

Evaluation of phylogenetic relationship among seabuckthorn (*Hippophae rhamnoides* L. spp. *turkestanica*) wild ecotypes from Pakistan using amplified fragment length polymorphism (AFLP)

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Abstract

Sea buckthorn (*Hippophae rhamnoides* L.) is a very potent medicinal and multipurpose plant which has gained global significance due to its medicinal and multipurpose utility. It bears yellow to orange berries which are known to human beings from centuries for their effects on health. The plant is widely distributed throughout Northern Areas of Pakistan. The phylogenetic relationship among these natural seabuckthorn ecotypes from Northern Areas of Pakistan is not established so for using reliable molecular markers. AFLP has been proved to be an effective tool for the determination of phylogenetic relationship among closely related species. To provide a population level genetic profile for investigation and exploitation of genetic diversity of Sea buckthorn (*Hippophae rhamnoides* sub spp. *turkestanica*), 25 plant samples selected from natural populations of seabuckthorn in Pakistan were analyzed using AFLP (Amplified Fragment Length Polymorphism) markers the University of Sussex, UK. Phylogenetic distance estimated revealed that the ecotypes expressed common heritage for their phylogenetic relationship with a considerable genetic diversity among them as well. Quite a few ecotypes showed close relationship irrespective of their geographic distances and morphological attributes. The research evolved a significant outcome to start a breeding program for the evolution of seabuckthorn varieties for the mountain areas of Pakistan and Azad Kashmir.

Introduction

Seabuckthorn (*Hippophae rhamnoides* L.) of the family *Elaeagnaceae* is a multipurpose shrub distributed in Asia, Europe and North America (Ercisli *et al.*, 2008). In Pakistan Seabuckthorn has natural populations found throughout Northern Areas (Shah *et al.*, 2007).

The broad geographical distribution and diversified ecological conditions may contribute to the extensive diversity of Seabuckthorn (Ercisli *et al.*, 2008). Seabuckthorn ecotypes of Pakistan do not only exhibit great diversity in plant morphology, physical attributes but also express diversity in biochemical constituents (Shah *et al.*, 2007; Sabir *et al.*, 2005). The morphological, physical and biochemical diversity of naturally occurring ecotypes requires a credible evidence to be declared as genetically diverse germplasm before exploiting them to start any breeding program for crop improvement.

The knowledge of genetic relationships among the germplasm available, helps in great deal to achieve desirable objectives (Vijayan *et al.*, 2005; Le *et al.*, 2000). The molecular approach for the estimation of genetic diversity has improved increasingly valuable in identification of germplasm (Singh *et al.*, 2006; Congiu *et al.*, 2000).

Different Molecular Markers have been used to assess phylogenetic relationships and genetic diversity in seabuckthorn including isozymes (Yao & Tigersted, 1993), randomly amplified polymorphic DNA (RAPD) (Ercisli *et al.*, 2008, Ercisli *et al.*, 2007, Sheng *et al.*, 2006; Singh *et al.*, 2006; Raun *et al.*, 2004; Bartish *et al.*, 2002; Sun *et al.*, 2002). In addition to RAPD and other molecular markers, AFLP (Amplified Fragment Length

Polymorphism) is a whole genome approach to study the genetic diversity which is gaining the popularity for lower level systematics (Brussell *et al.*, 2005). The use of restriction enzymes and involving PCR rounds proved to be extremely useful, as no prior sequence information is required for analysis. The AFLP technique has recently illuminated the details of phylogenetic relationships within different plant varieties (Mc Kinnon *et al.*, 2008, Bousios *et al.*, 2007, Pellmyr *et al.*, 2007, Joly & Bruneau 2007). The technique is very useful for the detection of genetic relationship among seabuckthorn cultivated varieties as well (Raun & Li. 2005).

Seabuckthorn is a potent multipurpose plant for the mountain areas of Pakistan and Azad Kashmir. The wild germplasm can be used as source of gene pool to start a breeding program to evolve new Seabuckthorn varieties for economical development in mountain areas of Pakistan. The advent of modern molecular techniques like AFLP has opened the new window of opportunity to know about the genetic diversity of existing gene pool to help in improving the efficiency and validity of breeding program. Seabuckthorn of Northern Areas of Pakistan has not been characterized so far, using any DNA based molecular marker. In present study we selected twenty-five (25) ecotypes of seabuckthorn collected from different localities of Northern Areas of Pakistan, showing morphological, physical and biochemical diversity among them, for AFLP analysis to determine the phylogenetic relationship among them.

