CONCLUSION

Based on these revision works of *Rhynchoglossum* in Malesia, there were six species of *Rhynchoglossum*. The six species were *Rhynchoglossum borneense* Merr., *R. celebicum* Karton. spec. nov., *R. klugioides* C.B.Clarke, *R. medusothrix* L. Burtt, *R. obliquum* Blume, and *R. spumosum* Elmer. *Rhynchoglossum celebicum* is a new species that newly described here beside the other five species.

Malesia have six species of *Rhynchoglossum* and five of them were endemic. *Rhynchoglossum obliquum* is a widespread and very common species distributed from Sumatra to New Guinea. *Rhynchoglossum klugioides* was previously only known from the Philippines currently distributed also to Seram Island, Moluccas. The other four species are endemic in each region. *Rhynchoglossum spumosum* was endemic to the Philippines from Negros Island and Mindanao Island, while the *R. celebicum* endemic to Sulawesi. *Rhynchoglossum borneense* and *R. medusothrix* are endemic to Borneo which is recorded only found in the eastern part of the island. *Rhynchoglossum* can be found from lowland areas to mountain areas of 1500 m above sea level at the edge of the forest, close to water shaded or in the rock of limestone area.

The phylogenetic relationships of the genus *Rhynchoglossum* in Malesia have been analyzed based on morphological characters. Sixty characters were used and selected for their apparent taxonomic values that are good to separate one taxon with the others. Phylogenetic analysis resulted 128 equally most parsimonious tree of 138 steps produce consistency index (CI) = 0.6562, homoplasy index (HI) = 0.3438 and retention index (RI) = 0.5769.

The ingroup was separated in two sister clades, one consist *R. obliquum*, *spumosum* and *R. celebicum*, another consist *R. klugioides*, *R. borneense* and *medusothrix*. The separation reflected that morphological characters are clearly arrange the affinity among the species and not the geographical pattern. It is clear that the morphological analysis needs to be complemented by an analysis of molecular data to provide a better resolution within a clade of *Rhynchoglossum* in Malesia and support the relationship proposed in this study.