

Preparation of Protein Extraction from *Metroxylon sagu* Rottb. for Two-Dimensional Electrophoresis Analysis



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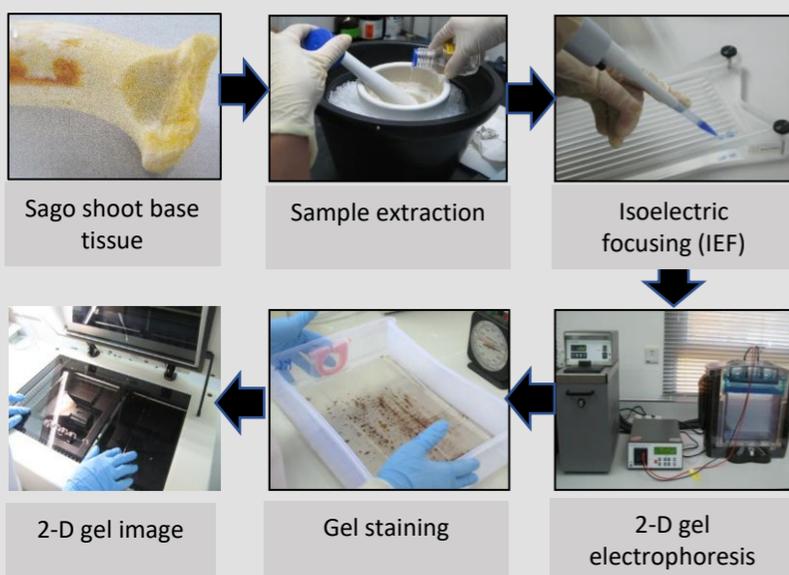


Metroxylon sagu Rottb.

3. PROBLEM STATEMENT

Two-dimensional gel electrophoresis (2-DE) is still a powerful approach to analyze protein differences between samples visually. The technique, nevertheless, demands a suitable sample preparation to produce reliable results. Sago contains compounds that would interfere with the 2-DE analysis. Among protein preparation methods, the phenol extraction/ammonium acetate precipitation method has been reported to produce satisfactory 2-DE gels from other recalcitrant plant tissues.

4. MATERIALS AND METHODS



1. INTRODUCTION

Sago palm (*Metroxylon sagu* Rottb.) is a potential commodity for the starch industry and a global food security solution. We have two varieties with different agronomic traits. MOL-03 is a high-yielding variety with a long maturity period, while KAR-01 is a low-yielding variety with a short maturity period. Molecular studies can be used to understand their genetic differences. The information gained would be beneficial for the development of fast-yielding sago palms.

2. OBJECTIVES

To evaluate the suitability of phenol extraction/ammonium acetate precipitation method for preparing protein from sago palm soft shoot base tissue for 2-DE analysis

5. RESULTS

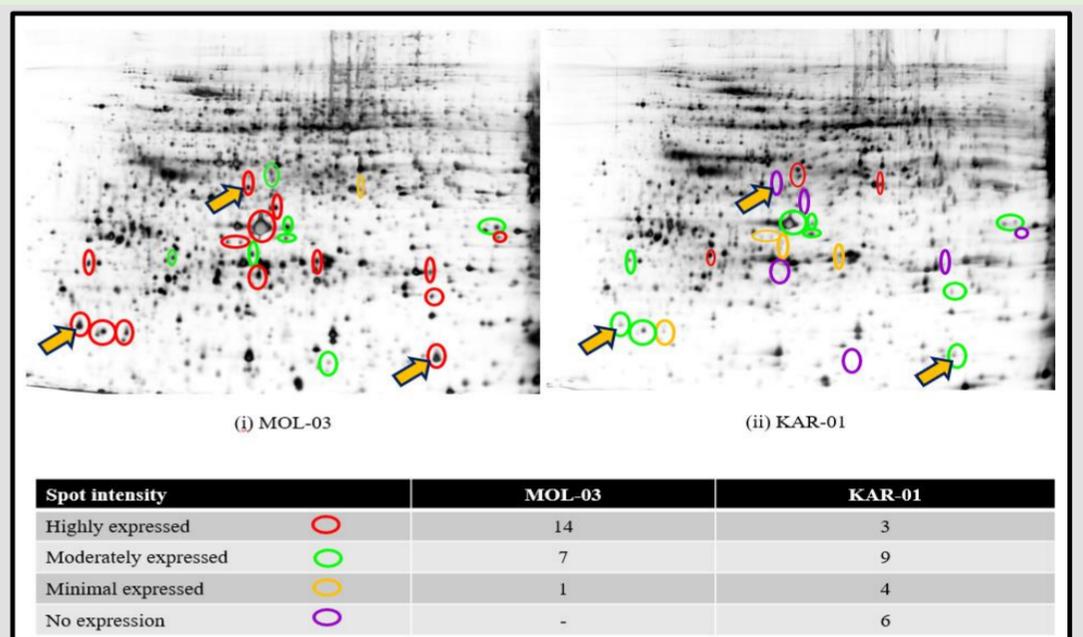


Fig. 1. Comparison of 2-DE representative gels, with protein spots visualization obtained from two different *Metroxylon sagu* using Silver staining.

6. DISCUSSION

Protein extraction

Protein extraction was performed using the phenol/ ammonium acetate precipitation method described by Awang *et al.*, (2010) and subsequently separated by 2-DE in the linear 4 to 7 pH range.

Protein spots visualization

Well-resolved 2-DE images with sharp protein spots and clear gel background was obtained. Protein spots with different expression intensity in both varieties could be observed clearly.

7. CONCLUSION

The phenol extraction/ ammonium acetate precipitation method produces good 2-DE gel images. The method can be used for further proteomic analysis.

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