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# Seed yield and essential oil content of fennel influenced by genetic variation and genotype × year interaction

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ABSTRACT

Common fennel (*Foeniculum vulgare* Mill.) is an important medicinal plant with considerable geographical distribution in Iran. Variation in eighteen populations of fennel collected from different regions of Iran and two European accessions was evaluated based on agro-morphological traits, ISSR markers, seed yield and essential oil content. Accessions were planted in the field and studied for two consecutive agronomic years. The analysis of data on all 20 accessions showed that mean squares of genotypes, years, and genotype × year interaction was significant for most of the traits indicating wide variation for the studied traits in the fennel accessions influenced by the environment. Coefficients of genotypic variability revealed high genetic variation for seed yield per plant and harvest index suggesting the possibility of improving seed yield by means of selection particularly in the first year. Seed yield per plant had positive correlations with the number of effective umbels per plant and 1000-seed weight as yield components. Cluster analysis based on agro-morphological traits classified populations into 4 major groups in the first year. Similarly the UPGMA (unweighted pair group method with arithmetic mean) dendrogram obtained from ISSR molecular data based on SM (simple matching) classified populations into four groups. Agro-morphological and ISSR data matrices were not correlated and did not correspond to the geographical variation of the populations. In general, the results of this research showed that there was a considerable genetic variation in terms of seed yield and the other agronomic and molecular traits among accessions and depending on the objectives, this variation may be utilized to select superior genotypes for medicinal purposes and in plant breeding programs.



## 1. Introduction

Plants have been used as a major source of medicine from thousand years ago. Plants of Apiaceae (=Umbelliferae) family are very important in medical, pharmaceutical and chemical industries. They usually grow in moderate climates and are adapted to low amounts of water (Omidbaigi, 2007). Common fennel (*Foeniculum vulgare* Mill.) as one of the most important medicinal plants in this family is a perennial that grows naturally in many different parts of the world (Akgul, 1986; Kafi, 2003). It is native to southern Europe and the Mediterranean area (Parsons, 1973). In Iran, fennel has a considerable geographical distribution and traditionally has been used as herb and spice (Heywood, 2002).

All plant parts of fennel are edible: roots, stalks and leaves, but the spice comes from dried seeds where an essential oil is also extracted for medicinal uses. The oil is composed of a mix of several monoterpenes and phenylpropanoids, with trans-anethole, estragole, fenchone and limonene as main constituents (Guillen and Manzanos, 1994). Essential oil of fennel has been reported to possess antifungal (Mimica-Dukic et al., 2003; Soylu et al., 2006; Kamble and Patil, 2008) antimycobacterial and anticandidal activities (Abed, 2007; Camacho-Corona et al., 2008).

Nowadays, wild medicinal plants are endangered because of destruction of natural habitats and inordinate harvest by the native people. Therefore, study and evaluation of genetic relationships of these plants at morphological as well as molecular levels is a crucial issue for enabling better exploitation and conservation of genetic resources (Fracaro and Echeverrigaray, 2006; Rahimmalek et al., 2009). Analysis of genetic relationships in crop species is an important component of crop improvement programs, as it serves to provide information on genetic diversity, and is a platform for stratified sampling of breeding populations. Recently, DNA-based marker data allows more reliable differentiation of plant genotypes (Mondini et al., 2009).

Due to their independence from age, physiological and environmental conditions, molecular markers are widely used to track

