

LIST OF FIGURES

| Figure No. | Title | Page |
|------------|---|------|
| 2.1 | Conceptual framework of spatial epidemiology data analysis using geographical information system (GIS) | 45 |
| 3.1 | Location of the study areas in Peninsular Malaysia | 59 |
| 5.1 | Representative of the amplicons derived from selected positive controls verified by 2% (w/v) gel electrophoresis | 143 |
| 5.2 | Sensitivity test by using 10-fold serial dilutions of well defined reference control DNA | 144 |
| 5.3 | Representative profiles of the melting curves (aligned melt curves) of ITS-2 amplicons for <i>Necator americanus</i> (black), <i>Ancylostoma duodenale</i> (blue), <i>A. ceylanicum</i> (red), <i>A. caninum</i> (green) and <i>A. braziliense</i> (purple) | 145 |
| 5.4 | Representative profiles of the melting curves (derivative melt curves) of ITS-2 amplicons for <i>Necator americanus</i> (black), <i>Ancylostoma duodenale</i> (blue), <i>A. ceylanicum</i> (red), <i>A. caninum</i> (green) and <i>A. braziliense</i> (purple). <i>N. americanus</i> (black) produced two peaks while single peak was produced for other <i>Ancylostoma</i> spp | 146 |
| 5.5 | Representative profiles of the melting curves (difference plot curves) of ITS-2 amplicons for <i>Necator americanus</i> (black), <i>Ancylostoma duodenale</i> (blue), <i>A. ceylanicum</i> (red), <i>A. caninum</i> (green) and <i>A. braziliense</i> (purple) | 147 |
| 5.6 | Calculation of the sensitivity and specificity for both conventional semi-nested PCR and HRM-real-time PCR assay | 150 |

| | | |
|-----|--|-----|
| 5.7 | The HRM profile (i.e., normalized fluorescence curves) (above) and derivative melt curve (below) of nine out of 11 samples in which hookworm-like eggs were seen via microscopy however failed to be amplified in our conventional PCR | 151 |
| 6.1 | Phenogram of the <i>A. ceylanicum</i> sequences of <i>cox 1</i> gene constructed using Neighbor-Joining (NJ) | 176 |
| 6.2 | Phenogram of the <i>A. ceylanicum</i> sequences of <i>cox 1</i> gene constructed using Maximum Parsimony (MP) | 177 |
| 6.3 | Multiple sequences alignment of <i>cox 1</i> gene for <i>A. ceylanicum</i> isolates from this study representing humans, dogs and cats together with reference sequences obtained from GenBank database | 180 |
| 7.1 | Conceptual framework of GIS study methodology | 201 |
| 7.2 | Map distribution of STH species at sub-district levels in Peninsular Malaysia (1970-2012) from available survey data | 236 |
| 7.3 | Predicted prevalence map of <i>A. lumbricoides</i> as derived from logistic regression model of the relation between observed empirical prevalence survey data and remote sensing (RS) - satellite sensor environmental variables | 237 |
| 7.4 | The continuous probability map shows the spatial distribution probability prevalence of <i>A. lumbricoides</i> exceeds 50% | 238 |
| 7.5 | Public health control planning maps | 239 |
| D.1 | Multiple sequence alignment of the second partial internal transcribed spacer (ITS-2) ribosomal RNA gene of five hookworm species employed in the primer design | 310 |
| J.1 | Maps shows the Land Surface Temperature (LST), Normalized Difference Vegetation Index (NDVI) and Digital Elevation Model (DEM) of Peninsular Malaysia | 320 |

| | | |
|-----|--|-----|
| M.1 | Maps of the actual geo-positioned location distribution of STH species at sub-district level in Peninsular Malaysia (1970-2012) from available survey data | 326 |
| N.1 | Plot of the model accuracy to predict areas with (denoted as 1) and without infections (denoted as 0) | 327 |
| N.2 | Result of Moran's I for distribution of <i>A. lumbricoides</i> as assessed using ArcGIS 9.3 software (ERSI, Redlands, CA, USA) | 327 |
