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Salivary Amylase Polymorphism Among Kotas and Badagas of the Nilgiri Hills, South India

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KOTA VE BADAGA (NILGIRI HILLS - GÜNEY HİNDİSTAN) TOPLUMLARI ARASINDA TÜKÜRÜK AMİLAZ POLİMORFİZMİ

Özet

Güney Hindistan' ın *Nilgiri Hills* bölgesinde yaşayan ve soyunu kabile-içi evlilikler (endogami) ile sürdüren *Kota* ve *Badaga* toplumlarındaki bireylerden 223 tükürük örneği alındı. Tükürükler amilaz polimorfizmi açısından incelendi. Bu işlem için, kesintili vertikal poliakrilamid jel elektroforezi yöntemi kullanıldı. *Badaga* ' da yaşayanlarda, Amy_1 değişkenlerinin fenotip frekansları çok yüksek (0.1282) bulundu. *Kota* toplumunda ise, yalnızca, sık görülen Amy_1A fenotipi bulundu, başka bir değişkene rastlanmadı. Bu bulgular, dünyanın öteki toplumlarında yapılmış çalışmaların verileriyle karşılaştırıldı.

Summary

Salivary samples from 223 individuals belonging to two endogamous populations namely the *Kotas* and the *Badagas* of the *Nilgiri Hills*, *South India* were screened for amylase polymorphism using discontinuous vertical polyacrylamide slab gel electrophoresis. The phenotype frequency of Amy_1 variants is found to be very high (0.1282) in *Badagas*. No variant phenotype other than the common Amy_1A was observed in *Kotas*. The results are compared with the existing data available on world populations.

Keywords: *Salviary amylase polymorphism - Kotas and Badagas - Nilgiri (India)*

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INTRODUCTION

Human salivary amlyase (EC.3.2.1.1) is the major constituent of saliva present at a concentration of about 40% of the total protein content in saliva (1). After polyacrylamide slab gel electrophoresis, amylase is visualized as 5-8 faintly and heavily stained bands occuring alternatively. Identical patterns have been obtained in fractions of submandibular, sublingual and parotid saliva (2). Earlier studies have shown that salivary amylase exhibits polymorphism with the occurence of both common and variant phenotypes (3, 4). The difference between the common and variant phenotype is shown by the presence of an extra pair of slow migrating bands in the latter at the cathodal end. The locus responsible for the human salivary amylase have been designated as Amy_1 with multipl alleles located on chromosone 1, along with Amy_2 locus for pancreatic amylase (1, 5).

The *Kota* tribes form one of the earliest inhabitants of the *Nilgiri Hills*. They are strictly endogamous in nature, living in isolation for many centuries, and now distributed in seven villages of the *Nilgiri* plateau. The *Badagas* constitute the single earliest largest community living in the *Nilgiris* over few centruies. They also practise endogamy and are widely distributed throughout the*Nilgiri* plateau.

The present study is concerned with the screening of salivary amylase polimorphism in the *Kota* and the *Badaga* groups of the *Nilgiri Hills, South India.* The present investigation is incidentally at first of its kind on an Indian population group.

MATERIAL AND METHODS

Whole salivary samples (1-3 mL; unstimulated) were collected in clean, dry, sterile test tubes from 223 unrelated individuals belonging the *Kota* (n : 106) and the *Badaga* (n : 117) groups. The processing of saliva samples, experimental procedure for vertical polyacrylamide slab gel electrophoresis and staining for amylase activity were essentially as described earlier (6).

RESULTS AND DISCUSSION

Figure 1 shows the human salivary amylase phenotypes observed in the *Kotas* and the *Badagas*. The phenotypes include the common Amy_1A (channels 1, 2 and 3) and variants Amy_1Vc (channels 4, 5, 6, 7, and 8). In general, variants are classified on the basis of the position of the extra bands and so far 12 phenotypes (1 common and 11 variants) have been cited in the literature (1).

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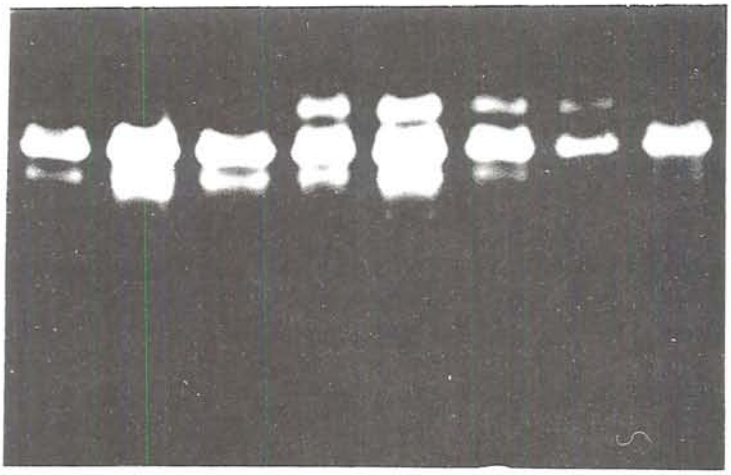

Fig. 1. Electrophoretic phenotypes of salivary amylase in the *Kotas* and the *Badagas*. Channels 1,2 and 3 correspond to Amy_1A and the rest, variant phenotypes (Amy_1Vc).

In the present study, two types of variants were encountered. These variant phenotypes however could not be assigned to any specific class of variants reported earlier in the literature for one of the reference samples. Therefore, in the present study, the two observed variants together are tentatively designated as Amy_1Vc as practised earlier (7, 8).

The distribution of salivary amylase phenotypes in the *Kotas* and the *Badagas* is shown in Table 1. The phenotype Amy_1A is found to occur with high value in both the groups. It is significant to note the total absence of amylase variants in the *Kotas* unlike the *Badagas* who are characterized with very high incidence of Amy_1 variants (12.82 %). In our earlier investigation on a heterogenous *Madras* city population (6) it was observed that Amy_1 variants occur with a percentage frequency of 6.8 which is also on the higher scale like the present findings on the *Badagas* of the *Nilgiris*. When compared to world populations, the frequency in *Badagas* accounts for the second highest value (next to black Nigerians) and also higher than for white Americans, Japanese and black Americans (1, 8).

In the light of the above interesting observation, it is reasonable to conclude that there exists genetic difference between the *Kotas* and the *Badagas* for the salivary amylase polymorphism. It however remains to be ascertained whether these two groups exhibit similar genetic heterogeneity for other loci before any firm generalization can be made on the underlying genetic diversity.

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Table 1. Distribution of Amy_1 phenotypes in the *Kotas* and the *Badagas*.

Population	Number tested	Amy_1 phenotype Amy_1A	Amy_1Vc
Kotas	106	106	0
Badagas	117	102	15
* Frequency of Amy1 phenotypes		Amy_1A :0.8718 Amy_1Vc :0.1218	
* Gene frequency		Amy_1A :0.9337 Amy_1Vc :0.0663	

A : Common; Vc : Variants combined; (*) Badagas

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