

# Distinct DC-SIGN and DC-SIGNR Genetic Polymorphism among the Chinese Han Population

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## ABSTRACT

DC-SIGN and DC-SIGNR efficiently bind and transmit HIV-1 to susceptible target cells in trans. Among the Caucasian population, we previously found that heterozygous DC-SIGN and DC-SIGNR 7/5 reduced the risk of HIV-1 infection in an Exposed-Seronegative cohort, while the homozygous DC-SIGNR 7/7 repeat is associated with an increased probability of HIV-1 transmission. Here we analyzed DC-SIGN/DC-SIGNR genotype and allele distribution among the Chinese Han population and compared them with those of the Caucasian population.

The studied cohort includes 520 healthy individuals of Chinese Han ethnicity which were confirmed negative for HBV, HCV, and HIV-1. Among the Chinese Han population, we found 6 genotypes in the DC-SIGN repeat region based on number of repeats. Allele 7 was most common with a frequency of 0.9808. Alleles 4, 5, 6, and 8 with low frequency were also found, while only 3 alleles were identified in Caucasians. While the DC-SIGNR genetic polymorphism frequency was high. We identified 16 genotypes in the DC-SIGNR repeat region of Chinese Han individuals. Of these 16 genotypes, 8/5, 8/8, 9/4, 9/6, and 9/9 were not previously found in the Caucasian population. We observed a significant difference of 6/5, 7/4, 7/5, 7/6, 7/7, 9/5, 9/7, 9/9 genotype distribution and 5-, 6-, 7-, 9- allele frequency between the Chinese Han and Caucasian populations (P<0.01).

DC-SIGN/DC-SIGNR genotypes and allele distribution in Chinese Hans were significantly different from those among Caucasians, and exhibited unique genetic characteristics previously unrecognized in the Caucasian population, which may help to find new polymorphism related to HIV-1/AIDS transmission and progression.

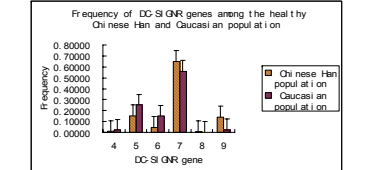
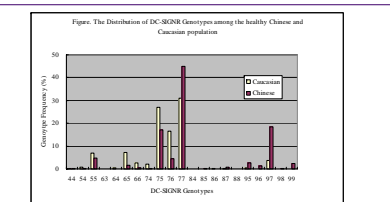
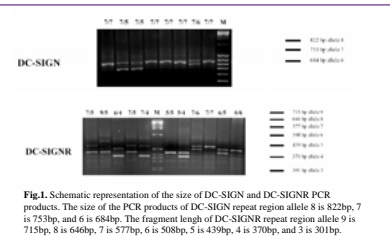
## INTRODUCTION

DC-SIGN and DC-SIGNR efficiently bind and transmit HIV-1 to susceptible target cells in trans. Among the Caucasian population, we previously found that heterozygous DC-SIGN and DC-SIGNR 7/5 reduced the risk of HIV-1 infection in an Exposed-Seronegative cohort, while the homozygous DC-SIGNR 7/7 repeat is associated with an increased probability of HIV-1 transmission. Here we analyzed DC-SIGN/DC-SIGNR genotype and allele distribution among the Chinese Han population and compared them with those of the Caucasian population.

## MATERIALS & METHODS

- 520 healthy individuals of Chinese Han ethnicity which were confirmed negative for HBV, HCV, and HIV-1.
- The DC-SIGN/DC-SIGNR repeat region was PCR amplified from genomic DNA extracted from PBMC.
- Alleles were distinguished by 3% agarose gel electrophoresis. Cloning and sequencing were performed to obtain sequences from allele 3 to 9.
- Fisher's exact test was used for statistic analysis. The  $\chi^2$  test was used to estimate the difference of genotypes and alleles between the Chinese Han and Caucasian populations. Polymorphism Information Content (PIC) of DC-SIGNR was calculated.

## RESULTS



**Fig.2.** The distributions of DC-SIGNR genotypes and allele-types among the Chinese Han healthy controls (n=520) were compared to American Caucasian population (N=698). **A.** The distribution of DC-SIGNR genotypes between the Chinese and the Caucasian populations were significantly different (p<0.001). The Chinese population had a significantly higher amount of 7/7 and 9/9 genotypes, but significantly lower amounts of 6/5, 7/5 and 7/6 genotypes than the Caucasian population (p<0.001). **B.** The Allele distribution in our normal Chinese controls was similar to the Eastern Asians, but significantly different from the Caucasians (p<0.001). The Chinese had more 7 and 9 alleles and less of 5 and 6 alleles compared to the Caucasians (p<0.001).

