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Using electrophoretic techniques in variation between 35 taxa of *Brassicaceae* Burnett

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Abstract
Seed protein diversity as revealed by variation in SDS-PAGE has been used to reassess the taxonomic relationships between 35 species related to 24 gemera of the Brassicaceae. A total of number of 82 protein bands with molecular weight ranging between 0.064 and 0.94 were recorded in the electropherograms. These bands were used as binary characters and analyzed by the STATISCA program package using the UPGMA clustering method. The produced dendrogram from SDS-PAGE analysis showed separation of the two species of genus Raphanus at taxonomoc level of 62% wherase the remainder are separated into two groups. Also, the dendrogram showed a close affinity between genus *Lepidium* and genus *Capsella*. The phenogram shows that eight species of genus *Brassica* from different geographical locations are not grouped together in one cluster.

Keywords: Brassicaceae (Cruciferae); Seed protein electrophoresis; Numerical analysis

1. Introduction

The *Brassicaceae* Burnett (=*Cruciferae* de Jussieu) is a large natural family of the *Brassicales*. The family is considered to be monophyletic on the basis of the elongate gynophore and elongate, exserted stamens (Rodman, 1991 and Judd *et al*., 1994) [17, 12]. The family is considered to be monophytic on the the basis of the elongate gynotype and elongate exserted stamens Judd *et al*., 1999) [12]. Electrophoretic separation of seed proteins is a useful technique in plant taxonomy. Polyacralyamide gel electrophoresis for protein and isozyme was used for identification of species, subspecies and variety level (Adrianse *et al*., 1969, Boulter *et al*., 1970, Evans and Abernethy, 1983) [1, 6, 9]. Comparing the major storage seed protein in different taxa have provided valid source of evidence for addressing taxonomic relationships at the different taxonomic levels (Nath *et al*., 1997; Kamel & El-Mashad, 1999; Badr *et al*., 2000; Hassan, 2001; El-Rabey *et al*., 2002; and Kamel, 2005) [16, 14, 4, 8, 13]. In Egypt, Tächolm (1974) reported 61 genera and 106 species and El-Hadidi & Fayed (1995) [7] reported 55 genera and 108 species. Kamel *et al*. (2003) studied characterization and the relationship between 17 egyption cruciferous taxa. Also, Amaal Hasan (2009) [3] studied the molecular systematic of 9 tribes of Brassicaceae in Egypt based on different electrophoretic techniques. Aim of the present work is to differentiate between different species gathered from different locations belonging to 24 genera by using seed protein profiles.

2. Materials and Methods

The seeds of 35 taxa representing 24 genera of Brassicaceae were obtained from the Royal Botanic Gardens at Kew, London, UK,), The Botanic Garden Berlin-Dahlem, Germany, and from different localities in Egypt. Studied local taxa were identified according to Tächolm (1974) and Boulos (1999). The studied taxa are given in Table 1.

Table 1: Localities of the studied taxa of the family

No.	Taxa	Serial number	origin	Collection Date
1	Brassica oleracea S.I.L	0070498	England	1988
2	B. oler. var. capitata L.	---	Egypt	2009
3	B. oler. var. botrytis L.	---	Egypt	2009
4	B. rapa L	0020747	Switzerland	1974
5	B.nigra (L.) koch	0070395	England	1988
6	B. tournefotii Gouan	0184696	Egypt	2002
7	Cardamine flexuosa	1071	England	1988
8	Cardamine hirsuta	387109	Brukina-Faso	2007
9	Capsella bursa-pastoris DC.	---	Egypt	2009
10	Coronopus didymus L	0076065	England	1989
11	Descurainia sophia (L.) Webb	0497413	Jordan	2008
12	Diplotaxis rucoides (L.)DC	0113946	Jordan	1996
13	D.harra (forssk) Boiss.	---	Egypt	2009
14	D. tenufolia (L.)DC	064824	England	1986
15	Eruca Sativa Miller	---	Egypt	2010

16	Erysimum cheiri (L.) Crantz	0026716	France	----
17	Farsetia aegyptia Turra	---	Egypt	2010
18	Hirschfeldia incana (L.) Lagr. Fossat	0115249	Lebanon	1996
19	Lepidium sativum L.	0071831	Oman	1987
20	Raphanus sativus L.	---	Egypt	2010
21	R. raphanistrum L.	0071853	Oman	1989
22	Moricandia sinaica (Boiss.) Boiss.	---	Egypt	2010
23	Matthiola longipetala (Vent) DC.	---	Egypt	2010
24	Sinapis alba L.	200095	Jordan	2003
25	S. arvensis L.	0115272	Lebanon	1996
26	S. allionii Jacq.	---	Egypt	2010
27	Sisymbrium orientale L.	0158808	Jordan	2001
28	S. altissimum L.	0175935	Belgium	1989
29	S. irio L.	---	Egypt	2009
30	S. officinale (L.) Scop	0053257	England	1984
31	Schouwia thebaica Webb.	---	Egypt	2010
32	Thlaspi perfoliatum L	0113876	Jordan	1996
33	Thlaspi caerulescens Presl	1322497	Germany	2004
34	Thlaspi montanum L.	1760604	Germany	2004
35	Thlaspi montanum Vahl	123456	Jordan	2002

