Trait Patterns and Genetic Resources of Dill (*Anethum graveolens* L.)

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Abstract

Dill (*Anethum graveolens* L.) is used fresh or processed for food seasoning and preservation. Production is concentrated in temperate regionsbut can be grown as a cool season crop in India and Thailand.Several secondary metabolites, among them essential oils are present in the plant andwith claimed health benefits. Despite the many potential benefits, dill is anunderutilized crop. The current study survey global and European genetic resources. Hence, accessions from the Nordic germplasm collectionwere evaluated, aiming at tracing trait patterns.The survey showed both gaps and overlaps in availablegenebank holdings. Accessions from outside Europe were highly under-represented in the global collections, as were wild material and crop wild relatives. The evaluation showed that important agro-botanical traits correlated, such as plant height, umbel size and other size characters. Furthermore, essential oil composition wasclearly influenced by high temperature stress. A discussion on access and use of genetic resources of minor crops such as dill was included.

Key words

Abiotic stress,*Anethum graveolens*, Conservation, Dill, Genebank evaluation,Genetic resource, Morphology

Introduction

Dill (*Anethum graveolens* L.)is cultivated for its taste and flavour. Fresh, tender leaves and crowns (young umbels with flower buds) are consumed as vegetables. Dried fruits (hereafter termed seeds) are used as food seasoning and preservative or for oil extraction (Zohary and Hopf,2000). Dillhas an annual(some places biennial) growth pattern. The umbels are holdingnumerous of small yellowish flowersandbrown fruits(Heywood, 1971). The plant belongs to the*Apiaceae* family, is a diploid (2*n*=22) species withoutcrossing,and pollinated by insects(Ma et al., 1984; Snell and Aarssen, 2005). Production is concentrated to the temperate region of the world and especially Europe and USA but the crop is grown all over the world, from the Arctic Circle in northern Norway (Schübeler, 1889) to tropical and subtropical sites with a significant production in Thailand and India.A related species, Indian dill (*Anethum sowa* Roxb.) is grown in Asia in addition to the common dill. Dill has a long tradition in Ayurvedic medicine(Jana and Shekhawat, 2010). One characteristic of dill plants is the odour, and the scientific name*Anethum* is derived from theGreek word of*strong smelling*(ibid). Furthermore, the common name *dill*can be traced back the old Nordic "*dilla*", which means to calm down. Here, the plantwas used asteacuring sleeplessness but also for seasoning dishes like gravlax that from the medieval time has been prepared byanglers by burying salmon in sand for a light fermentation before seasoning. Dill is part of the traditional flavours of the Scandinavian spirit Aquavit, a tradition that goes back to at least the 15th century (Lichine, 1987; Blue, 2004).Several secondary metabolites, among them essential oils, are present in the plant (Bailer et al., 2001).The oils caninhibit growth of bacteria and fungiandhave repellent effects on certain insects(Seo et al., 2009). Claimed health benefits are many (Kmiecik et al., 2001;Delaquiset al., 2002; Lazutka et al.,2001; Al-Ismailand Aburjai, 2004; Singh et al., 2005; Yazdanparast and Bahramikia, 2008).

Despite the widespread use and many potential benefits, dill is a minor or underutilized crop (Galambosi and Peura, 1996). The European Commission Plant Variety Database (available at https://ec.europa.eu) does not include dilland dill seeds may occasionally be sold without a cultivar name, or old cultivars are still sold, as their turnoveris slow. Most seed enterprises do not include breeding for dill. Future challenges are many, ranging from increased temperature to other abiotic or biotic stresses caused by climate change. A cold-season crop like dill would probably be affected by such changes. To be able to maintain or improve yield and quality, access to genetic resources is fundamental (Bellon and van Etten, 2014). Genetic diversity in germplasm collections is evident however without clustering due to geographical origin of the material (Suresh et al., 2013).However, desired traits may not necessarily be easy to breed into high-yielding genotypes, as unwanted traits may accompany the wanted ones. This is especially the case if a wild population or landraces are used as the genetic resource but would also count as a general challenge. Doubled haploid methods have been developed to speed up the breeding process and produce uniform lines for hybrid breeding (Thomas et al., 2003; Ferrie et al., 2011). The aims of this study were to examine available global genetic resources of dill and to study trait pattern in dill.

Material and methods

Global databases searches

The Global Biodiversity Information Facility, www.gbif.org(GBIF, 2017) was used to overview the occurrences of dill and its crop wild relatives. *Anethum graveolens*and*Anethum*were used as filters in the search function of the facility. Occurrences were given asobservations of natural populations, herbarium specimens, seed collects or similar. Georeferenced occurrences were used to trace region of diversity. These are records with known geographical origin indicated by geographical coordinates. Clusters of georeferenced occurrences were compiled using the map function in the facility.

The Global Gateway to Genetic Resources,www.genesys-pgr.org, (Genesys, 2017) and the ECPGR Umbellifer database (Allender, 2017) were applied to survey the global genebank and European holdings of dill and its wild relatives. A reported accession is a seed sample or any form of conserved propagation material.

