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Abstract
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Key words: Communities of Phytoplankton, Vertical Distribution, Water Quality, Gondang Reservoir
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Vertical Distribution of Phytoplankton Communities in Gondang Reservoir, Lamongan, East Java, Indonesia

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ABSTRACT: Human activity are increase recently around the Gondang Reservoir, Lamongan and cause increased of discharges waste that could potentially degrade the quality and function of the reservoir also changes the composition, abundance and distribution of phytoplankton communities. This study aims are to determine the vertical distribution of phytoplankton community and use it to assume the waters fertility rates in the Gondang Reservoir from January to February 2016. This study used survey method by taking samples of water and phytoplankton in three observation stations (inlet, middle and outlet) and 5 depth of 0 cm, 50 cm, 100 cm, 150 cm and 200 cm with 2 times of observation. Phytoplankton that has been found consist of 4 divisions, i.e. Chlorophyta (31 genera), Chrysophyceae (14 genera), Cyanophyta (7 genera) and Pyrrophyta (3 genera). Total abundance of phytoplankton ranged between 111-2.557 ind/liter. The highest abundance from all stations are at 50 cm depth where the light intensity is optimum and phytoplankton abundance decreased with increasing depth. Phytoplankton diversity index (H') ranged from 3,31755 to 7,82316 indicating that the diversity range is moderate to high. Water quality parameters such as temperature, brightness, pH, DO, nitrate and orthophosphate is good to support phytoplankton life. The overall observations indicated that Gondang Reservoir are including in mesotrophic waters. In conclusion, the vertical distribution of phytoplankton can be used as a parameter to asses the water quality in Gondang Reservoir.

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INTRODUCTION

Reservoir receives water input from the river that constantly flowing over it. The river water containing organic and inorganic material that can fertilize the waters of the reservoir [1]. Gondang Reservoir was built with the purpose for drinking water, rice field irrigation, tourism and aquaculture. Based on the various objectives and the utilization, tourism, agriculture and inland fisheries are the most activities that can provide overload input for the dam water itself. This reservoir is drained by three rivers, which is around that three rivers also have various of human activities that can also provide load input to the dam water.

The load input will be the source of additional nutrients for waters that can also cause a variety of water problems, such as eutrophication [2]. This process occurs when the the load input are excess and then causing the decline in water quality. The declining of water quality will also disrupt the lives of phytoplankton as primary producers waters. In addition, the burden of these inputs can also cause sedimentation resulting decline in the productive layer of water and can shorten the life of the reservoir [3, 4]. Changes in water conditions will also cause changes in community structure of phytoplankton in particular biological component [5].

The purpose of this study was to determine the phytoplankton community structure vertically so it can be used to predict the fertility level of the water in the Gondang Reservoir.

MATERIAL AND METHODS

The sample collection was conducted from January to February 2016. The phytoplankton community were taken vertically in Gondang Reservoir and the water quality that were measured including brightness, temperature, dissolved oxygen (DO), pH, nitrate and orthophosphate.

Gondang Reservoir is located in 113°15'56'' East Lon - 7°12'18" South Lat. The location map can be observed in Figure 1. This research was conducted by taking samples of water and phytoplankton samples vertically at three observation stations and 5 depth observations (0 cm, 50 cm, 100 cm, 150 cm and 200 cm). Station I is located in the area of the river water intake (inlet), station 2 is located in the middle of Gondang Reservoir and station 3 is located in the outlet of Gondang reservoir (Figure 1). Determination of the depth were

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conducted based on the preliminary studies using secchi disk at all three stations with the average brightness was 1.54 cm (based on the depth of the photic zone). Observations were conducted 2 times with an interval of the first and second observation was one week and the sampling time is at 9:00 to 12:00 pm. Sampling was done by filtering phytoplankton 25 liter of reservoir water at any depth. Water quality parameters measured include physical parameters such as temperature (thermometer Hg) and brightness (secchi disk), while chemical parameters were measured such as dissolved oxygen (DO meter Lutron DO-5510), pH (pH paper), nitrate and orthophosphate (titration).

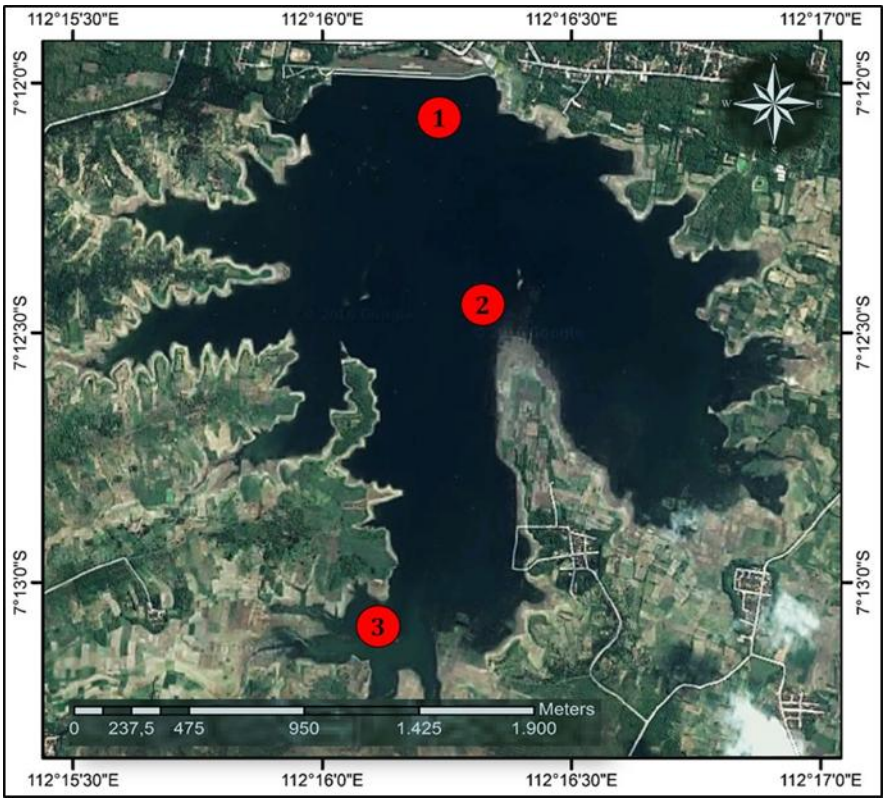

Figure 1. Location of study area and sampling stations Station 1 (Inlet), Station 2 (Middle) and Station 3 (Outlet)

Data analysis included the abundance of phytoplankton were observed using the "Lackey drop" method. The abundance of phytoplankton value (N) is calculated using the following formula with slight modification [6]:

$$N = \frac{T \times V}{L \times v \times P \times W} \times n$$

where : T = area of cover glass (20 x 20 mm^2)
L = area of the visual field in microscopy (mm^2)
V = Volume of plankton concentrate in the bottle container
v = Volume of plankton concentrate under the cover glass (ml)
W = Volume of filtered water with a plankton net (liter)
P = Total field of view (5)
n = number of phytoplankton present in the visual field
N = The abundance of phytoplankton (individuals/liter)

The relative density (KR) is calculated using the formula:

$$KR = \frac{ni}{N} x100\%$$

where : ni : number of individuals in the genus
N : total number of individuals

The values of relative density (KR) are between 1% to 100%. Low density percentage indicates the number of organisms that live in waters have little value.