3. Extraction and analysis of seed protein

Characterization of seed protein fractions are carried out by using one dimensional sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE). Preparation and running of gel were carried out according to Laemmli (1970) [15] and Stegeman *et al*. (1981). The gel was stained with coomassie brilliant blue stain R- 250. Bands were determined and scanned by using Hoefer Scanning densitometr GS 300. Protein gel bands scanned and photographed in Figure 1, 2 & 3.

4. Numerical Analysis

This study is dependent upon the application of a total of 87 comparative anatomical characters and their states as a binary character (0 &1), on each of the taxa studied. The characters and states have been subjected to numerical analysis under a program using similarity and dissimilarity assessment percentage method (Rohlf, 1989) [18]. The method applied is based on cluster analysis by using an UPGMA (unweighted pair-group method with arithmetic means) dendrogram illustrating the interspecific relationships of the studied species as percent similarity.

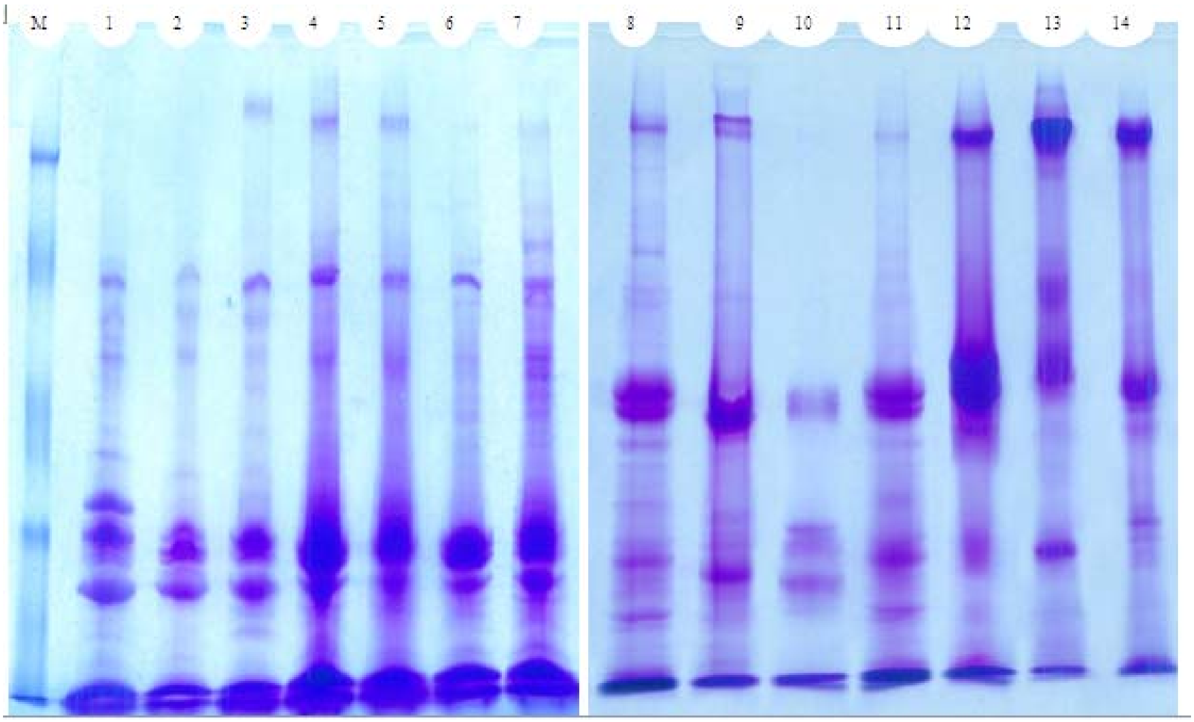

Fig 1: SDS-polyacrylamide gel electrophoresis illustrating storage seed protein of the studied species (1-14 as numbered and listed in Table 1)

