

Fig. 6. Schematic illustration of *CCR5* haplotypes. (a) A *CCR5* open reading frame (ORF) and polymorphisms in the neighboring DNA sequence that are tightly linked to the *CCR5* ORF define different *CCR5* haplotypes. Polymorphisms tightly linked to the *CCR5* ORF have been found within *CCR2* and in the *cis*-regulatory region of *CCR5*. In every cell there is a pair of *CCR5* haplotypes that differ from each other (i.e., heterozygous) or are identical to each other (homozygous). Different combinations of *CCR5* haplotype pairs (e.g., HHG*2/HHE) may be associated with varied susceptibility to HIV-1 infection and/or altered rates of disease progression in HIV-1-infected individuals. Wt, indicates wild type. To maintain uniformity in the numbering systems, it was proposed at the *CCR5*--AIDS symposium (held at the NCI-FCRDC, Frederick, MD, April 20, 1999), to designate the first nucleotide of the *CCR5* translational start site as +1 and the nucleotide immediately upstream as -1 (3, 4). For reference, we have provided the two commonly used numbering systems along with the new numbering system. (b) The cohorts were genotyped for polymorphisms indicated. Genotyping methods and haplotype classification were as described previously (1, 4). In this classification system, *CCR5* haplotypes are grouped into one of seven human haplogroups (HH) -A, -B, -C, -D, -E, -F (F*1 and F*2), -G (G*1 and G*2). The genotypic characteristics of haplotypes within each haplogroup at the polymorphic positions *CCR2*-V64I, and *CCR5* A-2733G, G-2554T, G-2459A, T-2135C, C-2132T, A-2086G, C-1835T, and $\pm\Delta 32$ is as shown. Differences from the ancestral *CCR5* haplogroup (HHA) are in bold. In this paper, homozygosity refers to two haplotypes of the same haplogroup and heterozygosity indicates two haplotypes from two different haplogroups. [Adapted from Mangano *et al.* (5).]