Trait pattern detection

A subset of accessionsfrom the Nordic germplasm collection (Table 1) was selected for the trait pattern detection. In 2014, the accessions were field cultivatedfor detailed morphological characterization. In 2010, the same accessions were compared under field (F)and greenhouse (G) conditions. The study was carried out at Alnarp, Sweden (55°39’N, 13°04’E).The soil was a loamy clay soil fertilized with around 50 kg ha-1 PROMAGNA 11-5-18™ (Yara, Norway). Plants were raised indoor, planted in late May with a row distance 50 cm and 25 cm between plants, and irrigated regularly. For greenhouse cultivation, plants were grown in 2 ½ L pots, 5 pots per accession, 3 plants per pot filled with a compost/peat-based soil (P-jord™ from Hasselfors, Sweden), overdressed with YaraMila 22-0-12™ (Yara, Norway)one month after planting, and irrigated on a daily basis. Climate data were recorded (SMHI, 2015).

Accessions were scored according to a standard set of agro-botanical descriptors developed by UPOV (1999)but by applying SI units(Table 2).Twelveindividuals per accession were scored, giving 12 replicate notations per accession. In 2010, scorings were based on one average registration per accession and seeds were analysed for essential oil composition. Before analysis, seeds were dried, packed in sealed bags and stored at -18 °C.A static headspace GC method was used, where the area of each resulting curve is proportionate to the concentration of the respective compound.These analyses were conducted in a private company in Copenhagen as part of a partnership agreement.

Table 1. Overview of the material included in the study.

Code	Accession name [a]	Accession number	Variety information [b] (year of release and breeders institute)
S1	Bouquet	NGB20377	Unknown breeder, delivered by Nelson Garden, Sweden
S2	Gold Crown	NGB20378	Unknown breeder, delivered by Nelson Garden, Sweden
S3	Mammut	NGB20376	Svalöf Weibull AB, Sweden, unknown year of relaese
S4	Johnsons	NGB20381	Unknown breeder, delivered by Johnsons Seeds, UK
S5	Hercules	NGB20380	Unknown breeder, delivered by Nelson Garden, Sweden
S6	Pikant	NGB13156	1956, Olson & Sons AB, Sweden
S7	Alm. Como	NGB531	Same variety as S9 (1974, Ohlsens Enke A/S, Denmark)
S8	Dura	NGB11686	1975, Olson & Sons AB, Sweden, crown type
S9	Como	NGB20379	1974, Ohlsens Enke A/S, Denmark
S10	Superdukat	NGB13157	1955, Ohlsens Enke A/S, Denmark
S11	Blanco	NGB12012	1983, Sluis & Groot Seeds, Netherlands
S12	Tuve	NGB7743	1978, Ohlsens Enke AS, Denmark
S13	Dukat	NGB12166	1976, Ohlsens Enke A/S Denmark
S14	Goda	NGB11687	1977, Olson & Sons AB, Sweden
S15	Hadi	NGB13962	1973, Olson & Sons AB, Sweden
S16	Arlöv	NGB20234	Naturalized population collected in redement garden

[a] More details are available from the database SESTO (2017).S15 and S16 were not included in the 2010 evaluation, S12 was not included in the 2014 evaluation. [b] For variety name, this was often the same as accession name

Table 2. Overview of morphological descriptors with code, character and details regarding scale. All characters recorded at the time of flowering (if nothing else stated).

Code	Character	Scale and details
Umb.Diam	Umbel diameter	In cm at flowering
Pl.Heigh	Plant height	In cm at flowering
Time.Umb	Time to umbel developing	Days from seeding to fully developed umbels
Time.Flow	Time to flowering	Days from seeding to main umbel in full flowering
Stem.Diam	Stem diameter	In mm, main stem, at flowering
Stem.Grcol	Stem green colour	3=light, 5=medium, 7=dark
Stem.Vax	Stem waxiness	1 to 9 scale, from absent or very weak to very strong
Leaf.Vax	Leaf waxiness	1 to 9 scale, from absent or very weak to very strong
Leaf.Den.F	Leaf density of feathering	3=loose, 5=medium, 7=dense
Leaf.Len	Leaf length	3=short, 5=medium, 7=long
Leaf.Wid	Leaf width	3=narrow, 5=medium, 7=broad
Pl.Dens	Plant density of foliage	3=loose, 5=medium, 7=dense
Bran.num	Number of branches	Actual number of primary branches
LeafWid.Seg	Leaf width of segments	3=narrow, 5=medium, 7=broad

Statistical analysis

The statistical analysis of variation was done with the aid ofR software (R Core Team, 2017). Initially, we produced boxplots and histograms to overview the distribution. Outliers were identified but not removed.A Pearson correlation matrix (*scatterplot*in R) was set up to describe the relationship between characters. Atwo-ways cluster analysis was made using the R function *heatmap*.The output showed a cluster illustration where both accessions and charactersare shown in the same picture.Dissimilarities were expressed as different colours from light yellow to dark red. Principal component analysis(PCA bi-plot) of the essential oil data was carried out using the *prcomp* command in R. ANOVA and Tukey multiple comparison of means were used to identify differences between field and greenhouse cultivation for the continuous, numeric characters at a 95% confidence level.