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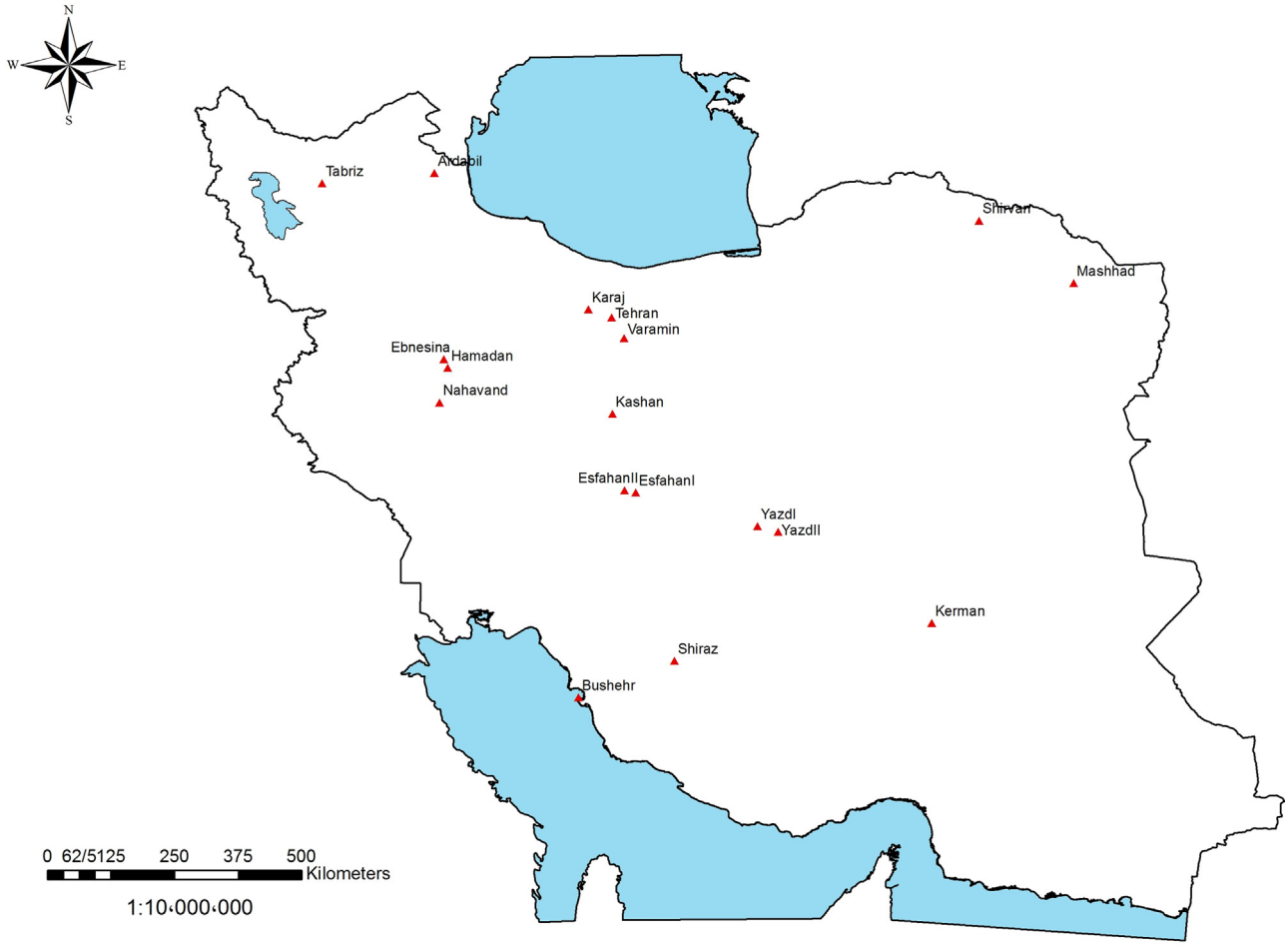


**Fig. 1.** Map of the collection sites for 18 fennel accessions generated by ArcGIS Ver. 10.2 software.

genetic diversity, to classify inheriting pools and to determine the genetic maps (Mondini et al., 2009). Inter simple sequence repeats (ISSR) as a dominant marker with a large number of polymorphic fragments per primer has been successfully employed to characterize genome diversity (Yang et al., 1996) and to reveal genetic variation in a range of different plant species (Zietkiewicz et al., 1994; Kantety et al., 1995; Joshi et al., 2000) including medicinal plants (Rahimmalek et al., 2009; Shaw et al., 2009). Recently, it has provided information on genetic diversity among cultivated fennel germplasm (Bahmani et al., 2012a; Bahmani et al., 2013; Abou El-Nasr et al., 2013).

Fennel is a perennial species and regenerates annually. It is essentially cross pollinated due to self-incompatibility, which result in a high degree of variation within each population and this offers the breeder to undertake screening and selection of plants to improve the population for the desired traits. It is therefore possible to observe agro-morphological variation and harvest seed that exist in plants regrown from a same rootstock in different years. Limited information is available on seed yield and yield components and seed essential oil content of *F. vulgare* by evaluation of traits in more than one agronomic year. Also, comparative studies between the two approaches of molecular and agro-morphological assessments of genetic variation in fennel are lacking. The objectives of the present investigation were (1) to estimate seed yield potential and essential oil content among diversified populations of fennel native to Iran and Europe evaluated in two consecutive years, and (2) to characterize fennel populations based on agro-morphological and ISSR molecular marker data.

## 2. Materials and methods

### 2.1. Plant materials and field experiment

Plant materials consisted of 18 populations from Iran and two European accessions (see Supplementary information Table S1). Iranian populations were collected from different geographical regions all over the country (Fig. 1). The experiment was conducted at the research farm of the Esfahan University of Technology, Esfahan (32° 32′ N and 51° 32′ E, 1630 m asl) at two agronomic years of 2011 and 2012. Seeds of all 20 populations were planted in mid-March 2010 at the depth of 2 cm using a randomized complete block design with 3 replications. Each plot consisted of four rows 40 cm apart and 2 m in length. The soil was a Typic Haplargid with clay loam texture, pH 7.5 and organic matter content of 1%. Fertilizers were applied at 100 kg N/ha and 100 kg P/ha prior to sowing and 100 kg N/ha top dressed in shooting stage in both years. The crop was irrigated as needed and weeds were manually controlled.

### 2.2. Phenotypic evaluation

Among agro-morphological characteristics, days to 50% emergence (DE), days to 50% flowering (DF) and days to 50% maturity (DM) were measured based on each plot performance. For the other observations, data were recorded on five randomly selected plants in each plot and their average was considered for analysis. The traits were, plant height (PH), number of effective umbels per plant (NEUM), umbel width (UMW), number of secondary branches per