

Figure 2: Evolutionary relationships of the viral sequences in *gag* gene

The evolutionary history was inferred using the Neighbor-Joining method. The tree is drawn to scale. The evolutionary distances were computed using the Maximum Composite Likelihood method. The rate variation among sites was modeled with a gamma distribution (shape parameter = 0.7166). Numbers at branch nodes refer to the bootstrap support (only values greater than 95% are shown.). The sequences of the patients considered dual infected in gag gene (DI 03, DI 06, DI 08, DI 16, DI 52, DI 56 and DI 72) are marked with brown, green, red, blue, pink, turkey and grey circle respectively; A and B letters identify the viral populations found in DI patients. Branch lengths are draw to scale.