TOTAL SEED STORAGE PROTEIN PATTERNS OF SOME *LATHYRUS* SPECIES GROWING IN TURKEY USING SDS-PAGE

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Abstract

Present study determined the variation of total electrophoretic seed protein patterns and protein amounts in some *Lathyrus* species viz., *L. tukhtensis, L. cilicicus, L. saxatilis, L. annuus, L. hierosolymitanus, L. gorgoni* var. *gorgoni, L. Lycicus and L. odoratus* collected from their natural habitats of different localities in Turkey. Electrophoretic data were documented by using a gel documentation system (Bio-Rad, USA) and analysed by using Quantity 1-D analysis software and also the dendogram were formed with 4.0% tolerance in UPGAMA (Unweighed Pair-Group Arithmetic Mean). The differences among species were observed and all 9 taxa were clearly identifiable from the protein patterns. The formed dendogram from SDS-PAGE analysis showed that all studied taxa constituted two clusters. The first one consisted of *L. saxatilis, L. gorgoni, L. annuus, L. hierosolymitanus, L. lycicus* and *L. gorgoni* were found to have higher similarity to each other. Also, it was reproted that quantities of total seed proteins in the present study. *L. lycicus* (79.906 µg/ml) has highest total protein content whereas *L. cilicicus* (65.860 µg/ml) has lowest total protein content.

Introduction

Genus *Lathyrus*, which is a member of the *Viciae* tribe (family *Leguminosae*), consists of about 160 anuual and perennial species and many of them are economically important, used as forage, human food or ornamental plant and have a long history as cultivated plants (Chtourou-Ghorbel *et al.*, 2001, Brahim *et al.*, 2002, Lewis *et al.*, 2005). Classification of *Lathyrus* has varied in the history of the genus (Brahim *et al.*, 2002). Kupicha's (1983) morphology-based monograph represents only worldwide treatment of genus. She proposed infrageneric classification with 13 sections (Kupicha, 1983; Asmussen & Liston, 1998). The *Lathyrus* L. genus is represented with 75 taxa in the level of species, subspecies and variety and it is divided into 10 sections in Turkey (Davis, 1970; Ertekin & Saya, 1990, Ertekin, 1994; Davis *et al.*, 1988; Maxted & Goyder, 1988; Guner & Ozhatay, 2000; Genç & Şahin; 2008; Genç, 2009).

The systematic methodology especially based on morphology chiefly has been improved by the incorporation of physiology, ecology or biochemical traits (Ayaz *et al.*, 1999; Przybylska *et al.*, 2000). It was reported that biochemical and molecular analysis, particularly of electrophoretic analysis of seed proteins as revealed by SDS-PAGE (Sodium Dodecyl Sulphate Polyacrilamide Gel Electrophoresis) have provided valid evidence for detecting intraspecific variation and assessing interspecific relationships (Ladizinsky & Hymowitz, 1979; Kamel *et al.*, 2003; Javaid *et al.*, 2004; Çelebi *et al.*,

2009; Hameed *et al.*, 2009). Many studies based on the electrophoretic analysis of seed proteins have been used to examine genetic variability and systematic problems in several legumes such as the genus *Astragalus* (Actk *et al.*, 2004), genus *Lupin* (Vaz *et al.*, 2004), genus *Pisum* (Jha & Ohri, 2002), genus *Lathyrus* (Przybylska *et al.*, 1999, 2000, Emre *et al.*, 2006; Emre *et al.*, 2007a, Emre, 2009), genus *Onobrychis* (Emre *et al.*, 2007b), genus *Phaseolus* (Przybylska & Przybylska, 1993) and genus *Vicia* (Przybylska & Zimniak-Przybylska, Z., 1997; Ayaz *et al.*, 1999; Mirali *et al.*, 2007; Emre, 2007; Emre *et al.*, 2007c). Present study reports the variation of total electrophoretic seed protein patterns and protein amounts in some *Lathyrus* species collected from their natural habitats of different localities in Turkey.

Materials and Methods

Dry seeds of *Lathyrus* species viz., *L. tukhtensis* Czecz., *L. cilicicus* Hayek&Siehe, *L. saxatilis* (Vent.) Vis., *L. annuus* L., *L. hierosolymitanus* Boiss., *L. gorgoni* Parl. var. gorgoni, *L. lycicus* Boiss., *L. phaselitanus* Hubb.-Mor&Davis, *L. odoratus* L., were collected from various areas of Turkey. Details about the seed materials are given in Table 1.