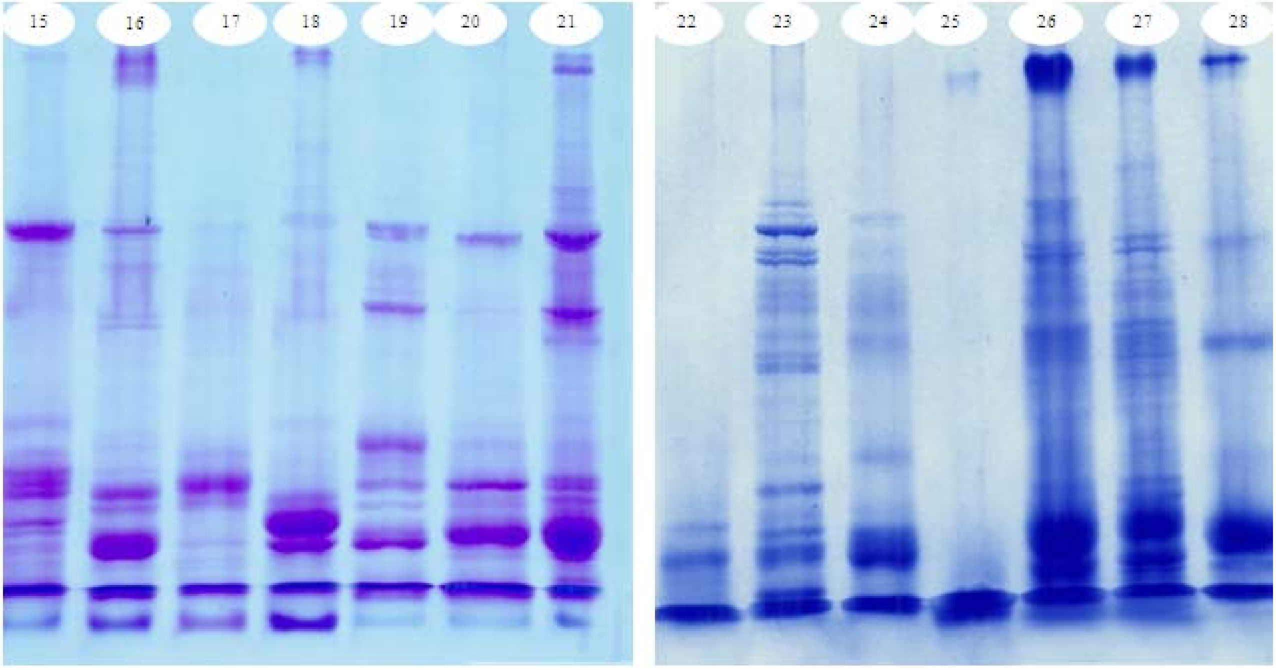

Fig. 2: SDS-polyacrylamide gel electrophoresis illustrating storage seed Protein of the studied species (15-28 as numbered and listed in Table 1)

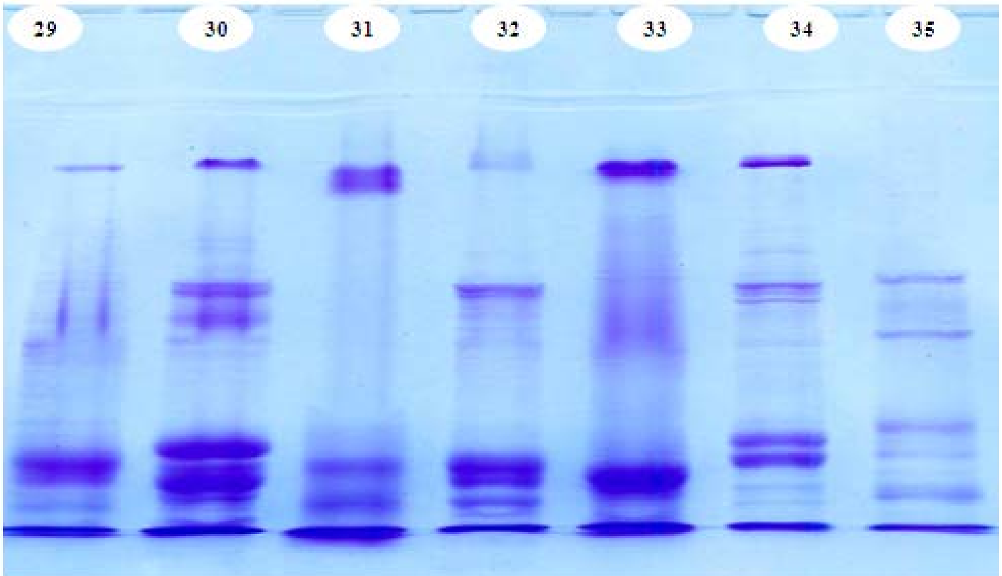

Fig 3: SDS-polyacrylamide gel electrophoresis illustrating storage seed Protein of the studied species (29-35 as numbered and listed in Table 1)