Results and discussion

Global occurrences and region of domestication

The Global Biodiversity Information Facility (GBIF, 2017) showed that dill (*Anethum graveolens*) wasrecorded with7580 occurrences and of these4935 were georeferenced. Europewas the main cluster of occurrences, followed byNorth America and Central Asia. According to the literature, dill is native to Mediterranean and Central Asian regions, also termed Eurasia(Zeven and Zhukovsky, 1975). High genetic diversity is expected in these areas where domestication took place.

Only two other *Anethum* species than dill were present with occurrences in GBIF (2017). One was Indian dill (*Anethum sowa* Roxb.) and also termed sowa.This planthadonly seven occurrences and four of thesewere georeferenced to South Asia(three hadan unknown origin).According to literature, the plant grows wild in India but the plant is also cultivated throughout South Asiaand from there to Malaysia and Japan(Malhotra and Vashishtha, 2005; Jana and Shekhawat, 2010).The other *Anethum* species with occurrences was *Anethum theurkauffii* Maire. This species had also a few occurrences in GBIF (2017) and only one was georeferencedto Morocco. Two more species; *Anethum patulum* L. ex B.D.Jacks., and *Anethum pusillum* Hort. ex Steud., were both recorded with no single occurrences, and*Anethum thodei*was recorded with two occurrences (South Africa) but with uncertain taxonomy and no taxonomic author. The results clearly show that dill has very few crop wild relatives and the genepool may as such be restricted.

Genetic resources and genebank holdings

The Global Gateway to Genetic Resources(Genesys, 2017) and the ECPGR Umbellifer crop database (Allender, 2017) were used to survey accessions maintained in genebanks (seedbanks). Such accessions, if available for distribution, are important genetic resources for crop improvement. The survey showed a total number of 1263 *Anethum graveolens*accessionsin Genesys (2017) while the ECPGR Umbellifer database showed that 1510 accessions are maintained in European genebanks. There is much overlap between the databases, as expected, as European genebanks report to Genesys (through the EURISCO catalogue, http://www.ecpgr.cgiar.org/resources/germplasm-databases/eurisco-catalogue).According to Genesys (2017), the largest collection(317 accessions) was at Plant Breeding and Acclimatization Institute in Poland (http://www.ihar.edu.pl), followed by

Leibniz Institute of Plant Genetics and Crop Plant Research in Germany(http://www.ipk-gatersleben.de) (208 accessions).Regarding country of origin, the majority of accessions had a European country of origin, in particular Eastern European countries (Poland, Hungary, Ukraine, Romania, and Germany as the top 5 countries of origin). Only a few accessions were from countries outside Europe (the top 5; Thailand 36, Azerbaijan 26, Turkey 23, and USA 17). Traditional cultivars and landraces counted forthe majority of the accessions (around 800), while 100 accessions wereadvanced cultivars and 64 were wild/natural or weedy populations.

In general, unwanted duplication among collection holders is a challenge (FAO, 2010). For the material included in the current study, cultivars like ‘Dukat’ and ‘Mammut’ were represented with eight end seven different accessions, respectively, which are maintained in different genebanks in Europe. On average, a cultivar is duplicated in three different collections (Table 3). Misspellings or synonyms were frequent, as indicated in Table 3.

Table 3. Duplication holdings of selected dill varieties according to the ECPGR Umbellifer drop database

Variety	accessions in ECPGR database	Synonyms or misspellings
Dura	2	
Goda	1	
Blanco	1	
Dukat	8	Ducat, Dukat leaf dill, Dukat dill, Dukat 3670 B
Pikant	5	Picant, Picant 2415 hg, Pikant HQ
Superdukat	3	Super-dukat OE, Superdukat O.E.
Hadi	2	
Arlöv	1	
Mammut	7	Mamoth, Mamouth, Manemuet ww
Bouquet	3	Bouguet, Bouquet dill
Gold Crown	1	
Como	2	Almindelig Como
Hercules	1	
Johnsons	1	

Regarding access to the germplasm, around 50 percent, or 623 out of the 1263 accessions in Genesys (2017),were not available for distribution under the multilateral system.Other*Anethum*species were not represented,except for one single accession of Indian dill [here classified as *Anethum graveolens* L. *subsp. sowa* (Roxb. ex Fleming) Gupta], and maintained at IPK Gatesleben (Germany). In addition, one single accession of*Anethum crispum*, a taxon not recognized by ITIS (http://itis.gov),and three accessions of *Anethum* sp. were reported.

The above numbers reflect status in genebanks reporting to the Global Gateway to Genetic Resources, which include collection holders from most European countries and the major international collections like the USDA genebanks, IPK Gatesleben, CGR (Netherland) and the VIR (Russia). However, many Asian national genebanks, like those in China and India are not included in Genesys. At least for Indian dill, such collections may provide useful genetic resources.

