

## **CHAPTER VI**

### **CONCLUSION**

#### **6.1 Analysis of proteome profile in renal cortex and medulla related with K status in subjects living in northeastern Thailand**

In conclusion, we performed gel-based, differential proteomics analysis of renal cortex and medulla obtained from the NKD and KD subjects. Using differential proteomics analysis, we successfully identified the alterations in expression of several proteins both in renal cortex and medulla. These altered proteins have demonstrated to be involved in the processes of several cellular functions, bioenergetics, and acid-base regulation. CA I, a metabolic enzyme was up-regulated in the KD group. Chronic K depletion is associated with the increase intracellular acidosis and thus its up-regulation is possibly to control the acid-base homeostasis. Acyl-CoA thioesterase and ADP.ATP translocase are important metabolic enzymes that involve in energy production. Their up-regulation might reflect the decrease of ATP production. GST class-pi and CAT are metabolic enzymes involve in the detoxification process. Their up and down regulation may relate to oxidative stress and lead to renal injury. SPARC-like 1 is signal protein and was down-regulated in the KD group. Its down-regulation might reflects renal enlargement in the low K condition. These finding may lead to an explanation for the pathogenic mechanisms and pathophysiology of chronic K depletion, which might be related with HN, commonly encountered among the Northeastern Thais.