



# ( F O F U J D % J W F S H F O D F J O & P S J B Q E S O N \$ M S J B J O V E " D D F T T J P O T

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## Abstract

Although Ethiopia is a center of diversity for many crops including Coriander little is known on the genetic divergence of this crop due to its negligence in the research program of the country in the past. The genetic divergence of 25 land races was assessed using SULQFLSDO FRPSRQHQQW DQG FOXVWHU DQDO\VLV EDVHG RQ FKDUDFWHUV 7KH DFFHVVLQR ODUJHVW FRQVLVWLQJ DFFHVVLQRV +LJK LQWHU FOXVWHU GLVWDQFH ZDV REVHUYH FOXVWHU , DQG ,9 LQGLFDWLQJ WKH SUHVHFH RI VXEVWDQWLDO JHQHWLF GLYHUVLW clusters. Accessions 16 and 8 having positive values for principal component 1 and 2 were of considerable breeding interest because of their good combination for the studied yield related traits.

**Keywords:** Coriander accessions; Genetic divergence; Cluster analysis; Principal component analysis

## Introduction

Coriander (*Coriandrum sativum* L.) is an annual spice herb that belongs to the family of Umbelliferae/Apiaceae. It is used as a spice for medicine and a raw material in food, beverage and pharmaceutical industries. Its green foliage, rich in vitamins and other minerals, is used in vegetables and salads while its seeds contain essential oils rich in linalool [1]. Although coriander is one of the several plant species for which Ethiopia is known as a center of origin and diversity [2] there is little information on its genetic divergence which in turn hinders the exploitation of the wealth of its diversity. The only work so far done on genetic divergence on Ethiopian coriander is that of Mengesha et al. [3], that focused on collections from different agro-ecological and geographical areas of the country. However, ecological and geographical diversifications are not the only causes of genetic divergence. For the changing of genetic material, genetic drift, natural variation and artificial selection also contribute to the genetic divergence [4] coriander accessions were diversified in different agro-ecologies of Ethiopia. Therefore, intensive collection focusing on the desired traits will benefit breeders by large for effective improvement in coriander [3]. Accordingly, target collection of the present coriander accessions was made from the potential growing areas of Arsi and Bale zones that were not well covered before and thus not well addressed by work of Mengesha et al. [3].

Genetic divergence is an essential prerequisite factor in any crop improvement programme to identify potential parents for hybridization and to obtain high yielding variety [5]. Therefore, having precise information and knowledge on the nature and degree of genetic divergence is helpful and fundamental to identify and organize the available genetic resources aiming at the production of promising cultivars [6]. For the selection of parents based on the extent of genetic divergence in different crop species multivariate methods have successfully utilized [7]. Target collection of coriander accessions was made from the present study was undertaken with the following objectives: a) to assess and evaluate genetic diversity of coriander accessions, b) to identify characters which contribute at maximum genetic diversity and c) to identify accessions for future use in breeding programs in coriander.

## Materials and Methods

The experiment was conducted at Sinana Agricultural Research Center in 2012 which is located at an altitude of 2400 m.a.s.l. Sinana has a range of mean annual rainfall of 563-1018 mm with minimum and maximum temperature of 7.9 °C and 24.3°C, respectively. The soil type is dark-brown with slightly acidic reaction [8].

Twenty five coriander accessions collected from Arsi and Bale potential growing areas were sown in RCBD with three replications on a plot of 2 meter length with spacing of 15 and 30 cm between plants and rows, respectively. The experiment was conducted under rain-fed condition. Three times hoeing and weeding were carried out without the application of chemicals and fertilizers. Five plants were randomly selected for the measurement of the characters. A total of 8 characters were recorded according to the descriptors of International Plant Genetic Resource Institute (IPGRI) as given by Diederichsen [2]. These are: number of basal leaves, length of basal leaf, length of the longest basal leaves, habitus of the basal leaves, blade shape of the upper stem leaves, blade shape of the longest basal leaves, foliation and branching habit. Recorded descriptors were subjected to principal component analysis and average linkage hierarchical method of cluster analysis to determine the common pattern of variation among the accessions using SAS version 9.2 (2008) [8]. Genetic divergences between clusters were calculated using Mahalanobis' [9] and clustering of accessions was done according to Tocher's method as described by Rao [10].

## Result and Discussion

The principal component analysis revealed that the majority of the total variation was contributed by component one and two (Figure 1). Principal component one and two contributed 35% and 19% of the total variation (Table 1) respectively. Maximum genetic variance was contributed by length of basal leaves (0.51) and foliation of the plant (0.49) to principal component 1 while number of basal leaf (0.62) and

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present study, the range of inter-cluster D2 values from 13.22 (cluster I and III) to 47.42 (cluster IV and V) was obtained. It is comparable to range of inter-cluster distance (13.8 to 91.3) reported by Singh et al.

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