

## ACE gene polymorphism among Panika and Baiga of Madhya Pradesh

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### ABSTRACT

*The present study was carried out to study the ACE gene polymorphism among the Panika and Baiga of Madhya Pradesh. A total number of 120 individuals (age group 12 to 50) i.e. 60 samples each from both the populations constitute the samples for the present study. The highest genotype frequency of ID i.e. 60% is found in both the populations. 20% each of II and DD homozygous genotype were found in Panika whereas 28.33% and 11.66% for II and DD homozygous genotype were found respectively in Baiga. However, both the populations show non-significant difference from each other having p-value of 0.33 ( $\chi^2 = 2.18$ ) at 95% confidence interval. Hence, it follows Hardy Weinberg Law.*

**KEYWORDS:** Angiotensin Converting Enzyme, Polymorphism, Panika, Baiga, ACE gene

### INTRODUCTION

Angiotensin I-converting enzyme (ACE), a zinc metallopeptidase, cleaves angiotensin I to angiotensin II (octapeptide) which is a potent vasoconstrictor and at the same time activates the vasodilator, bradykinin (Ward 1995). It plays an important role in blood pressure regulation and maintenance of salt and water homeostasis in the body (Murry et al. 2011).

Though the human ACE gene contains a number of variable polymorphic regions that can be of potential use in genetic analysis of populations (Rieder et al. 1999), the insertion/deletion (I/D) polymorphism present in intron 16, in particular has been extensively investigated with reference

to many diseases including heart disease, hypertension, diabetes and diabetic nephropathy (Doi et al. 1996, Ohno et al. 1996, Yoshida et al. 1996, Staessen et al. 1997, and Kennon et al. 1999).

A group of alleles of some genetic variants are expected to have a combined negative or positive effect in a single Mendelian population of a specific geographical area. ACE is one of the candidate genes for various complex disorders like IgA Nephropathy (Yoshida et al. 1995), Meningococcal disease (Harding et al. 2002), Preterm Cardio-respiration (Harding et al. 2003), Alzheimer disease (Elkins et al. 2004), and Severe Acute Respiratory syndrome (Itoyama et al. 2004). Polymorphism of the ACE gene also varies from population to population. Hence, it is important to have a baseline data on the frequency distribution of known and clinically important mutation of the particular gene among various population especially Tribal population of Madhya Pradesh, where the highest number of tribes in India inhabited in this state, which is under reported for both clinical and genetic data. Therefore, in the present study, an attempt is made to understand the extent of ACE gene polymorphism among Panika and Baiga tribes of Madhya Pradesh.

The Baiga and Panika Tribes are one of the backward tribe in Madhya Pradesh. According to 2001 census, the population of Baiga was 250,000 and population of Panika ranging from 47,806 to 81,335 ([http://censusindia.gov.in/Tables\\_Published/SCST/dh\\_st\\_madhya\\_pradesh.pdf](http://censusindia.gov.in/Tables_Published/SCST/dh_st_madhya_pradesh.pdf)). Baiga belong to the Austro-asiatic linguistic group, while Panika belong to Dravidian linguistic group (Yadav et al. 2012). In terms of population size, Baiga are more than Panika, but Baiga are found to be the more primitive. They still retain their hunting and gathering feature and depend a lot on forests for their food, medicine and their living.

## **MATERIALS AND METHODS**

A total of 120 blood samples with the age group varied from 12-50 years constitute the sample size of the study. The samples were collected by using the finger prick method randomly from individuals unrelated up to 1<sup>st</sup> cousin after a prior informed written consent. DNA was isolated using the High yield Genomic DNA isolation kit from 300 µl of blood sample (Real Biotech Corporation) and quantified by Nanodrop spectrophotometer. The ACE gene mutation was detected by the polymerase chain reaction (PCR) amplification analysis (Majumder et al. 1999) and fragments of about 190 bp (D allele) and 490 bp (I allele) were separated on 2% agarose gel electrophoresis and the genotypes were visualized with long wave UV light with ethidium

bromide as a staining agent. The statistical analysis was performed using the software POPGENE version 1.31. (Yeh and Yang 1999). Genotype distribution differences between the two populations were assessed using Chi-square contingency test.