Morphological trait patternsin dill

Ageneral characteristic of the species *Anethum graveolens* isillustrated in Figure 1 (boxplots), wherea lower and an upper percentile define a box in which most of the observations are found and with a thick line is drawn at the median value. Whiskers from each side of the box are drawn to more distant observations(one step away from the upper and lower percentiles, respectively) and outliers (two steps from the percentiles) are plotted as small circles. For umbel diameter, the box ranged from 14 to 19 cmwith a mediandiameter of16.6 cm. For time to flowering, the box ranged from 61 to 72 days with a mediantime of 67 days. For plant height, the box ranged from 60 to 80 cm with a median height of 71 cm and some outliers. Among the categorical descriptors, stem green colourranged from 5 (medium) to 7 (dark) with a median score at 5. For stem waxiness, almost all plants were given the score 7 on a 1-9 scale. For leaf waxiness, the box ranged from 5 to 7, with median score at 5. For leaf density of feathering, the scores ranged from 5 to 7 with a median score 5. Both leaf length, leaf widthand plant density ranged from 3 to 7 with a median score 5. For leaf width of segments, almost all plants were scored 3 (narrow).The data were based on more than a hundred characterized plants from fourteen different accessions the Nordic germplasm collection. One could argue that a broader geographical origin could have been included. However, studies have shown no or very little influence of geographical origin (Suresh et al., 2013) except for landrace material (Ninouet al., 2017). In our study, variation was detected inimportant yield component traits such as leaf length, leaf width and the diameter of main umbel, which all are traits thateasily can be exploited in breeding programs. Variation was also detected in agronomic traits such as plant height and flowering time.Morphological characters are highly influenced by environmental factors. For example, umbel size and number of branches do increase with spacing between plants (Garrabrants and Craker, 1987; Gupta, 1977). Our morphological data were gathered from plants spaced25cm apart, grown in rows, and fertilized and irrigated according to contemporary cultivation standards.

Correlations among the characters are illustrated in the Pearson correlation matrix (Figure 2). The upper right triangle shows the scatter plots between all pairs of descriptors with lowest smoothers. The lower left triangle shows the linear correlation coefficient with significance levelsmarked as being different from zero. A Pearson correlation coefficient of 1 was found between leaf length and leaf width, which means that these two characters are totally correlated, showing a general pattern that leaves that were broad also were long, vis a versa. A high correlation coefficient (0.889 was detected between time to umbel development and time to flowering, showing that these characters are closely related. Furthermore, high correlationcoefficientswere also noted between stem diameter and leaf length or leaf width (0.75 for both) and between stem diameter and umbel diameter and plant height (0.56 for both), showing a pattern where plants with thick stems generally have large leaves and tall. Such plants also tend to flower late (correlation coefficient between stem thickness and flowering time = 0.47).Several other size parameters were also positively correlated.Negative correlation coefficients were observed between stem green colour and the same size parameter (correlation coefficient around – 0.50).