Analysis of the value of individual plankton diversity (H') used the Diversity Indices formula adapted from Shannon - Weaver as follows:

$$H' = -\sum Pi \ln Pi$$

$$Pi = \frac{ni}{N}$$

where : Pi : The proportion of species to the I to the total number

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ni : Number of cells / head of taxa biota i
N : Number of cells / head of taxa biota in the cell

Based on the above formulation, the diversity index range is categorized as follows [7]:

H ' < 2.3 : Low diversity, low community stability
2.3 < H ' > 6.9 : moderate diversity, medium community stability
H ' > 6.9 : high diversity, high community stability

RESULT AND DISCUSSION

The abundance of phytoplankton

Based on observations of phytoplankton in Gondang Reservoir in January - February 2016, we found 4 divisions of phytoplankton, consist of Chlorophyta, Chrysophyta, Cyanophyta and Pyrrhophyta. Phytoplankton that are classified in Chlorophyta found as many as 31 genera, namely *Chlorella, Scenedesmus, Tetraedron, Pediastrum, Asterococcus, Genicularia, Ulothrix, Uronema, Granulochloris, Roya, Eramosphaera, Schizochlamys, Actinastrum, Staurastrum, Golenkinopsis, Oocystis, Chlorococcum, Cylendrocystis, Closterium, Triploceras, Planktospaeria, Crucigenia, Closteridium, Dicellula, Groenbladia, Cosmarium, Gloeocystis, Raphidonema, Ankistrodesmus, Mesotaenium,* and *Polytoma*. Division of Chrysophyta were found that as many as 14 genera, consist of *Navicula, Frustulia, Chrysosphaera, Achanthes, Epithemia, Mastogloia, Cymbella, Ellipsoidon, Chlorobotrys, Tetradriella, Synedra, Cylindrotecha, Nitzchia,* and *Surirella.* Division Cyanophyta found as many as 7 genera, among others, *Gomphosphaeria, Microcystis, Anabaena, Merismopedium, Synechococcus, Spirulina,* and *Synechococystis.* Division Pyrrophyta found as many as 3 genera namely *Ceratium, Cystodinium, and Gymnodinium.* Total genus of phytoplankton found as many as 55 genera. The high composition of phytoplankton allegedly caused by the organic and inorganic input materials to Gondang reservoir, that is able to fertilize waters and contain enough nutrients for phytoplankton. The composition of phytoplankton community reflects the environmental conditions of the ecosystem, among which nutrient availability plays a significant role [8, 9].

The total abundance of phytoplankton ranged between 111-2557 individuals/liter. The lowest total abundance of phytoplankton was found at Station 2 in the second observation at a depth of 200 cm and the highest was found at Station 3 on the second observation at a depth of 50 cm. The pattern of vertical distribution of phytoplankton was shown in Figure 2 as follows:

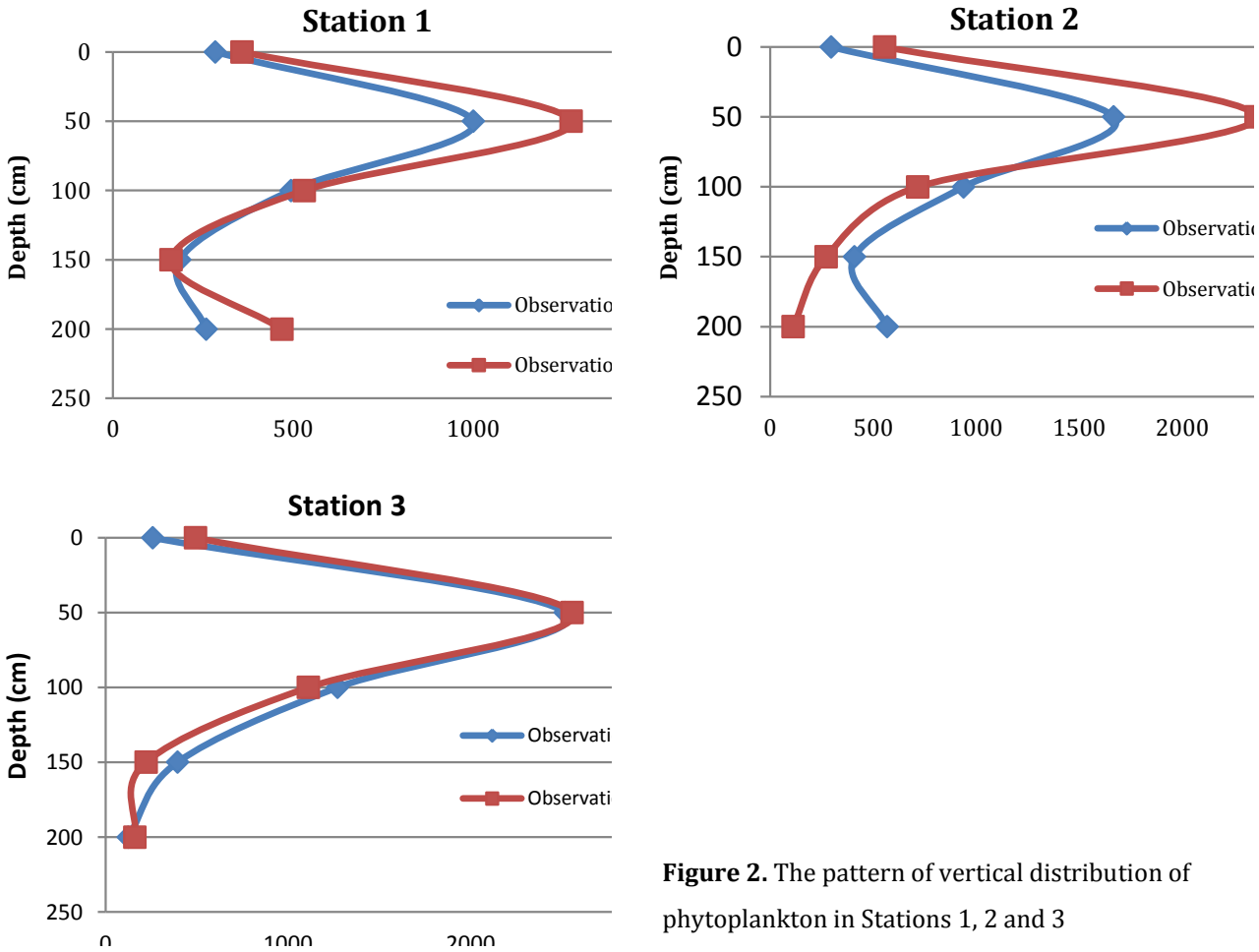
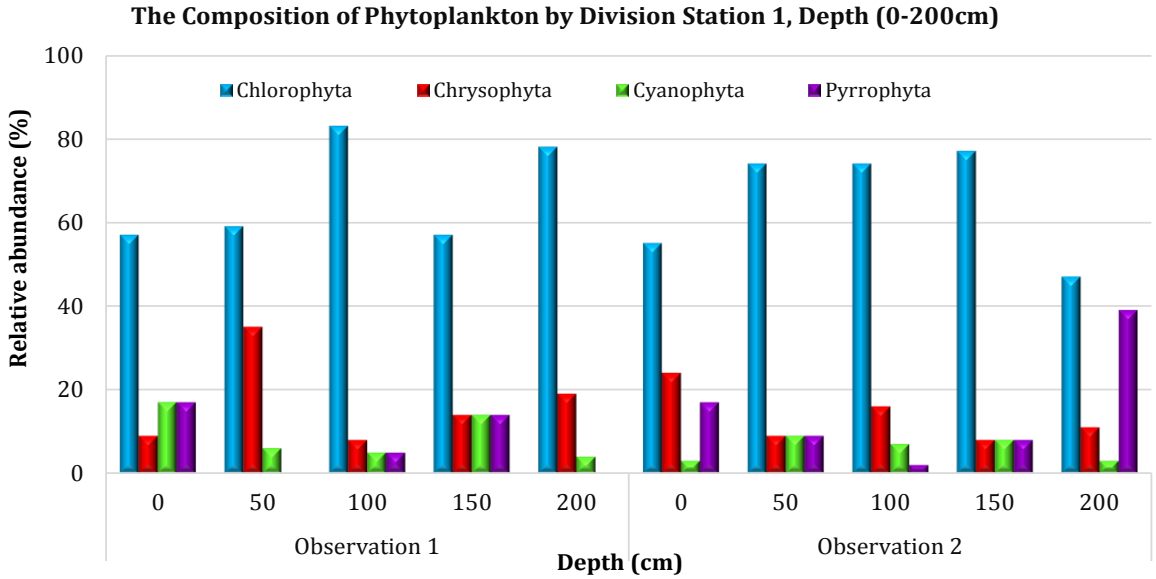