Materials and Methods

Twenty-five seabuckthorn ecotypes were used in this study. The leaf samples were taken from wild seabuckthorn populations from Skardu, Hunza Gilgit, Hussainabad, Murtazabaad, Nagar, Shigar, Sadpara, Khaploo, Sust and Jaglot areas of Northern Pakistan represented as dots in Fig. 1. All these ecotypes were showing diversity in some morphological parameters like tree shape, fruit color and tree height. The already frozen leaf samples were immediately subjected to -80°C before transporting them to the University of Sussex, School of Life Sciences United Kingdom for further studies. The experiment was conducted in Plant Molecular Biology laboratory, John Maynard Smith Building, University of Sussex, UK.

DNA extraction: Genomic DNA was extracted from frozen leaf tissue using *DNeasy Plant Mini Kit* (Qiagen). The purity and quantity of extracted DNA were measured with the help of spectrophotometer in 260 and 280 nm wavelengths (Thermo Nicolet 100 UV, London, UK). The quantity of DNA was in between 1.3 (E7) and 1.6 (E15). Extracted DNA is shown in Fig. 2.

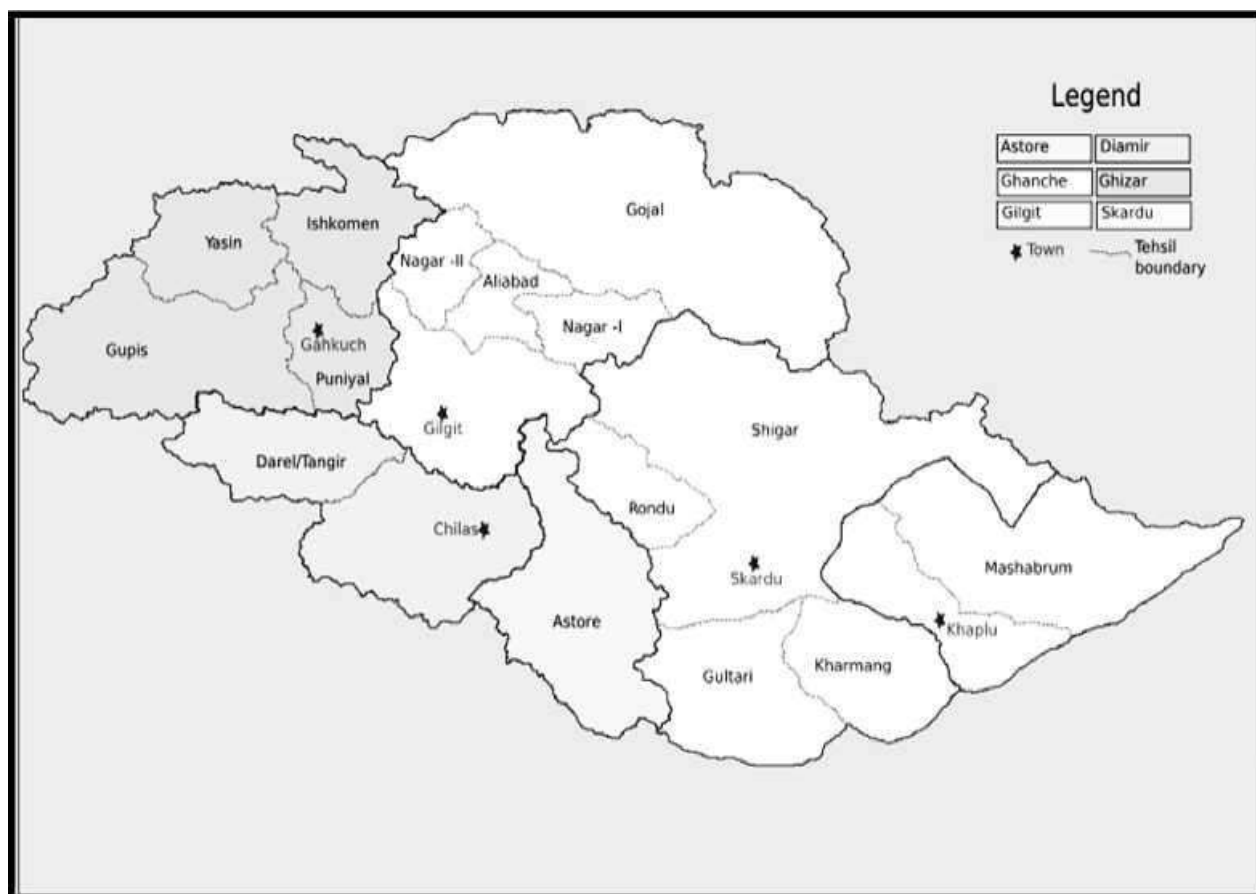


Fig. 1 – Sampling sites from Northern areas of Pakistan.

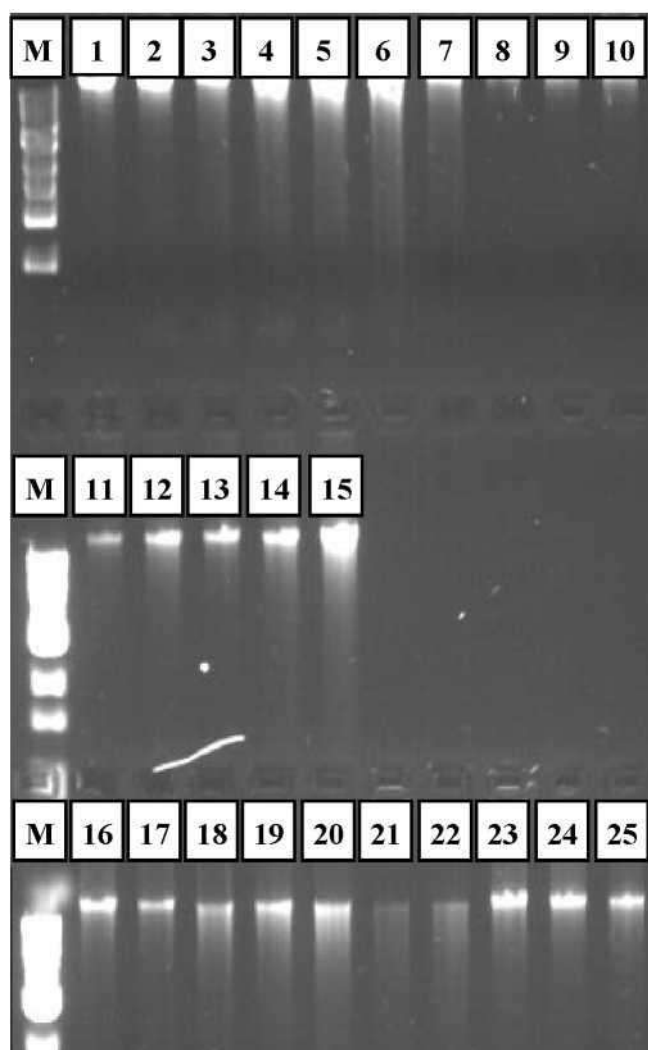


Fig. 2 – Genomic DNA of seabuckthorn ecotypes.

AFLP analysis

Digestion of genomic DNA: Genomic DNA was digested with reagents and enzymes in the ratio as follows. Water 37pl, genomic DNA 2pl, 10 times Ligase buffer 5pl, MSe I adopter (50pM): 1pl, EcoRI adopter (5pM) 1pl, Mse I (10p/pl) 1pl, EcoRI 1 pl, Ligase 2pl to make the final volume 50 pl. The mixture was vortexed and kept overnight at 50°C for over night.

Preamplifications: For preamplification reaction reagents were mixed as follows: Water 15.3pl, 10 X PCR buffer 2.5 pl, dNTPs (1.25 mM each) 4pl, EcoRI(+A) 5CTCGTAGACTGCGTACC-30.15g/pl)1pl,MseI(+C) 3 CAT CT GAGACGCAT GG TTAA- 5 (0.15pg/pl), template ligation 1pl, taq polymerase 5u/pl 0.2pl and the total volume was made up to 25ul. The PCR conditions were 50°C for 2 minutes to get infill and at 94°C for 30 seconds, 56°C for 60°C and 72°C for 60 seconds.