## RESULT

Table 1 shows the distribution of genotype and allele frequency of ACE I/D polymorphism among the Panika and Baiga of Madhya Pradesh. A total number of 120 individual samples i.e.60 sample each in both the population were screened for ACE I/D polymorphism among the Panika and Baiga. All the locus of ACE I/D genotype were found to be polymorphic. The ogenotype frequency of I/D is found to be very high i.e. 60% in both the population. 20% each of II and DD homozygous genotype were found in Panika whereas 28.33% of II and 11.66% of DD homozygous genotype were found in Baiga. The D allele frequency among the Panika and Baiga is 0.50 and 0.42 respectively. While applying Hardy Weinberg law, the expected and (observed) genotypic frequencies of II, ID, and DD are as 25% (20%), 50% (60%) and 25% (20%) respectively in Panika whereas in Baiga, the expected and (observed) genotypic frequencies of II, ID, and DD are as 33.8% (28.3%), 49% (60%) and 17.2% (11.7%) respectively. The chi-square and (p-value) for Panika and Baiga is 2.203 (0.138) and 3.065 (0.080) respectively. The p value of both the population is not less than 0.05. Hence, Panika and Baiga follow Hardy Weinberg Law and the observed frequencies differences may be due to chance factor.

**Table-1:** The genotype and allele frequency distribution of ACE I/D polymorphism among Panika and Baiga of Madhya Pradesh.

| POPULATION         | GENOTYPE  |         |           | ALLELE FREQUENCY |      | $\chi^2$ | P-value |
|--------------------|-----------|---------|-----------|------------------|------|----------|---------|
|                    | II        | ID      | DD        | I                | D    |          |         |
| <b>PANIKA (60)</b> | 12(20.0%) | 36(60%) | 12(20.0%) | 0.50             | 0.50 | 2.18     | 0.337   |
| <b>BAIGA (60)</b>  | 17(28.3%) | 36(60%) | 07(11.7%) | 0.58             | 0.42 |          |         |

The comparison between Panika and Baiga on applying chi square tests show that p value = 0.33 which is > 0.05 level. Hence, there is no significant difference at 95% confidence interval in the distribution of ACE genotypes among both the population on the basis of genotypic frequencies. Hence, it follows Hardy Weinberg Law.

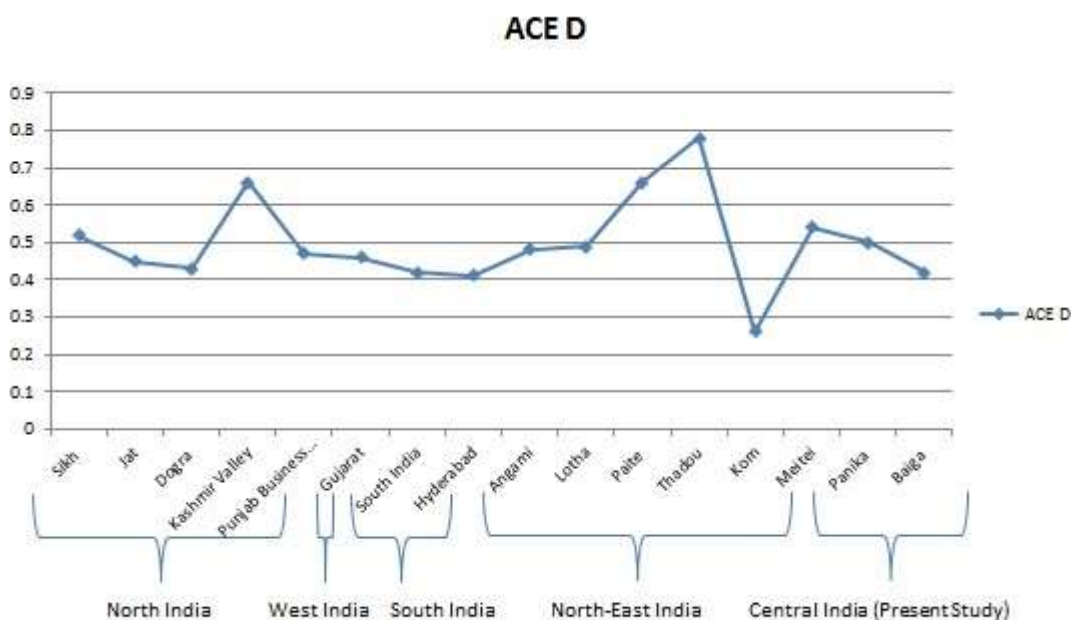
## DISCUSSION

The frequency of D allele of ACE ID polymorphism is relatively higher among the Panika (50%) as compared to that of the Baiga (42%). However the difference between the two tribal groups is statistically not significant with respect to the genotype distribution (Chi-square value- 2.18, p-value 0.33).

