

Annexure IV

Seed biophysical characteristics of 187 RILs based on NBPGR minimal descriptors for green gram (*V. radiata*) and (PPV & FRA, 2007)

RILs Line No.	*Seed Colour	*Seed Lustre	*Seed Shape	*Seed Texture	*Seed Size	*100 seeds wt. (in g)	* Coat Thickness (in mm)	*Seed Hardness (in kgf)
1	BG7	D	D	R	Large	5.390	0.067	1.400
2	BG7	S	D	S	Large	7.660	0.050	2.833
3	BG7	S	D	S	Large	5.977	0.050	1.867
4	LG1	D	D	R	Medium	4.329	0.070	2.700
5	BG7	S	O	S	Medium	4.917	0.057	1.967
6	LG1	S	D	S	Medium	4.827	0.060	2.700
7	BG7	D	D	R	Medium	4.042	0.070	2.033
8	BG7	D	D	R	Medium	4.647	0.057	2.567
9	GY3	S	O	S	Medium	4.795	0.063	2.733
10	DGM6	D	D	R	Large	5.033	0.057	2.000
11	DG2	S	D	S	Medium	4.371	0.053	2.800
12	BG7	D	D	R	Medium	4.682	0.060	2.600
13	BG7	D	D	R	Medium	4.353	0.057	1.767
14	LG1	D	D	R	Medium	4.022	0.053	2.033
15	DGM6	D	D	R	Medium	4.432	0.057	1.900
16	B5	D	D	R	Medium	3.728	0.063	1.667
17	DGM6	D	D	R	Medium	4.157	0.063	2.233
18	BG7	D	D	R	Medium	4.192	0.050	2.200
19	DGM6	D	D	R	Medium	3.671	0.063	1.567
20	DGM6	D	D	R	Medium	3.977	0.043	2.267
21	DG2	D	D	S	Medium	3.877	0.077	2.333
22	DG2	D	D	S	Medium	3.706	0.053	2.633
23	GY3	S	D	S	Medium	3.756	0.053	2.767
24	GY3	D	D	S	Medium	4.002	0.070	2.333
25	GY3	D	D	S	Medium	3.474	0.050	1.867
26	DG2	D	D	S	Medium	3.583	0.053	2.333
27	B5	D	D	R	Medium	3.411	0.057	1.467
28	B5	D	D	R	Medium	3.748	0.070	1.467
29	B5	D	D	R	Medium	3.740	0.043	1.467
30	BG7	D	D	R	Medium	3.645	0.060	2.067
31	BG7	D	D	R	Medium	3.848	0.060	1.667
32	DG2	D	D	R	Medium	3.300	0.047	2.467
33	BG7	D	D	R	Medium	3.682	0.063	2.633
34	BG7	D	D	R	Medium	3.724	0.057	1.833
35	BG7	D	D	R	Medium	3.792	0.053	1.100
36	BG7	D	D	R	Medium	3.301	0.057	1.933
37	BG7	D	D	R	Medium	3.390	0.067	2.867
38	GY3	D	D	R	Medium	3.928	0.057	2.600
39	BG7	D	D	R	Medium	3.354	0.077	2.067
40	BG7	D	D	R	Medium	3.183	0.057	1.633
41	BG7	D	D	R	Medium	4.780	0.060	1.467
42	DGM6	D	D	R	Medium	3.354	0.053	2.100

43	BG7	D	D	R	Medium	3.897	0.057	2.267
44	BG7	D	D	R	Medium	3.954	0.057	1.933
45	DGM6	S	D	S	Medium	3.357	0.053	1.433
46	DGM6	S	D	S	Small	2.950	0.050	1.867
47	B5	D	D	R	Medium	3.625	0.053	1.933
48	DGM6	S	D	S	Small	2.877	0.067	2.867
49	DG2	D	D	R	Medium	3.538	0.067	2.333
50	BG7	D	D	R	Small	2.932	0.053	1.933
51	GY3	D	D	R	Medium	3.970	0.057	2.033
52	DG2	D	D	R	Medium	3.675	0.057	1.633
53	BG7	D	D	R	Medium	3.882	0.057	2.067
54	DG2	D	D	S	Medium	3.534	0.057	1.633
55	GY3	D	D	S	Medium	4.197	0.060	1.900
56	BG7	D	D	R	Small	2.975	0.060	1.800
57	BG7	D	D	S	Medium	3.280	0.060	1.300
58	DG2	D	D	R	Medium	3.788	0.067	1.533
59	LG1	D	D	R	Small	2.703	0.070	1.933
60	BG7	D	D	R	Medium	3.664	0.053	1.767
61	GY3	D	D	R	Medium	4.968	0.057	2.667
62	BG7	D	D	R	Medium	3.956	0.070	1.433
63	DGM6	D	D	R	Small	2.976	0.070	1.500
64	DGM6	D	D	S	Medium	3.674	0.073	2.633
65	BG7	D	D	R	Medium	3.876	0.063	1.933
66	DG2	S	D	S	Medium	3.125	0.063	1.267
67	GY3	S	O	S	Medium	3.772	0.057	1.567
68	BG7	D	D	R	Medium	3.339	0.070	1.233
69	GY3	D	D	R	Medium	3.476	0.057	1.500
70	B5	D	D	R	Small	2.954	0.047	1.633
71	BG7	S	D	S	Medium	3.927	0.060	1.700
72	DGM6	D	D	R	Medium	3.579	0.063	1.633
73	DGM6	D	D	R	Medium	3.417	0.070	2.233
74	B5	D	D	R	Small	2.978	0.060	1.633
75	GY3	D	D	R	Medium	4.139	0.053	2.033
76	BG7	D	D	R	Small	2.803	0.053	1.500
77	BG7	D	D	R	Medium	3.576	0.057	1.667
78	LG1	D	D	R	Medium	3.555	0.057	1.800
79	GY3	S	D	R	Medium	3.664	0.063	2.233
80	B5	D	D	R	Medium	3.138	0.057	1.300
81	DGM6	D	D	R	Small	2.975	0.057	2.500
82	GY3	D	D	R	Small	2.274	0.063	1.600
83	BG7	D	D	R	Medium	3.330	0.070	2.200
84	BG7	D	D	R	Medium	3.528	0.063	1.833
85	DG2	D	D	R	Medium	3.610	0.053	1.967
86	BG7	D	D	R	Medium	3.255	0.050	1.700
87	DG2	S	D	S	Medium	3.716	0.060	2.667
88	GY3	S	D	S	Medium	3.845	0.057	5.100
89	GY3	S	D	S	Medium	3.987	0.053	1.867
90	B5	D	D	R	Medium	3.476	0.057	1.567
91	DGM6	D	D	R	Medium	3.404	0.070	2.000
92	LG1	D	D	R	Medium	3.350	0.057	2.033
93	BG7	D	D	R	Medium	3.619	0.060	1.300