5. Results and Discussion

In the present study, SDS-PAGE seed storage proteins analysis was conducted to elucidate the taxonomic relationship between 35 taxa of the family. 82 different bands ranged between 0.06-0.97 (Table 2, charac., no 1-82). A maximum number of 26 bands, which were not necessarily present in all the studied taxa was detected in *Raphanus sativus* (Egypt), while the lowest one was recorded in samples of *Moricandia sinaica* (Egypt). On the other hand, the 11 bands have been recorded in *Lepidium campestre* (Germany), *Mathiola tricuspidata* (Greerce) and *Thlaspi montanum* (Germany). 14 bands have been recorded in *Brassica fruticulosa subsp. fruticulosa* (Spanien), *Erysimum crepidifolium* (Czech Republic) and *S. arvensis* (Lebanon). 20 bands have been recorded in *Lepidium sativum* (Oman) and *Raphanus raphanistrum* (Oman). 23 bands have been recorded in *B. rapa* (Switzerland) and *B. tournefotii* (Egypt). 13 bands have been recorded in *Brassica* nigra (England), *Erysimum cheiri* (France), *Erysimum heritieri var. hierrense* (Spain) and *Sisymbrium irio* (Egypt). 9 bands have been recorded in *Brassica geniculata* (Greece), *Erysimum bicolor* (Portugal) and *Farsetia aegyptia* (Egypt).

Table 2: The relative percentages and position of protein bands of the total protein in the studied taxa (1-17 as numbered and listed in Table 1)

No.	Taxa / RF	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	0.060	---	--	--	--	--	--	--	--	--	--	--	--	1.0	--	--	--	--
2	0.090	---	--	--	--	--	--	--	--	1.0	--	--	1.0	1.0	--	--	--	--
3	0.10	---	--	--	--	--	--	--	1.58	4.29	--	--	3.54	--	--	--	--	--
4	0.11	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
5	0.12	---	--	--	--	--	--	--	6.89	2.58	--	--	--	15.62	--	--	8.28	--
6	0.13	---	--	7.95	--	--	--	--	--	--	--	2.53	10.82	--	19.26	--	--	--
7	0.14	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	6.83	--
8	0.15	---	--	--	6.38	6.26	2.58	--	--	--	--	--	--	--	--	--	--	--
9	0.16	---	--	--	--	--	--	2.61	--	--	--	--	--	--	--	--	--	--
10	0.17	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
11	0.18	---	--	--	--	--	--	--	1.45	--	--	--	--	--	--	--	--	--
12	0.20	---	--	--	--	--	--	--	--	--	--	--	--	6.72	--	--	--	--
13	0.21	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
14	0.24	---	--	--	--	--	--	--	1.29	--	--	--	--	--	--	--	--	--
15	0.25	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
16	0.27	---	--	--	--	3.97	--	2.38	1.1	--	--	--	--	--	--	--	2.51	--
17	0.28	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
18	0.30	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	2.49	--
19	0.31	---	--	--	2.55	--	--	--	2.81	--	--	--	--	--	--	--	--	--
20	0.32	---	--	--	--	--	--	2.95	--	--	--	2.77	--	6.46	--	--	--	--
21	0.33	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
22	0.34	2.77	--	--	--	--	2.06	--	--	--	--	--	--	--	--	--	--	--
23	0.35	---	--	--	--	--	--	--	--	--	--	1.98	--	--	5.38	--	--	--
24	0.36	---	--	--	2.67	--	--	--	--	--	--	1.39	--	--	--	--	--	--
25	0.37	6.57	7.89	--	5.62	8.52	5.73	--	1.61	--	--	--	--	13.99	--	--	--	--
26	0.38	---	--	10.33	--	--	--	4.69	--	3.47	--	--	--	--	--	--	--	--
27	0.39	---	--	--	--	--	--	--	2.81	--	--	2.16	--	--	--	--	--	7.55
28	0.40	---	--	--	3.8	--	2.43	--	--	--	--	--	--	--	--	18.69	6.29	--
29	0.41	---	--	--	--	--	--	2.49	--	--	--	--	--	--	--	--	--	--
30	0.42	---	14.32	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
31	0.43	7.32	--	6.56	--	--	3.25	1.44	--	--	--	--	--	--	--	--	2.56	--
32	0.44	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
33	0.45	---	--	--	--	--	--	1.73	2.42	--	--	--	--	--	--	--	--	--
34	0.46	5.05	--	--	--	--	--	--	--	5.11	--	2.18	--	--	5.05	4.12	6.57	8.6
35	0.47	---	--	6.23	--	--	--	2.76	--	--	--	--	--	--	--	--	--	--
36	0.48	---	8.99	--	--	--	8.17	--	--	--	--	--	--	--	--	--	--	--
37	0.49	4.36	--	--	6.54	10.85	--	2.86	--	--	--	--	20.92	--	--	--	--	--
38	0.50	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
39	0.51	---	--	--	--	--	--	--	9.9	--	--	--	--	--	--	--	--	--
40	0.52	4.9	--	--	--	--	--	1.77	--	--	--	--	--	--	--	7.03	--	8.6
41	0.53	---	--	4.12	--	--	--	--	16.84	--	--	15.86	18.15	--	18.45	--	--	--
42	0.54	--	--	--	5.05	--	--	3.81	--	8.14	--	--	--	--	--	--	3.67	--
43	0.55	--	--	--	--	--	4.74	--	10.84	--	26.35	--	--	--	--	--	3.67	--
44	0.56	--	--	--	2.82	--	--	--	--	--	--	10.27	--	--	--	--	--	--
45	0.57	--	--	--	--	9	6.06	2	--	10.3	--	--	--	--	--	--	--	--
46	0.59	3.95	--	2.81	--	--	--	--	--	--	--	--	16.12	--	--	--	--	--
47	0.60	--	--	--	--	--	--	2.03	4.87	7.44	--	--	--	--	6.7	--	--	---
48	0.61	--	--	--	--	--	7.57	--	--	--	--	3.7	--	--	--	--	--	--
49	0.62	4.43	--	--	--	--	--	1.69	--	3.66	--	--	--	--	--	--	--	--
50	0.64	--	--	5.83	--	--	--	3.2	2.72	--	--	2.74	--	--	--	--	--	--
51	0.65	--	5.95	--	--	--	--	--	--	--	--	--	--	--	2.21	--	--	--
52	066	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
53	0.67	--	--	--	--	--	--	4.22	--	--	--	--	--	--	--	--	--	--
54	0.68	--	--	8.18	--	--	--	--	--	--	--	--	--	--	--	--	--	--

