

EFFECT OF STAINING METHOD ON THE EFFICIENCY OF PROTEIN ELECTROPHORESIS IN QUANTIFYING RESISTANCE OF FLAX TO POWDERY MILDEW DISEASE

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ABSTRACT

Seed proteins of ten flax genotypes, having different levels of susceptibility to powdery mildew (PM), were separated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Gels were stained with Coomassie Brilliant Blue R-250 (CBB) or silver nitrate (SN). Data for PM severity and amounts of protein fractions were entered into a computerized stepwise multiple regression. Using the predictors supplied by stepwise regression, a two-factor model was constructed to predict PM severity when the gel was stained with CBB. This model showed that PM severity differences were due largely to the protein fractions no_s. 24 and 3, which accounted for 76.18% of the total variation in severity ratings. On staining the gel with SN, a five-factor model was constructed. This model showed that PM severity differences were due to largely to the protein fractions no_s. 36, 22, 32, 2, and 21, which accounted for 96.03% of the total variation in PM severity. These results indicate that the SN regression model was superior, compared with that of CBB, in predicting PM severity from banding patterns. This superiority was attributed to the higher R^2 value of the model. Therefore, SDS-PAGE of proteins and staining with SN may provide a supplementary assay to field trials to distinguish between PM resistant or susceptible genotypes quantitatively.