94	GY3	D	D	R	Medium	3.657	0.063	2.200
95	B5	D	D	R	Medium	3.138	0.063	2.367
96	B5	D	D	R	Small	2.355	0.057	1.867
97	BG7	D	D	R	Medium	3.847	0.060	2.000
98	GY3	D	D	R	Medium	3.364	0.043	1.400
99	LG1	D	D	R	Medium	3.604	0.053	2.200
100	DG2	D	D	R	Medium	3.318	0.060	1.467
101	BG7	D	D	R	Medium	3.106	0.073	1.733
102	DG2	D	D	R	Medium	3.844	0.070	2.433
103	BG7	D	D	R	Medium	3.159	0.027	1.833
104	LG1	D	D	R	Medium	3.546	0.053	2.167
105	GY3	S	D	R	Medium	4.024	0.047	1.633
106	BG7	D	D	R	Medium	3.545	0.063	2.533
107	BG7	D	D	R	Medium	3.299	0.057	1.833
108	BG7	D	D	R	Medium	3.482	0.053	1.367
109	LG1	D	D	R	Small	2.389	0.047	2.233
110	BG7	D	D	R	Medium	3.692	0.067	1.800
111	BG7	D	D	R	Medium	3.329	0.060	1.433
112	BG7	D	D	R	Medium	3.093	0.070	1.400
113	B5	D	D	R	Medium	3.165	0.063	0.900
114	DG2	D	D	R	Medium	4.028	0.060	2.633
115	GY3	D	D	R	Medium	3.663	0.060	2.200
116	BG7	D	D	R	Medium	4.107	0.073	2.733
117	DG2	D	D	R	Medium	3.586	0.060	2.933
118	B5	D	D	R	Medium	3.355	0.063	1.600
119	B5	D	D	R	Medium	2.855	0.063	1.867
120	BG7	D	D	R	Medium	3.360	0.080	1.233
121	BG7	D	D	R	Medium	3.775	0.063	1.600
122	BG7	D	D	R	Medium	3.506	0.050	2.867
123	DG2	D	D	R	Medium	4.864	0.057	2.133
124	DGM6	S	D	R	Medium	3.053	0.053	1.867
125	B5	D	D	R	Medium	3.964	0.050	1.667
126	DGM6	S	D	R	Medium	3.010	0.053	1.400
127	BG7	D	D	R	Medium	3.532	0.067	1.833
128	B5	D	D	R	Medium	3.493	0.050	1.867
129	BG7	S	D	R	Medium	3.583	0.057	2.000
130	DGM6	S	D	S	Small	2.568	0.053	1.567
131	GY3	S	D	S	Medium	4.654	0.063	2.300
132	GY3	S	D	S	Medium	3.946	0.053	2.500
133	DGM6	S	D	S	Small	2.880	0.050	1.733
134	DG2	S	D	S	Medium	3.983	0.053	2.800
135	BG7	D	D	R	Medium	3.774	0.067	2.000
136	BG7	D	D	R	Medium	3.356	0.063	1.867
137	BG7	D	D	R	Medium	3.010	0.060	1.700
138	GY3	D	D	R	Medium	3.672	0.053	2.867
139	DGM6	D	D	R	Medium	3.289	0.050	1.967
140	DGM6	D	D	R	Medium	3.384	0.053	2.000
141	BG7	D	D	R	Medium	3.289	0.057	2.000
142	DGM6	D	D	R	Medium	3.271	0.057	1.400
143	BG7	S	D	R	Medium	3.121	0.050	2.067
144	LG1	D	D	R	Medium	4.118	0.057	3.067

145	GY3	D	D	S	Medium	3.849	0.057	2.833
146	GY3	S	D	S	Medium	3.539	0.060	1.900
147	BG7	D	D	R	Medium	3.243	0.063	1.933
148	DG2	S	D	S	Medium	4.411	0.067	2.467
149	DG2	S	D	S	Medium	4.232	0.047	2.433
150	B5	S	D	R	Small	2.927	0.060	2.433
151	GY3	D	D	S	Medium	3.076	0.033	2.000
152	B5	D	D	R	Medium	3.871	0.077	1.667
153	BG7	D	D	R	Medium	4.013	0.060	1.333
154	BG7	D	D	S	Medium	3.374	0.057	1.933
155	BG7	D	D	R	Small	2.990	0.067	1.967
156	DGM6	D	D	R	Medium	3.377	0.063	1.767
157	B5	D	D	R	Small	2.829	0.057	1.767
158	B5	D	D	R	Small	2.136	0.067	1.800
159	B5	D	D	R	Medium	3.376	0.053	1.600
160	BG7	D	D	R	Medium	3.178	0.063	1.467
161	GY3	S	D	S	Medium	3.579	0.067	2.667
162	BG7	D	D	R	Medium	3.712	0.047	1.700
163	BG7	S	O	S	Medium	3.561	0.073	2.000
164	DGM6	D	D	R	Medium	3.159	0.067	1.833
165	DGM6	D	D	R	Medium	3.197	0.063	2.700
166	GY3	S	D	S	Medium	3.312	0.063	1.633
167	DGM6	S	D	S	Medium	3.215	0.050	1.633
168	BG7	D	D	R	Small	2.905	0.020	1.967
169	B5	D	D	R	Small	2.069	0.073	1.333
170	DGM6	S	D	S	Medium	3.501	0.050	1.800
171	B5	D	D	R	Small	2.550	0.047	1.500
172	DGM6	S	D	S	Small	2.625	0.030	2.433
173	DGM6	D	D	S	Small	2.688	0.083	1.433
174	BG7	D	D	R	Medium	3.283	0.070	1.833
175	LG1	D	D	R	Medium	3.478	0.087	1.867
176	LG1	D	D	R	Small	2.972	0.033	2.267
177	DGM6	D	D	R	Medium	3.043	0.060	2.867
178	B5	D	D	R	Small	2.946	0.060	1.367
179	DGM6	S	D	S	Medium	3.098	0.050	2.800
180	DGM6	S	D	S	Small	2.574	0.030	1.800
181	DGM6	S	D	S	Small	2.896	0.063	2.100
182	DGM6	D	D	R	Medium	3.526	0.060	2.333
183	DGM6	D	D	R	Small	2.433	0.067	1.667
184	BG7	D	D	R	Small	2.819	0.067	2.400
185	GY3	D	D	R	Medium	3.183	0.050	2.500
186	DGM6	D	D	R	Medium	3.433	0.063	2.033
187	DGM6	D	D	R	Medium	3.679	0.070	3.233
Mean	-	-	-	-		3.565	0.059	2.003
VRM	LG1	Shiny	Drum	Smooth	Medium	4.197	0.060	3.367
TNAU	Deep red	Shiny	Kidney	Smooth	Small	4.490	0.070	2.667

