INTRODUCTION
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Population genetics deals with consequences of Mendelian laws on the composition of the population with special reference to the effects of mutation, selection, migration and chance fluctuation of gene frequencies (Vogel & Motulsky, 1982). All these factors determine the genetic structure of the population under consideration. The structure and gene pool of human populations are studied by considering gene frequencies of marker genes. Further, it involves the study of conditions of stability in a population and determine modes of change in gene frequencies. Change in the genetic composition of a population is known as evolution. The gene frequency differentiation plays an important role in microevolution of man. A geneticist can approach macroevolutionary phenomena only by the inferences drawn from the known microevolutionary ones. Since Darwin's theory of natural selection was synthesized in modern genetic terms, the development in genetics from gene to population level has advanced further. During the last few decades, population genetics has contributed much to the understanding of both long term human evolution and ongoing biological differentiation of the local populations.

The recent trend is to study the population 'Variation' in respect of several genetic markers. A large
number of different enzymes and proteins are made in the human organism and there are now good reasons to believe that the amino-acid sequence of each of their polypeptide chains is coded in the DNA of a separate gene locus. So there is a vast array of the so called 'structural' gene loci in the genetic constitution of each individual. Further, it has been shown that, at certain loci, many different alleles determining structurally distinct versions of the corresponding polypeptide may exist in human populations. Most of these are quite rare. But in some cases certain alleles at a particular locus may be sufficiently frequent as to give rise to what is often referred to as 'genetically determined polymorphism'. That is a situation in which individual members of the population can be categorized into two or more separate types, each relatively common and characterized by the distinctive manner in which they synthesize the particular enzyme or protein (Harris, 1972). 'Protein polymorphism' signals the existence of 'allelism', and it has been estimated that from 20 to 50 percent of all structural gene loci in a given species exist in two or more allelic forms in any given population (Goodenough, 1978).

Interest is now focussed on the distribution of genes within a population and differences in their frequencies in different populations. With the discovery of electrophoretic and biochemical techniques it is now possible to detect many
hereditary variants of blood and other tissues. Since most of serological, biochemical and other genetic characters have a distinct mode of inheritance, and majority of them are perhaps little influenced by environment they are the obvious choice for comprehending, evolutionary divergence and genetic differences between population groups.

India has been peopled from pleiostocene time and has been the seat of early urban civilization of Indus Valley. The ecology varies from snow bound Himalayas in the North, to the arid Thar desert in the north-west, to the coast line about 6083 km around peninsula. (Balakrishnan, 1978). The variety of flora and fauna consequent on different physical features of geography have a bearing on the habitations of human populations. The complexities of race, religion, caste and color make India an 'Ethnological museum' wherein one can study the mankind in various perspectives.

About 1500 studies (Gupta and Dutta, 1966) on over 800 populations to describe morphologically the people of Indian subcontinent were listed as mostly endogamous. In the last two decades, however there is a marked shift from the morphological studies to genetic investigations. A large number of populations have been studied for example ABO system (an estimated 800 studies are available – Majumdar & Roy, 1982). Similarly large number of populations are tested
for MN, Rh, serum proteins especially Transferrin (Kamboh & Ferrel, 1987), Haptoglobins (Bakshi et al; 1977) and Albumin (McDermid, 1971) and red cell enzymes. A few populations mostly caste Hindus have also been studied for a number of markers (Ananthakrishnan and Kirk, 1969; Ananthakrishnan 1972; Bhalla, 1966; Blake et al, 1971; Kirk, 1968).

A number of both morphological and genetic studies revealed considerable heterogeneity among the people of India, and at least 4 broad morphological types, namely Australoids, Caucasoids, Mongoloids and Negroids who have contributed to the biological composition of India (Malhotra et al, 1978). Dravidians, now concentrated in South India, have probably come through the North-west either from Central (or) West Asia (Balakrishnan, 1978).

While considering the genetic relationships among the populations of the region the most important feature to be taken into account is the caste, which is basic to the Hindu society and has influenced other religions also. Its most important characteristic being the endogamy, which would have helped to preserve to a considerable extent the characteristics of original gene pool in the absence of drift (Balakrishnan, 1978).
The large heterogeneous people of India, living in various ecological zones are bound for centuries to a variety of specific mating patterns due to religion and tradition. This has resulted in division of population into a number of endogamous groups (Dobzhansky, 1965), whose members have to adhere to the social laws. The endogamous groups contribute the framework of social organization known as caste system (Karve, 1961).

Many theories have been put forward to explain the origin of caste system. According to classical interpretation, the castes are supposed to have been formed by splitting of the 4 varnas through occupational specialization (Malhotra, 1974). According to Karve (1961), the subcastes are not always segments split off from the same caste and, in most cases, are probably the result of the lack of fusion of different racial elements.

The endogamous groups varying enormously in terms of language, pattern of marriage, rituals, food habits, and many aspects of culture provide human geneticists with a variety of important and rare material for specific enquiries in the field of population genetics (Roychoudhury, 1977).

In the present work an attempt is made to study the genetic relations between the two endogamous populations namely Reddy and Kamma of Nellore District. The
investigation extends detailed examination to 6 genetic markers: (1) A_1A_2BO (2) Rh(D) blood group systems (3) Transferrin (4) Haptoglobin (5) Ceruloplasmin (6) Albumin. The specific aims are: - 

1. To study the genetic constitution of Reddis (Panta, Pokanati, Pedakanti - three subcastes of Reddies) and Kammass (Gampachatu Kammass).

2. To examine the genetic diversity and gene differentiation among Reddy and Kamma Castes.

3. To assess the genetic affinities among these populations (Reddy & Kamma) under study, and to a limited extent with the other castes of Andhra Pradesh.