UNIVERSITI PUTRA MALAYSIA

MORPHOLOGICAL, BIOCHEMICAL AND GENETIC DIVERSITY OF CUMIN FROM IRANIAN PROVINCES

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FP 2011 52
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DOCTOR OF PHILOSOPHY
UNIVERSITI PUTRA MALAYSIA
2011
MORPHOLOGICAL, BIOCHEMICAL AND GENETIC DIVERSITY OF CUMIN FROM IRANIAN PROVINCES

By

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Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Doctor of Philosophy

November 2011
MORPHOLOGICAL, BIOCHEMICAL AND GENETIC DIVERSITY OF CUMIN FROM IRANIAN PROVINCES

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November 2011

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In order to assess the genetic diversity of cumin and determine the traits effective on seed yield and cumin-aldehyde production, forty nine cumin ecotypes which are sub-populations belonged to nine populations from different provinces of Iran were evaluated based on morphological and biochemical traits. Results indicated a significant variation for all the measured traits among and within populations derived from different provinces. Kerman and Esfahan populations showed the best performance based on the phenotypic data, while Yazd had almost the lowest levels of traits. Correlation analysis showed number of seed per umbel and umbel per plant had highest relationship with seed yield. Path analysis also demonstrated that number of umbel per plant and number of seed per umbel had the most direct effects on seed yield and were identified as the most effective factors on seed yield. Cumin aldehyde was mostly correlated by number of umbel per plant. The present study showed that different qualitative characteristics such as seeds with light color and without trichome and leaves without trichome, alternate and large pods of petiole tend to produce high seed yield. Pattern analysis of different populations based on first two main principal components categorized the measured genotypes in to three groups:
Pars, Northern_Khorasan, Golestan, Semnan and Yazd (Group1), Southern_Khorasan and Khorasan_Razavi (Group2) Kerman and Esfahan (Group3), where the third group are high yielding genotypes with different genetic background can be advised for cultivation and used in breeding programs. So the available genetic diversity among the Iranian cumin populations can be utilized to produce high yielding population of cumin.

Moreover the phenotypic diversity as well as molecular variability among the populations, a significant variation was seen within the populations. It proves that during the years so many variations due to sampling and also cross pollination as well as crossing over produce different ecotypes within each population some of the populations such as Kerman have shown more variability within the population. It can be due to higher evolution speed as compared to other populations. Therefore, there is a high potential for cumin breeding in Iran and introducing these ecotypes to other countries.

Cumin ecotypes showed different variation for the measured traits, the highest variation belonged to cumin-aldehyde. As these view Kerman and Esfahan populations had the best performance on cumin-aldehyde. Correlation analysis showed number of seed per umbel and umbel per plant had highest relationship with seed yield. Path analysis also demonstrated that number of umbel per plant and number of seed per umbel had the most direct effects on seed yield and were identified as the most effective factors on seed yield. Cumin aldehyde was mostly correlated by number of umbel per plant. The present study showed that different qualitative characteristics such as seeds with light color and without trichome and leaves without trichome, alternate and large pods of petiole tend to produce high seed yield. Evaluation of molecular variance using three joint molecular markers and phylogenetic relationship of ecotypes was done for the first time. Within population
variance showed the highest proportion of variation, the ecotypes in each population were different. AFLP markers showed more polymorphism than the other markers (RAPD and SSR). The highest PIC value belonged to E+AGT (0.66). Since this crop is cross pollinated and SSR is a codominant marker and AFLP has higher efficiency for assessing the polymorphism, using of SSR as well as AFLP can increase the impact of genetic survey. If genetic diversity is done based on a good coverage of AFLP & SSR markers in genome then the extreme genotypes based on distance can be chosen for hybrid production. Totally, based on all molecular markers clustering showed Yazd population has the biggest distance from the other populations, also Kerman and Khorasan populations which might have some ancestor had almost the close distance. Cluster of 49 cumin ecotypes, showed Zarand has arranged almost separately, it means that it may have different background than the others. The measured ecotypes were divided almost into five groups based on joint markers and comparison of phenotypic and molecular cluster therefore it can be confirmed that there is a good relation between the phenotypic and molecular clusters.
Abstrak tesis yang dikemukakan kepada senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