*mean of 3 replications; g – gram, mm – millimetre, kgf – kilogram force,

Annexure V

Callosobruchus maculatus (Thanjavur populations) resistance evaluation on 187 RILs of VRM(Gg)1 and TNAU Red

RILS	Eggs laid	Eggs Hatched	Hatch %	Adults emerged	No. of Males	No. of Females	% Damage	Score (W&T)	Score (Sun)	Survival %	Log % Survival	MDP (days)	Index of Suitability
1	15.00	12.00	80.00	9.00	5.00	4.00	90.00	HS	S	60.00	1.78	22.56	0.079
2	25.00	17.00	68.00	10.00	4.00	6.00	100.00	CS	S	40.00	1.60	28.40	0.056
3	27.00	11.00	40.74	5.00	2.00	3.00	50.00	MS	MR	18.52	1.27	22.50	0.056
4	18.00	18.00	100.00	8.00	2.00	6.00	80.00	HS	S	44.44	1.65	23.38	0.070
5	53.33	35.00	62.93	6.33	2.67	3.67	63.33	MS	MR	11.88	1.14	32.49	0.035
6	29.00	28.00	96.55	7.00	4.00	3.00	70.00	MS	MR	20.69	1.32	22.33	0.059
7	20.00	12.00	60.00	5.00	2.00	3.00	50.00	MS	MR	25.00	1.40	22.60	0.062
8	13.00	9.00	69.23	9.00	3.00	6.00	90.00	HS	S	69.23	1.84	24.33	0.076
9	42.67	28.67	69.51	4.00	2.67	1.33	40.00	MS	MR	9.38	0.99	31.46	0.034
10	24.00	18.00	75.00	10.00	2.00	8.00	100.00	CS	HS	41.67	1.62	27.90	0.058
11	27.00	15.33	57.39	7.67	5.33	2.33	76.67	HS	S	28.40	1.45	28.58	0.051
12	21.00	10.00	47.62	5.00	4.00	1.00	50.00	MS	MR	23.81	1.38	24.40	0.056
13	19.67	14.33	68.63	6.33	3.00	3.33	63.33	MS	MR	32.20	1.57	31.80	0.049
14	25.00	20.00	80.00	10.00	5.00	5.00	100.00	CS	HS	40.00	1.60	29.00	0.055
15	26.33	18.33	60.68	5.33	3.00	2.67	53.33	MS	MR	20.25	1.34	31.38	0.043
16	18.00	10.67	60.14	6.33	2.67	4.00	63.33	MS	MR	35.19	1.57	30.14	0.052
17	12.00	10.00	83.33	5.00	3.00	2.00	50.00	MS	MR	41.67	1.62	28.20	0.057
18	17.00	16.00	94.12	9.00	4.00	5.00	90.00	HS	S	52.94	1.72	25.56	0.067
19	53.00	29.00	54.72	0.00	0.00	0.00	0.00	CR	HR	0.00	0.00	0.00	0.000
20	13.00	8.33	65.47	3.67	1.00	3.00	36.67	MS	MR	28.21	1.48	31.97	0.047
21	52.33	35.00	67.85	8.67	4.33	4.67	86.67	HS	S	16.56	1.24	29.70	0.042
22	51.00	17.33	33.49	5.00	2.00	3.00	50.00	MS	S	9.80	0.98	28.14	0.035
23	23.00	19.00	82.61	8.00	3.00	5.00	80.00	HS	S	34.78	1.54	22.63	0.068
24	23.00	13.00	56.52	6.00	4.00	2.00	60.00	MS	MR	26.09	1.42	23.17	0.061
25	21.00	15.00	71.43	5.00	2.00	3.00	50.00	MS	MR	23.81	1.38	25.20	0.055
26	58.67	32.33	56.31	7.67	4.33	3.33	76.67	HS	MR	13.07	1.11	27.75	0.040
27	13.00	7.00	53.85	7.00	5.00	2.00	70.00	HS	S	53.85	1.73	23.29	0.074
28	19.00	10.00	52.63	8.00	4.00	4.00	80.00	HS	S	42.11	1.62	27.50	0.059
29	8.00	3.00	37.50	3.00	2.00	1.00	30.00	MS	R	37.50	1.57	24.00	0.066
30	8.00	1.00	12.50	1.00	1.00	0.00	10.00	MS	R	12.50	1.10	24.00	0.046

