



KEMENTERIAN RISET, TEKNOLOGI DAN PENDIDIKAN TINGGI
UNIVERSITAS HASANUDDIN
FAKULTAS PERTANIAN
DEPARTEMEN BUDIDAYA PERTANIAN

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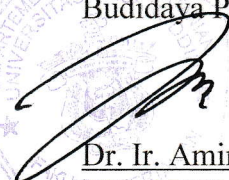
SURAT KETERANGAN
No. 209/UN4.10.7.1/DA.01.04/2019

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Makassar, 9 Juli 2019

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Budidaya Pertanian


Dr. Ir. Amir, M.Si
NIP. 195911031991031002

No	Nama Dosen	Status pada Artikel	Anggota Penulis Lain:	Judul Publikasi	Nama Jurnal/Prosiding
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		Ketua	Laode Asrul Iradhatullah Rahim Tutik Kuswinanti Burhanuddin Rasyid Andi Nasruddin	Effect of Cocoa Pod Husk Compost Produced Using Rot Fungi on the Growth of Cocoa Seedlings	Online Journal of Biological
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		Anggota	Fachirah Ulfa	The growth and production of soybean (Glycine max L.) using nitrogen fixing bacteria and phosphate solubilizing bacteria	Suranaree J. Sci. Technol.
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Dr. Ir. Amir, M.Si
NIP. 19591103 199103 1 002

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Local Rice Genotypes of Tana Toraja and North Toraja Regencies: Kinship Relations and Character Interaction

M Riadi¹, Kasmianti², I Saputra², R Sjahril³ and Rafiuddin⁴

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IOP Conference Series: Earth and Environmental Science, Volume 270, The 1st Biennial Conference on Tropical Biodiversity 20–21 September 2018, Makassar, Indonesia

rinaldi-sjahril@agri.unhas.ac.id

¹ Laboratory of Plant Breeding and Seed Science Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

² Alumni, undergraduate course, Agro-technology, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

³ Laboratory of Plant Bio-science and Reproduction Biotechnology, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

⁴ Laboratory of Plant Physiology and Nutrition, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

M Riadi *et al* 2019 *IOP Conf. Ser.: Earth Environ. Sci.* **270** 012039

<https://doi.org/10.1088/1755-1315/270/1/012039>

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Abstract

Tree, The Regency of Tana Toraja and North Toraja, are two regencies in the Province of South Sulawesi where even though both are not the center of rice crop development, but in both regencies we can find many cultivated local rice genotypes. This study aims to determine the relationship between

local rice genotypes found in the two regencies based on panicle and grain characteristics and the correlation between these characters. The characters observed are panicle length, grains number per panicle, panicle density, awn length, grain length, grain width, grain thickness, grain length to width ratio and 100 seeds weight. Results showed that 49 local rice genotypes were found (27 local rice genotypes from Tana Toraja regency and 22 local rice genotypes from North Toraja regency) with various rice colors, i.e. from white to purple. These local rice genotypes can be grouped into three groups with a similarity rate of 67.56%, namely group I consists of 41 local rice genotypes, group II consists of 3 local rice genotypes (all local rice genotypes from Tana Toraja regency) and group III consists of 5 local rice genotypes and these characters can be grouped into two groups with a similarity rate 48.71%, namely group I consists of two characters (panicle length and grains number per panicle) and groups II consists of 7 characters (panicle density, awn length, grain length, grain width, grain thickness, grain length to width ratio and 100 seeds weight). There was a very significant positive correlation between the characters, namely panicle length and grains number per panicle, panicle length and panicle density, panicle length and awn length, grains number per panicle and panicle density, awn length and grain width, grain length and grain length to width ratio, grain length and 100 seeds weight, grain thickness and 100 seeds weight and grain length to width ratio and 100 seeds weight, with the correlation coefficient values 0.630**, 0.406**, 0.470**, 0.960**, 0.428**, 0.821**, 0.609**, 0.591** and 0.365**, respectively and there was also a very significant negative correlation between the characters, namely awn length and grain length to width ratio and grain width and grain length to width ratio, with the correlation coefficient values -0.401 ** and -0.770 **.