55	0.70	10.22	--	--	--	10.13	--	--	4.13	--	--	11.53	--	--	--	--	--	--
56	0.71	--	--	--	--	--	--	--	2.4	--	--	--	--	--	--	7.82	--	--
57	0.72	--	--	--	--	--	--	--	0	5.43	--	--	--	--	4.15	--	--	--
58	0.73	--	13.54	--	--	--	--	--	2.58	--	--	--	--	--	--	--	--	--
59	0.74	16.01	--	16.11	--	--	--	--	--	--	16.5	--	--	--	--	--	--	--
60	0.75	--	--	--	36.99	29.72	16.36	13.2	--	--	--	--	--	--	6.69	--	4.14	--
61	0.76	--	9.74	7	--	--	--	--	4.8	5.8	17.9	4.93	--	--	--	4.39	--	8.14
62	0.77	7.68	--	--	--	--	14.83	--	--	--	--	--	16.8	--	4.44	--	--	--
63	0.78	--	--	--	--	--	--	4.65	9.77	--	--	--	--	10.22	--	--	--	--
64	0.79	--	5.85	--	--	--	--	--	--	--	--	14.07	--	--	--	9.87	3.41	--
65	0.80	--	--	--	6.9	9.69	--	--	--	--	--	--	--	--	3.8	--	--	--
66	0.81	--	--	17.72	--	--	9.3	--	2.02	12.78	--	3.65	--	--	2.48	9.88	--	35.73
67	0.82	6.6	17.35	--	--	--	--	8.65	--	--	29.42	--	--	--	--	1.0	1.0	--
68	0.83	--	--	--	7.64	--	--	--	6.92	--	--	4.83	--	--	--	--	--	--
69	0.84	--	--	1.77	--	5.83	5.36	--	--	6.25	--	--	--	--	--	--	1.0	1.0
70	0.85	--	--	--	--	--	4.87	4.36	--	--	--	--	--	--	--	--	--	--
71	0.86	--	--	--	--	--	--	--	--	--	9.83	--	--	--	--	--	--	--
72	0.87	--	--	5.39	--	--	--	3.22	3.68	--	--	5.36	--	--	--	8.61	--	--
73	0.88	--	---	--	--	--	--	--	--	4.46	--	2.83	6.06	4.64	4.36	--	--	--
74	0.89	3.9	--	--	--	--	--	--	4.53	--	--	-	--	--	--	5.32	--	--
75	0.90	--	--	--	4.16	6.05	--	--	--	--	--	--	--	--	--	--	--	3.97
76	0.91	--	8.38	--	--	--	5.06	3.67	--	3.47	--	--	--	--	--	6.83	23.1	--
77	0.92	6.25	--	--	--	--	--	--	2.15	--	--	2.36	--	--	--	--	--	--
78	0.93	--	--	--	--	--	--	--	--	--	--	--	3.32	--	--	5.01	--	4.83
79	0.94	--	--	--	--	--	--	--	--	4.66	--	--	4.28	2.52	--	--	3.01	4.73
80	0.95	--	--	--	--	--	--	--	--	--	--	4.86	--	--	--	--	--	--
81	0.96	--	--	--	--	--	--	19.66	--	--	--	--	--	--	6.7	--	--	--
82	0.97	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
Total		14	9	13	12	10	15	23	23	16	5	18	9	13	14	13	16	9