31	39.00	28.00	71.79	5.00	1.00	4.00	50.00	MS	MR	12.82	1.11	25.00	0.044
32	9.00	5.00	55.56	6.00	4.00	2.00	60.00	MS	MR	66.67	1.82	29.00	0.063
33	40.67	28.00	74.02	6.67	3.33	3.00	66.67	MS	S	16.39	1.33	30.28	0.044
34	24.00	16.00	66.67	8.00	6.00	2.00	80.00	HS	S	33.33	1.52	26.38	0.058
35	46.00	25.67	57.53	7.00	4.00	3.00	70.00	HS	S	15.22	1.14	26.92	0.042
36	42.00	22.33	52.90	8.00	4.00	4.00	80.00	HS	S	19.05	1.32	29.99	0.044
37	21.00	16.00	76.19	9.00	3.00	6.00	90.00	HS	S	42.86	1.63	23.89	0.068
38	20.00	13.00	65.00	9.00	4.00	5.00	90.00	HS	S	45.00	1.65	22.44	0.074
39	48.67	20.67	43.41	6.00	2.67	3.33	60.00	MS	MR	12.33	1.11	28.55	0.039
40	20.33	12.67	67.01	6.00	2.67	3.67	60.00	MS	MR	29.51	1.50	30.52	0.049
41	37.00	22.00	59.46	5.00	2.00	3.00	50.00	MS	MR	13.51	1.13	27.00	0.042
42	53.33	26.00	36.27	3.33	1.33	2.00	33.33	MS	R	6.25	0.56	31.60	0.027
43	21.00	16.00	76.19	9.00	1.00	8.00	90.00	HS	S	42.86	1.63	24.78	0.066
44	18.00	10.00	55.56	8.00	3.00	5.00	80.00	HS	S	44.44	1.65	24.13	0.068
45	26.33	14.00	57.56	6.67	4.00	2.67	66.67	MS	S	25.32	1.44	27.44	0.053
46	8.00	6.00	75.00	7.00	3.00	4.00	70.00	HS	MR	62.50	1.80	25.40	0.071
47	42.33	24.33	64.00	8.00	3.67	4.33	80.00	HS	S	18.90	1.29	31.67	0.041
48	23.00	12.00	52.17	7.00	1.00	6.00	70.00	HS	S	30.43	1.48	30.00	0.049
49	19.00	11.00	57.89	9.00	4.00	5.00	90.00	HS	S	47.37	1.68	22.56	0.074
50	24.00	17.00	70.83	7.00	4.00	3.00	70.00	HS	S	29.17	1.46	25.57	0.057
51	13.00	12.00	92.31	9.00	4.00	5.00	90.00	HS	S	69.23	1.84	25.89	0.071
52	17.00	15.00	88.24	10.00	7.00	3.00	100.00	CS	HS	58.82	1.77	28.60	0.062
53	64.00	12.00	18.75	0.00	0.00	0.00	0.00	CR	HR	0.00	0.00	0.00	0.000
54	27.00	20.00	74.07	9.00	7.00	2.00	90.00	HS	S	33.33	1.52	29.78	0.051
55	18.00	14.00	77.78	8.00	4.00	4.00	80.00	HS	S	44.44	1.65	23.00	0.072
56	21.00	14.33	70.26	5.00	3.00	2.00	50.00	MS	MR	23.81	1.32	32.07	0.042
57	42.00	26.33	64.68	6.67	3.33	3.33	66.67	MS	S	15.87	1.19	28.79	0.041
58	16.00	10.00	62.50	4.00	3.00	1.00	30.00	MS	R	18.75	1.40	28.25	0.049
59	10.67	7.33	63.64	7.00	4.33	3.00	70.00	HS	S	65.63	1.83	30.87	0.059
60	37.00	26.00	70.27	10.00	4.00	6.00	100.00	CS	HS	27.03	1.43	25.40	0.056
61	28.67	22.33	79.01	7.67	3.67	4.00	76.67	HS	S	26.74	1.45	28.10	0.051
62	57.00	28.00	49.12	5.00	3.00	2.00	50.00	MS	MR	8.77	0.94	27.80	0.034
63	12.00	8.00	66.67	8.00	6.00	2.00	80.00	HS	S	58.33	1.77	24.00	0.074
64	25.00	18.00	72.00	10.00	4.00	6.00	100.00	CS	HS	40.00	1.60	29.30	0.055
65	14.00	11.00	78.57	8.00	3.00	5.00	80.00	HS	S	57.14	1.76	24.63	0.071
66	52.33	36.33	68.78	9.33	4.67	4.67	93.33	HS	HS	17.83	1.25	26.52	0.047

67	29.00	19.33	68.05	9.00	4.33	4.67	90.00	HS	HS	31.03	1.53	26.19	0.059
68	23.67	16.33	67.78	8.00	3.67	4.33	80.00	HS	S	33.80	1.53	30.99	0.050
69	17.00	12.00	70.59	9.00	7.00	2.00	90.00	HS	S	52.94	1.72	24.56	0.070
70	21.67	5.33	23.41	5.00	2.00	3.00	50.00	MS	MR	23.08	1.22	29.88	0.040
71	20.00	13.00	65.00	7.00	3.00	4.00	70.00	HS	S	35.00	1.54	22.71	0.068
72	26.00	22.00	84.62	10.00	5.00	5.00	100.00	CS	HS	38.46	1.59	29.90	0.053
73	28.00	17.00	60.71	10.00	5.00	5.00	100.00	CS	HS	35.71	1.55	30.20	0.051
74	32.00	12.00	37.50	0.00	0.00	0.00	0.00	CR	HR	0.00	0.00	0.00	0.000
75	31.00	20.00	64.52	10.00	3.00	7.00	100.00	CS	HS	32.26	1.51	30.00	0.050
76	20.33	13.67	55.09	5.33	2.67	2.67	53.33	MS	MR	26.23	1.33	28.49	0.048
77	42.00	19.67	52.72	6.33	3.67	2.67	63.33	MS	MR	15.08	1.21	27.56	0.044
78	11.00	11.00	100.00	6.00	4.00	2.00	60.00	MS	MR	54.55	1.74	22.17	0.078
79	24.00	22.00	91.67	9.00	5.00	4.00	90.00	HS	S	37.50	1.57	24.44	0.064
80	23.00	19.00	82.61	8.00	2.00	6.00	80.00	HS	S	34.78	1.54	23.63	0.065
81	22.00	15.00	68.18	6.00	2.00	4.00	60.00	MS	MR	27.27	1.44	29.17	0.049
82	19.00	8.33	42.44	4.00	2.33	1.67	40.00	MS	MR	21.05	1.34	31.75	0.042
83	32.00	13.00	40.63	0.00	0.00	0.00	0.00	CR	HR	0.00	0.00	0.00	0.000
84	37.33	20.00	63.77	4.67	1.67	3.00	46.67	MS	MR	12.50	1.27	34.46	0.038
85	33.00	28.00	84.85	7.00	2.00	5.00	70.00	HS	S	21.21	1.33	24.43	0.054
86	18.33	12.33	73.84	8.33	5.67	2.67	83.33	HS	S	45.45	1.69	26.78	0.064
87	26.00	15.00	57.69	10.00	6.00	4.00	100.00	CS	HS	38.46	1.59	27.60	0.057
88	22.00	18.00	81.82	10.00	6.00	4.00	100.00	CS	HS	45.45	1.66	29.10	0.057
89	19.00	17.00	89.47	9.00	2.00	7.00	90.00	HS	S	47.37	1.68	30.56	0.055
90	17.00	2.00	11.76	2.00	2.00	0.00	20.00	MS	R	11.76	1.07	28.00	0.038
91	27.00	22.33	84.43	8.00	3.67	4.33	80.00	HS	S	29.63	1.54	28.17	0.057
92	8.00	6.00	75.00	6.00	4.00	2.00	60.00	MS	MR	62.50	1.80	23.80	0.075
93	24.00	18.00	75.00	10.00	5.00	5.00	100.00	CS	HS	41.67	1.62	30.00	0.054
94	38.33	27.67	69.04	7.33	3.67	3.67	73.33	HS	S	19.13	1.30	33.66	0.039
95	14.00	9.00	64.29	7.00	4.00	3.00	70.00	HS	S	50.00	1.70	21.71	0.078
96	13.67	6.67	49.25	3.00	2.33	0.67	30.00	MS	R	21.95	1.26	31.98	0.040
97	15.00	9.00	60.00	5.00	3.00	2.00	50.00	MS	MR	33.33	1.52	22.00	0.069
98	21.00	19.00	90.48	8.00	5.00	3.00	80.00	HS	S	38.10	1.58	23.25	0.068
99	22.00	7.00	31.82	7.00	4.00	3.00	70.00	HS	S	31.82	1.50	23.86	0.063
100	59.67	43.33	73.11	8.67	4.00	4.67	86.67	HS	S	14.53	1.18	28.36	0.042
101	32.00	22.00	68.75	8.00	6.00	2.00	80.00	HS	S	25.00	1.40	32.13	0.044
102	17.00	9.00	52.94	7.00	3.00	4.00	70.00	MS	MR	41.18	1.61	32.00	0.050