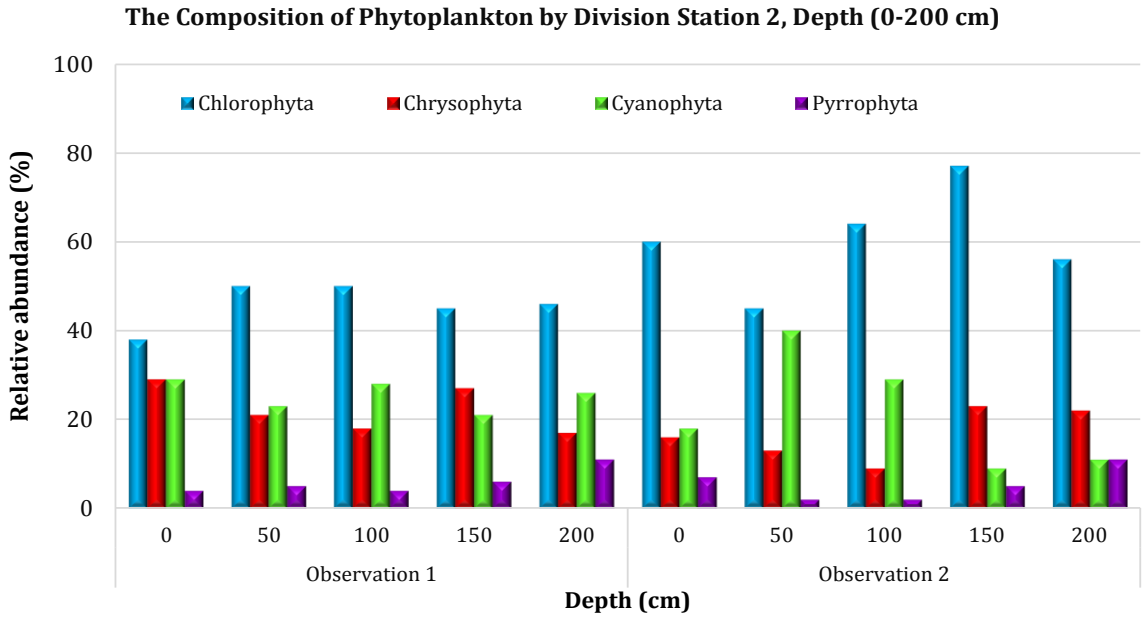
Figure 2. The pattern of vertical distribution of phytoplankton in Stations 1, 2 and 3

Based on the observations, it shown that the highest phytoplankton abundance in all the stations are at a depth of 50 cm where the light intensity is optimum and the abundance were decreased with the increasing of water depth. Phytoplankton need sunlight to life, so that the area where the light intensity is very low, the phytoplankton cannot live and breed well [10]. Light is in greatest supply at the top of the water layer and phytoplankton are hypothesized to exist there when there is adequate nutrient supply [11, 12].

The Composition of Phytoplankton based on Division

The composition of phytoplankton is the percentage of the phytoplankton, which occupies a body of water. In this study showed that the composition of the phytoplankton at each station with five different depths with different genus (Figure 3). Overall, the percentage of the abundance of phytoplankton in Gondang Reservoir are most commonly found at each station and depth respectively are Chlorophyta, Cyanophyta, Chrysophyta and Pyrrophyta. In the tropics lake in the Philippines, it was found that Chlorophyceae, Dinophyceae, Cyanophyceae has a higher abundance due to high lighting conditions [13]. Gondang Reservoir waters, which are in the tropics area also have optimum solar lighting. Thus expected if the Chlorophyceae, Dinophyceae and Cyanophyceae division were more often found in greater numbers.





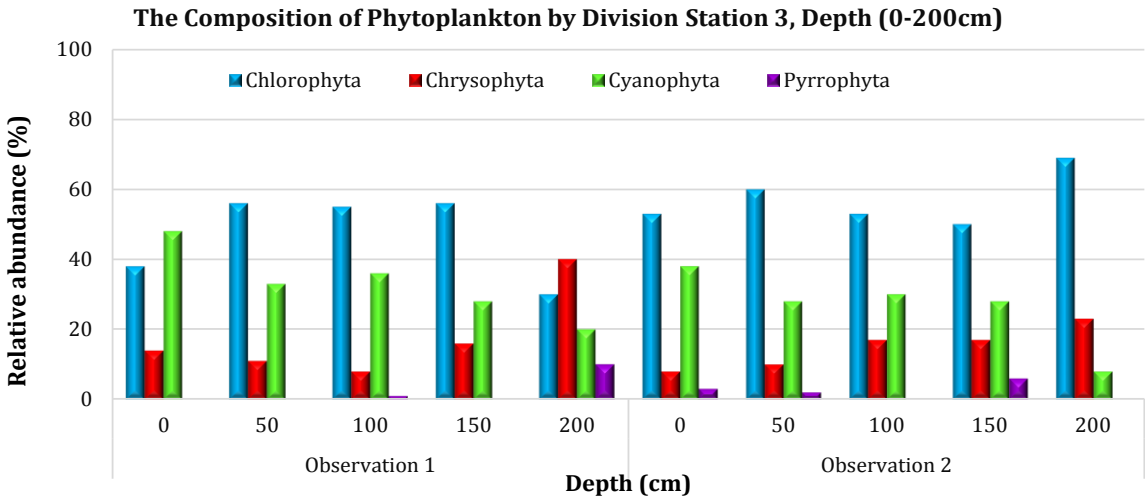


Figure 3. The composition of phytoplakton based on Division in Station 1, 2 and 3

The Composition of Phytoplankton based on Genus

The most common genus that has been found were *Chlorella, Spirulina, Staurastrum, Ulothrix, Genicularia, Achnanthes* and *Ceratium*. In some depth also found *Closterium, Nitzchia, Synedra* and *Gleocystis* genus at a depth of 150 cm and 200 cm at Station 1 (inlet) and 3 (outlet).

Overall, the percentage of the highest genus that has been found at the most depth in 3 stations (inlet, middle and outlet) owned by *Chlorella* on the first observation and the second observation, this is because *Chlorella* is a cosmopolitan organism or can live everywhere during the environmental conditions are appropriate and supportive for their life. *Chlorella* is cosmopolitan genus that can grow everywhere, except in a very critical environment for life [14]. The highest percentage of the genus in 3 stations and 5 depth is 39%. This result shows that no species is dominates. The percentage of composition of phytoplankton can be determined as follows, if the percentage more than 70% the species are dominance, 50-65% are spread domination and <50% there is no domination [15].

Analysis of Diversity Index

Based on analysis of the diversity index of phytoplankton, in Station 1 first observation, the diversity index ranged from 4.11614 to 5.90092 and the second observation between 5.44641 to 6.21286. At station 2 the first observation, the diversity index ranged from 5.46581 to 7.82316 and the second observation between 4.37093 to 7.8062. At station 3 first observation, the diversity index ranged from 4.05097 to 6.87702 and the second observation between 3.31755 to 6.65959 (Figure 4).

Overall, the value of phytoplankton diversity index (H') in Gondang Reservoir ranged from 3.31755 to 7.82316. The result showed that the diversity of waters were moderate to high or it can be said that the Gondang Reservoir have a degree of order or stability of the organisms were quite good (moderate).

Analysis of Water Quality Parameters

Waters parameters such as brightness, temperature, dissolved oxygen (DO), pH, nitrate and orthophosphate have been measured. The results of waters brightness measurement ranged from 1.34 to 1.64 meters. Brightness values during the study is still good for phytoplankton to perform photosynthesis.

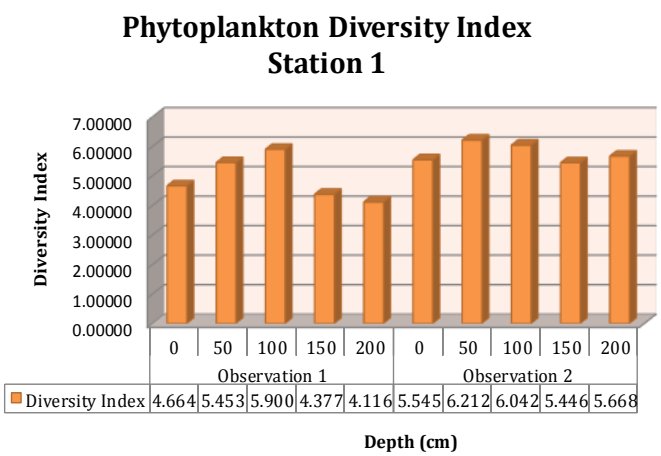
Water temperature at 3 stations and 5 depths ranging between 27-32^{o}C. Temperatures tend to be high in the surface (at a depth of 0 cm) and a concomitant with the increasing of water depth, the water temperature were decreases. This is due to the increasing depth then the light intensity wil also decrease so that the water temperature will decline as well. Usually, the deeper water has the lower temperature [16]. The water temperature that is good for phytoplankton growth ranged between 20 - 30^{o}C. Each type of phytoplankton has its own optimum temperature [17]. Overall, the water temperature in Gondang Reservoir are optimal for the growth of phytoplankton at a depth of 50 cm - 200 cm is 27-30^{o}C.