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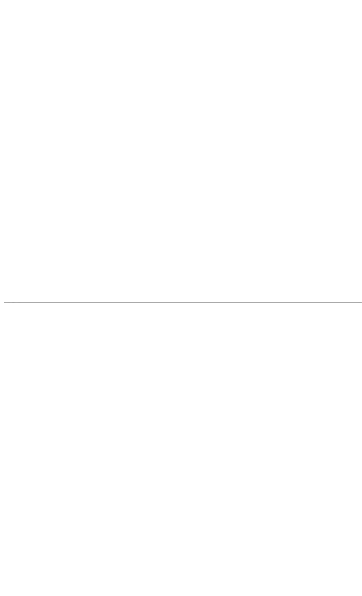
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Local Rice Genotypes of Tana Toraja and North Toraja Regencies: Kinship Relations and Character Interaction

M Riadi¹, Kasmianti², I Saputra², R Sjahril³, Rafiuddin⁴

¹ Laboratory of Plant Breeding and Seed Science Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

² Alumni, undergraduate course, Agro-technology, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

³ Laboratory of Plant Bio-science and Reproduction Biotechnology, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

⁴ Laboratory of Plant Physiology and Nutrition, Faculty of Agriculture, Hasanuddin University, Makassar 90245, Indonesia

E-mail: rinaldi-sjahril@agri.unhas.ac.id

Abstract. Tana Toraja and North Toraja, are two regencies in the Province of South Sulawesi where even though both are not the center of rice crop development, but in both regencies we can find many cultivated local rice genotypes. This study aims to determine the relationship between local rice genotypes found in the two regencies based on panicle and grain characteristics and the correlation between these characters. The characters observed are panicle length, grains number per panicle, panicle density, awn length, grain length, grain width, grain thickness, grain length to width ratio and 100 seeds weight. Results showed that 49 local rice genotypes were found (27 local rice genotypes from Tana Toraja regency and 22 local rice genotypes from North Toraja regency) with various rice colors, i.e. from white to purple. These local rice genotypes can be grouped into three groups with a similarity rate of 67.56%, namely group I consists of 41 local rice genotypes, group II consists of 3 local rice genotypes (all local rice genotypes from Tana Toraja regency) and group III consists of 5 local rice genotypes and these characters can be grouped into two groups with a similarity rate 48.71%, namely group I consists of two characters (panicle length and grains number per panicle) and group II consists of 7 characters (panicle density, awn length, grain length, grain width, grain thickness, grain length to width ratio and 100 seeds weight). There was a very significant positive correlation between the characters, namely panicle length and grains number per panicle, panicle length and panicle density, panicle length and awn length, grains number per panicle and panicle density, awn length and grain width, grain length and grain length to width ratio, grain length and 100 seeds weight, grain thickness and 100 seeds weight and grain length to width ratio and 100 seeds weight, with the correlation coefficient values 0.630**, 0.406**, 0.470**, 0.960**, 0.428**, 0.821**, 0.609**, 0.591** and 0.365**, respectively and there was also a very significant negative correlation between the characters, namely awn length and grain length to width ratio and grain width and grain length to width ratio, with the correlation coefficient values -0.401 ** and -0.770 **.

1. Introduction

Rice is an important type of cereal crops and is the main staple food for most Indonesian people. The government continues to improve efforts to increase rice production, both through improved cultivation techniques and through breeding activities to produce new varieties with high yield potential.



South Sulawesi province is one of the regions in Indonesia known as the national food barn. Some Regency in this region, are central areas for rice cultivation, but there are several other agencies that are not centers of rice cultivation, two of which are Tana Toraja and North Toraja regencies. The two regencies are the result of the development of the Tana Toraja regency which is known as one of the tourist visit areas [1].

Although the regencies of Tana Toraja and North Toraja are not centers of rice development, in both regencies, we can find many local rice genotypes that have been cultivated by farmers from generation to generation. The long history of rice cultivation and variations in environmental conditions that occur can contribute to the diversity of existing local rice genotypes. Through time, local rice genotypes that have been and continue to be cultivated by farmers will be adapt well to specific environmental conditions. [2] showed a significant variability concerning the seed morphological characteristics and adaptation to local environment, [3] showed a high phenotypic variation of agro-morphological properties in the population of local rice genotypes and [4] showed the presence of local rice genotypes tolerant to drought stress.

