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MOLECULAR VARIABILITY OF ZUCCHINI YELLOW MOSAIC VIRUS (ZYMV) ISOLATES FROM TURKEY

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BACKGROUND and OBJECTIVES

Cucurbits are widely grown in different provinces of Turkey. However their production is restricted by plant viruses. ZYMV is one of the most economically important viruses of cucurbit crops worldwide, including in Turkey. Several strains have been defined based on their biological, serological and molecular variability – particularly in the coat protein (CP) coding region (Lecoq & Desbiez, 2012). One molecular cluster (A1) appears highly prevalent worldwide, but other clusters (A4, A5) have been observed recently in several European and Mediterranean countries, probably in relation to recent introductions (Lecoq & Desbiez, 2012). However the situation in Turkey remains unknown. The aim of this research was thus to characterize the molecular variability of ZYMV in Turkey and look for the presence of emerging strains.

MATERIAL and METHODS

During the years 2010-2012, 230 cucurbits samples were collected from different provinces of Turkey and tested by ELISA for the presence of ZYMV. 22 ZYMV-positive isolates from Adana, Antalya, Muğla, Antakya and Anamur in 1994 were also included in the analysis. After RNA extraction and RT-PCR, the partial CP sequences of ZYMV isolates from Ankara, Antalya, Konya and Karaman provinces of Turkey were obtained and compared to the worldwide diversity of the virus using MEGA6 software.

RESULTS

According to ELISA results, 37% of the samples were infected with ZYMV. Full CP sequences were obtained for 43 isolates collected from different provinces of Turkey in 2010-2012. The CP coding regions of Turkish ZYMV were 837 nt long and encoded 279 amino acids (aa). Forty isolates of different region were classified in the subgroup A1 and these isolates showed 99 % sequence identity with Fars, Iraq and Germany isolates. Three isolates collected from Antalya region in 2011 were classified in subgroup A4 and showed 99 % sequence identity isolates from the same subgroup that have emerged recently in France. Based on partial CP sequences, the 22 isolates from 1994 belonged to subgroup A1.

CONCLUSIONS

The CP coding region is the most frequently used for studies of genetic diversity in Potyviruses. In this study, sequence analysis of ZYMV isolates of Turkey showed that most isolates belonged to a major molecular group (A1), the most widespread worldwide. However three isolates from Antalya region belonged to a different molecular group (A4) that has been observed in several countries including China and Poland and seems to be now emerging in south-eastern France. Further surveys are required to determine if group A4 is now emerging in Turkey.

REFERENCES

Lecoq, H. and Desbiez, C. (2012) Viruses of cucurbit crops in the mediterranean region: an ever-changing picture. *Advances in Virus Research*, 84, 67-126.

Building bridges between disciplines for sustainable management of plant virus diseases



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