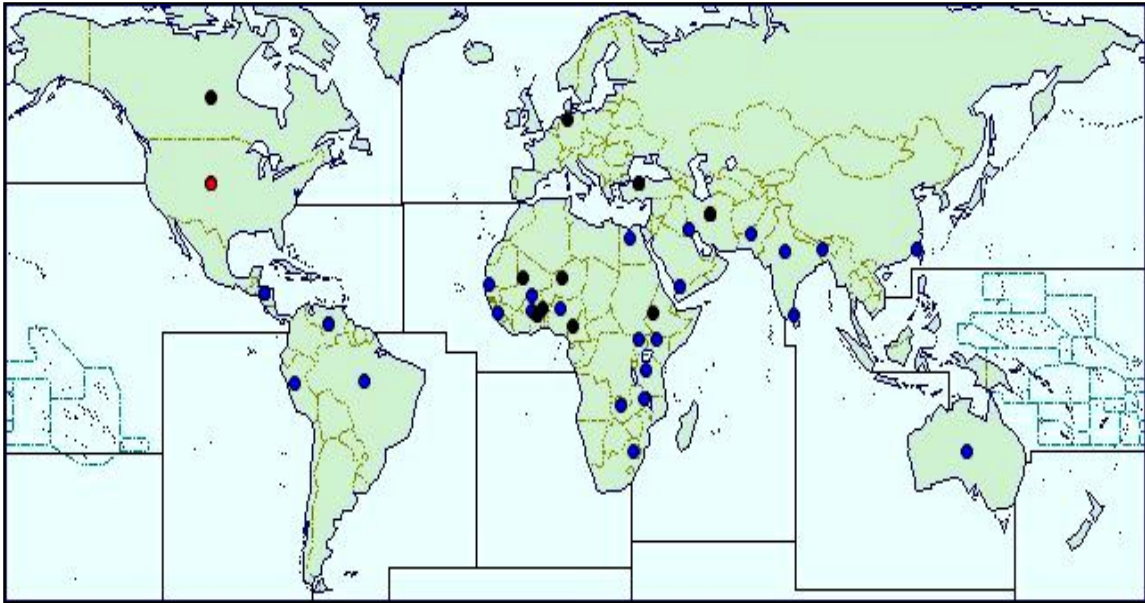
103	25.00	17.00	68.06	7.00	3.67	3.67	70.00	HS	S	28.00	1.46	29.04	0.050
104	20.00	12.00	60.00	6.00	4.00	2.00	60.00	MS	MR	30.00	1.48	24.67	0.060
105	16.00	11.00	68.75	5.00	2.00	3.00	50.00	MS	MR	31.25	1.49	26.00	0.057
106	19.00	8.00	51.05	8.33	5.00	3.33	83.33	HS	S	43.86	1.70	28.21	0.061
107	31.67	19.00	61.36	8.33	5.67	2.67	83.33	HS	S	26.32	1.45	26.53	0.055
108	59.00	33.33	55.02	8.00	2.67	5.33	80.00	HS	S	13.56	1.14	27.33	0.042
109	34.00	22.67	69.16	8.67	4.00	5.00	86.67	HS	S	25.49	1.45	28.37	0.052
110	23.00	6.00	26.09	6.00	4.00	2.00	60.00	MS	MR	26.09	1.42	26.50	0.053
111	14.00	9.00	64.29	9.00	5.00	4.00	90.00	HS	S	64.29	1.81	22.33	0.081
112	11.00	8.00	72.73	10.00	3.00	7.00	100.00	HS	S	72.73	1.86	21.25	0.088
113	16.00	12.00	75.00	9.00	6.00	3.00	90.00	HS	S	56.25	1.75	22.56	0.078
114	17.00	9.00	52.94	7.00	2.00	5.00	70.00	MS	MR	35.29	1.55	22.50	0.069
115	30.67	16.33	54.91	8.00	3.00	5.00	80.00	HS	S	26.09	1.45	28.72	0.051
116	13.00	11.00	84.62	10.00	7.00	3.00	100.00	CS	HS	76.92	1.89	25.50	0.074
117	56.00	6.00	10.71	4.00	3.00	1.00	40.00	MS	MR	7.14	0.00	32.00	0.027
118	9.00	7.00	77.78	8.00	4.00	4.00	80.00	MS	MR	55.56	1.74	26.40	0.066
119	17.33	12.00	73.67	7.33	5.00	2.33	73.33	HS	S	42.31	1.60	27.17	0.059
120	32.00	0.00	0.00	0.00	0.00	0.00	0.00	CR	HR	0.00	0.00	0.00	0.000
121	50.00	11.00	22.00	10.00	5.00	5.00	100.00	CS	HS	20.00	1.30	34.80	0.037
122	40.00	6.00	15.00	4.00	2.00	2.00	40.00	MS	MR	10.00	1.00	28.75	0.035
123	27.00	16.00	59.26	10.00	4.00	6.00	100.00	CS	HS	37.04	1.57	25.30	0.062
124	15.00	12.00	80.00	8.00	5.00	3.00	80.00	HS	S	53.33	1.73	25.13	0.069
125	101.00	58.00	57.43	2.00	1.00	1.00	20.00	MS	R	1.98	0.30	28.50	0.010
126	14.00	5.00	35.71	7.00	3.00	4.00	70.00	MS	MR	50.00	1.70	32.43	0.052
127	17.00	8.00	47.06	7.00	2.00	5.00	70.00	MS	MR	35.29	1.55	22.50	0.069
128	63.00	38.00	60.32	6.00	3.00	3.00	60.00	MS	MR	9.52	0.98	28.00	0.035
129	20.00	16.67	81.99	6.33	2.33	4.00	63.33	MS	MR	31.67	1.54	31.91	0.049
130	42.67	8.00	20.87	2.00	1.33	0.67	20.00	MS	R	4.69	0.65	31.78	0.020
131	26.00	21.00	80.77	6.00	5.00	1.00	60.00	MS	MR	23.08	1.36	23.33	0.058
132	20.00	11.00	55.00	5.00	2.00	4.00	50.00	MS	MR	25.00	1.48	28.00	0.053
133	11.00	7.00	63.64	5.00	2.00	3.00	50.00	MS	MR	45.45	1.66	22.80	0.073
134	15.00	10.00	66.67	7.00	4.00	3.00	70.00	HS	S	46.67	1.67	23.00	0.073
135	18.00	15.00	83.33	6.00	2.00	4.00	60.00	MS	MR	33.33	1.52	22.83	0.067
136	17.00	13.00	76.47	9.00	6.00	3.00	90.00	HS	S	52.94	1.72	23.78	0.072
137	26.00	7.00	26.92	8.00	3.00	5.00	80.00	HS	S	30.77	1.49	34.63	0.043
138	24.00	5.00	20.83	5.00	2.00	3.00	50.00	MS	MR	20.83	1.32	25.60	0.052