Local rice genotypes that are maintained and cultivated by farmers are germplasm sources that can be used in new rice varieties development breeding programmes. Characterization of germplasm is very important and can help breeders to utilize appropriate characters in rice yield improvement programmes [5]. Gunasekaran [6] stated that the success of plant breeding depends on the availability of genetic diversity, knowledge of the desired character, and efficient selection strategies that make it possible to exploit existing germplasm sources.

Until now, information about the morphological characters of local rice still cultivated in Tana Toraja and North Toraja Regency, particularly related to the characters of panicle and grain was not widely reported. This study aims to determine the kinship relations and character interaction between local rice genotypes found in the two regencies based on panicle and grain characteristics and the correlation between these characters.

2. Material and Method

This The study took place from March to August 2018. A sampling of panicles of local rice genotypes was carried out in the regencies of Tana Toraja and North Toraja. Determining the location (village) of sampling in each regency was done by purposive sampling, which is based on information on the presence of local rice obtained from the Office of Agriculture and District Offices. Characterization of panicles was carried out at the Laboratory of Plant Breeding and Seed Sciences, Department of Agriculture, Faculty of Agriculture, Hasanuddin University, Makassar.

Panicle characters measured: (1) quantitative characters, including panicle length (cm), grains number per panicle (seeds), panicle density (seeds cm^{-1}), awn length (mm), grain length (mm), grain width (mm), grain thickness (mm), grain length to width ratio, and 100 seeds weight (g); and (2) qualitative characters, including the color of the husk, the color of rice and the form of grain. Characterization follows the guidance of rice plant characterization and evaluation system. Quantitative characters data tabulated through MS Excel 2007 for windows. Descriptive analysis was used to determine the average level and standard deviation of each character, while to find out groupings between genotypes, groupings between characters, and the correlation between characters was done using Minitab software version 16. The analysis results are displayed in the dendrogram and correlation matrix.

3. Results and discussion

Local rice genotypes found were 49 genotypes, 27 local rice genotypes originated from Tana Toraja regency, and 22 local rice genotypes originated from North Toraja Regency. The descriptive analysis of the quantitative characters observed and measured from all local rice genotypes are presented in Table 1. Table 1 shows that there are three characters that have high standard deviation values, namely panicle length, grains number per panicle and awn length, with a standard deviation value 28.39, 54.10 and 17.24 respectively.

Table 1. Maximum, minimum, mean and deviation standard of the panicle and grain characters

Characters	Code	Maximum	Minimum	Mean	Deviation Standart
Panicle Length	PL	323.90	199.20	259.00	28.39
Grains Number	GN	304.70	68.20	140.30	54.10
Panicle Density	PD	1.12	0.33	0.53	0.17
Awn Length	AL	53.40	0.00	1.16	17.24
Grain Length	GL	9.86	7.09	8.27	0.60
Grain Width	GW	3.66	2.73	3.18	0.20
Grain Thickness	GT	2.32	1.98	2.13	0.07
Grain Lenght to Width Ratio	GL/W-R	3.34	2.11	2.61	0.29
100 Seeds Weight	100SW	3.43	2.24	2.78	0.27

The dendrogram of the local rice genotypes are presented in Figure 1. In Figure 1 shows that at the level of similarity 67.56%, these local rice genotypes can be grouped into three groups, i.e., group I consists of 41 local rice genotypes, group II consists of 3 local rice genotypes and group III consists of 5 local rice genotypes. Only in group II, all local rice genotypes originated from Tana Toraja regency. According to [7] that, using cluster analysis, the found genotypes can be grouped based on the level of similarity that exists. With this grouping, it can be used by plant breeders to determine and select local rice genotypes as the crossing parent in the breeding programmes of new rice varieties development.

Each local rice genotype found has a degree of similarity between panicles and grains. The level of similarity can be used to determine the proximity of the kinship between genotypes. The higher the level of similarity, the closer the relationship. Conversely the more difference, the more distant kinship. [2] stated that information produced through the study of seed morphology, cluster analysis, and diversity studies could be used efficiently in different seed quality character improvement programs. This is in line with the opinion of [8] that information generated through cluster analysis based on phenotypic and genotypic data can be used efficiently in rice breeding related to a genetic improvement for grain or seed quality characteristics.