Table 3: The relative percentages and position of protein bands of the total protein in the studied taxa (18-35 as numbered and listed in Table 1)

No	Taxa / RF	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
1	0.060	--	--	--	--	--	1.0	--	--	--	--	--	--	--	--	--	--	--	--
2	0.090	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
3	0.10	--	--	--	--	--	2.91	--	--	--	--	--	--	--	--	--	--	--	--
4	0.11	3.53	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
5	0.12	2.53	--	--	1.88	--	--	--	--	11.6	7.11	8.36	--	--	--	--	--	--	--
6	0.13	--	--	--	4.26	--	--	--	39.4	--	--	--	--	--	--	--	--	--	--
7	0.14	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.94	--	3.08	--
8	0.15	--	--	--	--	--	--	--	--	--	--	--	--	3.76	--	--	--	--	--
9	0.16	--	--	--	--	--	--	--	--	--	--	--	2.53	--	--	3.44	--	7.31	--
10	0.17	--	--	--	--	--	2.03	--	--	--	--	--	--	--	12.45	--	9.88	--	--
11	0.18	--	--	--	--	--	--	--	--	--	1.20	--	--	--	--	--	8.74	--	--
12	0.20	--	--	--	--	--	--	--	--	--	--	--	--	--	14.24	--	-	--	--
13	0.21	--	--	--	--	--	--	--	--	1.26	1.38	--	--	--	--	--	--	--	--
14	0.24	--	--	--	--	--	--	--	--	--	-	--	--	--	--	--	--	--	2.4
15	0.25	--	--	--	1.34	--	--	--	--	2.68	--	--	--	0.79	--	--	--	--	--
16	0.27	3.7	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
17	0.28	--	--	--	--	--	1.51	--	--	--	1.93	1.87	--	--	--	--	2.76	--	--
18	0.30	--	--	--	--	--	--	--	--	2.5	--	--	--	--	--	--	1.47	--	--
19	0.31	--	--	--	--	--	-	--	--	--	--	--	--	--	--	--	--	1.42	--
20	0.32	--	--	--	--	--	--	--	--	--	--	--	--	1.53	--	--	--	--	--
21	0.33	1.7	--	--	3.4	--	2.21	--	--	--	--	--	--	--	--	--	--	--	--
22	0.34	--	2.01	--	--	--	--	--	--	2.39	1.68	--	--	2.5	--	--	--	--	--
23	0.35	--	--	--	--	--	1.95	3.09	--	--	1.84	--	--	--	--	--	--	--	--
24	0.36	--	--	--	2.31	--	--	1.64	--	2.96	--	--	--	--	--	1.81	--	4.51	--
25	0.37	--	--	--	--	--	6.95	--	--	--	--	--	--	--	--	--	1.98	--	--

