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## MENU

- [About Us](#)
- [Author/Submission Guideline](#)
- [Abstracting & Indexing](#)
- [Types of Articles](#)
- [Editorial Team/Board](#)
- [Focus and Scope](#)
- [Current Volume](#)
- [Archive](#)
- [Announcement and Call for Paper](#)
- [Publication Ethics](#)
- [Open Access Licences Policy](#)
- [Review and Scanning](#)
- [Plagiarism Policy](#)
- [Contact Us](#)

## IJAS | DECEMBER 2013 | VOL 1 ISSUE 2

Filter by:

---

### **Mineralogy and Micromorphology Characteristic of Vertisol Lying on Limestone Parent Rocks at Jeneponto District of South Sulawesi Province, Indonesia** [92-97]

Ulfiyah A. Rajamuddin, Christianto Lopulisa, Hernusye Husni, Muhammad Nathan

[\[Full Text\]](#) [\[Abstract & References\]](#)

---

### **Potential of Plant Extracts as Growth Exogenous Regulators of Potato Seeds** [98-103]

Fachirah Ulfa, Enny Lisan Sengin, Baharuddin, Syatrianti Andi Syaiful, Nadira R. Sennang, Rafiuddin, Nurfaida, Ifayanti

[\[Full Text\]](#) [\[Abstract & References\]](#)

---

### **Assessment of Trees Outside Forest (TOF) in Selected Makiling Subwatersheds** [104-111]

Jan Joseph V. Dida, Joseph C. Paquit, Cheamson Garret K. Boongaling, Gemmalyn E. Magnaye, Nathaniel C. Bantayan

[\[Full Text\]](#) [\[Abstract & References\]](#)

---

### **Germination Viability of Maize M1 Seeds (*Zea mays* L.) after Gamma Ray Irradiation** [112-118]

Rafiuddin, Dahliana Dahlan, Yunus Musa, Burhanuddin Rasyid, Muh. Farid Bdr

[\[Full Text\]](#) [\[Abstract & References\]](#)

---

### **Effectiveness of Fungal and Bacterial Isolates from Rhizosphere of Passion Fruits againsts *Fusarium oxysporum* f. sp *passiflorae* in Vitro** [120-126]

Hilda Karim, Tutik Kuswinanti, Ade Rosmana, Burhanuddin Rasyid

[\[Full Text\]](#) [\[Abstract & References\]](#)

---

### **Productivity of Local Goat Fed Corn Stover Treated with Fungi *Trichoderma* sp. and Supplemented *Gliricidia*** [128-134]

Rohmiyatul Islamiyati, Asmuddin Natsir, Sjamsuddin Rasjid, Ismartoyo

[Full Text](#) [Abstract & References](#)

---

**Genetic Relationship amongst *Marica*, *Kacang Goat* and *Capra* species**

[136-143]

Rosdiana Ngitung, Herry Sonjaya, Syamsuddin Hasan, Wempie

[Full Text](#) [Abstract & References](#)

---

**Tagging and Mapping of Mixed Dipterocarp Mountain Forest at Species Level using an Airborne Hyperspectral Imager [144-161]**

Kamaruzaman Jusoff

[Full Text](#) [Abstract & References](#)

---



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## Genetic Relationship amongst *Marica*, *Kacang* Goat and *Capra* species

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**Abstract:** *Marica* goat is an endemic species that can be found only in South Sulawesi, Indonesia. It has been reported by the FAO as endangered species because its number of population has been significantly decreased. Domestication by local people has been done by cultivating them with *Kacang* goat that leads to an interbreeding process. Conservation of the goats must be done immediately due to its rapidly decreasing population. However, accurate identification and quantification of the goat by DNA analysis is highly important. The objective of this study is to determine the differences amongst *marica*, *kacang* and *Capra hircus*, *C. caucasica* and *C. falconeri* from the GenBank. The sequence of the mitochondrial DNA (mtDNA) at d-loop region of 30 *Marica* goats and five *Kacang* goats from three districts in South Sulawesi were investigated. Their nucleotide sequences were compared with the sequence of the GenBank's *Capra sp* and were analyzed using Dendogram neighbor joining tree. The results showed that there were a few nucleotide differences between some *Marica* and *Kacang* goat that were located at 20, 840 and 980bp. In addition, both nucleotides sequence have short genetic distance compared to *C. hircus*. However, comparing with other *Capra sp*, the distance was significantly far. Meanwhile, according to the dendogram, it was found that all Goats and *Capra sp* came from the same ancestral lineage. It can be concluded that *Marica* and *Kacang* goats could be very closely related with *C. hircus* but they were different from the *C. caucasica* and *C. falconeri*.