**Table 2:** ACE D allele frequency among the Panika and Baiga with other Indian population.

| Population                | ACE D | References             | Geography        | Linguistic group |
|---------------------------|-------|------------------------|------------------|------------------|
| Sikh                      | 0.52  | Pasha et al. 2002      | North India      | Indo European    |
| Jat                       | 0.45  | Pasha et al. 2002      | North India      | Indo European    |
| Dogra                     | 0.43  | Pasha et al. 2002      | North India      | Indo European    |
| Kashmir Valley            | 0.66  | Syeed et al. 2010      | North India      | Indo European    |
| Punjab Business community | 0.47  | Badarudoza. 2009       | North India      | Indo European    |
| Gujarat                   | 0.46  | Dwivedi et al. 2012    | West India       | Indo European    |
| South India               | 0.42  | Deeba et al. 2009      | South India      | Dravidian        |
| Hyderabad                 | 0.41  | Bhavani et al. 2005    | South India      | Dravidian        |
| Angami                    | 0.48  | Murry et al. 2011      | North East India | Tibeto-Burman    |
| Lotha                     | 0.49  | Murry et al. 2011      | North East India | Tibeto-Burman    |
| Paite                     | 0.66  | Saraswathy et al. 2009 | North East India | Tibeto-Burman    |
| Thadou                    | 0.78  | Saraswathy et al. 2009 | North East India | Tibeto-Burman    |
| Kom                       | 0.26  | Saraswathy et al. 2009 | North East India | Tibeto-Burman    |
| Meitei                    | 0.54  | Saraswathy et al. 2009 | North East India | Tibeto-Burman    |
| Panika                    | 0.50  | Present Study          | Central India    | Dravidian        |
| Baiga                     | 0.42  | Present Study          | Central India    | Austro-Asiatic   |

The distribution of D allele is found to vary in Indian population based on geography and the linguistic group i.e. it is found to be highest in north-east India with an average frequency (0.54), followed by north India (0.51), west India and Central India (0.46), and South India (0.42). The average D allele frequency of the present study is found to be exactly similar with West India (0.46). Linguistically, Tibeto-Burman group is found with the highest average D allele frequency (0.54), followed by Indo-European group (0.50), Dravidian (0.44), and Austro-Asiatic (0.42).



**Figure 1:** Graphical representation of D allele frequency in different population of India.

The frequency of D allele of ACE ID polymorphism vary considerably across the world population ranging from 0.000 among the Nasioi Melanesian (ALFRED database, extracted from Kenneth K.K et al., data unpublished submitted at Yale University) to 1.000 among the Abazians in Europe (Romualdi et al. 2002). Here, factors other than genetic such as natural selection or social factors may be conducive for the survival of more mutated alleles though not really selecting against the wild type allele (Murry et al. 2011). It is reported that the D allele behaves as a marker of atherosclerotic cardiovascular complications (Staessen et al. 1997), Hypertrophic

cardiomyopathy patients with the DD genotype of the ACE gene polymorphism revealed greater progression of the Left Ventricular hypertrophy (Doolan et al. 2004). Other studies have found out that the D allele is an independent risk factor for diabetic nephropathy (Doi et al. 1996, Ohno et al. 1996, Yoshida et al. 1996, Kennon et al. 1999, and Fujisawa et al. 1998), Myocardial infarction (Cambien et al. 1992) and metabolic syndrome (Das et al. 2009).

Panika and Baiga though speak dialects belonging to different linguistic groups are known to be having a similar protoaustraloid ethnic element (Chandiok et al. 2014), thus relatively lower frequency of ACE D allele among them coincides with that of Indian population of West who speak Indo-European linguistic group. Thus, suggesting that genes and language do not go hand in hand.

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