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**United States Patent****F6,635,271****Acosta, et al.****May 28, 2000**

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A combination of genes and a unique human genome that comprises 46 complete DNA sequences and uses thereof.

**Abstract**

The present invention relates to the discovery of an isolated genetic composition and a combination of isolated nucleic acid sequences that can confer a resistance to Human Immunodeficiency Virus (HIV). This invention provides useful tools for research into HIV infection and for the development of diagnostics, screening assays, and drug discovery.

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**CLAIMS**

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What is claimed is:

1. An isolated genetic composition comprising:  
a first nucleic acid sequence comprising SEQ ID NO. 1 (Chromosome 1);<sup>1</sup>  
a second nucleic acid sequence comprising SEQ ID NO. 2 (Chromosome 2);  
...  
a twenty-second nucleic acid sequence comprising SEQ ID NO. 22 (Chromosome 22);  
a twenty-third nucleic acid sequence comprising SEQ ID NO. 23 (X chromosome);  
a twenty-fourth nucleic acid sequence comprising SEQ ID NO. 24 (Chromosome 1);<sup>2</sup>  
...  
a forty-sixth nucleic acid sequence comprising SEQ ID NO. 46 (Y chromosome).
2. A combination of isolated nucleic acid sequences comprising SEQ ID NOs: P1-P10.
3. An immortalized human cell line comprising the genetic composition of Claim 1.

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**DESCRIPTION**

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**BACKGROUND OF INVENTION***1. Field of the Invention*

The present invention relates to in vitro and in vivo studies of the infective processes of the Human Immunodeficiency Virus (HIV) and to the development of screening assays, diagnostics, anti-HIV therapeutics, and preventive measures. Human white blood cells

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1. SEQ ID NO:1 is the complete DNA sequence of chromosome 1 and the sequence is hypothetically disclosed in the written description.

2. Since each body cell has two sets of chromosomes, there are actually 46 nucleic acid sequences, SEQ ID NOs 1-46 that comprise the complete nuclear genome.

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whose outer membranes display the human CD4 receptor are normally susceptible to infection by HIV. The present invention is noteworthy because this identified genome provides HIV resistance even in the presence of the human CD4 receptor. The identification of this genome, gene combination, and stable cell line provides noteworthy new tools to explore the intracellular mechanisms of resistance to HIV replication and its infective processes. The HIV infection process begins with attachment of human immunodeficiency virions to human cell membranes, followed by the take-over of a cell's protein synthesis machinery by the inserted viral genome.

## *2. Related Background Art*

Although other individuals have demonstrated resistance to HIV, the present invention includes an immortalized human cell line that will facilitate research and development into anti-HIV therapies such as gene replacement therapy. Although drug therapy has prolonged the lives of many who are able to tolerate a strict regime of powerful protease inhibitors and/or reverse transcription inhibitors, greater understanding of individual resistance provided by this invention will significantly increase therapeutic and preventive treatments and efforts to limit an epidemic threat to the well-being of millions of potential and existing AIDS patients.

## SUMMARY OF THE INVENTION

Therefore, an object of the present invention is to provide a stable human cell line whose cells contain an HIV resistant genome and a gene combination (P1-P10) that confers heightened HIV resistance.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a combination of genes and to a unique human genome (hereinafter the Dolly Genome) that comprises 46 complete DNA sequences. The Dolly Genome was isolated and sequenced from an individual who is completely resistant to HIV infection and resistant to developing AIDS. Thus, the Dolly Genome represents a valuable diagnostic, screening assay, and research resource to combat deadly HIV infection and AIDS.

A cell line (CL100) carrying the Dolly Genome has been developed from tissue samples obtained from the individual completely resistant to HIV. CL100 can grow indefinitely in vitro. Thus, it is a continuous source of the Dolly Genome.

A combination of genes P1-P10, with corresponding SEQ. ID. NOs. P1-P10, was also isolated from the Dolly Genome. One or more genes in combination P confer a dominant trait, i.e., only one copy is needed and thus useful for gene therapy. Although gene combination P does not completely confer HIV resistance, it increases the resistance of cells and animals that carry this gene.

### EXAMPLES

The following examples illustrate selected aspects of the present invention, yet the offering of these specific examples is in no way intended to limit the scope of the invention as defined by the claims.

#### Example 1

The genome of an uninfected individual at risk for infection is extracted from white cells from a whole-blood sample and compared to the Dolly genome to determine the degree of HIV susceptibility.

#### Example 2

Gene region P1-P10 of an uninfected individual at risk for infection is isolated from a whole-blood sample and compared to the P1-P10 sequence to ascertain the degree of HIV susceptibility.

The above genome and gene combination have been deposited under the terms of the Budapest Treaty in the following International Deposition Authority.

Name: National Institute of Bioscience and Cytology

Address: HG C-9361 on May 12, 1999