**Core proteins in exocytosis and endocytosis**

Investigator Names

Secretory is a very important cell function, especially for the secretory cells, such as chromaffin cell and goblet cells. Besides, secretory pathway plays a very important role in the neuron signal transport. There are also many diseases related to dysfunction in secretory pathway. Overall, Secretory is very important for cell, organism and human body. However, there are many unsolved questions in the secretory pathway regulation, especially the regulation between exocytosis and endocytosis. Exocytosis is a process in which an intracellular vesicle moves to the plasma membrane and subsequent fusion of the vesicular membrane and plasma membrane ensues. Endocytosis is an energy-using process by which cells absorb molecules by engulfing them. Endocytosis is used by all cells of the body because most substances important to them are large polar molecules that cannot pass through the hydrophobic plasma or cell membrane. Per the definition of exocytosis and endocytosis, we can say endocytosis is the opposite process of exocytosis. There are many cross talks between exocytosis and endocytosis. First, exocytosis and endocytosis share many proteins and molecules during their regulation pathways. Second, both exocytosis and endocytosis are involved in secretory pathway, their main function is transport, these two process transport many same or associated molecules. Third, many organelles are involved in both exocytosis and endocytosis, such as ER, Golgi, endosome and lysosome. However, the regulation between exocytosis and endocytosis is very complicated. There are more than 200 different proteins in the regulation of exocytosis pathway. Therefore, we want to find the core proteins in exocytosis and endocytosis, trying to give a better understand of regulation between exocytosis and endocytosis.

**We aim to find the core proteins in the exocytosis and endocytosis.** We will search all the proteins involved in exocytosis and endocytosis pathway in KKEG website and search every protein’s interaction from protein-protein interaction website, then build up the protein-protein interaction database in exocytosis and endocytosis. First, we will utilize the rich-club coefficient to determine if our network has a “rich-core”. Second, we will use multiple methods to determine the core proteins. Besides, we will build up the spatial connection among these core proteins to achieve a complete picture of core proteins in the exocytosis and endocytosis.

Exocytosis and endocytosis are responsible for the regulation of synapse function, which is the main fundamental basics for the neuron signal transport in body. However, many questions remain unsolved in the regulation between exocytosis and endocytosis. There are more than 200 different kinds of proteins in the exocytosis and endocytosis pathway, which make the regulation of exocytosis and endocytosis very complicated. Therefore finding the core proteins in the exocytosis and endocytosis provides us a systematic picture to illustrate the regulation between exocytosis and endocytosis, which will lead us to find the important proteins in the regulation between exocytosis and endocytosis. We will use the rich-club coefficient to determine if our network has a “rich-core”. This method is first time employed for the analyze core proteins in the exocytosis and endocytosis, which will provide us a better understanding of the regulation between exocytosis and endocytosis.

**Significance**

We aim to find the core proteins in the exocytosis and endocytosis from this project. We notes that since the first exocytosis event was found in 1963, more than 50 years has passed. However, there are many questions remain unsolved, especially the regulation between the exocytosis and endocytosis. We try to find the core proteins in the exocytosis and endocytosis, which will provide us a better understanding of the secretory regulation picture.

There are many papers report the important proteins in the regulation in the exocytosis and endocytosis. For example, Protein scaffolds in the coupling of synaptic exocytosis and endocytosis (Stephan J. Sigrist 2011). We can obtain some proteins related to the exocytosis and endocytosis from some literature, but we cannot obtain all the important proteins from the literature. We can obtain most of the proteins related to exocytosis and endocytosis from KKEG website. However, we cannot obtain the core proteins from the website. Therefore, our project will set up the protein-protein interaction related to the exocytosis and endocytosis from KKEG website and systematically analyze the database, trying to find the core proteins in the regulation of the exocytosis and endocytosis.

We will use rich-club coefficient method to determine if our network has a “rich-core”. This method is first time to use in determine the core proteins in exocytosis and endocytosis. Besides, we will use multiple methods to determine the core proteins and set up the spatial relation between these core proteins. All these methods we will use above will provide us a convincing list of the core proteins in the exocytosis and endocytosis. Our project will give a better understanding on the regulation of the exocytosis and endocytosis.

**Innovation**

We read lots of papers related to the analyze method of finding the core proteins in the exocytosis and endocytosis. The paper “Models of core/periphery structures” provide us the new sight of analyzing database. “rich-club” is a powerful method to analyze the core proteins (Harel, N, 2014; Zhou, W.-X, 2008; Caetano, T.S, 2007). However, no paper use the “rich-club” concept to analyze the core proteins in exocytosis and endocytosis. Besides, we will use multiple measurements to find the core proteins and compare these proteins in spatial. We will use a new method to test our results, which is that we use another secretory pathway proteins other than exocytosis and endocytosis to see if there are strong connection between these proteins and the core proteins in the exocytosis and endocytosis. All above, we use very new and meaningful methods to analyze our data.

We are the first one to use rich-club coefficient method to find the core proteins in the exocytosis and endocytosis. We are the first one to try to use multiple methods to analyze the whole exocytosis and endocytosis pathway regulation, from ER, Golgi, Endosome and plasma membrane. We are the first one to search the spatial connection between the core proteins we will find from the exocytosis and endocytosis database.