## **CHAPTER V**

## CONCLUSIONS AND SUGGESTIONS

## 5.1. Conclusion

Based on the research that has been carried out, it can be concluded that:

- 1. The microflora found in the three Cangkuak samples in Kuantan Mudik were dominated by bacteria with the highest number of microflora obtained in the DKR (177.0 x  $10^5$  cfu/g) then DR (69.0 x  $10^5$  cfu/g) and DK (48.0 x  $10^5$  cfu/g).
- The highest proportion of bacterial groups in the three cangkuak samples is in fermentative bacteria (2.0 6.30x10<sup>5</sup> cfu/g), cellulolytic bacteria (3.30 5.90x10<sup>5</sup> cfu/g), amylolytic bacteria (1.70 4.40x10<sup>5</sup> cfu/g), proteolytic bacteria (0.12 7.90x10<sup>5</sup> cfu/g), lipolytic bacteria (0.08 0.12x10<sup>5</sup> cfu/g).
- 3. There were six potential fermentative isolates in the three cangkuak samples, namely DK-I<sub>1</sub>, DR-I<sub>1</sub>, DR-I<sub>2</sub>, DR-I<sub>3</sub>, DKR-I<sub>1</sub>, and DKR-I<sub>2</sub>.
- 4. Pathogenic bacteria were found in DR and DKR samples, while no pathogenic bacteria were found in DK.

## 5.2. Suggestions

1. For further research, it is recommended to conduct research on identifying and characterizing potential fermentative bacteria in traditional fermented meat products from Kuantan Mudik District.

2. Conducting research on cangkuak fermentation in a controlled manner by using potential fermenting bacteria as cultures/starters in the manufacture of cangkuak.