Seed proteins were extracted as described by Jha & Ohri (2002). Seed coats were removed prior to extraction and cotyledons were obtained. These were homogenised in 0.1M Tris-HCl buffer (pH: 7.5). Total protein was extracted after centrifugation at 17.600 g for 20 min., at 4°C and supernatants were used for analysis. Proteins in the supernatants were quantified using Bio-Rad DC protein assay (Bio-Rad Laboratories, UK) and on the gel, Fermentas (116.0 kDa (kilodalton), 66.2 kDa, 45 kDa, 35 kDa, 25 kDa, 18.4 kDa) used as marker. The samples were boiled for 5 minutes prior to loading, then average 200 µg protein of each sample was loaded on to the 12% SDS-PAGE (Laemmli, 1970). Electrophoresis was performed in the Protean II electrophoresis cell (Bio-Rad Laboratories, UK) at 20 mA until the bromophenol dye (BDH Laboratory Supplies Poole, England) front had reached the bottom of the gel. The gels were stained in Coomassie Brilliant Blue (Sigma Aldrich Chemie, Germany) solution for 30 min., at 67°C and destained in destaining solution for 3-4 h at 67°C to visualise the proteins.

Statistical analysis

Electrophoretic data were documented by using a gel documentation system (Bio-Rad, USA) and analysed by using Quantity 1-D analysis software and also the dendogram were formed with 4.0% tolerance in UPGAMA (Unweighed Pair-Group Arithmetic Mean).

Results and Discussion

Kupicha's (1983) classification based on morphological characters proposed 153 species of Lathyrus into four great sections viz., Orobus (54), Lathyrus (33) Notolathyrus (23) and Lathyrostylis (20); other four sections comprises two to seven species (Aphaca, Linearicarpus, last five Clymenum, Pratensis) and sections are monotypic (Orobon, Nissolia, Viciopsis, Neurolobus, Orobastrum) (Asmussen & Liston, 1998; Badr et al., 2002). Furthermore, Doğan et al., (1992) determined 54 Lathyrus species grown in Turkey to nine sections based on forty morphological characters. They suggested that there are basically nine sections (Orobus, Lathyrostylis, Aphaca, Nissolia, Orobon, Gorgonia,

Species	(Davis <i>et al.</i> , 1970)	Kupicha (1983)	Doğan <i>et al.</i> , (1992) Locality	Locality
L. tukhtensis Czecz.	Platystylis	Lathyrosthylis	Lathyrosthylis	Karaman, Ermenek Gülnar road, 1340 m
L. cilicicus Hayek&Siehe	"	Lathyrosthylis	Lathyrosthylis	Trabzon, Araklı, 1950 m.
L. saxatilis (Vent.) Vis.	Orobastrum	Viciopsis	Nissolia	Isparta, Eğirdir, edge of Kovada lake, 900 m
L. annuus L.	Cicercula	Lathyrus	Lathyrus	Mugla Osmaniye village, 500 m
L. hierosolymitanus Boiss.	¥	Lathyrus	Lathyrus	Muğla, Marmaris, İçmeler- Bozburun road 3rd km, 450 m
L. gorgoni Parl. var. gorgoni	¥	Lathyrus	Gorgonia	Antalya, Ünsallar district, around Prison, 40 m
L. lycicus Boiss.	3	Lathyrus	Cicercula	
L. phaselitanus HubbMor & Davis	3	Lathyrus	Not examined	Antalya, Kemer, Phaselis, 20m,
L. odoratus L.	Lathyrus	Lathyrus	Not examined	Muğla,Dalyan, İztuzu road, 10m,

Clymenum, Cicercula and *Lathyrus*) which are grouped in two subgenera, viz., subgenus *Lathyrus* and subgenus *Orobus* (Doğan *et al.*, 1992). In addition, Davis (1970) recognized 58 *Lathyrus* species from Turkey under ten sections viz., *Orobus, Platystylis, Pratensis, Lathyrus, Orobastrum, Cicercula, Clymenum* and *Aphaca,* in addition to monotypic sections *Orobon* and *Nissolia* in flora of Turkey (vol. III) (Table 1). In this study, SDS-PAGE it was used the as a tool for assessing genetic variation and determining the relationships among distinct species belonging to genus *Lathyrus* including three sections *Lathyrus* (*L. tukhtensis* and *L. cilicicus*), *Viciopsis* (monotypic section; *L. saxatilis*), *Lathyrus* (*L. annuus, L. hierosolymitanus, L. gorgoni, L. lycicus, L. phaselitanus* and *L. odoratus*). *Linearicarpus* and *Orobastrum* (monotypic section) (Kupicha, 1983). The differences among species were observed and all 9 taxa were clearly identifiable from the protein patterns. The total seed protein banding patterns of 9 taxa are illustrated in Fig. 1 and protein amounts of *Lathyrus* species were given Table 2.