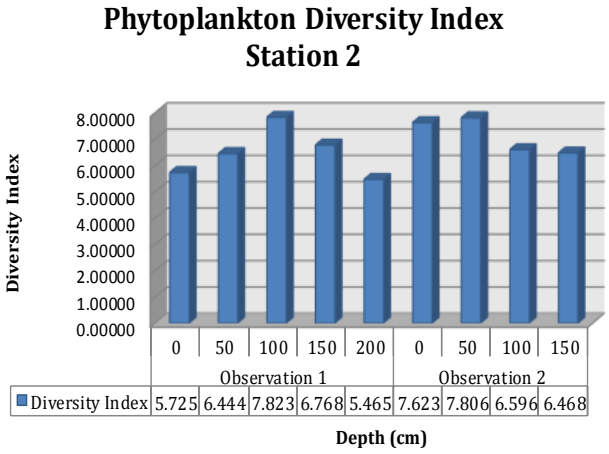
The levels of dissolved oxygen (DO) in this resent study were ranged from 4.91 to 6.86 mg/l. Good water quality is water that the contains of dissolved oxygen levels between 5-7 mg/l [18]. The values obtained that dissolved oxygen in waters Gondang Reservoir is still within the normal range and good to support life of aquatic organisms. Based on the observations, dissolved oxygen levels decline rapidly with depth. It is strongly related to the abundance of phytoplankton and their influence direct diffusion of oxygen into the water thereby affecting the levels of dissolved oxygen in waters Gondang Reservoir.

The degree of acidity (pH) in Station 1, 2 and 3 either on the first or second observation observation are 7. During the observation the pH value was stable at 7 and was good for phytoplankton. Most aquatic biota are sensitive to changes in pH and the optimum pH value are about 7 to 8 [18].

The levels of nitrate ranged from 0.033 to 0.214 mg/l, the values are still optimum for the growth of phytoplankton. Based on further review the nitrate levels which are good for the growth of phytoplankton is 0.01 to 0.43 mg/l [19] if the values are more than a preset range, it can lead to eutrophication. The result indicated that Gondang Reservoir waters including in mesotrophic water.

The levels of phosphate which are good for the growth of phytoplankton is ranged from 0.02 to 0.16 mg/l [20]. The levels of phosphate were obtained during the study ranged from 0.018 to 0.098 mg/l, in this case the phosphorus content is obtained that the Gondang Reservoir pertained mesotrophic. Overall the water quality parameters such as temperature, brightness, pH, DO, nitrate and orthophosphate classified as good for supporting the phytoplankton life.





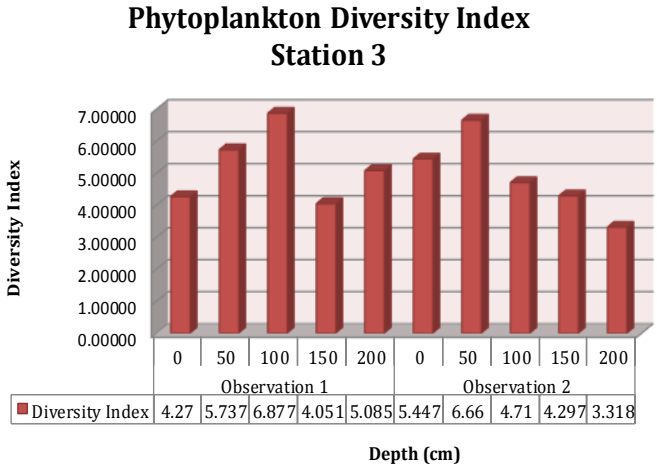


Figure 4. Phytoplankton Diversity Index in Station 1, 2 and 3

CONCLUSION

The vertical distribution of phytoplankton in Gondang Reservoir showed that the the water quality is still good for phytoplankton and classified as mesotrophic water. In the future, the observation of vertical distribution of phytoplankton can be used as a one of parameter to evaluate the water quality.

Recommendation

For future researches we suggest to use another parameter from phytoplankton such as chlorophyll *a* as water indicator quality.

Competing interests

The authors declare that they have no competing interests.

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A Review on Current Knowledge of Genetic Diversity of Domestic Goats (*Capra hircus*) Identified by Microsatellite Loci: How those Efforts are Strong to Support the Breeding Programs?

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ABSTRACT: Genetic characterization requires knowledge of genetic variation that can be effectively measured within and between populations. It is considered as an important tool for sustainable management or conservation of a particular population. Presence of limited diversity may hamper the possibility of populations to adapt the local environment in the long term, but loss of genetic diversity can also more immediately lead to decrease fitness within populations. In this paper, genetic diversity of more than 120 domestic goat populations found in various parts of the world has been summarized. The paper is limited only to the diversity study conducted by microsatellite loci. In all the goat populations reviewed, the within population genetic diversity is extremely higher than between population variation which might be due to the uncontrolled and random mating practiced among the breeding flock. However, the technical as well as statistical data management deficiencies, like selection of microsatellites and other sampling biases, observed in the reports could have their own influences on the limited and weak variations obtained within and among populations. The genetic distance among populations is very narrow especially populations found within states. In general, goats are the most transported animals during the lengthy commercial and exploratory journeys took place in the old world long time ago. This contributed the goat to have narrow genetic differentiation compared to other ruminant livestock. The technical fissures observed in the past efforts on identification and structure analyses of the goat populations might also demand further works to design appropriate conservation and breeding management programs.

Keywords: Domestic goat, Genetic distance, Heterozygosity, Microsatellite marker, Polymorphic information content

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INTRODUCTION

Genetic diversity has been shaped by past population processes and will also affect the sustainability of species and populations in the future [1]. Maintenance of genetic diversity in livestock species requires adequate implementation of conservation priorities and sustainable management programs [2]. It is also a key to the long-term survival of most species [3] and widely used to categorize animals in the world [4]. However, isolation-by-distance [5], historical and geological factors [6], physical barriers [7,8] and ecological factors through morphological adaptation to local conditions [9] are some of the factors which are suspected in disrupting patterns of genetic structure and gene flow of a given population. Especially in domestic animals, the gene flow disruption is overseen more by human intervention than by physical barriers [10].

Farm animal genetic diversity is required to meet current production needs in various environments, to allow sustained genetic improvement, and to facilitate rapid adaptation to changing breeding objective and serves as a tool for animal breeding and selection [11- 13]. However, classifying the genetic diversity based on historical, anthropological and morphological evidences [14] as well as their geographical origin are not satisfactory and enough for the purpose of conservation and utilization of these resources. In addition, phenotypic characterization provides a crude estimate of the average of the functional variants of genes carried by a given individual or population, and the appropriateness of phenotypic traits to study the genetic variation between populations is very limited [15]. Hence, comprehensive knowledge of the existing genetic variability is the first step for the conservation and exploitation of domestic animal diversity [16].

Goats are considered the most prolific ruminant among all domesticated ruminants especially under harsh climatic conditions [17]. The high versatility, moderate size and hardy nature of goats made them ideal as a food resource in the lengthy commercial and exploratory journeys that took place in the old world a long time ago [18]. Today, there are >1,000 goat breeds (www.fao.org/corp/statistics/en/), and recently >861.9 million goats are kept around the world with the respective continental share in Million: Asia (514.4), Africa (291.1), South America (21.4), Europe (18.0), Central America (9.0), Caribbean (3.9), Northern America (3.0) and Oceania (0.9) [19]. The existence of such a large gene pool is important for the potential future breed preservation and for the development of a sustainable animal production system [2].

The absence of well-managed conservation genetics programs and the uncontrolled introgression between indigenous as well as foreign breeds are seriously threatening the future of many populations in various parts of the world [20]. The high gene flow and the admixture of the breeds can result low level of genetic differentiation [21]. This has also an implication of the presence of terrible risk that most breeds may perish before they have been exclusively recognized and exploited. Microsatellite marker is the main molecular markers employed to identify and characterize genetic diversity of domestic goats found in various corners of the world by various scholars. However, following financial and other reasons, most of the efforts conducted may not be as supportive as expected in revealing the required information for designing appropriate and sustainable goat breeding programs. Therefore, given the limited number of efforts conducted on domestic goats, strength and gaps (with emphasis) of past efforts have been summarized and possible 'the way forward' is suggested in this paper.