**Table1. Distribution of DC-SIGN genotypes among the healthy Chinese Hans and the Caucasian population**

DC-SIGN genotype	Chinese Han population (n=520)		Caucasian population (n=698)	
	Subjects	Frequency	Subjects	Frequency
Wild Type 7/7	506	0.9730	0	0.0000
8/8	2	0.0038	0	0.0000
7/6	0	0.0000	1	0.0014
7/5	0	0.0000	4	0.0057
6/6	2	0.0038	0	0.0000
7/4	2	0.0038	0	0.0000

**Table 2** Frequency of DC-SIGN alleles among the healthy Chinese Han and the Caucasian population. **Table 3** Distribution of DC-SIGNR alleles among the healthy Chinese Han and Caucasian population.

DC-SIGN alleles	Frequency		DC-SIGNR Alleles		Frequency	
	Chinese Han population (n=520)	Caucasian population (n=698)	Chinese Han population (n=520)	Caucasian population (n=698)	Chinese Han population (n=520)	Caucasian population (n=698)
4	2 (0.0038)	0 (0.0000)	6a	0.0000	0.0000	
5	2 (0.0038)	0 (0.0000)	5a	0.1000	0.2403	
6	4 (0.0077)	1 (0.0012)	6a	0.0462	0.1483	
7	102 (0.1962)	116 (0.1662)	7a	0.6000	0.5094	
8	18 (0.0346)	4 (0.0057)	8a	0.0000	0.0014	
9	0	0	9a	0.1014	0.0215	
Total	184 (0.1000)	1150 (0.1000)	Total	1.0000	1.0000	

Note: \* Compared with the Caucasian population, \* P<0.01

**Table 3. Distribution of DC-SIGNR genotypes among normal Chinese Hans and Caucasian population.**

DC-SIGNR genotype	Chinese Han population (n=520)		Caucasian population (n=698)	
	numbers	frequency	numbers	frequency
4/4	2	0.0038	2	0.0029
5/4	—	—	6	0.0086
5/5	23	0.0442	49	0.0702
6/4	2	0.0038	3	0.0043
6/5*	8	0.0154	51	0.0731
6/6	6	0.0115	18	0.0258
7/4*	1	0.0019	15	0.0215
7/5*	90	0.1731	109	0.2708
7/6*	23	0.0423	116	0.1662
7/7*	212	0.4077	217	0.3109
8/5	1	0.0019	—	—
8/6	—	—	—	—
8/7	—	—	1	0.0014
8/8	2	0.0038	—	—
9/5*	12	0.0212	4	0.0057
9/6	4	0.0077	—	—
9/7*	97	0.1865	26	0.0372
9/9*	15	0.0288	—	—
Total	520	1.0000	698	1.0000

Note: \* Compared with the Caucasian population, P<0.01.

## SUMMARY

Within the Chinese Han population

DC-SIGN:

- There are 6 genotypes in the DC-SIGN repeat region based on number of repeats.
- Allele 7 was most common with a frequency of 0.9808.
- Alleles 4, 5, 6, and 8 with low frequency were also found, while only 3 alleles were identified in Caucasians.

DC-SIGNR:

- The DC-SIGNR genetic polymorphism frequency was high; its PIC was 0.5312.
- There are 16 genotypes in the DC-SIGNR repeat region of Chinese Han individuals.
- Of these 16 genotypes, 8/5, 8/8, 9/4, 9/6, and 9/9 were not previously found in the Caucasian population.
- We observed a significant difference of 6/5, 7/4, 7/5, 7/6, 7/7, 9/5, 9/7, 9/9 genotype distribution and 5-, 6-, 7-, 9- allele frequency between the Chinese Han and Caucasian populations (P<0.01).
- More inserted mutation was found in Chinese Hans than Caucasian population.

## CONCLUSIONS

DC-SIGN/DC-SIGNR genotypes and allele distribution in the Chinese Hans were significantly different from those among the Caucasians, and exhibited unique genetic characteristics previously unrecognized in the Caucasian population, which may help to find new polymorphism related to HIV-1/AIDS transmission and progression.

## REFERENCE

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