2 d-electrophoresis separation of the wheat leaf proteome - lab report example

Science, Biology

2 D-Electrophoresis Separation of the Wheat Leaf Proteome

The paper " 2 D-Electrophoresis Separation of the Wheat Leaf Proteome" is a perfect example of a lab report on biology. In the experiment, the aim was to carry out a 2 D-electrophoresis separation of the wheat leaf proteome. There are two gels produced in the experiment, in figure 1 the gel was ideal as it is evident by the spots that represent the proteins. In figure 2, the gel was not produced as expected; it was black with no spots. This means the gel was bad and it is recommended that the experiment be run again. Discussion By definition, the proteome is the entire protein complement that includes the modifications made to a given set of proteins by a cellular system or an organism (Ferry et al. 2002). Basing on the results of figure 1(2 D ideal gel), it is observed that the proteins were separated as expected; this implies that all the conditions were carefully maintained and the laboratory procedures were also followed accordingly. The dots indicate that the proteins were separated and their kDa could be identified from the left side using a ladder or the marker. In this case, the protein of interest could be identified, and then cut out from the strip so that it could be measured by spectrophotometer. At this point, the OD is then determined which could be extrapolated on the standard curve to get the concentration of this protein of interest. The concentration could be got by using the equation of the standard curve, hence calculating X value. The dark staining in this ideal gel could be due to incomplete solubilization of the sample before application. In figure 2, it is observed that there were no dots in the gel (no proteins on the gel) indicating that the experiment may have not been carried out accordingly. This could be due to the conditions of the protocol were not

adhered to. It is known that the same sample used to produce results as shown in figure 1 was the one used to produce the results in figure 2. In this regard, the black gel could be due to the samples did not completely solubilize before application. In this case, it is necessary to ensure that the samples are stable and completely solubilized. Repeated precipitation-resolubilization cycles result in horizontal streaking. The samples could be poorly soluble in the rehydration solution: In this case, the concentration of the solubilizing component should be increased. Also, increase the IPG buffer concentration. In order to produce expected results, it is recommended to trouble shout and identify why the results came out as what was not expected then follow the right procedure to generate the expected results

Proteomics is known to be a large scale study of protein functions and characteristics. The aim of proteomics research involves obtaining an integrated view of an abnormal and normal organism or cellular processes at their constituent proteins level, for instance, on the basis of post-translational modifications, protein-protein interactions, protein abundance as well as their regulatory networks (Ferry et al. 2002). Proteomics is classified into 2 major subgroups: Protein profiling that includes identification of specific markers and targets as well as functional proteomics that include the structure definition, function, and interactions. 2-D PAGE is mostly suitable for studies related to protein profiling. It is also suitable to target or functional proteomic research, where the modification or expression of the given proteins is followed in the course of the alteration in growth conditions or systematic treatment regimens (Ferry et al. 2002)

Protein profiling such as the one carried out in the lab entails 2-D gels

comparison in order to understand different biological processes through the determination of the absence or presence, modification states and down or up-regulation of proteins. In this case, Profiling hence acts as a technique of '' discovering putatively causal correlations'' between modification states or protein abundance and biological processes that are of interest. The aim of functional proteomics is to test predictions that are specified through detailed proteins structures analysis, cellular locations, roles as well as interactions with other proteins. In this experiment, the aim was to determine if the wheat plant was resistant to the aphids through protein profiling. In this case, 2D electrophoresis was employed.