The all studied taxa of genus *Lathvrus* cluster together on the basis of seed protein similarities as designed by previous morphological classification. The formed dendogram from SDS-PAGE analysis showed that all studied taxa constituted two clusters (Fig. 2). The first one consisted of L. saxatilis, L. gorgoni, L. annuus, L. hierosolymitanus, L. lycicus and L. phaselitanus second one by L. tukhtensis, L. cilicicus and L. odoratus. In cluster I, L. saxatilis and L. gorgoni were found to have higher similarity to each other. Present study demonstrated that L. saxatilis, which is member of monotypic section was gathered together with members of section Lathyrus. Davis (1970) Viciopsis. indicated that L. saxatilis is a species of doubtful systematic position. Kupicha (1983) stated that L. saxatilis resembles the fruit of some members of the section Lathyrus. But findings of Doğan conflict with current results. Doğan et al., (1992) indicated that L. saxatilis placed different cluster from elements of section Lathyrus (L. annuus, L. hierosolymitanus) and it was nested together with members of section Nissolia. Furthermore, present findings determined L. gorgoni grouped together with elements of section Lathyrus and section Viciopsis (L. saxatilis). It was found that L. gorgoni has exhibited closer similarity with L. saxatilis than members of section Lathyrus. Doğan et al., (1992) proposed a new section Gorgonia to accomadate L. gorgoni in addition to L. rotundifolius and L. undulatus. But L. gorgoni has been placed in section Lathyrus by Kupicha (1983) and also it has been placed in section *Cicercula* by Davis et al., (1970). Results of present study was supported by several other studies such as chloroplast DNA restriction site data (Asmussen & Liston, 1998), electrophoresis of seed storage proteins (El Shanshoury, 1997), AFLP data (Badr et al., 2002), seed surface characters (Abu El Enain et al., 2007) which reported that L. gorgoni has been clustered together with elements of section Lathyrus.

Taxa	Total protein amounts (µg/ml)
L. tukhtensis	69.674
L. cilicicus	59.860
L. saxatilis	65.209
L. annuus	75.395
L. hierosolymitanus	65.627
L. gorgoni var. gorgoni	75.279
L. lycicus	79.906
L. phaselitanus	73.395
L. odoratus	65.441

Table 2. Protein amounts of investigated Lathyrus species.

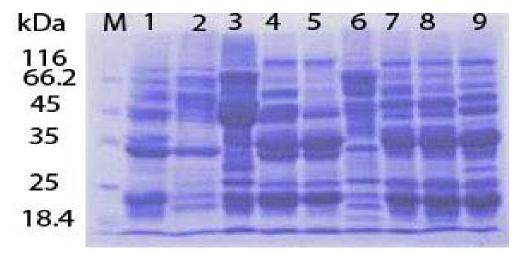


Fig. 1. SDS-PAGE of total seed proteins in studied *Lathyrus* taxa. M: Marker; 1: L. tukhtensis; 2: L. cilicicus; 3: L. saxatilis; 4: L. annuus; 5: L. hierosolymitanus; 6: L. gorgoni; 7: L. lycicus; 8: L. phaselitanus; 9: L. odoratus

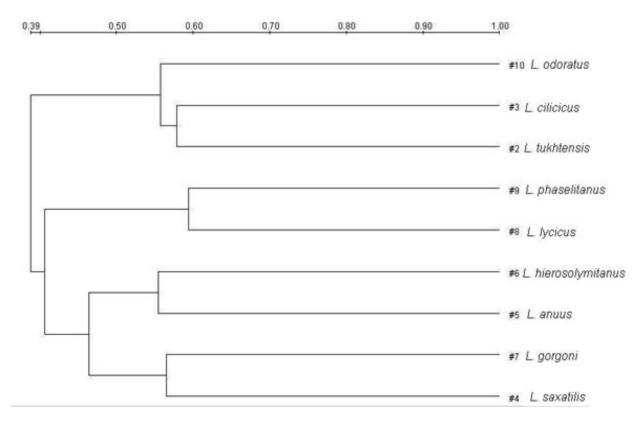


Fig. 2. Dendogram of Lathyrus species based on total seed protein profiles.

Present study demonstrated that *L. annuus* and *L. hierosolymitanus* were closest each other. A study done by Asmussen & Liston (1998) demonstrated that *L. annuus* and *L. hierosolymitanus* exhibited close affinity each other based on chloroplast DNA. El-Shanshoury (1997) found that most of species from section *Cicercula* are seperated into three groups according to findings obtained from electrophoresis of total seed proteins. Results of study done by El-Shanshoury (1997) showed that *L. annuus* and *L. hierosolymitanus* had close similarity. The affinity between some species of section *Lathyrus*, especially *L. annuus* and *L. hierosolymitanus*, is supported by both AFLP and isozyme data in addition to cpDNA restriction site data and cluster analysis of the seed

characters (Asmussen & Liston, 1998; Badr *et al.*, 2002; Abou-Ebu-El Enain *et al.*, 2007). Also, *L. lycicus was* clustered with *L. phaselitanus* when the results of cluster I were compared. Davis (1970) indicated that *L. phaselitanus* is allied to *L. Lycicus*. In cluster II, *L. tukhtensis* and *L. Cilicicus* were closer to each other. In addition, it was found that *L. odoratus*, placed in cluster II, was nested together with these two species. Also, it determined that quantities of total seed proteins in the present study (Table 2). *L. lycicus* (79.906 µg/ml) has highest total protein content whereas *L. cilicicus* (59.860 µg/ml) has lowest total protein content.

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