26	0.38	6.86	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
27	0.39	--	6.8	--	--	--	--	--	--	--	--	--	1.34	3.19	--	--	--	2.58	--
28	0.40	--	--	--	--	--	3.36	4.52	--	1.82	2.32	8.29	--	--	--	--	3.37	--	--
29	0.41	--	3.19	11.81	9.46	--	--	--	--	--	--	--	1.38	--	--	--	2.6	2.41	--
30	0.42	--	--	--	--	--	3.72	--	--	2.71	1.77	--	--	4.21	--	--	--	--	8.5
31	0.43	--	--	--	2.51	--	--	--	--	1.06	--	--	1.99	--	--	6.7	--	7.49	--
32	0.44	3.46	--	--	--	--	--	--	--	--	--	--	--	6.18	--	--	--	--	--
33	0.45	--	--	--	--	--	3.44	5.37	--	--	2.55	--	1.87	--	--	8.02	--	4.04	--
34	0.46	--	8.04	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
35	0.47	--	--	--	4.04	--	4.02	--	--	--	2.66	--	--	--	--	--	--	3.58	--
36	0.48	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	8.9
37	0.49	3.64	4.88	--	--	--	5.44	8.79	--	3.89	3.12	--	--	--	--	5.04	--	--	--
38	0.50	--	--	--	--	--	--	--	--	--	--	--	4.9	11.27	--	--	--	2.55	--
39	0.51	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
40	0.52	--	12.7	--	--	--	--	--	--	--	--	--	--	--	--	3.57	--	--	--
41	0.53	5.45	--	--	1.0	1.0	--	--	--	--	--	--	--	--	--	--	--	--	--
42	0.54	--	--	--	--	--	1.0	--	--	--	1.0	--	--	--	--	--	--	--	9.8
43	0.55	--	--	--	4.8	--	--	9.19	--	5.91	4.57	--	7.78	2.24	--	--	--	1.63	--
44	0.56	--	--	--	--	--	--	--	--	--	--	--	--	--	--	6.41	--	2.01	--
45	0.57	--	--	--	3.59	--	3.16	--	--	--	--	13.86	3.74	3.17	--	--	4.58	--	--
46	0.59	--	--	--	--	--	4.66	--	--	4.75	2.63	--	4.72	--	--	5.04	--	--	--
47	0.60	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
48	0.61	--	--	--	--	--	--	--	--	--	--	--	--	1.78	--	--	--	3.24	--
49	0.62	--	--	--	0.91	--	--	--	--	2.9	--	--	--	--	--	--	--	--	--
50	0.64	--	--	--	--	--	4.14	4.74	--	--	--	--	--	--	--	--	--	--	--
51	0.65	--	--	--	0.99	--	--	--	--	--	1.73	--	--	--	--	--	--	--	--
52	066	--	--	--	--	--	--	--	--	--	--	--	2.94	--	--	3.42	--	--	--
53	0.67	--	--	--	--	--	--	--	--	--	2.82	--	--	--	--	--	--	---	--
54	0.68	--	--	--	--	--	--	--	--	4.0	--	--	--	--	--	--	--	--	--
55	0.70	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
56	0.71	6.56	--	--	2.75	--	--	--	--	--	--	--	--	--	--	3.42	--	--	--
57	0.72	--	--	4.03	--	--	--	--	--	--	3.48	--	4.81	--	--	--	--	--	--
58	0.73	--	--	--	--	-	3.57	--	--	5.91	--	--	--	--	--	--	--	3.64	--
59	0.74	--	--	--	--	--	--	8.98	--	--	2.67	--	--	--	--	--	--	--	--
60	0.75	--	15.6	6.56	6.04	--	--	--	--	--	--	7.39	6.84	--	--	--	--	--	1.7.
61	0.76	--	--	--	--	--	--	--	--	--	1.59	--	--	--	13.88	--	--	--	--
62	0.77	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
63	0.78	--	--	--	--	--	6.89	--	--	--	3.74	--	--	--	--	--	--	18.4	6.9
64	0.79	--	--	--	--	--	--	--	--	5.01	--	--	--	--	--	--	--	--	--
65	0.80	--	--	--	3.47	--	--	--	--	--	--	--	--	20.55	--	--	--	--	--
66	0.81	--	11.87	18.07	--	--	--	--	--	--	4.89	--	--	--	--	--	--	--	9.7
67	0.82	--	--	--	5.16	--	--	6.27	--	--	--	--	30.83	--	--	--	--	20.2	--
68	0.83	10.27	--	--	--	--	2.77	--	--	--	--	--	--	7.42	29.89	24.33	--	--	--
69	0.84	--	1.0	6.34	4.39	29.5	--	--	--	--	--	--	--	--	--	--	--	--	--
70	0.85	--	--	--	--	--	6.84	14.3	--	9.34	--	--	--	--	--	--	-	-	7.8
71	0.86	--	--	--	--	--	--	--	--	--	20.35	--	18.46	--	--	13.37	34.08	--	--
72	0.87	34.49	--	--	--	--	--	--	--	--	--	--	--	16.1	--	--	--	--	--
73	0.88	--	--	--	--	--	14.5	--	--	16.3	--	44.37	--	--	--	--	--	7.13	6.5
74	0.89	--	11.58	--	26.88	55.1	--	--	--	--	--	--	--	--	--	--	--	--	--
75	0.90	--	--	42	0	--	--	33.0	--	--	--	--	--	6.71	--	--	9.14	--	17.6
76	0.91	17.96	17.26	--	--	--	--	--	--	--	10.55	--	7.89	--	29.54	12.95	--	4.6	--
77	0.92	--	--	7.77	--	--	--	--	--	9.22	--	15.86	--	2.3	--	--	--	--	--
78	0.93	--	--	--	--	15.3	--	--	60.5	--	3.76	--	--	--	--	--	--	--	--
79	0.94	--	--	--	--	--	--	--	--	--	2.2	--	--	--	--	3.95	7.98	--	--
80	0.95	--	--	--	--	--	8.63	--	---	--	--	--	--	5.58	--	--	--	--	--
81	0.96	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	0
82	0.97	--	--	--	3.07	--	--	--	--	--	--	--	--	--	--	--	--	-	0
Band Total		12	11	8	20	3	22	11	2	20	26	7	15	17	5	14	13	18	11