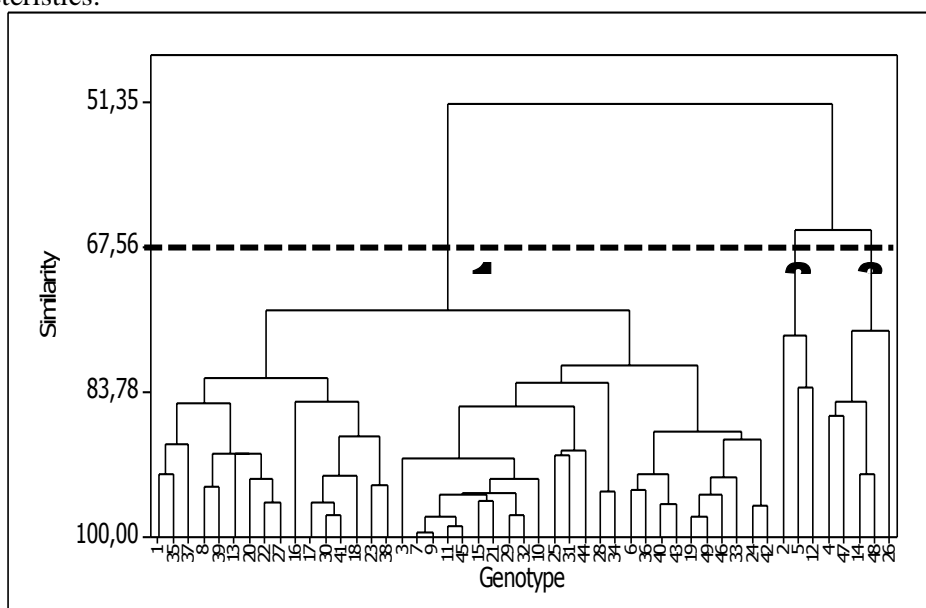


Figure 1. Dendrogram of the local rice genotypes is found (genotypes 1-27 originated from Tana Toraja regency and genotypes 28-49 originated from North Toraja regency).

The dendrogram of the quantitative characters is presented in Figure 2. In Figure 2 shows that at the level of similarity 48.71%, these characters can be group in two groups, group 1 consisted of two characters namely panicle length and grains number per panicle, while in group 2 consists of seven characters, namely panicle density, awn length, grain length, grain width, grain thickness, grain length to width ratio and 100 seeds weight.

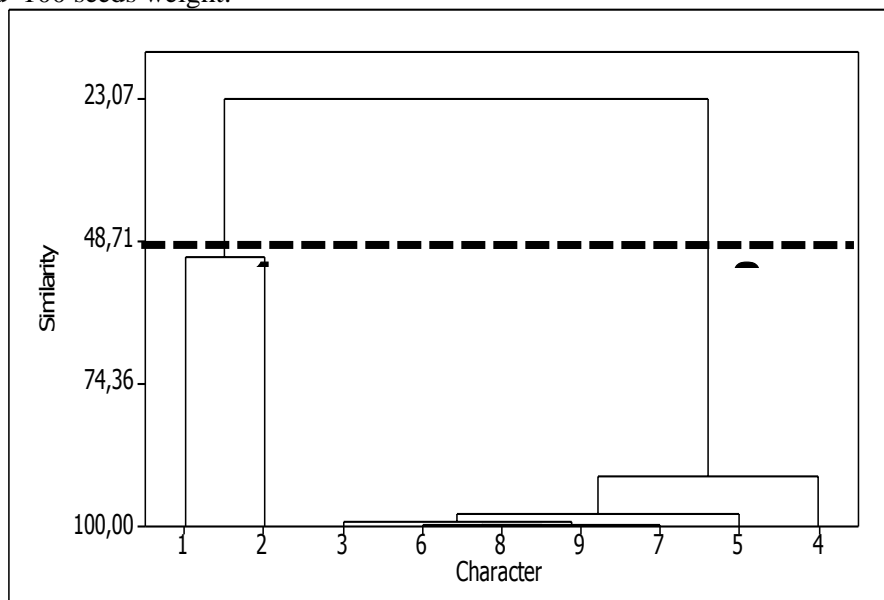


Figure 2. Dendrogram of the quantitative characters are measured (1 = Panicle Length, 2 = Grains Number, 3 = Panicle Density, 4 = Awn Length, 5 = Grain Length, 6 = Grain Width, 7 = Grain Thickness, 8 = Length to Width Ratio, and 9 = 100 Seeds Weight).