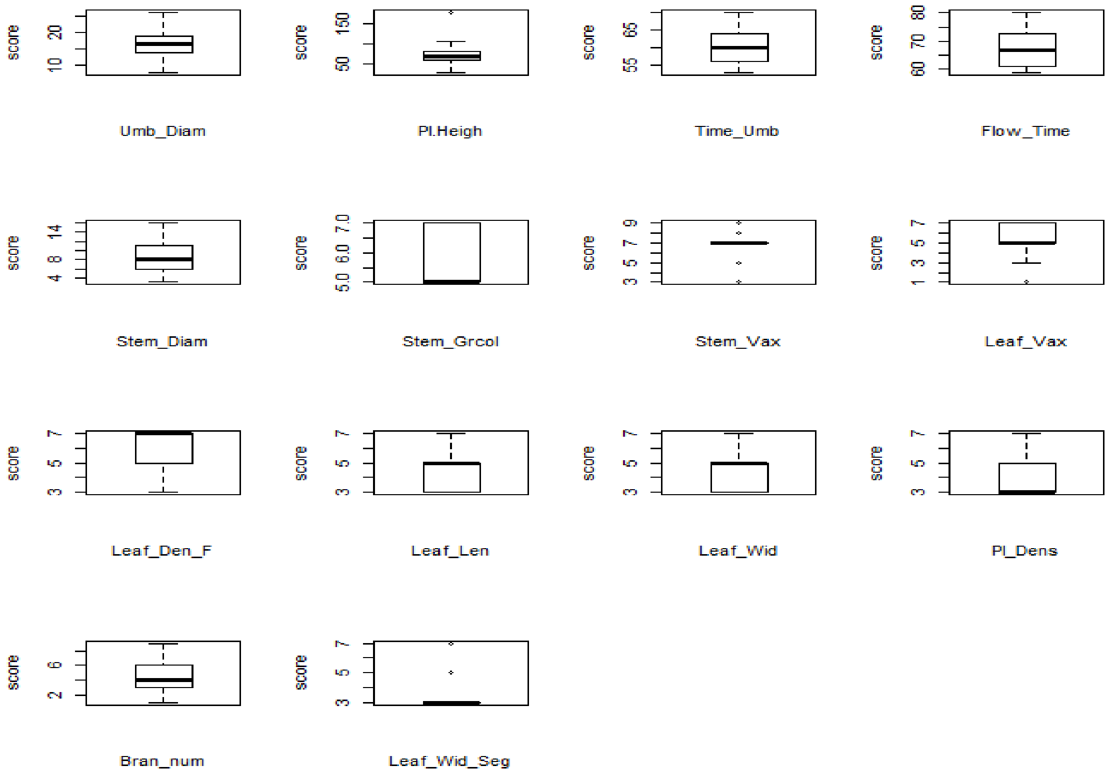

Figure 1. Boxplots showing the scores of the various descriptors are illustrated in Figure 1.

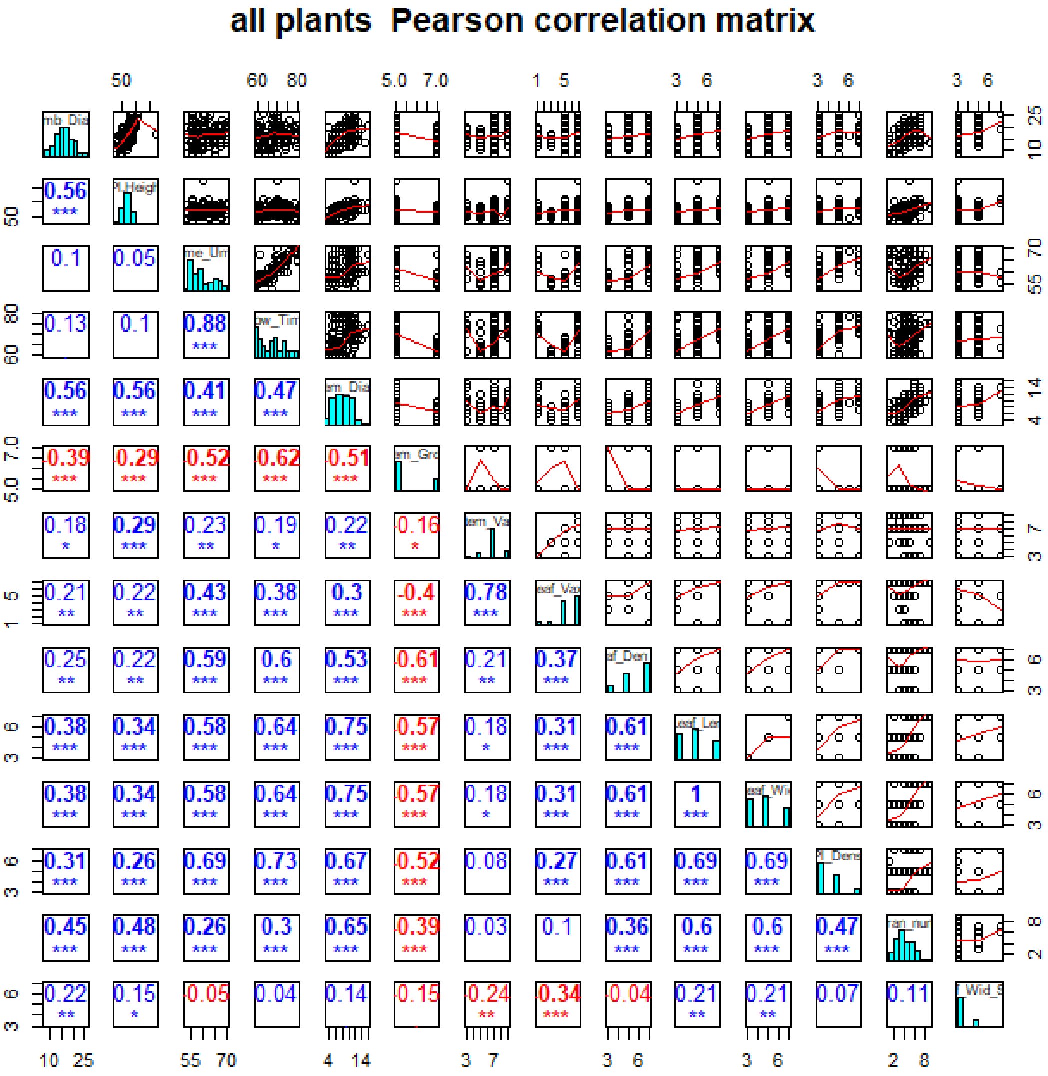

Figure 2. Pearson correlation matrix showing the relationship among dill characters

Differences among accessions

The different accessions varied in several important characteristics: such as plant height, umbel diameter, stem diameter and time to flowering (*P*<0.001 for all, Table 4). The earliest flowering accessions were ‘Dura’ (NGB11686) and ‘Como’ (NGB20379),flowering 60 days after seeding.‘Goda’ (NGB11687), ‘Blanco’ (NGB12012), ‘Hadi’ (NGB13962), Mammut (NGB20376), and Herculus (NGB20380) were the latest and needed 72 to 75 days from seeding to flowering. Plant height varied among the accessions, from an average of 55 cm in the naturalized population (NGB20234) to 84 cm in the cultivar ‘Hadi’ (NGB13962).

