber showed higher carbon to nitrogen ratio (C:N) in seeds of large seeded type SML 668 as compared to small seeded ML 818 indicating massive diversion of excess carbon in growing sink of large seeded type (Table 2). As sucrose synthase is one of the rate limiting steps towards conversion of carbon to starch in grains and its low activity in small seeded mungbean restricts starch biosynthesis and in otherway accelerate protein synthesis. It has been reported that enhancing SuSy activity results in increased levels of starch in transgenic potato tubers (Baroja-Fernández et al. 2009).

In attempting to identify biochemical indicators of sink strength, it was proposed that the activity of SS can serve as an indicator of active sink growth (Sun et al. 1992). That hypothesis was derived from studying plant sinks such as developing tomato fruits, bulking potato tubers, and developing lima bean seeds (Sun et al.1992; Xu et al. 1989).Particularly with lima bean seeds and tomato fruits, the activity of SS was strongly related to growth .

. As breeders developed many short duration early maturing varieties of pulses, these varieties quickly trap atmospheric CO2 as favourable conditions for high photosynthesis prevails during mungbean crop season i.e. the warmer temperature, and .higher solar radiation. Many short duration varities have been attributed by rapid grain filling and shorter maturity period. The higher atmospheric CO2 is largely drained off into the developing grains because seeds are the ideal dumping platform to store excess CO_2 derived products as carbohydrates i.e. mainly starch. The present findings indicated that elevated CO_2 increased accumulation of sugar ,total carbohydrates and less protein , as a result C:N ratio increased (Table 2). High CO2 levels in the atmosphere lower the nitrogen concentration in plants, which in turn affects the protein content in food. Loladze (2014)was able to show that, when averaged across very different plant and tissue types, experimental approaches and locations, elevated CO_2 reduced the overall mineral content of plants by about 8%.

At the same time, elevated CO_2 was shown to strongly increase the ratio of soluble carbohydrates (starch and sugars) to proteins. Since climatic condition affects photosynthesis, therefore, significant genotype x environment interaction persists in pulses across the diverse climatic condition. Here taking decision is very critical, whether we need attractive commercially viable large seeded pulses having short maturing type with less quality traits or long duration small seeded varieties with high protein and micronutrients content.

It remains a great challenge for breeders to combine both the traits (Large seed size and high protein) which are antagonistic to each other and also under the changing scenario of climate change associated with increasing CO_2 and temperature

Table 1 : Per cent seed protein (dry weight basis) and test weight of different

Genotype	Protein %	Test weight (g)	Genotype	Protein %	Test weight (g)
		100 Seed wt			100 Seed wt
IPM 409-4	22	2.50	PDM-818	14.4	3.65
Sona yellow	16.5	3.41	PDM-281	15.3	3.48
COGG-912	15.2	3.39	PDM 191	13.2	4.08
VBG-04-008	16.8	2.71	PPM 262	21.1	2.34
IPM 205-7	15	3.58	IPM-2-23	13.3	4.67
IPM 99-115	12.5	3.48	SML 668	14.7	5.00
PDM 139	11.8	4.10	IPM S-2-8	9.8	3.57
TARAN-18	12.7	3.56	PPM -2	17.2	2.64
Pusha Vishal	13.8	3.83	Pant U-31	11.2	4.30
IPM 06-5	11.7	6.43	IPM 2-17	14.6	4.05
Pusha 9531	14.7	4.17	IPM-02-10	13.2	4.06
Pratiksha Nepal	16.5	4.66	PDM-54	16.4	3.41
IPM 2-14	19.5	3.43	AKM 99-4	12.6	4.06
ML-818	19.6	3.20	JBT 46123	12.8	4.95
Correlation Seed size and protein		-0.615**			