GENETIC DIVERSITY AND POLYMORPHIC INFORMATION CONTENT

Genetic diversity refers to the total number of genetic characteristics in the genetic makeup of a species that serves as a way for populations to adapt to changing environments. It represents diversity within a population [22] and it is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offsprings bearing that allele. The population will continue for more generations because of the success of these individuals (http://genetics.nbii.gov/GeneticDiversity.html).

Choosing the appropriate breed or population for conservation is one of the most important problems in the conservation of genetic diversity in domestic animals. Some of the parameters which can help the study of genetic diversity within a population are expected heterozygosity estimates and allelic distribution; and they are believed as they are good indicators of genetic polymorphisms within a population [22-24]. On the other hand, the precision of estimated genetic diversity is a function of the number of loci analyzed, the heterozygosity of these loci and the number of animals sampled in each population [25].

Estimation of heterozygosities

Estimations of expected and observed heterozygosities are measures of genetic variability within a given population [23]. The expected heterozygosity is the proportion of heterozygotes expected in a population; whereas, observed heterozygosity is the percentage of loci heterozygous per individual or the number of individuals heterozygous per locus [26].

As it is indicated in the table, several reports confirmed the status of genetic variability of different goat populations (Table 1) and genetic diversity (H_E and H_O) estimates observed in goat of Sri Lanka, Australia, Korean, Botswana and in some Indian and Brazilian goat populations were below 0.5. This is because of maintaining microsatellite loci which had registered heterozygosity estimates below 0.5 in the respective breeds during the analysis. Literatures suggest that heterozygosity estimates having greater than 0.5 heterozygosity estimates are believed to be appropriate for genetic diversity study [44, 45]. Similarly, some of the estimated values were also closer to the margin. These low estimates imply that there might have been high selection pressure, small population size, minimal or null immigration of new genetic materials into the populations. Similar low genetic diversity estimates were reported for Argentinean and Chilean goat populations despite the small sample sizes used in the analysis [18].

Whereas the remaining estimates conclude that the studied populations have substantial and high amount of within population genetic diversity. This might be due to low selection pressure, large population size and immigration of new genetic materials [41]. High value of average expected heterozygosity within the populations could also be attributed to the large allele numbers detected in the tested loci [46]. In most of the above diversity estimates, the observed heterozygosity (H_O) and expected heterozygosity (H_E) estimates for each locus and goat population are closer to each other indicating no overall loss in heterozygosity (allele fixation) [40]. However, few

of the microsatellites studied by various scholars (e.g. [41]) had higher observed heterozygosity than expected heterozygosity estimates that probably indicate the existence of sampling bias [45].

Table 1. Estimation of genetic heterozygosity of indigenous goats

Breed	Country	H_E	H_O	No.MS	Author
Sri Lanka and Australian goats (12)	Sri Lanka-Australian	0.45-0.49	--	22	[27]
Korean goats	Korean	0.38	0.36	9	[28]
Indian goat populations	India	0.54-0.79	0.505	17- 25	[29-32]
Swiss goats (11)	Swiss3-24	0.66	--	47	[13]
Canary Island goats	C. Islands	0.62	--	27	[33]
Kalahari Red goats	--	0.63	--	8	[34]
Sub-Saharan breeds	*	0.54	0.56	11	[35]
Spanish Guadrrama goat	Spain	0.81	0.78	10	[36]
Croatian spotted goat	Croatia	0.77	0.76	20	[37]
Chinese ten goat populations	China	0.54-0.64	0.55-0.62	14	[38,39]
Brazilian goats and herds	Brazil	0.50-0.70	0.61-0.70	11	[40]
Guinea Bissau goat	W. Africa	0.60	0.61	14	[39]
Iranian goat populations	Iran	0.65-0.80	--	13	[2]
Ardi	S.Arabia	0.68	0.55	11	[41]
Twelve Chinese breeds	China	0.61- 0.78	0.60 - 0.78	17	[16]
Three Egyptian and two Italian goat breeds	Egypt and Italy	0.67- 0.79	--	7	[42]
Tswana goat	Botswana	0.16	0.12	12	[43]
Ethiopian goat populations	Ethiopia	0.55-0.69	0.52-0.68	15	[22,24]

MS=Microsatellite;* Uganda (4), Tanzania (5), Kenya (2), Mozambique (2), Nigeria (3), Mali (1) and Guinea Bissau (1)

On the other side, heterozygosity estimates of nine domestic Swiss goat herds were higher than Wild Ibex goats and Bezoar goats with the mean H_E ranging from 0.51 to 0.58 for domestic herds and from 0.17 to 0.19 for the wild species [47]. The lowest heterozygosity, the lowest genetic variation within the population, estimates are comparable with the mean observed (H_O=0.12±0.16) and expected heterozygosity (H_E=0.16±0.20) values of Tswana goat population [43] which is because of the effects of inbreeding and selective breeding in small and closed population. This idea is supported by Caňón et al. [48] who stated the positive correlation (r = 0.35) of population size with heterozygosity estimates. Low amounts of genetic diversity increase the vulnerability of populations to catastrophic events such as disease outbreaks that indicates high levels of inbreeding with its associated problems of expression of deleterious alleles or loss of over-dominance [2]. It can also destroy local adaptations and break up co-adapted gene complexes ultimately leading to the probability of population or species extinction [2].

Estimation of allelic distribution and locus variability

The allelic distribution is the other measure of genetic variability in a given population [23, 43]. The primary disadvantage of using allelic richness, i.e. the corrected mean number of alleles reflected in the standardized sample size [49], as a measure of genetic diversity is that it is highly dependent on sample size: large samples are expected to contain more alleles than small samples [50]. Similarly, more alleles are expected to be found in a region sampled many times than in a region sampled few times. Private allelic richness has the same problem: large samples are expected to have more private alleles than small ones. On the other hand, intensive sampling of genetically similar populations may reduce the number of private alleles to any population. Therefore, a region that has been sampled intensively may appear to have fewer private alleles than a region sampled less intensively. These problems have a straightforward statistical solution: rarefaction can be used to compensate for differences in sample size and number [50]. The mean number of alleles and expected heterozygosities are very accurate indicators of the genetic polymorphism within a population [41]. Mean observed alleles (n_a) that explain high level of polymorphism of the studied microsatellites were reported for several goat populations (Table 2).

Though the mean number of alleles (MNAs) indicated in table 2 showed the suggested minimum estimates, except some Ethiopian, Brazilian, Egyptian, Italian and Iran goat populations, comparatively the average as well as the range of alleles estimated were the highest estimation (14.9 mean number of alleles with a range of five to 43 alleles per locus for 45 breeds) for the 45 goat populations studied in the Mediterranean regions [48] (Table 2). In addition to this, all the microsatellites (30 microsatellites, which is the maximum coverage) were covered during the study. One of the reasons for the lowest estimates of MNA per locus, in many of the studies, might be because

of using very few bucks, e.g. 3-5 bucks per year for Tswana goat for 16 years of almost closed breeding program at BCA farm [43]; and it might also be because of directional selection for parasite resistance/tolerance coupled with increased productivity [51] that possibly accumulates inbreeding. Similarly, among the 26 loci of twelve Chinese goat populations, 17 were polymorphic and the number of alleles varied between 4 (ILSTS005) and 19 (BM2113); the remaining nine loci (excluded from the analysis) tested had less than four alleles or non-specific PCR products [16]. The later screening procedure was not undertaken by many of the authors. For studies like genetic distance, microsatellite loci should have no fewer than four alleles to reduce the standard errors of distance estimates [25].

For the other goat populations relatively encouraging estimates of MNA were reported. However, though those reports explain the existence of high polymorphism, the average number of alleles depends on sample size, number of observed alleles tends to increase with increasing population size and the number of sires used in a breeding program. This is because of the presence of unique alleles in populations which occur at very low frequencies [41, 43].

In general, heterozygosity deficiency may be resulted because of the presence of a null allele which is the allele that fails to multiply during PCR using a given microsatellite primer due to a mutation at the primer site [25, 53], small sample size where rare genotypes are likely to be included in the samples [2], Wahlund effect, that is presence of fewer heterozygotes in population than predicted on account of population subdivision and decrease in heterozygosity because of increased consanguinity (inbreeding) [11]. Higher heterozygosity provides better assignment performance [54] and the loss of alleles is probably the consequence of repeated founder effects during migration events [55].