139	40.00	25.67	64.26	6.33	2.67	3.67	63.33	MS	MR	15.83	1.20	31.84	0.038
140	12.00	8.00	66.67	9.00	2.00	7.00	90.00	HS	S	58.33	1.77	25.00	0.071
141	13.00	11.00	84.62	8.00	5.00	3.00	80.00	HS	S	61.54	1.79	25.25	0.071
142	12.00	7.00	58.33	6.00	4.00	2.00	60.00	MS	MR	50.00	1.70	29.50	0.058
143	22.00	20.00	90.91	5.00	0.00	5.00	50.00	MS	MR	22.73	1.36	33.60	0.040
144	18.00	15.00	83.33	9.00	6.00	3.00	90.00	HS	S	50.00	1.70	22.56	0.075
145	21.00	16.00	76.19	7.00	4.00	3.00	70.00	MS	MR	28.57	1.46	22.83	0.064
146	39.00	14.00	28.97	2.33	1.00	1.33	23.33	MS	R	5.98	1.15	27.00	0.043
147	24.00	21.00	87.50	6.00	4.00	2.00	60.00	MS	MR	25.00	1.40	24.17	0.058
148	27.00	23.00	85.19	9.00	4.00	5.00	90.00	HS	S	33.33	1.52	23.67	0.064
149	25.00	1.00	4.00	0.00	0.00	0.00	0.00	CR	HR	0.00	0.00	0.00	0.000
150	13.00	11.00	84.62	5.00	3.00	2.00	50.00	MS	MR	38.46	1.59	23.40	0.068
151	38.33	17.67	45.92	5.00	2.33	2.67	50.00	MS	MR	13.04	1.06	31.38	0.035
152	36.67	26.33	71.92	3.00	2.33	0.67	30.00	MS	R	8.18	0.92	29.64	0.031
153	35.00	7.00	20.00	9.00	3.00	6.00	90.00	MS	MR	14.29	1.15	24.40	0.047
154	27.67	18.00	69.40	8.33	6.00	2.33	83.33	HS	S	30.12	1.58	25.33	0.063
155	22.00	12.67	59.16	4.67	2.33	2.33	46.67	MS	MR	21.21	1.21	31.23	0.039
156	36.00	24.67	67.93	8.00	3.67	5.00	80.00	HS	S	22.22	1.40	29.21	0.048
157	39.00	23.33	60.65	7.33	3.67	3.67	73.33	HS	S	18.80	1.26	29.40	0.044
158	19.33	10.00	49.40	0.67	0.67	0.00	6.67	R	HR	3.45	0.67	33.00	0.020
159	15.00	11.00	73.33	6.00	2.00	4.00	60.00	MS	MR	40.00	1.60	21.83	0.073
160	19.67	12.67	67.62	6.67	4.33	2.33	66.67	MS	S	33.90	1.55	29.37	0.053
161	30.33	24.33	77.58	7.00	3.00	4.00	70.00	HS	S	23.08	1.37	34.09	0.040
162	15.00	12.00	80.00	8.00	6.00	2.00	80.00	HS	S	53.33	1.73	22.13	0.078
163	29.00	17.00	58.62	10.00	6.00	4.00	100.00	CS	HS	34.48	1.54	26.40	0.058
164	15.00	15.00	100.00	9.00	7.00	2.00	90.00	HS	S	60.00	1.78	22.56	0.079
165	23.00	9.33	42.44	1.00	0.33	0.67	10.00	MS	HR	4.35	0.98	34.00	0.029
166	27.00	16.00	59.26	10.00	5.00	5.00	100.00	CS	HS	37.04	1.57	27.20	0.058
167	77.00	18.00	23.38	6.00	4.00	3.00	70.00	MS	MR	7.79	0.72	28.29	0.034
168	43.00	28.33	64.69	9.00	4.67	4.33	90.00	HS	S	20.93	1.33	27.26	0.049
169	46.33	24.33	56.06	0.33	0.00	0.33	3.33	R	HR	0.72	0.60	35.00	0.017
170	73.00	52.00	71.23	8.00	6.00	2.00	80.00	HS	S	10.96	1.04	26.63	0.039
171	23.67	11.67	50.09	6.00	3.00	3.00	60.00	MS	MR	25.35	1.40	28.36	0.049
172	29.00	21.33	72.31	3.33	1.33	2.00	33.33	MS	R	11.49	1.09	30.69	0.036