Table 4. Mean value with standard deviation of the numeric descriptors in dill accessions.

Genotype	Time from seeding to umbel fully developed (days)	Time from seeding tofull flowering (days)	Plant heigt (cm)	Umbel Diameter (cm)	Stem diameter (mm)
Dura (NGB11686)	56 ± 1	60 ± 2	68 ± 9	15 ± 2	8 ± 1
Goda (NGB11687)	67 ± 3	75 ± 3	79 ± 13	18 ± 3	12 ± 2
Blanco (NGB12012)	63 ± 3	73 ± 3	68 ± 15	17 ± 3	10 ± 3
Dukat (NGB12166)	62 ± 4	70 ± 5	71 ± 18	17 ± 5	10 ±3
Pikant (NGB13156)	58 ± 3	63 ± 3	62 ± 13	13 ± 2	6 ± 1
Superdukat (NGB13157)	63 ± 3	71 ± 3	71 ± 11	17 ± 4	10 ± 2
Hadi (NGB13962)	63 ± 3	73 ± 5	84 ± 27	19 ± 3	10 ± 2
Arlöv (NGB20234)	56 ± 1	61 ± 1	55 ± 9	15 ± 2	5 ± 1
Mammut (NGB20376)	64 ± 4	73 ± 5	69 ± 14	19 ± 4	9 ± 3
Bouquet (NGB20377)	58 ± 1	63 ± 2	75 ± 11	17 ± 3	7 ± 1
Gold Crown (NGB20378)	63 ± 4	71 ± 6	76 ± 10	17 ± 4	9 ± 3
Como (NGB20379)	56 ± 1	60 ± 1	77 ± 8	17 ± 2	7 ± 1
Hercules (NGB20380)	63 ± 2	72 ± 2	72 ± 14	17 ± 3	11 ± 1
Johnsons (NGB20381)	58 ± 1	62 ± 2	57 ± 9	13 ± 4	6 ± 1
Alm. Como (NGB531)	56 ± 1	64 ± 3	80 ± 16	19 ± 4	8 ± 2
P level (ANOVA)	*P*<0.001	*P*<0.001	*P*<0.001	*P*<0.001	*P*<0.001

As expected, some clustering of accessions was detected (Figure 3). The heatmap graphicscontain two dendrograms; one for accessions and one for descriptors, shown on either side of the graph. The plotted grinds illustrate the extent of dissimilarity between each combination. Identical colour indicates the same response. In dill, the distinct clusters were detected, one containing eight accessions (NGB20378, NGB12166, NGB20380 NGB20376 NGB13157, NGB13962, NGB11687 and NGB12012) and the other seven accessions (NGB20234, NGB20381, NGB13156, NGB20377, NGB20379, NGB11686, and NGB531). The different descriptors also fell into two main clusters. The tree descriptors; stem waxiness, leaf waxiness and stem green colour clustered together. In a second, and a large cluster, the rest of the descriptors were present. For example, time from planting to flowering and time from planting to the umbels development clustered very close as did leaf length and leaf width.

Temperature effects on morphology and essential oil composition

On average (across accessions), dill plants grown in greenhouse were 17 cm taller than plants grown in field (*P*<0.001) and the plants were lodging more easily than field plants. Greenhouse temperature was 4-6º C higher than outdoors with the highest differences on sunny days. The result correspond well to Fraszczak (2012) that has shown stem elongation in dill grown at 25°C compared to 20°C.