Estimation of polymorphic information content (PIC)

Literatures state that the polymorphic information content (PIC) values depict the suitability of the markers and their primers used in the study for analyzing the genetic variability of a given population. Hence, microsatellite markers having greater than 0.5 PIC value are considered as highly informative and highly polymorphic [56, 57]. Therefore, highly polymorphic markers were employed for the goat populations indicated in Table 2.

In contrast to this, lower PIC values of microsatellites (for instance Korean goats PIC = 0.35, [28]; for Egyptian and Italian goats of few loci PIC=0.221, 0.482 & 0.389 [42] and for India goat having 28% of the loci <0.5 PIC [58]) which were expected to be excluded were included in the analysis. In fact, the PIC is determined by heterozygosity and number of alleles [41] and this makes microsatellite markers the choice for genetic characterization and diversity studies. In particular, the high PIC values of a particular marker suggest its usefulness for genetic polymorphism and linkage mapping studies in goats and 60% of microsatellite loci had significant hardy-Weinberg equilibrium (HWE).

Level of inbreeding (F_{IS})

F_{IS} is a measurement of the reduction in heterozygosity of an individual as a result of non-random mating within its subpopulation [59]. It is an average increase of homozygous loci by decreasing the heterozygous loci with the same proportion [43]. It is less suited to reflect historical processes because it has a different, more rapid dynamic than does gene diversity [59]. A high positive F_{IS} indicates a high degree of homozygosity and vice versa [45]. Inbreeding coefficients is estimated for populations which show significant deviation from the HWE [26]. This indirectly implies that inbreeding coefficient (F_{IS}) [59] is significant for significant HWE estimation; but it may not work for all loci of a population.

Based on this background, moderate and high level of inbreeding coefficients were reported by various scholars for different goat populations; for instance, for Marwari (F_{IS}=0.26; [32]), Jamunapari (F_{IS}=0.19; [66]), Mehsana (F_{IS}=0.16; [60]) and Kutchi (F_{IS}=0.23; [31]) breeds of India, Ardi goat breed (F_{IS} =0.18 with only 50% of the markers under HWE; [41]) of Saudi Arabia, Tswana goat breed (F_{IS} =0.12; [43]) of Botswana are some of the reports having high level of inbreeding. However, particularly for Tswana goat breed, the F_{IS} estimate ranged from -0.2340 (INRA006) indicating low levels of inbreeding at that marker locus to 0.8772 (MCM527) depicting high levels of inbreeding. This might be because of the small population size, closed breeding system and very limited number of breeding bucks used for many consecutive years in the farm [43]. The lowest heterozygosity and MNA estimates indicated in table1 and 2 above strengthen this rationale. However, tolerable mean value of F_{IS} (0.03) with the range of -0.223 to 0.220 was obtained for 17 microsatellites (with 12 MNA per locus and a range of 0.586 to 0.790 H_E estimates) of 12 Chinese indigenous goat populations [16].

The moderate level of inbreeding may be a result of moderate levels of mating between closely related individuals under field conditions and may be the uncontrolled and unplanned mating that caused high level of

inbreeding. On the contrary, very low inbreeding value (F_{IS}=0.10) were reported within 45 rare breeds of 15 European and Middle Eastern countries [48] compared with the above reports and the discrepancy between the observed and expected heterozygosities and the difference between the observed and effective number of alleles could confirm the existence of inbreeding [48]. Still the level of inbreeding estimates in all the 45 breeds studied except the two populations (St. Gallen Booted goat breed of Switzerland, F_{IS} = 0.048 and Thuringian forest goat breed of Germany F_{IS} =0.049) are not tolerable because the estimated values obtained were higher than 0.05.

Table 2. Estimated mean number of alleles and polymorphic information content

Breed	Country origin/Region	MNA per breed	MNA per MS	PIC per locus	Author	MS (No.)
Egyptian and Italian goat breeds (5)	Italy	6.48	3.8-9.8	0.22 -0.87	[42]	7
Indian goat breeds (10) f	India	6.33-9.7	4-24	0.08-0.90	[23,40,59,60]	17-25
Taleshi goat	Iran	6.7	2.4-5.2	0.54-0.81	[61]	9
Iranian goat breeds (6)	Iran	6.46 -8.15		0.71-0.86	[2,62]	13
Croatian spotted goat	Croatia	8.1	8.1	0.74	[37]	20
Ardi goat	Saudi Arabia	6.64		0.63	[41]	
Brazilian goat breed (3)	Brazil	3.5 -7.2	3-11	NA	[40]	11
Namibian goat breeds (4)	Namibia		4.67 – 6.00		[63]	18
Kalahari Red goat	South Africa	7.77	7.77	NA	[34]	18
Tete goat	Mozambique	5.58			[64]	
Pafuri goat	Mozambique	6.94			[64]	
45 breeds	Mediterranean regions	5.2-9.1	5-43	NA	[48]	30
Chinese goat populations (22)	China	5.24 -9.1	4-19	0.62-0.88	[16,65]	17-20
Tswana goat	Botswana		1.83	0.58	[43]	12
Indigenous goat populations (17)	Ethiopia	5.13 -6.73	2.06-23	NA	[22,24]	15

Key:- MS=Microsatellite

From thirty microsatellites used, twenty-four of them were in H–W equilibrium (p>0.05) and is more than 90% of the total 45 populations of European and Middle East goats studied [48]. However, small number of loci which were in Hardy-Weinberg Equilibrium: only seven loci (ILSTS011, SPS113, ILSTS029, SRCRSP3, MAF70, ILSTS005 and OarAE54) i.e., only 50% of the total fourteen microsatellite markers, showed Hardy Weinberg Equilibrium (HWE) (p>0.05) in Ardi goat population of Saudi Arabia [41]. Similarly, only 55% of the total microsatellites used showed HWE (P>0.05) in Alpine Saanen and Moxotó dairy goat populations in Brazil [40]. Such findings indicate the presence of effect of selection or uncontrolled breeding practice in the study populations [41]. Huge deviation from HWE (16 out of 20 loci), i.e. only 20% showed HWE (P>0.05), was observed on Kanniadu goats of India [67]; the possible reasons for the deviations pointed out were existence of "null" alleles, high mutation rate and size of homoplasy of microsatellite loci, besides the small study population. On the other hand, four out of the 12 loci (SRCRSP5, MCM527, ILST087 and INRA006) that differed significantly from the Hardy-Weinberg equilibrium (HWE) were observed indicating subjection of, particularly, those loci to systematic selection and dispersive forces such as genetic drift and inbreeding [43]. In this study, five out of the total 12 loci were monomorphic (fixed allele) that could be linked to genes responsible for parasitic resistance, and this goes in line with the study made by Beh et al. [68].

The large proportion of loci without of HWE might be because of those loci being under within major histocompatibility complex [69] and under strong natural selection pressure [70]; or it might be because of the presence of null or non-amplified alleles, allele grouping defects, a sampling structure effect, selection against heterozygotes or inbreeding [40]. In other study, it is also stated that deviations from Hardy-Weinberg equilibrium could also be due to a variety of causes including: excess of heterozygote individuals than homozygote individuals [71] in contrast Mahmoudi et al. [2] who stated heterozygosis deficiency is one of the parameters underlying departure from HWE), migration, high mutation rate at microsatellite loci and artificial selection .

GENETIC DISTANCE AMONG POPULATIONS

The simplest parameters for assessing diversity among breeds are the genetic differentiation or fixation indices. Several estimators have been proposed (e.g. F_{ST} and G_{ST}), the most widely used being F_{ST} [72], which measure the degree of genetic differentiation of subpopulations through calculation of the standardized variances

in allele frequencies among populations. Statistical significance can be calculated for the F_{ST} values between pairs of populations [73] to test the null hypothesis of lack of genetic differentiation between populations and, therefore, partitioning of genetic diversity [74]. Hierarchical analysis of molecular variance (AMOVA) can be performed to assess the distribution of diversity within and among groups of population [75].

In relative to other markers, microsatellite data are commonly used to assess genetic relationships between populations and individuals through the estimation of genetic distances [76-80]. The most commonly used measure of genetic distances is Nei's standard genetic distance (D_S) [81]. However, the modified Cavalli-Sforza distance (D_A) is recommended for closely related populations where genetic drift is the main factor of genetic differentiation, as is often the case in livestock populations particularly in the developing world [82].

