

Letter to the Editor

High incidence of nasopharyngeal cancer: similarity for 60% of mitochondrial DNA signatures between the Bidayuh of Borneo and the Bai-yue of Southern China

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Abstract

Populations in Southern China (Bai-yue) and Borneo (Bidayuh) with high incidence of nasopharyngeal cancer (NPC) share similar mitochondrial DNA signatures, supporting the hypothesis that these two populations may share the same genetic predisposition for NPC, which may have first appeared in a common ancestral reference population before the sea levels rose after the last ice age.

Key words Nasopharyngeal cancer, incidence, DNA signatures

Among the proposed etiological factors for nasopharyngeal carcinoma (NPC), genetic factors have been considered to be the most important by recent studies^[1,2]. An exploration of NPC susceptibility genes in high risk populations has been launched at the genomic level^[3,4], although the exact carcinogenic mechanism(s) of this susceptibility remains unclear.

Devi *et al.*^[5] have previously reported the high prevalence of NPC among the Bidayuh of Borneo, whose NPC incidence is higher than that of the Cantonese in Southern China. The migration history of the people in this region has been linked to the high NPC incidence in certain ethnic groups residing in Southern China and Southeast Asia^[6]. Here, we refer to our article, “Is nasopharyngeal carcinoma really a Cantonese cancer?”, in the May 2010 issue of the *Chinese Journal of Cancer*^[7]. In our hypothetical article, we postulated that the Bidayuh and the Bai-yue share the same ancestral origin in the period before the sea

levels rose and drowned much of Sundaland; we further postulated that any genetic NPC susceptibility factors may have been inherited from this reference population.

Mitochondrial DNA (mtDNA) is considered a maternally inherited genetic material that is transmitted from mother to daughter. We would like to bring to the attention of our readers a recent study by Jinam *et al.*^[8], examining mtDNA signatures. They found that the mtDNA lineages of the Bidayuh (Temuans and Seletars) and of the populations from mainland Southeast Asia near Indochina or Southern China may have been linked before the Austronesian expansion. This similarity is characterized by the mtDNA haplogroups M21a, N9a6, N21, N22, and F1a'c, which account for more than 60% of the mtDNA lineages in the three Austronesian groups. This is in addition to the haplogroups M74b, M22, G1c, M7b1, B5b2, M7c2, and B4c2, which also have roots in mainland Southern China. All these haplogroups are either absent or very infrequently found in the populations near Taiwan (the origins of the Austronesians), and their ages range from approximately 30 000 to 10 000 YBP (years before the present), corresponding to the late Pleistocene to early Holocene period—the period before the sea levels rose.

We believe this finding adds credence to our hypothesis of a common genetic origin of NPC in a reference population that later gave rise to the Bidayuh and the Bai-yue. Furthermore, any such genes are possibly transmitted maternally.

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