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CS123A – Bioinformatics

**Hands On Exercise #13 – Origins of HIV**

**Part A:** Below is the consensus tree for the 12 HIV/SIV env sequences:

+------HIV2 D205

+-------100.0-|

| +------HIV2 UCI e

|

+100.0-| +------SIV Mm251

| | +100.0-|

| | | +------SIV SMM en

| +-58.0-|

+100.0-| | +------HIV2 ROD e

| | +100.0-|

| | +------HIV2 ST en

+100.0-| |

| | +---------------------------SIV AGM en

| |

+------| +----------------------------------SIV CPZ en

| |

| | +-------------HIV1 BRU e

| +----------------------87.0-|

| | +------HIV1 NDK e

| +-99.0-|

| +------HIV1 ELI e

|

+------------------------------------------------HIV1 MAL e

**Part B:**

1. GAG Consensus Tree

+------HIV2 D205

+-------100.0-|

| +------HIV2 UCI g

|

+100.0-| +------HIV2 ST ga

| | +100.0-|

| | | +------HIV2 ROD g

| +-70.0-|

+100.0-| | +------SIV SMM ga

| | +100.0-|

| | +------SIV Mm251

+100.0-| |

| | +---------------------------SIV AGM ga

+-73.0-| |

| | +----------------------------------SIV CPZ ga

| |

+------| +-----------------------------------------HIV1 MAL g

| |

| | +------HIV1 NDK g

| +------------------------------------97.0-|

| +------HIV1 ELI g

|

+-------------------------------------------------------HIV1 BRU g

1. POL Consensus Tree

+------HIV1 NDK p

+-64.0-|

+100.0-| +------HIV1 ELI p

| |

+100.0-| +-------------HIV1 BRU p

| |

+100.0-| +--------------------HIV1 MAL p

| |

+100.0-| +---------------------------SIV CPZ po

| |

| +----------------------------------SIV AGM po

+100.0-|

| | +------HIV2 ROD p

| | +100.0-|

| | | +------HIV2 ST po

+------| +----------------------57.0-|

| | | +------SIV SMM po

| | +100.0-|

| | +------SIV Mm251

| |

| +------------------------------------------------HIV2 D205

|

+-------------------------------------------------------HIV2 UCI p

**Part C:**

1. SIV/HIV2 shared a common ancestor. It later split into a group contain HIV1 and another group containing SIV/HIV2.
2. SIV shares a common ancestor with both HIV1 and HIV2.
3. For the sooty mangabey, HIV2 is more closely related than HIV1. Chimpanzees are more closely related HIV1. What this tree shows is that HIV shared a common ancestor. The sequences split with HIV1 on one side and then SIV/HIV2 on the other side. It appears that HIV either jumped back and forth between apes and humans or jumped to humans at multiple points in its evolution.