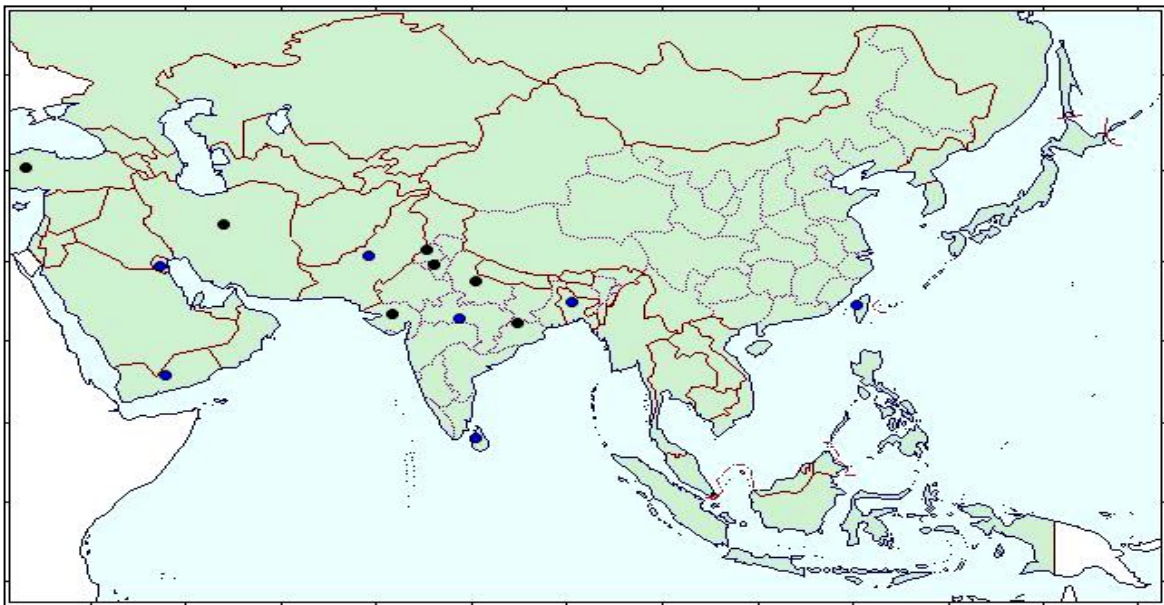
173	29.33	13.00	45.39	3.33	1.67	1.67	33.33	MS	R	11.36	1.05	31.22	0.034
174	23.00	19.00	82.61	9.00	5.00	4.00	90.00	HS	S	39.13	1.59	26.56	0.060
175	27.00	15.00	55.56	10.00	4.00	6.00	100.00	CS	HS	37.04	1.57	26.90	0.058
176	16.67	10.33	62.59	9.00	5.33	3.67	90.00	HS	S	54.00	1.74	28.30	0.062
177	26.00	21.00	80.77	4.00	2.00	2.00	40.00	MS	MR	15.38	1.19	29.50	0.040
178	35.33	18.00	54.37	6.33	4.33	2.00	63.33	MS	MR	17.92	1.24	27.38	0.046
179	66.00	45.33	69.18	7.67	4.33	4.00	76.67	HS	S	11.62	1.11	30.38	0.037
180	15.67	10.67	67.71	4.00	2.67	1.33	40.00	MS	MR	25.53	1.37	32.64	0.042
181	29.00	22.00	75.86	6.00	4.00	2.00	60.00	MS	MR	20.69	1.32	27.17	0.048
182	16.00	10.00	62.50	5.00	1.00	4.00	50.00	MS	MR	31.25	1.49	24.20	0.062
183	13.00	10.00	76.92	10.00	4.00	6.00	100.00	HS	S	69.23	1.84	23.78	0.077
184	14.00	8.00	57.14	3.00	3.00	0.00	30.00	MS	R	21.43	1.33	24.00	0.055
185	19.00	11.00	57.89	9.00	6.00	3.00	90.00	HS	S	47.37	1.68	22.56	0.074
186	28.33	21.00	71.33	7.67	4.33	3.33	76.67	HS	S	27.06	1.45	28.70	0.051
187	33.00	30.00	90.91	9.00	5.00	4.00	90.00	HS	S	27.27	1.44	29.56	0.049
Mean	27.10	16.18	62.72	6.70	3.32	3.23	66.95	-	-	30.78	1.38	26.42	0.052
Min.	8.00	0.00	0.00	0.00	0.00	0.00	0.00	-	-	0.00	0.00	0.00	0.000
Max.	101.00	58.00	100.00	10.00	7.00	8.00	100.00	-	-	76.92	1.89	35.00	0.088
St.Dev	14.65	8.92	19.36	2.49	1.58	1.67	25.01	-	-	17.34	0.39	5.88	0.017

Data from free-choice and no-choice tests. W and T – Weigand and Tahan (1990), Sun – Sun *et al.* (2008)

APPENDICES



1. Map showing distribution of *Callosobruchus maculatus* (Fab.) in different regions of the world
Black dot - present, no further details; blue dot - widespread; red dot - localised



2. Map showing distribution of *Callosobruchus maculatus* (Fab.) in South and South-east Asia including India
Black dot - present, no further details; blue dot - widespread; red dot - localised

(Source: Invasive Species Compendium Datasheets, maps, images, abstracts and full text on invasive species of the world, www.cabi.org; <http://www.cabi.org/isc/datasheet/10987>, last updated on 07 November 2014)

3. Classification of individual starch granules: (Winton and Winton, 1945)

Sl. No.	Shape	Examples
1.	Globular	Peanut, floury part of maize)
2.	Lenticular	Wheat, rye, barley
3.	Ellipsoidal	Legumes, pulses
4.	Pear-shaped	Potato, canna, banana
5.	Truncated	Cassava, sago
6.	Polygonal	Maize, rice, sorghum
7.	Bone-shaped	Latex of euphorbia

Bold font - relevant to present study

4. Morphological types of sensilla in *Callosobruchus chinensis* and *C. maculatus*

Types of sensilla	Tip	Wall	Shape	Socket
BB	Blunt	Smooth	Straight	Wide
ST 1	Sharp	Grooved	Straight or slightly curved	Tight
ST 2	Blunt	Smooth	Straight	Tight
SC	Blunt	Grooved	Straight	Wide
SB 1	Blunt	Smooth	Straight	Tight
SB 2	Blunt	Grooved	Curved	Wide
GP	Blunt	Grooved	Straight	Wide
SCa	-	-	-	-

(Source: Hu *et al.*, 2009)

BB - Bohm bristles; ST1 - Sensilla trichoid 1; ST2 - Sensilla trichoid 2; SC - Sensilla chaetica;

SB1 - Sensilla basiconic 1; SB2 - Sensilla basiconic 2; GP - Grooved pegs and SCa - Sensilla cavity

5. Steps for candidate gene annotation using the mungbean genome database (Eg.)

The screenshot shows the main page of the Crop Genomics Lab website. The navigation menu on the left includes 'Main page', 'Recent changes', 'Random page', and 'Tools'. The main content area features a 'Main Page' section with a welcome message and contact information for Professor Suk-Ha Lee. Below this, there is a 'Genome assembly data' section with several links: 'Mungbean Genome Jbrowse' (circled in red), 'Mungbean Assembly FTP', 'Adzuki bean Genome Jbrowse', 'Adzuki bean Assembly FTP', 'Web BLAST', 'Jatropha Genome Browse', 'Jatropha Assembly FTP', and 'Lactuca indica FTP'. A red arrow points from the 'Mungbean Genome Jbrowse' link to the next screenshot.