The results of the correlation analysis among quantitative characters are presented in Table 2. In Table 2 shows that there was a very significant positive correlation between the characters, namely panicle length and grains number per panicle, panicle length and panicle density, panicle length and awn length, grains number per panicle and panicle density, awn length and grain width, grain length and grain length to width ratio, grain length and 100 seeds weight, grain thickness and 100 seeds weight and grain length to width ratio and 100 seeds weight, with the correlation coefficient values (r) 0.630**, 0.406**, 0.470**, 0.960**, 0.428**, 0.821**, 0.609**, 0.591** and 0.365**, respectively and there was also a very significant negative correlation between the characters, namely awn length and grain length to width ratio and grain width and grain length to width ratio, with the correlation coefficient values (r) -0.401** and -0.770**. There was a significant positive correlation between the characters, namely between grain width and grain thickness with the correlation coefficient value (r) 0.314* and there was also a significant negative correlation between the characters, namely between grain length and grain width with the correlation coefficient value (r) -0.277*.

The correlation value between one character and another character shows the closeness of the relationship between the two characters. On the results of correlation analysis, the closeness of the relationship between two characters is expressed as a positive relationship or a negative relationship. A positive relationship indicates that an increase in the value of one character will increase the value of other characters in pairs, while a negative relationship indicates that an increase in the value of one character will decrease the value of other characters in pairs [9].

Table 2. The matrix of phenotypic correlations among quantitative characters

Characters	PL	GN	PD	AL	GL	GW	GT	GL/W-R
GN	0.630**							
PD	0.406**	0.960**						
AL	0.470**	0.162ns	0.057ns					
GL	-	-	-	-				
GW	0.070ns	0.228ns	0.247ns	0.222ns	-0.277*			
GT	0.180ns	0.082ns	0.042ns	0.428**		0.314*		
GL/W-R	0.026ns	0.101ns	0.128ns	0.070ns	0.176ns			
100SW	-	-	-	-	-	-	-	-
	0.154ns	0.191ns	0.177ns	0.401**	0.821**	0.770**	0.062ns	
	0.075ns	0.092ns	0.137ns	0.009ns	0.609**	0.049ns	0.591**	0.365**

(**) = significantce at 1%, (*) = significance at 5%, ns = non significance.

PL (Panicle Lenght), GN (Grains Number), PD (Panicle Density), AL (Awn Lenght), GL (Grain Lenght), GW (Grain Width), GT (Grain Thickness), GL/W-R (Lenght to Width Ratio), 100SW (100 Seeds Weight).

Based on the results of observations of qualitative characters, namely: (a) the color of the husk showed that there were 4 genotypes (8.16%) with brown-colored straw, 6 genotypes (12.24%) yellowish brown, 13 genotypes (26.53%) yellow straw with brown stripes, 4 genotypes (8.16%) were golden yellow and 22 genotypes (44.90%) were straw yellow, (b) the rice color shows that 2 genotypes (4.08%) were dark purple, 6 genotypes (12.24%) were brownish purple color, 7 genotypes (14.29 %) were red, 22 genotypes (44.90%) were white and 12 genotypes (24.49%) were milky white and (c) the form of grain shows that there were 3 genotypes (6.12%) in the form of slender, 39 genotypes (79.59%) in medium shape and 7 genotypes (14.29%) were medium to slim. The diversity of rice colors from local rice genotypes was found to be in line with those reported by Sinha (2018). Indrasari (2006) stated that the different colors of rice are genetically regulated characters, due to differences in genes that regulate aleurone color, endosperm color, and starch composition in endosperms. The color of rice indicates that the rice contains polyphenols and anthocyanins which can be useful as antioxidants [10]. Umadevi [11] stated that extracts from brown rice had been used to treat breast and stomach cancer and warts. And it has also been used to treat digestive disorders, nausea, and diarrhea

According to [12], black (purple) rice became popular in Indonesian society not only for the development of functional foods, but also because of genetic variability of cultivars which caused diversity in pigmentation, nutritional value, and phytochemical properties. The black rice was included in the *Oryza sativa* L. species, which is the same species as white rice and brown rice. Information on genetic diversity and mating system is a major part of maintaining diversity [13,14].