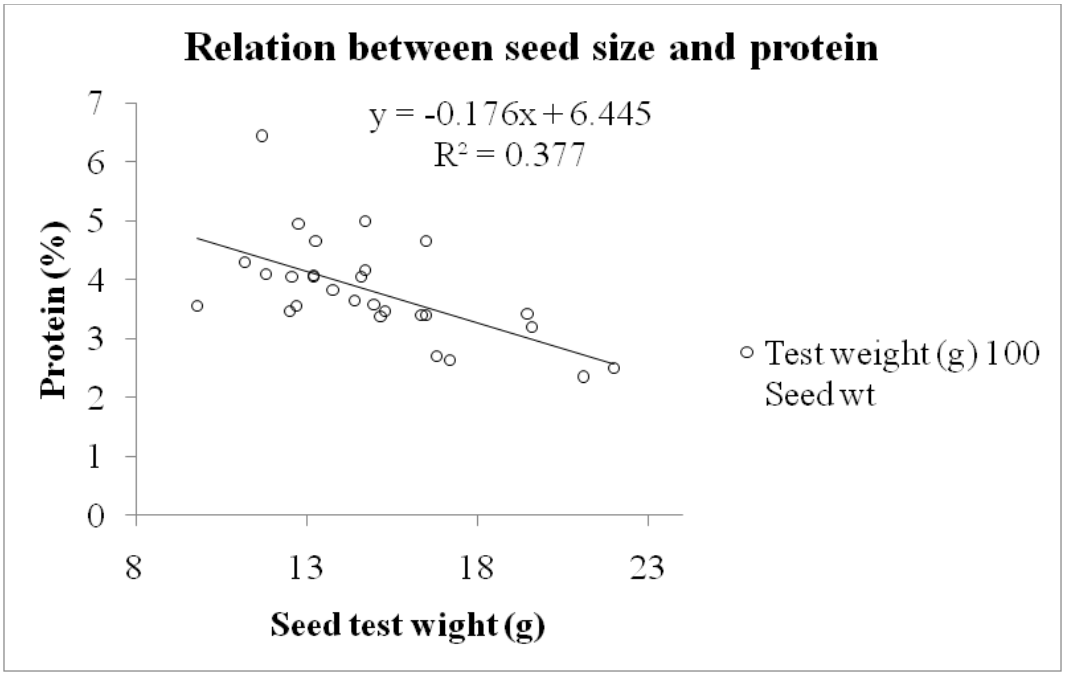

Fig 2: Liner regression line showing relationship of seed size and protein percent in seeds

Fig 3: Sucrose synthase and protein content in two contrasting seed size mungbean genotypes

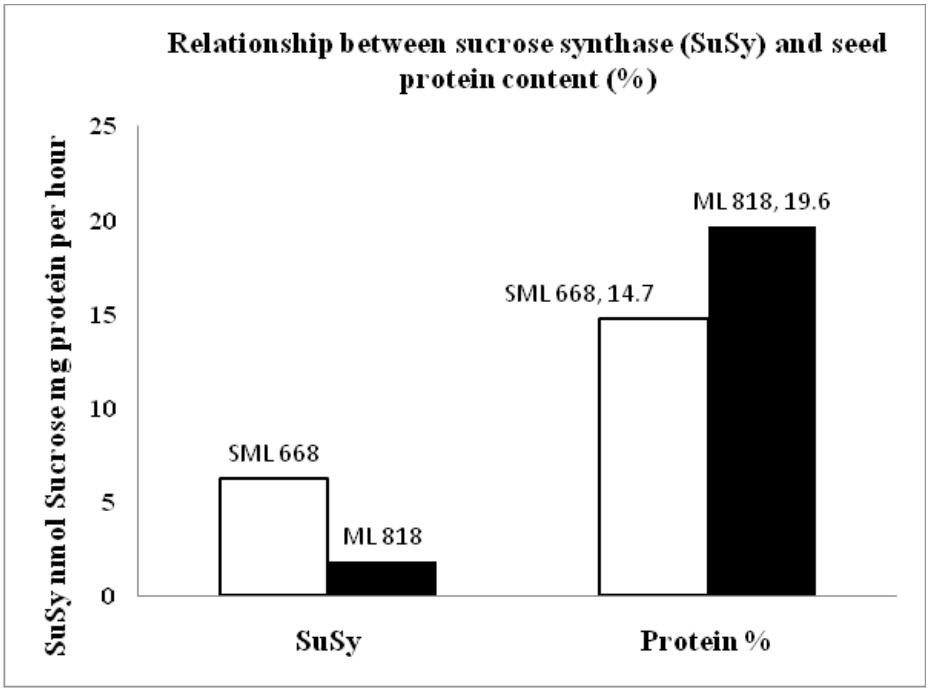

Table 2: C:N ratio of the contrasting seed sized mungbean as affected by increasing CO_2 concentration

CO_2 (ppm)	Total sugars	Starch	Total carbohydrates	Overall C:N ratio	C:N ratio ML 818	C:N ratio SML 668
350	4.0	63	75	3:1	3:1	3:1
450	6.5	68	82	4:1	3:1	5:1
550	7.0	73	86	6:1	4:1	7:1

CONCLUSION

In mungbean seed size is genetically controlled ,perhaps through key enzyme sucrose synthase. High rate of grain filling enhances more carbohydrate accumulation over protein through higher activity of sucrose synthase activity in seeds. Similar situation was also observed when more carbohydrates starch and total sugars with more C:N ratio and less protein detected under elevated CO2 . The results showed a negative correlation with seed size and protein content. New breeding strategies need to be explored to combine both the traits together to make mungbean commercially viable with enriched protein content.

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