The screenshot shows the JBrowse genome browser interface. The 'Genome' track is selected, and the 'Vr08' dropdown menu is circled in red. The 'Genes' track shows the gene 'Vradi08g19320' circled in red. The 'Reference sequence' track is also visible. A red arrow points from this screenshot to the next one.

The screenshot shows the gene details window for 'Vradi08g19320'. The 'Region sequence' section is highlighted in yellow. The sequence is displayed in FASTA format. A red arrow points from this section to the next screenshot.

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ATGTTTCATTTTCIGCTACTATGTTTCCTCCTTCITTTGTTTCCTGCTCAAACACTTCCTCTC
AAAGCCCTCTCCCATTTACCTTGTTGATTTCTCAIGTCTGAAGCCACCAACCCATTGCAGGG
TGCCCTTTTGACGCAATTTGTTGAAAATGCTTCTTGTGGCAAGTTTTTGACACTGAAAGCATA
GCTTTCATGGACAAAATCCTCCGTTCCCTCAGGGCAAAGTGAAGAGACTTAACCTCCTCCCTGC
CTTGCACACTACATTCTCCTAAGACTCACACACTGAATCCATCAAAGAGGTGCAAAATGGTTC
TGTTCCTCCATCGTCGACGATCTCTTGGCAAAAATAACGTTTCACCGCTTGATATAGACATA
CTTATCATAAACTGCAGTGGCTTTTGCCCTCACCTCTTTAACCTCCGTTGTTATTGAAAA
ATACTCAATGAGAACGACATCAAGAGCTAATGTCTCTGGCATGGGGTGCAGTGCAGGTG
CCCTTTGATTGATATGGCTCAGAACTCTCTGAGGGTACACATGAACCTCAATGCOCTTGT
  
```

blastx: search protein datab... JBrowse Vr08:41272255...4: X

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastx&PAGE_TYPE=BlastSearch&L

Apps Bookmarks Search insect flight ppt

BLAST >> blastx

Translated BLAST: blastx

blastn blastp **blastx** fblastn tblastx

BLASTX search protein databases using a translated nucleotide query sequence

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear Query subrange

ATGTTTCATTTTCGCTACTATGTTTCCTCCTCTCTGTTTCCTGCTCAAACACATTCCTCCTC
 AAAGCCCTCTCCCATTTACCTTGTGGATTTCTCATGTCTGAAGCCACCAACCCATTGCAGGG
 TGCCTTTTGGAGCATTTGTTGAAATGCTTCTCTGTCAGGCAAGTTTTCACACTGAAAGCAIA
 GCTTTCATGGACAAAATCCTCCGTTCTCAGGGCAAAGTGAAGAGACTTACCTCCCCCTGC
 CTTGCCTACATTCCTCCTAAGACTCACCACACTGAAATCCATCAAAGAGGTGCAAAATGGTTC

Or, upload file No file chosen

Genetic code: Standard (1)

Job Title:

Align two or more sequences

Choose Search Set

Database: Non-redundant protein sequences (nr)

Organism: Exclude

Exclude Optional: Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query Optional: [YouTube](#) [Create custom database](#)

BLAST Search database Non-redundant protein sequences (nr) using Blastx (search protein databases u

NCBI Blast:Nucleotide Sequ... NCBI Conserved Domain Se... Crop Genomics Lab... X

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Apps Bookmarks Search insect flight ppt

BLAST Results

Edit and Resubmit Save Search Strategies Formatting options Download

Job title: Nucleotide Sequence (1290 letters)

RID: CW6YJ543015 (Expires on 04-12 22:29 pm)

Query ID: Id|Query_38891

Description: None

Molecule type: nucleic acid

Query Length: 1290

Database Name: nr

Description: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program: BLASTX 2.8.0+ [Citation](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

Graphic Summary

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

RF +1 Superfamilies

PLN03169 super-family

Distribution of the top 100 Blast Hits on 100 subject sequences

Color key for alignment scores

■ <40 ■ 40-50 ■ 50-80 ■ 80-200 ■ >=200

1 250 500 750 1000 1250

Questions/comments

https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi?RID=CW6YJ543015&mode=all

Search insect flight ppt

Conserved domains on [lcl|Query_12963]

View Standard Results

Local query sequence

Graphical summary Zoom to residue level show extra options

RF +1

Non-specific hits

FAE1_CUT1_RppA

CHS_like

BH0617

Superfamilies

cond_enzymes super-family

FabH super-family

PLN03169 super-family

List of domain hits

Name	Accession	Description	Interval	E-value
[H] PLN02377	PLN02377	3-ketoacyl-CoA synthase	61-1275	1.66e-141
[H] FAE1_CUT1_RppA	pfam08392	FAE1/type III polyketide synthase-like protein; The members of this family are described as ...	64-915	9.00e-99
[H] CHS_like	cd00831	Chalcone and stilbene synthases, plant-specific polyketide synthases (PKS) and related enzymes ...	226-1203	6.14e-44
[H] BH0617	COG3424	Reducted naringenin-chalcone synthase [Secondary metabolites biosynthesis, transport and ...]	322-1110	2.47e-11

Blast search parameters

Data Source: Live blast search RID = CW6YJ543015

User Options: Database: CDSEARCH/cdd v3.16 Low complexity filter: yes Composition Based Adjustment: yes E-value threshold: 0.01 Maximum number of hits: 500

References:

- Marchler-Bauer A et al. (2017), "CDD/SPARCLE: functional classification of proteins via subfamily domain architectures.", *Nucleic Acids Res.*45(D)200-3.
- Marchler-Bauer A et al. (2015), "CDD: NCBI's conserved domain database.", *Nucleic Acids Res.*43(D)222-6.
- Marchler-Bauer A et al. (2011), "CDD: a Conserved Domain Database for the functional annotation of proteins.", *Nucleic Acids Res.*39(D)225-9.
- Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", *Nucleic Acids Res.*32(W)327-331.

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