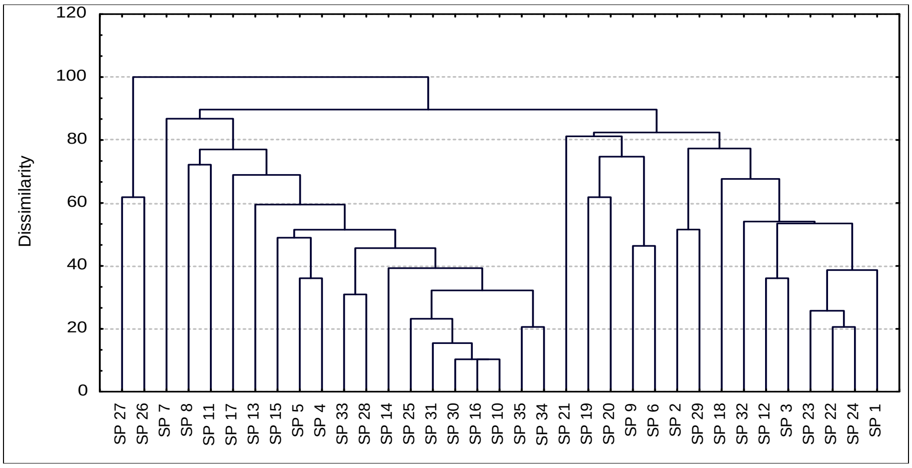

Fig 4: UPGMA-dendrogram based on 82 protein characters illustrating similarity and dissimilarity distances Between the studied taxa as numbered and listed in Table 1.

The phenogram of Fig. 4 produced from the numerical analysis for 82 seed protein characters between 35 taxa of Brassicaceae showed that, all the studied taxa are separated at taxonomic level of 100 %. Two species of genus *Raphanus* (*R. raphanistrum* and *R. sativus*) are separated in single cluster of 62%. Rest of the taxa are separated into two groups the first separated at 85 % dissimilarity level. This group included the two species of genus *Sinapis* (*S. alba* and *S. allionii*), *B. Tournefotii* (Egypt) and *Diplotaxis* (Egypt) are grouped at taxonomic level of 72%, three species of *Erysimum (E. Cheiri, E.crepidifolium* and *E. heritieri var. Hierrense)* and the two species of *Thlaspi caerulescens* and *Thlaspi montanum* which are collected from Germeny. On the other hand, *B. Rapa* has separated in single disimilarity level of 85%. Ther are a great affinity between B. *oleracea. var. capitata* and *B. oler. var. Botrytis* which are separated at taxonomic levels of 30%. The second group delimited at 82%; at this group the remainder of the studied taxa are recognized; in which the highest similarity was between three species of *genus Mathiola (M. fruticulosa, M. incana* and *M. tricuspidata*). Also, *Capsella bursa-pastoris* (Egypt) is corellate with *Brassica oleracea*(England) which in turn shared with the three species of *Lepidium* (*L. campestre, L. densiflorum* and *L. sativu*m) such group is separated at dissimilarity level of 80%.

It is obvious that, the four species belong to genus *Erysimum* were collected from different localaties as showen in Table 1 showed a great variations in the number of bands in their protein profile patterns (Figs. 1, 2 &3). From the results, *B. oler. var. Capitata* (Egypt) and *B. oler. var. Botyrtis* (Egypt) are shared in 6 bands (Table 2, bands, no.8,25,37,60,65 &75) in turn shared with *Brassica oleracea* (England) in three bands (Table 2, bands, no. 8, 25 & 60). The most eight species of genus *Brassica* shared in band no.25 with migration distance of 0.37. The low level of protein polymorphism could be attributed to the conservative nature of the seed protein. This conclusion was in accordance with Bonfitto *et al*. (1999) [5] who used SDS-protein profiles to identify nine cultivars of melons. Although the electrophoretic method shows good reproducibility, it failed to identify all of the examined taxa. The detected of the intraspecific polymorphism in the resulted protein profiles could be attributed to some environmental stress (Sammour *et al*., 1993) [19]. *Brassica* genotypes of each species from different geographical locations in most cases are not grouped together in one cluster (Fig. 4), such result was in accordance with Kamel (2005) [13]. In addition *Capsella bursa-pastoris* (Egypt) grouped with three species of *Lepidium* at taxonomic level of 80%. On the other hand the two species of genus *Raphanus* are separated in single cluster of 62%. Such cluster grouped with most studed taxa of Tribe *Brassiceae* such as genus *Brassica*, genus *Diplotraxis*, genus *Sinapis* and genus *Raphanus*. This conclusion in accordance with Al-Shehbaz, *et al*. (2006) [2].

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