MORFOLOGI, BIOKIMIA DAN KEPELBAGAIAN GENETIK JINTAN DARI WILAYAH IRAN

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populasi yang berbeza berdasarkan dua komponen utama mengkategorikan genotip diukur kepada tiga kumpulan: Pars, Northern_Khorasan, Golestan, Semnan dan Yazd (kumpulan1), Southern_Khorasan dan Khorasan_Razavi (kumpulan2) Kerman dan Esfahan (kumpulan3), dimana kumpulan ketiga adalah terdiri dari genotip yang mempunyai hasil yang tinggi dengan latar belakang genetik yang berbeza dan boleh disarankan untuk program penanaman dan pembiakbakaan. Jadi kepelbagaian genetik yang ada di antara populasi jintan di Iran dapat digunakan untuk menghasilkan populasi jintan yang unggul.

Selain itu kepelbagaian fenotipik serta variabiliti molekul antara populasi, perbezaan ketara dapat dilihat di dalam populasi. Hal ini menunjukkan bahawa selama bertahun-tahun variasi kerana sampling dan juga pendebugan kacuk serta persilangan ecotypes yang berbeza di dalam setiap populasi, sebahagian populasi seperti Kerman telah menunjukkan lebih variabiliti dalam populasi. Hal ini mungkin terjadi kerana kecepatan evolusi yang dibandingkan dengan populasi lain. Oleh kerana itu, ada potensi tinggi untuk pembiakbaikan jintan di Iran dan memperkenalkan germplasma ini ke negara lain.

ACKNOWLEDGEMENTS

Praise to Almighty Allah the most Benevolent, Merciful and Compassionate, for giving me the utmost strength, patience and guidance to have this work completed. I would like to express my most sincere gratitude and deepest appreciation to the chairman of my supervisory committee, Assoc. Prof. Dr. Mihdzar Bin Abdul Khadir, Department of Agriculture Technology, Faculty of Agriculture, UPM for his invaluable contribution, inputs and careful supervision. Without his constant encouragement this thesis would have never been written.

I am indebted to member of my supervisory committee, Associate Professor Dr. Mohd Rafii Bin Yusop, Department of Crop Science, Faculty of Agriculture, UPM, and Assistant Professor Dr. Ghasem Mohammadi-Nejad Central of Horticulture research of Kerman University, Iran for their encouragement, constructive suggestion and guidance.

Furthermore, I would like to acknowledgment ABRI Central cooperation programmers for Support for the research. I would also like to extent my heartfelt appreciation to my friend who was to help during field experiment, Mr. Alagi Bah, Ph.D student of Agronomy, Faculty of Agriculture.

Words are not enough to express my heartfelt feeling my wife Mahrokh, my son Amir Mehrshad, My father and my mother for their constant support and concern and motivation thought the study period.
I certify that an Examination Committee has met on …………. To conduct the final examination of Ali Reza Bahraminejad on his Doctor of Philosophy thesis entitled “GENETIC DIVERSITY OF CUMIN IN IRAN AS DETERMINED BY MOLECULAR, BIOCHEMICAL AND MORPHOLOGICAL MARKERS” accordance with University Pertanian Malaysia (High Degree) Act 1980 and University Pertanian Malaysia (High Degree) Regulation 1981. The Committee recommends that the candidates be awarded the relevant degree. Members of the Examination Committee are as follows:

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DECLARATION

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously, and is not concurrently, submitted for any other degree at Universiti Putra Malaysia or any other institution.

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ALIREZA BAHRAMINEJAD

Date: 16th November 2011
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