Retrovirology

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A major susceptibility locus for HTLV-1 infection in childhood maps to chromosome 6q27

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from Fourth Dominique Dormont International Conference. Host-Pathogen Interactions in Chronic Infections
Paris, France. 13-15 December 2007

Published: 9 April 2008

Retrovirology 2008, **5**(Suppl 1):O6 doi:10.1186/1742-4690-5-S1-O6

This abstract is available from: http://www.retrovirology.com/content/5/S1/O6

Background

Human T-cell leukemia/lymphoma virus type 1 (HTLV-1) is a human oncoretrovirus causing adult T-cell leukemia/lymphoma (ATL) and chronic neuromyelopathy. We showed previously, by segregation analysis, that a dominant gene controls HTLV-1 infection through breast-feeding in children of African origin.

Materials and methods

To map this locus, we performed a genome-wide linkage analysis, based on the genetic model provided by segregation analysis, in five pedigrees (46 subjects with available DNA) of African origin with HTLV-1-seropositive children. A total of 382 microsatelites markers spanning the whole genome were typed. Two attractive positional genes located within the linked regions were further studied through an association analysis in an independent sample of 59 cases (24 HTLV-1 infected children and 25 ATL) and 48 controls (27 HTLV-1 seronegative but exposed children and 21 HTLV-1 seronegative young individuals) of African origin.

Results

Significant evidence for linkage (lod-score of 3.36, p=0.00004) was obtained for chomosomal region 6q27. Another maximum lod-score of 2.79 (p=0.0002) was obtained for chomosome 2p25. This result was entirely due to the largest pedigree of our sample, which alone gave a lod-score of 2.90 (p=0.00013). The role of exonic variants of *CCR6* on 6q27 and *ID2* on 2p25 was excluded.

Conclusions

Our results, mapping a major susceptibility locus to chromosome 6q27 and suggesting genetic heterogeneity with another locus at 2p25, pave the way to determination of the molecular basis of predisposition to HTLV-1 infection in children. [1]

References

1. Plancoulaine S, *et al.*: **A major susceptibility locus for HTLV-1 infection in childhood maps to chromosome 6q27.** *Hum Mol Genet* 2006, **15:**3306-3312.