

**STUDIES ON THE COMMON SMUT DISEASE OF CORN**

**A Thesis**

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**By**

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## VI. SUMMARY

Investigation was conducted at the Plant Pathology Laboratories of Plant Pathology Department, Faculty of Agriculture (El-Shattby), Alexandria University and at the Plant Pathology Department, Faculty of Agriculture, Damanshour University during successive seasons of 2006 until 2009.

### Results of the present investigation revealed that:

1. A total of 75 diseased samples of maize plants showing common smut disease symptom were collected from different corn cultivars in three localities in El-Beheira governorate (Abou Elmatamer, Haush Essa and Etai Elbaroud) during the summer seasons of 2007 and 2008. Many isolates of *U. maydis* the causal of common smut is recovered from this diseased samples.
2. No differences were found between isolates of *U. maydis* according to teliospores and basidiospores morphology under light microscope.
3. Results showed that there were great variations between the different culture phenotypes of *U. maydis*. Twenty three culture phenotypes were recognized. Seventeen phenotypes (No. 3, 52, 94, 96, 98, 104, 105, 115, 120, 123, 124, 128, 131, 133, 137, 138 and 139) were similar to phenotypes identified in previous study by Abou Elseoud (1999). However the other sex phenotypes were different than 151 phenotypes mentioned in Abou Elseoud's manual, they were giving the numbers 152, 153, 154, 156 and 157.
4. Variations were observed between the phenotypes concerning nature of culture, growth rate, colour, edge type, margin shape, surface texture, zonation, center modifications, culture elevation and culture center size, culture center colour, culture elevations.
5. Data of Phenotypes Distribution and Frequency of *U. maydis* in the surveyed area of El-Beheira governorate showed that the highest frequency of *U. maydis* phenotypes at all tested localities were phenotypes, No 152, 94, 115, 120, 153, 154, 157, 128 and 156. So

that, these phenotypes were chosen to be tested in the next experiments.

6. Data also indicate that the phenotypes No. 115, 94 and 152 were isolated from the three localities. While phenotypes 128 and 153 were isolated from two localities (Etai Elbaroud and Housh Essa for phenotypes No. 128 and Etai Elbaroud and Abou Elmatamer for phenotypes No. 153). On the other hand, there were 18 phenotypes; each was isolated once from one locality.
7. The virulence of 9 *U. maydis* phenotypes on maize cv. Balady were studied. Data showed that the highest infection percentage 38.5 % was obtained by phenotype No. 153 followed by phenotype No. 157 (23.1%), and phenotype No. 154 (18.0%). Meantime, the other six phenotypes (No. 94, 115, 120, 152, 128 and 156) were not pathogenic and failed to produce disease symptoms in the corn cv. Balady. In case of mixed cultures (mixing inoculum of the nine Phenotypes together) the infection percentage was the highest and reached 97.4%.
8. The compatibility between *U. maydis* phenotypes were also studied under greenhouse condition. In case of the combinations between the two pathogenic phenotypes (No. 157, 154 and 153), the infection percentage was increased in combination between phenotype No. 157 and 153 and reached to 92% .while, in combination between phenotype 157 and phenotype No. 154 increased to 79.5%. On the other hand, the combination between phenotype No. 153 and phenotype No. 154 caused 38.5 % infection percentage similar to phenotype No. 153 alone.
9. An increase in infection percentage was found in combination between between the pathogenic phenotypess (No. 157, 154 and 153) and the non-pathogenic phenotypes (No. 94, 115, 120, 152, 128 and 156) compared to the infection percentage caused by pathogenic phenotypes alone.
10. In case of the combinations between the non-pathogenic phenotype 94, with non-pathogenic phenotypes No. 115 and 156 were compatible and produced diseased symptoms on maize cv. Balady with infection percentages (43.6 and 20.5%, respectively). On the other hand non-pathogenic phenotype No. 152 and 115 were compatible and gave 23.1% infection percentage. In this respect, the

non-pathogenic phenotypes No. 128 and 156 were compatible and gave 25.6% infection percentage. In contrast, all other combinations between non-pathogenic phenotypes were not compatible and failed to produce disease symptoms on maize cv. Balady.

11. RAPD technique was used to investigate the variations between the nine phenotypes of *U. maydis*. Results indicated that 315 DNA fragment (bands) were produced by seven positive primers. The number of amplified products produced by each primer varied from 33 with primer I to 56 with primer BAR.
12. Cluster analysis of RAPD revealed that phylogeny tree divided the tested 9 phenotypes of *U. maydis* into two clusters. The first cluster divided into 5 subclusters included 8 phenotypes of *U. maydis*, while the second cluster included only phenotype 128. Pathogenic phenotypes 157 and 153 were present in very close to each other in subclusters and the non-pathogenic phenotypes (152, 156 and 115) were present in the same subcluster.
13. The susceptibility of 6 maize cultivars to *U. maydis* was studied under greenhouse condition. The obtained results showed that all tested cultivars were susceptible to *U. maydis*. The lowest infection percentage 12.83% was recorded on the white cultivar S.C.122, followed by white cultivar S.C.10 (28.17%). On the other hand, the highest infection percentages 64.07% was recorded with the white cultivar T.W.C.310 and 51.23% with T.W.C.314. The tested two yellow cultivar S.C.155 and T.W.C.352 were also susceptible.
14. Effect of Three chemical fungicides in controlling the three pathogenic phenotypes 153, 154 and 157 of *U. maydis in vitro* was investigated. Data showed that Vitavax was effective than Somi-eight and Premis at all the tested concentrations in inhibiting growth of *U. maydis*, except for phenotype No. 157, Somi-eight was very effective on all tested concentrations in inhibiting growth of this fungus compared with the other two fungicides (Vitavax, Premis).
15. Results also showed that Vitavax had an inhibitory effect on phenotypes 153 and 154 *U. maydis* at all tested concentrations. On the other hand, Vitavax had no effect on the phenotype 157 at low concentrations (0.01 and 1 ppm). While, it had 100% colonies inhibition at concentration of 5 ppm on phenotypes 153 and 154 of *U. maydis*. In case of phenotype 157, the colonies inhibition at concentration of 5 ppm was 9.77% only. In this respect, Somi-eight

**gave the maximum inhibitory effect (80.33%) on phenotypes No. 157 at the concentrate 400 ppm.**