

List of figures

| Figure | Page No |
|--|----------------|
| Figure 3.1 Workflow of Whole metagenome sequencing | 29 |
| Figure 3.2 The workflow of 16S rRNA metagenome sequencing | 32 |
| Figure 4.1 Procedure of traditional method of preparation of <i>napham</i> | 37 |
| Figure 4.2 Gel profile of the samples S1 (lane-3), S2 (lane-2) and one year (lane-1) sample in 2 % Agarose | 46 |
| Figure 4.3 (a) Base quality distribution of sample S1 (replicates R1 & R2) | 48 |
| Figure 4.3(b) Base quality distribution of sample S2 (replicates R1&R2) | 49 |
| Figure 4.4(a) Base composition distribution of sample S1 (replicates R1 &R2) | 50 |
| Figure 4.4 (b) Base composition distribution of sample S2 (replicates R1 &R2) | 51 |
| Figure 4.5(a) GC distribution of sample S1 | 52 |
| Figure 4.5(b) GC distribution of sample | 52 |
| Figure 4.6(a) Contig Length distribution of sample S1 | 54 |
| Figure 4.6(b) Contig Length distribution of sample S2 | 54 |
| Figure 4.7 Rarefaction curves created in MEGAN | 55 |
| Figure 4.8 SEED based annotation showing top10 functional diversity and predicted protein coding sequences in <i>napham</i> fermentation metagenome of two samples S1 and S2 | 67 |
| Figure 4.9 Statistical analysis of the tags and OTUs number of samples S3 and S4 | 70 |
| Figure 4.10(a) S3 OTU annotation tree construct by GraPhlAn | 71 |
| Figure 4.10(b) S4 OTU annotation tree construct by GraPhlAn | 72 |
| Figure 4.11 The evolutionary tree in genus | 73 |
| Figure 4.12(a) Phylogenetic tree –S3 | 74 |
| Figure 4.12(b) Phylogenetic tree – S4 | 75 |
| Figure 4.13(a) KRONA Graph of S3 showing dominant species <i>Staphylococcus</i> sp. | 78 |
| Figure: 4.13(b) KRONA Graph of S4 KRONA Graph of S4 showing dominant species <i>Enterococcus</i> sp. | 79 |
| Figure 4.14(a & b) Relative abundance of bacterial communities in two different | |

| | |
|---|----|
| stages of fermentation (S3 and S4) in <i>napham</i> 16 SrRNA metagenome at (a) Phylum level (b) Class level | 80 |
| Figure 4.14(c & d) Relative abundance of bacterial communities in two different stages of fermentation (S3 and S4) in <i>napham</i> 16 SrRNA metagenome at (c) Order level (d) Family level | 81 |
| Figure 4.15(a) Alpha diversity: Chao1 index in S3 and S4 | 83 |
| Figure 4.15(b) Alpha diversity: Shannon index in S3 and S4 | 83 |
| Figure 4.15(c) Alpha diversity: PD_whol_tree in S3 and S4 | 84 |
| Figure 4.15(d) Observed species in S3 and S4 | 84 |
| Figure 4.16 Rarefaction curve observed at 97 % similarity | 85 |
| Figure 4.17 Rank Abundance curve observed at 97 % similarity | 86 |
| List of Appendix | |
| List of published paper | |
| List of conference attended | |
| Chromatogram report | |
| Culture media used | |
| Accession report of B1 and B2 | |
| Accession report of WGS | |
| Accession report of 16srRNA | |
| Plant identification report from BSI, Shillong, Meghalaya | |
| Fish identification report from ZSI, Shillong, Meghalaya | |
| PHOTO PLATE I | |
| PHOTO PLATE II | |
| PHOTO PLATE III | |
| Abbreviation | |