

Effect of subculture number on pineapple *in vitro* multiplication and somaclonal variation

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ABSTRACT

This research was conducted to study the effect of subculture number on multiplication rate, and occurrence of somaclonal variation in pineapple plants (Ananas comosus). Repeating subcultures decreased the multiplication rate in subcultures 1 and 2 (20 times and 9 times, respectively) as it was 6 times in all next subcultures. Repeating subcultures over 5 subcultures decreased the normal plant percentage, it was 95%, 85%, 25% and 8% for subcultures 6, 7, 8 and 9, respectively, and also decreased surviving percentage to reach 85%, 62%, 43% and 21% for subcultures 6, 7, 8 and 9, respectively. SDS protein analysis dendrogram showed two subgroups, where first subgroup included subcultures 2, 3, 4 and 5 subcultures and the second subgroup included subcultures 6, 7, 8 and 9. This subgroup contained a category of subcultures 8 and 9 which were closely related together, whereas subculture 7 was further than this irrelativeness. Subculture 6 resulted in the highest number of shoots with best uniformity (95%) and surviving rate (85%).

Key words: Pineapple, Somaclonal variation, Subcultures, Multiplication.

INTRODUCTION

Micropropagation is necessary to preserve genetic uniformity of the plant material. Shoots multiplied clonally are a source of plantlets of a known genotype for breeding purposes and for economic culture. Clonal multiplication of a novel material regenerated from breeding procedures is also desirable to be uniformly and rapidly produce clonal plants for variety release. There are several published media for micropropagation of pineapple by Kiss *et al.* (1995); Escalona *et al.* (1999); Firoozabady and Gutterson (2003) and Be and Debergh (2006).

Somaclonal variation occurs in micropropagated plants, which could be

distinguished morphologically. Chen *et al.* (1998) evaluated 1360 flowering somaclones (produced plants) of *Phalaenopsis* (True Lady "B79-19") derived from tissue culture; no apparent difference was found in the shape of the leaves, whereas flowers in some somaclones were deformed. They also used 38 selected random primers to generate amplified segments of genomic DNA and to estimate polymorphism of somaclonal variations in *Phalaenopsis*. The random amplified polymorphic DNA (RAPD) data indicated that normal and variant somaclones were not genetically identical. Banding patterns of aspartate aminotransferase (AAT) showed that three distinct banding patterns were found in normal somaclones and only two-banded phenotypes were detected in variant