Genetic relationship between populations is often visualized through the reconstruction of a phylogeny, most often using the neighbor joining (N-J) method [83]. However, a major drawback of phylogenetic tree reconstruction is that the evolution of lineages is assumed to be non-reticulated, i.e. lineages can diverge, but can never result from crosses between lineages. This assumption will rarely hold for livestock where new breeds often originate from cross-breeding between two or more ancestral breeds. The visualization of the evolution of breeds provided by phylogenetic reconstruction must, therefore, be interpreted cautiously.

Multivariate analysis and more recently Bayesian clustering approaches have been suggested for admixture analysis of microsatellite data from different populations [84]. Probably the most comprehensive study of this type in livestock is a continent-wide study of African cattle [85], which reveal the genetic signatures of the origins, secondary movements, and differentiation of African cattle pastoralism.

Based on comparison of genetic distances that measure genetic drift, with microsatellite data set, the Reynolds distances underestimate the divergence of eastern Mediterranean goat populations (Saudi Arabia, Turkey, Albania and Cyprus) with a high heterozygosity [48]. Model-based clustering [84] of the goat microsatellite genotypic values indicates that the most significant subdivision is at the level of breeds or groups of closely related breeds [48]. Analysis at lower *K*-values may indicate a subdivision of the goat population [86] that preceded breed formation.

In relative to other reports, lower average values of F_{ST} for the four goat populations clusters (East Mediterranean: F_{ST}=0.033, Central Mediterranean: F_{ST}=0.040, West Mediterranean: F_{ST}=0.051 and Central-north European: F_{ST}=0.069) were obtained [48] than the values of 0.14 recorded for Asian goats [27], of 0.17 for Swiss goat populations [49] and of 0.10 for a set of Chinese goat populations [16]. Similar low estimate of mean differentiation among populations (F_{ST} = 0.0717) was also reported that indicates presence of mixing among population and the most variability occurs within a population [40]. This might be because of gene flow among most breeds has probably been restricted by geographical isolation rather than adherence to pedigree; i.e. a geographical restriction of genetic contacts of population may cause geographical clines or maintain clines that predate breed formation [48].

F_{ST} values for each pair of the goat populations in Ethiopia varied from 0.001 to 0.040 [22]. The average F_{ST} values over all microsatellite loci was 0.026, indicating that a 2.6% of total genetic variation corresponded to differences among populations, whereas 97.4% was explained by difference among individuals. Similarly, it was also noted that 5% of the total variation occurred due to population subdivision, while the remaining 95% of the variation existed among individuals within the goat ecotypes [24].

It was recommended that the highest genetic distance (F_{ST}) to be higher than 0.25, moderate to be between 0.05 and 0.25 and the lowest estimate below 0.05 [46, 87]. In general, the genetic distance between populations obtained by many of the scholars [16, 21, 22, 24, 40] is almost negligible (<0.05) and/or moderate ($0.05<F_{ST}<0.25$) values. Some of the authors revealed significant genetic distance estimates among populations. This implies that, despite the limitations of sampling and other related statistical management limitations stated above there is relatively moderate genetic sub-differentiation among the goat populations. A fixation index (F_{ST}) of about 0.15 is considered to be an indication of significant differentiation among populations [88]. In line with this, as an indirect way to measure quantitative genetic diversity, a fixation index (F_{ST}) of about 0.25 total genetic variance could be explained among-breed genetic variance [49].

In the phylogeny tree analysis employing both the NJ and UPGMA trees might be good. However, it would have been more informative if the fitness of the trees were statistically tested. This limitation makes the result blurred and difficult to arrive at certain conclusion with either of the phylogenetic tree analyses. In addition, besides to the polymorphic nature of microsatellites there might be a chance to face monomorphic nature of them. Hence, this demands some techniques to isolate such loci. However, there is no clear methodology that describes whether such techniques were employed or not. Monomorphic microsatellite loci were obtained while studying the Indian domestic goat populations and dropped out from the analysis [30]. Probably, the minimum

estimates of MNA per locus obtained in the microsatellite loci genotyped might be an indication of absence of employing some screening techniques. Such limitations were seen in many of the studies.

GAPS IDENTIFIED

Apart from the least sample size used in some of the studies, e.g. Halima et al [24] who used eight animals to represent a population and which is quite far from FAO recommendation for SSR marker analysis [89], the number of samples used for a study was not equal which leads the genetic diversity parameters like HWE and MNA to be sensitive for biasness; or there is no any technique indicated in the papers which was employed to handle such a limitation [90]. Large samples are expected to have more alleles than small samples [91]; however, the degree of influence of small sample size is weak as compared with the size of number of markers to be used [90].

In addition to the procedures to be followed in handling unequal sample size, selection of microsatellite loci which are efficient in polymorphism and techniques of screening monomorphic loci [93] and design of statistical genetic analysis in general are not clearly indicated in the papers and might bias the readers. This ultimately could have their own influence on implementation of further activities of improvement and conservation breeding programs. On the other hand, only very few or no microsatellite loci used in the analysis showed higher observed heterozygosity values than expected heterozygosity values [16, 22, 24, 39, 40]. This probably implies the existence of sampling bias [45]. In addition, some of the microsatellite loci (table 1) had shown H_E and H_O estimates of less than 0.5; however, it was suggested that such loci having values less than 0.5 are not appropriate for heterozygosity evaluation [44,45]. Similarly, the number of alleles found per locus is the other indicative in evaluating the efficiency of loci; hence, though it was not seen in some of the studies found in table 2, the number of alleles to be found per locus for remarkable genetic diversity of a population should be equal or greater than four [25, 92]. These all points remark as the microsatellites could be dropped out or could require to be prudent in selecting microsatellite. Apart from that it is important to note to be keen in selecting microsatellites to deliver strong recommendation that serves for effective sustainable conservation and breeding management strategies.

CONCLUSIONS AND RECOMMENDATION

Genetic diversity studies carried out on domestic goat at various parts of the world were compiled in this paper. More than 120 goat populations were included in the review. These all goat populations were studied with microsatellite markers. The results indicated that there is high within population genetic variations and very narrow population differentiation among the goat populations studied. On the other side, limited sample sizes which are not equal for the populations included in the respective studies, weak efficiency of the markers employed for the analysis (e.g. few numbers of alleles per marker, very low heterozygosity estimate per marker, etc) which lead to bias the parameters measured or absence of handling techniques to capture those limitations are observed in most of the studies. In general these all demand further works to support the goat breeding interventions.

Competing Interests
The authors have declared that there is no competing interest

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Biological Basis of Personality: A Brief Review

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ABSTRACT: This brief review discusses the research on biology-based personality and personality theories with biological basis. These theories include Eysenck's three factor model of personality, Gray's reinforcement sensitivity theory, and Cloninger's model of personality. The biology-based personality research is a relatively new topic in the field of psychology and there is a lot of scope for further research in the future specially in the field of neuroscience. Although it is a relatively new topic, but growing in interest and number of publications. Only recently in August 2004, there was a conference specifically on this topic, called "The Biological Basis of Personality and Individual Differences". This was a good forum for presenting and sharing of ideas between psychologists, psychiatrists, molecular geneticists, and neuroscientists. Recently it was named as the field of 'Personality. Therefore, further research on the biological basis of personality, especially in the field of 'Personality Neuroscience' is recommended.
Keywords: Biology-based Personality, Personality Theories, Personality

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INTRODUCTION

Biological Basis of Personality

Personality is derived from the Latin word, persona, where it originally referred to a theatrical mask [1]. The study of personality started with Hippocrates' four humors and gave rise to four temperaments [2]. Personality is the dynamic organization within the individual of those psychophysical systems that determine his characteristics behavior and thought [3]. Weinberg and Gould [4] defined personality as the characteristics or blend of characteristics that make a person unique. The American Psychological Association defines personality as individual differences in characteristic patterns of thinking, feeling, and behaving [5].

The study of personality focuses on two broad areas: [1] understanding individual differences in particular personality characteristics, such as sociability or irritability and [2] understanding how the various parts of a person come together as a whole [5].

Biological Basis of Personality

The biological perspective on personality emphasizes the internal physiological and genetic factors that influence personality. It focuses on why or how personality traits manifest through biology and investigates the links between personality, DNA, and processes in the brain. It is primarily accomplished through correlating personality traits with scientific data from experimental methods such as brain imaging and molecular genetics [6].