**Keywords:** *Marica* goat; *Kacang* goat; *Capra hircus*; South Sulawesi; mtDNA

### 1. Introduction

One of Indonesian's germplasm commodities are goats. Goats spread in different regions with different climates and separated in a long time. Various selections of environmental factors and treatment cause genetic changes in goat's population (Rout

*et al.*, 2008).

*Marica* goat is a type of local goat that can be found only in South Sulawesi Province, especially in the district of Maros, Jeneponto, Soppeng and Makassar (Fitra *et al.*, 2009). The goats are genetically potential to adapt in the dry land with a very low annual

rainfall. *Marica* goats can survive in the dry season although they only eat dry grass in the rocky ground. Unfortunately, according to Food and Agriculture Organization (2000) Report, its population is very low and is categorized as endangered species.

Traditionally, local communities raise various kinds of goats in the same field and cages. It also happened on *Marica* goat that was reared together with *Kacang* goat, consequently interbreeding and genetic mixing among goat are inevitable. According to previous observation and interview with a local traditional breeder, *Marica* goats have strong characteristic even they resulted from the combinations of *Marica* and *Kacang* goats. Thus, even the goats have strong characteristic of *Marica* goat, it does not guarantee that they are original *Marica* goats.

Molecular genetic studies within and across breeds are essential for the population management (Hall and Bradley, 1995; Ruane, 2000; Simianer, 2005). Performing such purpose, it is believed that using mitochondria DNA (mtDNA) is simply enough than using circular DNA. Mamalian mtDNA shows several special features such as absences of intron, material inheritance, lack of recombination events and a high mutation rate (Irwin *et al.*, 1991). Furthermore, it brings enough information to figure out goat ancestries (Chen *et al.*, 2005). Complete sequences of bovine mtDNA were published by Anderson *et al.* (1982), so the mtDNA have widely used for genetic diversity and phylogenetic analysis among different cattle breeds (Bradley *et al.*, 1996; Troy *et al.*, 2001). Specifically, D-loop area at mtDNA, non coding area, has nucleotide sequence that is useful to

determine phylogenetic relationship (Hou *et al.*, 2006). Meanwhile, the preservation of *Marica* goats should be done immediately considering the number of its population has declined sharply. However, before conducting conservation effort, determining the original *Marica* goat is essential. This study is therefore conducted to determine the kinship between *Marica* and *Kacang* goats and the original *Marica* from *Kacang* goats.

## 2. Materials and Methods

### 1.1 Animal Sample

DNA was obtained from whole blood sample because the DNA have specific genetic characteristic and the size is smaller than nucleus DNA (Chen *et al.*, 2005). It was impossible to find a number of *Marica* goats that have the same characteristic due to the lack of its number. All *Marica* goats comprising of seven goats from Maros (TB5, TB4, S1, S3, S2, TB6 and TB8), three goats from Makassar (MK3, MK4 and MK5) and 20 goats from Jenepono (JNP induk, JNP anak, MCJ2, MCJ3, I, Btg1, Btg2, Btg3, Btg4, TB VIII, B1, B2, B3, K1, K2, K3, Mks7, Mks8, Mks10, Mks7Jantan) were analysed. Almost all the goats were female except Mks7Jantan which was male. On the other hand, five *Kacang* goats were taken from Makassar.

### 1.2 DNA isolation

A total of 10 ml of blood were taken aseptically from the jugular vein of each *Marica* and *Kacang* goats and placed in vacuum glass tubes containing anticoagulant ACD (acid citrate dextrose). All samples were stored in a cooler and brought to laboratory for further analysis (Yadav and Yadav, 2008).