[15] stated that the availability of genetic diversity enables breeders to choose genotypes that have a superior character. Germplasm in the form of genotypes that have superior character can be used as gene donors in the development of new genetic diversity. The availability of plant germplasm that functions as a gene donor for characters that is the target of improving existing varieties or developing new varieties is absolutely necessary.

4. Conclusion

1. Freshness There were 27 local rice genotypes found in Tana Toraja regency and 22 local rice genotypes in North Toraja Regency. With a similarity level of 67.56%, these local rice genotypes can be grouped into three groups, i.e. group I consists of 41 local rice genotypes, group II consists of 3 local rice genotypes and group III consists of 5 local rice genotypes. Only in group II, all local rice genotypes originated from Tana Toraja Regency.
2. Based on the characters observed, with a similarity level of 48.71%, these characters can be grouped into two groups, i.e. group I consists of 2 characters, namely panicle length and grains number per panicle and group II consists of 7 characters, namely panicle density, awn length, grain length, grain width, grain thickness, grain length to width ratio and 100 seeds weight.
3. There were a very significant positive correlation between characters of panicle length and grains number per panicle, panicle length and panicle density, panicle length and awn length, grains number per panicle and panicle density, awn length and grain width, grain length and grain length to width ratio, grain length, and 100 seeds weight, grain thickness and 100 seeds weight and grain length to width ratio and 100 seeds weight, with correlation coefficient values 0.630**, 0.406**, 0.470**, 0.960**, 0.428**, 0.821**, 0.609**, 0.591** and 0.365**, respectively and there were also a very significant negative correlation between the characters, namely awn length and grain length to width ratio and grain width and grain length to width ratio, with the correlation coefficient values -0.401** and -0.770**.
4. The color of the husk is dominated by straw yellow (44.90%), the color of the rice is dominated by white (44.90%) and the grain shape is dominated by the medium (79.59%).

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PREFACE

The 1st Biennial Conference of Tropical Biodiversity (BCTB 2018) was held in Makassar, Indonesia on September 20 to 21, 2018 at the the Rinra Hotel, Makassar. BCTB 2018 is dedicated to address issues related to multidisciplinary field on tropical biodiversity management, hosted by Forestry Faculty of Universitas Hasanuddin.

The conference is aimed to benefit participants in terms of research development, networking initiation, and disseminating science and knowledge to broader context in particular in the area of biodiversity conservation and management. We are hoping that through the information discussed and developed in this conference bring positive contribution and significant changes in countering and addressing problems as well as challenges in the area concern as well as finding suitable solutions to protect and conserve our biodiversity from declining. It is also expected that the conference will give an impact on providing a platform for exchange of ideas and information amongst scientists, practitioners, and students; and in providing a media for promoting the international publications for Indonesian and worldwide researchers.

The last session of the conference was also attended by the Governor of Sulawesi Selatan Province, he delivered a very enthusiastic speech and welcome the participant and key note speakers. The conference is also attended by some conservation agencies. Therefore, this conference is also benefit for the related practitioner on managing biodiversity.

All papers submitted and presented in the conferences were subjected to peer-reviews. The selected papers is consolidated in this proceedings and presents recent researches in the field related to multiple aspects of tropical biodiversity. There are five categories in this biodiversity conference such as (i) global biodiversity assessment: climate change impacts for biodiversity, (ii) the existence of genetic diversity for biodiversity maintenance, (iii) conserving tropical biodiversity: current challenges for management, (iv) biodiversity and utilization: techno science and economics, (v) community partnership for biodiversity conservation : social and policy

We would like to appreciate all authors and respected keynote speakers who have contributed to this proceedings, the conference committee, speakers, attendees, organizing committee and sponsors who have made the 1st BCTB 2018 a succes. We wish the conference and the proceeding resulted will have significant contribution in field of tropical biodiversity literature.

Astuti Arif
Chair of Organizing Committee BCTB 2018.