The biological basis of personality is the theory which states that the anatomical structures located in the brain contribute to personality traits. This is derived from neuropsychology, a branch of science which studies how structure of the brain is related to various psychological processes and behaviors. For instance, in human beings, the frontal lobes are responsible for foresight and anticipation, and the occipital lobes are responsible for processing visual information. In addition, certain physiological functions such as hormone secretion also affect personality. For example, the hormone testosterone is important for sociability, affectivity, aggressiveness, and sexuality [7]. Other studies also show that the expression of a personality trait depends on the volume of the brain cortex it is associated with [8].

Personality neuroscience involves the use of neuroscience methods to study individual differences in behavior, motivation, emotion, and cognition. Personality psychology has contributed much to identifying the important dimensions of personality, but relatively little to understanding the biological sources of those dimensions. However, the rapidly expanding field of personality neuroscience is increasingly shedding light on this topic. DeYoung [8] provided a survey of progress in the use of neuroscience to study personality traits, based

on the Big Five dimensions: extraversion, neuroticism, agreeableness, conscientiousness, and openness or intellect.

The biological approach to personality has also identified areas and pathways within the brain that are associated with the development of personality. A number of theorists, such as Hans Eysenck, Gordon Allport, and Raymond Cattell, believe that personality traits can be traced back to brain structures and neural mechanisms, such as dopamine and serotonin pathways [6]. One of the best known biological theorists was Hans Eysenck, who linked aspects of personality to biological processes. Eysenck argued that introverts had high cortical arousal, leading them to avoid stimulation. On the other hand, he believed that extroverts had low cortical arousal, causing them to seek out stimulating experiences [9].

The emphasis is placed on the biochemistry of the behavioral systems of reward, motivation, and punishment. This has led to a few biologically based personality theories such as Eysenck's three factor model of personality, Grey's reinforcement sensitivity theory, and Cloninger's model of personality. The Big Five model of personality is not biologically based, but still some studies provided biological support for this model [10]. The most influential scientists in the field of biology-based personality theories are Hans Eysenck and Jeffrey Alan Gray. Eysenck used both behavioral and psychophysiological methodologies to test and develop his theories [11].

History of Biology-based Personality Research

It has been, since the ancient Greek time, attempted to explain personality through spiritual beliefs, philosophy, and psychology. Historically, studies of personality have traditionally come from the social sciences and humanities, but in the past two decades neuroscience has begun to be more influential in the understanding of human personality [12]. Eysenck published a book called "Dimensions of Personality," describing the personality dimensions of extraversion and neuroticism. He has many publications in this field [13-18]. Gray, his student, studied personality traits as individual differences in sensitivity to rewarding and punishing stimuli [11]. The significance of Gray's work and theories was the use of biology to define behavior, which stimulated a lot of subsequent research [19].

The biology-based personality research is a relatively new topic and recently, in 2004, there was a conference entitled "The Biological Basis of Personality and Individual Differences". This resulted in the publication of a book "The Biological Basis of Personality and Individual Differences" [20].

Personality Theories with Biological Basis

The following theories of personality have a biological basis. It will provide, in addition, a biological support for a popular non-biologically based personality theory, the Five Factor Model.

Eysenck's Three Factor Model of Personality: It was based on activation of reticular formation and limbic system in the brain [21]. The reticular formation is a region in the brainstem that is involved in mediating arousal and consciousness. The limbic system is involved in mediating emotion, behavior, motivation, and long-term memory. The three factors are extraversion (interaction with people), neuroticism (emotional instability), and psychotism (aggression and interpersonal hostility) [11].

Gray's Reinforcement Sensitivity Theory: This theory is based on the idea that there are three brain systems that all differently respond to rewarding and punishing stimuli [11]. These are (a) fight-flight-freeze system which mediates the emotion of fear (not anxiety) and active avoidance of dangerous situations. The personality traits associated with this system is fear-proneness and avoidance; (b) behavioral inhibition system which mediates the emotion of anxiety and cautious risk-assessment behavior when entering dangerous situations due to conflicting goals. The personality traits associated with this system is worry-proneness and anxiety; and (c) behavioral approach system which mediates the emotion of anticipatory pleasure, resulting from reactions to desirable stimuli. The personality traits associated with this system are optimism, reward-orientation, and impulsivity [11].

Cloninger Model of Personality: It is based on the idea that different responses to punishing, rewarding, and novel stimuli are caused by interaction of three dimensions: (a) novelty seeking which deals with the impulsiveness of people and is correlated with low dopamine activity; (b) harm avoidance which deals with the anxiousness of people and is correlated with high serotonin activity; and (c) reward dependence which deals with the approval seeking of people and is correlated with low norepinephrine activity (20).

Five Factor Model of Personality: It describes five core traits that a person possesses: (a) openness (enjoyment after experiencing new stimuli); (b) conscientiousness (dutiful and goal-oriented); (c) extraversion (people who seek stimuli outside of themselves); (d) agreeableness (aim to cooperate and please others); and (e) neuroticism (people who are emotionally unstable) [10; 22].

Hegerl et al. [23] in an article entitled “Sensory cortical processing and the biological basis of personality” concluded that their results support the concept that the serotonergic brain system, which is supposed to modulate sensory processing in primary auditory cortices, is an important factor underlying individual differences in sensation seeking. Action-oriented personality traits such as sensation seeking, extraversion, and impulsivity have been related to a pronounced amplitude increase of auditory evoked scalp potentials with increasing stimulus intensity [23]. The biological approach to personality has also identified areas and pathways within the brain, as well as various hormones and neurotransmitters, that are associated with the development of personality [6].

CONCLUSION AND RECOMMENDATIONS

As mentioned earlier, the biology-based personality research is a relatively new topic in the field of psychology and there is a lot of scope for further research in the future specially in the field of neuroscience. Although it is a relatively new topic, but growing in interest and number of publications. Only recently in August 2004, there was a conference specifically on this topic, called “The Biological Basis of Personality and Individual Differences”. This was a good forum for presenting and sharing of ideas between psychologists, psychiatrists, molecular geneticists, and neuroscientists. A book entitled “The Biological Basis of Personality and Individual Differences” was later on published [22]. Recently, DeYoung has gone further to name it as the field of 'Personality Neuroscience' [8].

Therefore, further research on the biological basis of personality, especially in the field of 'Personality Neuroscience' is recommended.

Competing interests

The authors declare that they have no competing interests.

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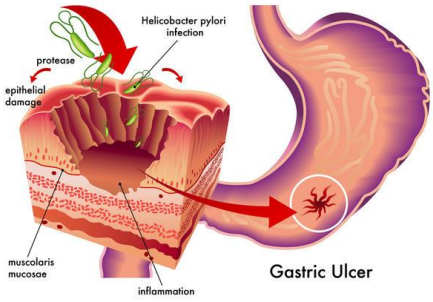

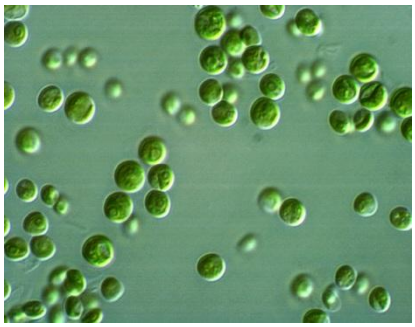

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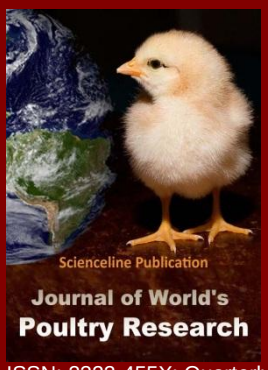

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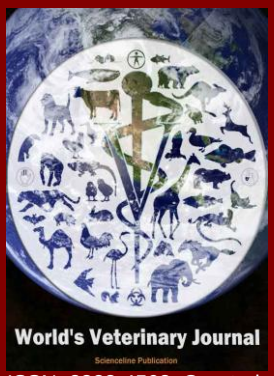

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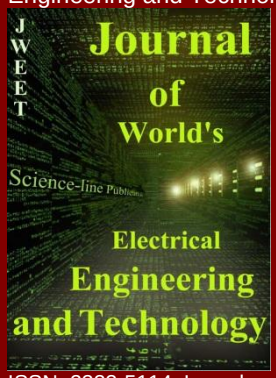

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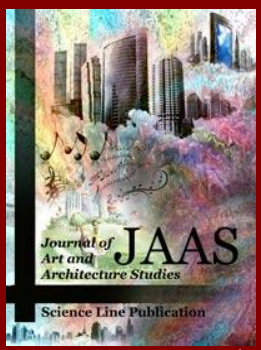

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