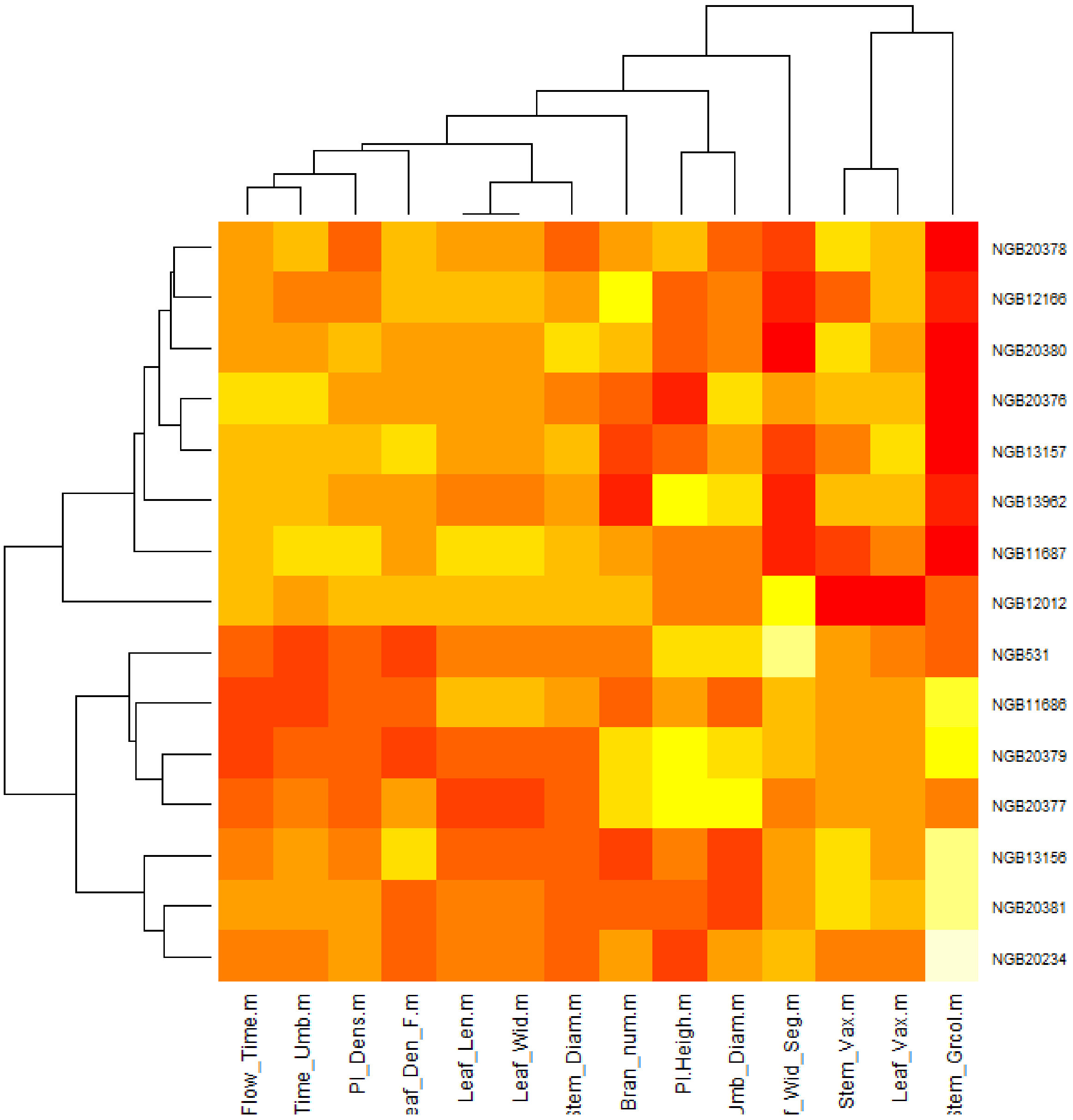

Figure 3. Two-way cluster diagrams (heatmap) of dill accessions and descriptors (see text for explanation).

In our study, twenty-sixessential oil compounds were detected in the dill seeds. The PCA bi-plotdemonstrated overall differences between field and greenhouse plants along the first principal component (Figure 4). Growing location was more important than genotype in explaining the variation. The two first principal components represented 47% and 19% of the total variation, respectively. The different variables are marked as red arrows, numbered fromup to30 in the bi-plot.Variable number 1 to 4 are plant height, time to flowering, leaf density of feathering and leaf width of segments, respectively, and the chemical compounds are numbered from 4 to 30. Chemical compound 13, 29, 6 and 11 were detected in levels of 30%, 23%, 10% and 6% of the total peak area, respectively. The other chemical compounds had lower or much lower content (minor compounds). Literature shows that limonene and carvone are the two most important major compounds of dill seed essential oil (e.g. Bailer et al., 2001). Singh et al. (2005) identified 35 compounds, where carvone (55.2%), limonene (16.8%), dill-apiole (14.4%), linalool (3.7%), trans-dihydrocarvone (2.8%), and cis-dihydrocarvone (2.6%) were the six compounds with the highest concentrations. The compounds in our study could not be identified due to lack of standards included but clearly demonstrated an influence of growing location.From related crops like caraway, growing locations is known to be of importance for essential oil composition(Valkovszki and Nemeth-Zambori, 2011; Solberg et al., 2017). Differences among genotypes have also been reported(Bailer et al., 2001; Said Al-Ahl and Omer, 2016; Galambosi and Peura, 1996; Msaada et al., 2009). We could see that some compounds were more influenced than others by the greenhouse versus field cultivation. Further studies are needed to clarify such patterns.