Labeling of primers: Water 6.25ul, Radiolabel (ICN 58404.2) 1ul, 10X kinase buffer 1ul, EcoRI (+AGG) primer 5 - GACTGCGTACCAATTCAGG-3' (0.05ug/ul) 1.5ul, T4 polynucleotide kinase (10u per pl) 0.25 pl. The mixture was incubated for one hour in hot block then 70°C for ten minutes to stop reaction.

The products of preamp reaction were analyzed visually in agarose gel and strong preamps were selected for further reaction in the following order. Water 387.2 pl, PCR buffer 64pl, dNTPs102.4pl Mse (+CAG primer 5 - GATGAGTCCTGAGTAACAG-3) 0.05pg/pl) 19.2pl, Taq Polymerase 5u/pl) 3.2pl, labeled primer 3.2pl and diluted preamp with PCR conditions 94°C for 30 seconds, 65°C for 30 seconds, 72°C for 60 seconds, (30 cycles) and 94, 56 and 72°C for 30, 30 and 60 seconds respectively with 27 cycles.

Preparation of acrylamide gel solution (6%): Following reagents were mixed as follows:

Urea 306g, 5 X TBE 66.6ml, and 500 ml water to dissolve urea.

Acylamide stock 40% was taken and water was added to 666 ml volume. The stock was kept in room temperature in the dark.

Making of gel: To make one gel, 80 ml of gel solution, 90pl of 25% ammonium persulphate (made fresh) and 90pl TEMED were mixed with each other.

Making of gel case: Plates were washed thoroughly with detergent under hot running water and dried with towels. Gel was pored in the spaces of plates and comb was inserted in 4mm depth. The gel was left to set for one hour. The bulldog clips and cling film were removed and the gel was put into the electrophoresis apparatus. The tank was filled with 0.5% TBE. Comb was removed by pulling it upwards. The top was washed of the gel with hypodermic needle and syringe. The comb was replaced with shark's teeth pointing down. It was pushed down until the teeth just touched the surface of the gel and made small indents. Gel was run till the dye reached to the end of the gel. Drained the gel and was placed in 10% methanol and 10% acetic acid. Gel was allowed to fix for at least 30 minutes. The acrylamide was with clingfilm and dried in gel drier.

Autoradiography: The Clingfilm was removed and the gel was put in automated cassette. A piece of X-Ray film was put on the gel and closed the cassette down firmly. The gel was exposed for overnight in darkroom.

Results and Discussion

The DNA profile among 25 populations of Seabuckthorn is compared in Fig. 3. Marker data for AFLP were scored and phylogenetic relationships were determined. The UPGMA dendrogram based on genetic distances among populations shows very clear picture of species evolutionary pattern in relationship and variability shown in Fig. 4. The dendrogram shows that three groups of the populations separated very early from each other in past to form discrete populations. The ecotypes E1, E2, E8, E9, E15, E18, E21, E24 and E25 were observed in a unique cluster, providing some common phylogenetic relationship among them. Ecotypes E1 and E2 originating from same ancestors but separated in near past to make a discrete cluster. Similarly E9 and E19 also grouped them in a separate group. Seabuckthorn ecotypes E24 and E18 were found be close in phylogenetic relationship. The ecotypes E9 and E19 were found to be in a distinct relation showing that they were separated from their ancestor in near past. E21 and E15 also behaved differently among the other phylogentic relatives. The ecotypes E3, E4, E5, E6, E14, E16, E22 and E23 were genetically similar and clustered together. E22 and E23 are most similar in their genetic make up. Same behavior of genotypic similarity was expressed by ecotypes E5 and E6, E4 and E16 and E3 and E14 who have some common genetic make up respectively.

The third cluster includes E7, E10, E11, E12, E13, E17 and E20. These ecotypes expressed genetically common behavior. The ecotypes E7 and E17 expressed close genetic relationship along with E11 and E12 who are very similar in their genetic make up. E10 and E13 were separated from E20 to express distinct genetic behavior.

