Biology case study

Business

In other Norms, we can get some partial or complete amino sequences of the targeting routines or information about likeness. Second, in order to further confirm the information about characteristics and function of the targeting protein that we have obtained from the bioinformatics database, we can actually introduce the virus into the cell, comparing it with a non- infected cell. SD-PAGE or 2-dimensional electrophoresis can be used to detect the differences between the two: targeting proteins will exist in the non-infected cell but Nil not exist in the infected cell.

Two-dimensional gel electrophoresis will separate proteins on the basis of charge and mass. Finally, we can obtain the pure targeting protein, and final step is to identify the amino sequence of the protein in order to determine its type and name. Since many proteins in vital cell survival has been identified and listed in the web database, all Nee need is to identify the amino sequence of the protein, and match this sequence in the database. We can also reconfirm the finding by using immunoassay in order to confirm whether the protein is actually degraded by the virus.

Step 2: How will you identify the ubiquity aliases responsible for visualization of he Metal” protein? (3 pets.) Ubiquity aliases combine with an ubiquity-containing E Pub-carrier protein, and targets specific protein substrates for degradation.

Its important function is to determine specificity. Therefore, if it were not to function correctly, the targeting protein would not be degraded. In order to determine which ubiquity aliases is responsible for the obfuscation of the

protein, we can obstacle the function of each type of ubiquity aliases in different cells.

Since we have already known the amino sequence of the protein in previous tepee, we can narrow down the targeting ubiquity aliases based on existing research data such as papers, INCUBI data. There are many types of ubiquity aliases in cells.

However, we can make some candidate groups of targeting E based on the bioinformatics database. Nee will use antibodies which specifically bind to each type of ubiquity aliases and impede its function. For example, the antibodies may covalently bind to the targeting ubiquity aliases, and therefore, impede its function. Then, we will measure the amount of targeting protein.

If we find that the amount of targeting protein is not Changed in a cell, we can identify the target ubiquity aliases. This is because only Nee the function of the target ubiquity aliases is impeded, the degradation of the targeting protein will not be occurred.

Step 3: What protein will be your drug target? What property of that protein will you target? Design an assay/approach to identify an antidote for “ degree”. (4 pets.) Since “ degree” targets a vital cellular protein for ubiquity-dependent degradation, if Nee block its process of degradation, we can effectively turn off its effect.

As mentioned earlier, ubiquity aliases brings specificity. Since we have already known Inch ubiquity aliases is responsible for degrading the targeting protein, a drug that targets the aliases will be a good antidote.

Will target the ubiquity aliases which brings specificity for reducing side effects of the antidote. In order to design the antidote: First, it should specifically bind to the target aliases. Protein structure and binding domain of the target aliases will be carefully determined to design the antidote. Second, the antidote effectively impedes the essential function of the aliases.