Concluding remarks

The current study showed that important traits such as essential oil composition is affected by enhanced temperature. Furthermore, correlations were detected between traits such as stem diameter and leaf size, umbel size and plant height, showing that plants with thick stems generally were large leafed and were tall. These plants also tended to flower late. Such knowledge is relevant for breeding, although dill is a minor crop and breeding in such crops tend to be neglected (Ochatt and Jain, 2007; Stamp et al., 2012; Solberg and Breian, 2015). The current investigation highlights both gaps and overlaps in the global holdings of dill genetic resources. There was a limited number of accessions with origin outside Europe. Overlaps were especially clear for old commercial cultivars such as ‘Mammut’ and ‘Dukat’. In Europe, a process on duplication reduction has started, identifying most appropriate accessions based on passport data(Engels and Maggioni, 2015). By reducing the number of duplicates, genebanks can rather focus on gaps. Especially interesting would be to have more accessions from Central Asia, as this is part of the region of diversity for dill (Zeven and Zhukovsky, 1975). Another gap was wild relatives, where less than 5% of the accessions (globally only around 60 accessions) were from wild or natural populations of dill and *Anethum* species other than dill were almost absent in genebanks. In general, as demonstrated for other vegetables, crop wild relatives may harbour genes relevant for future breeding programmes (Daunay et al., 2001; Syfert et al., 2016). For example, Indian dill has shown larger umbel size, higher seed yield and different essential oil composition that dill (Malhotra and Vashishtha, 2007). What comes to resistance to biotic and abiotic stresses, very little is known regarding dill wild relatives.

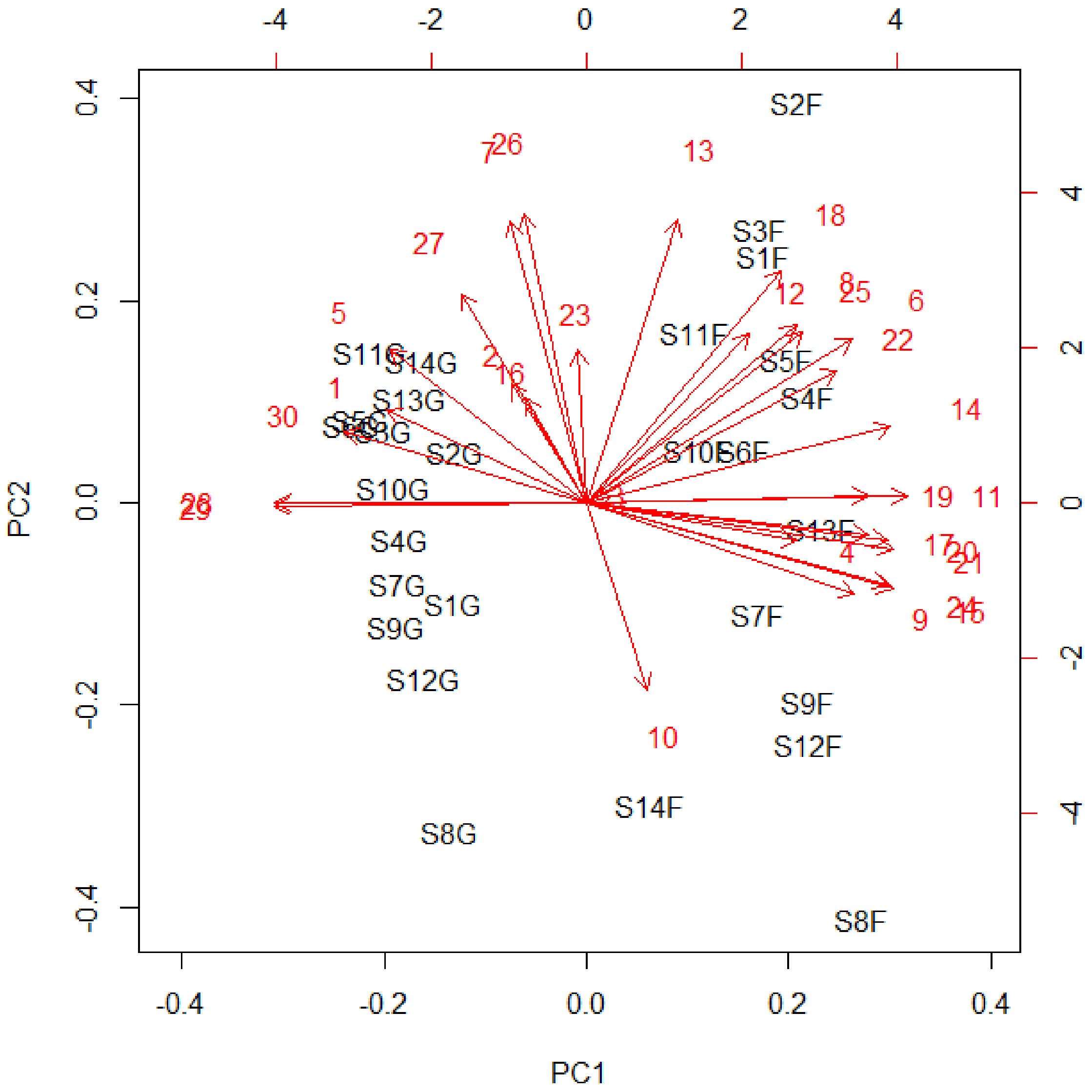

Figure 4: PCA biplot of dill accessions grown in field (S1F to S14F) and greenhouse (S1G to S14G), respectively with respect to morphology and essential oil components. Morphological characters are given as red arrows numbered from 1 to 4 while essential oild components argiven as red arrows numbered 5 to 30).

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