The common ancestor of all these ecotypes justifies the reporting of (Rongsen, 1992) that Seabuckthorn in Pakistan belongs to only one sub specie i.e., *turkestanica*. The genetic diversity and similarity among the ecotypes under this research further confirms that geographic distances and diverse climatic conditions along with different altitudes had no significant effect on the phylogenetic relationship of plant populations. Tian *et al.*, (2004) also reported that geographic distances had no visible effect in genetic differentiation. In an other studies for Autumn olive plant populations, Ahmed *et al.*, (2008) found that Autumn olive natural stands behaved quite differently when compared in phylogenetic relationship irrespective of their geographic distance.

The common heritage of Seabuckthorn populations collected from diverse locations of Northern Areas of Pakistan could be due to the fact that birds consume Seabuckthorn berries and thus play a major role in seed dispersal at variable altitudes and distant areas. Moreover Seabuckthorn is mostly found near the river belts of Northern Areas and seed dispersal is also facilitated by rivers coming from higher altitudes to valleys downwards. The study provides evidence that geographic distances and locations have least effect on the genetic behavior of plant populations. The diversity in Seabuckthorn ecotypes on the basis of biochemical constituents (Shah *et al.*, 2007) has to be linked with genetic diversity. Seabuckthorn has tremendous potential to fulfill the objectives of nutritional, economical and environmental significance. It is full of nutritional and biochemical constituents and becoming very popular around the globe due to its multipurpose utility (Yao & Tigerest, 1993). The naturally occurring Seabuckthorn populations of Northern Pakistan require to be improved by evolving new multipurpose varieties. The knowledge of distribution of genetic diversity provides a guide to the wise management of the genetic resources (Barret & Kohn, 1991). This study provided the base to launch a breeding program for seabuckthorn improvement to exploit the potential of this magic shrub for sustainable economic development in mountain environments of the country in particular and for the world in general.



Fig. 3. AFLP profile of genomic DNA of 25 ecotypes separated on Polyacrylamide gel.

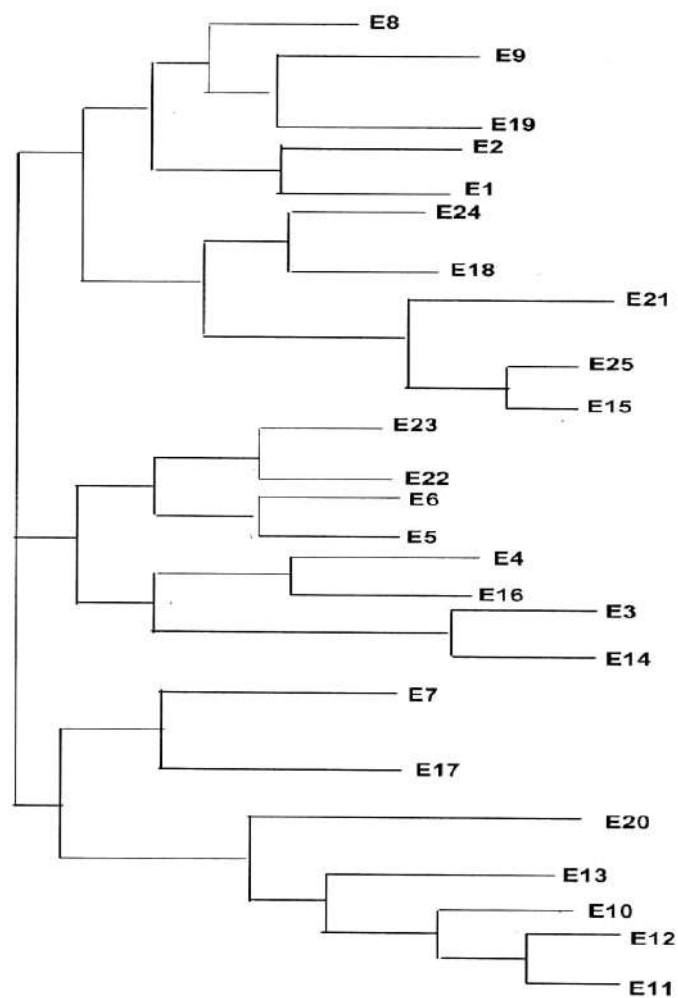


Fig. 4. Dendrogram of 25 seabuckthorn ecotypes.

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