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**Please note that if you use SimPlot in a publication, you can use the reference to the Lole<sup>1</sup> paper (for which I developed SimPlot)**

#### **A. Eubacteria**

1. *Borrelia burgdorferi*
  - i) Earnhart<sup>2</sup>
2. *Clostridium botulinum*
  - i) Hill<sup>3</sup>
  - ii) Hill<sup>4</sup>
  - iii) Luquez<sup>5</sup>
  - iv) Raphael<sup>6</sup>
3. *Escherichia coli*
  - i) Pimenta<sup>7</sup>
4. *Helicobacter pylori*
  - i) Oleastro<sup>8</sup>
  - ii) Pride<sup>9</sup>
5. IncP-1 plasmid
  - i) Norberg<sup>10</sup>
6. *Mycoplasma genitalium*
  - i) Ma<sup>11</sup>
7. *Pseudomonas syringae*
  - i) Sarkar<sup>12</sup>
8. *Rhizobium spp*
  - i) Gaunt<sup>13</sup>
9. *Staphylococcus aureus*
  - i) Olsen<sup>14</sup>
  - ii) Zhang<sup>15</sup>
10. *Streptococcus agalactiae*
  - i) Tettelin<sup>16</sup>

#### **B. Eukaryotes**

1. *Arabidopsis*
  - i) Marco<sup>17</sup>
2. *Carassius auratus* (fish)
  - i) Yang<sup>18</sup>
3. *Chlamydia trachomatis*
  - i) Gomes<sup>19</sup>
  - ii) Gomes<sup>20</sup>
  - iii) Nunes<sup>21</sup>
  - iv) Nunes<sup>22</sup>
  - v) Somboonna<sup>23</sup>
4. *Cryptosporidium spp*
  - i) Zhou<sup>24</sup>
5. *Cyclotella* (protist)
  - i) Beszteri<sup>25</sup>
6. Genet
  - i) Gaubert<sup>26</sup>
7. Hexapoda (springtails, distinct from Insectae)
  - i) Janssens<sup>27</sup>
8. Humans and other mammals
  - i) Costas<sup>28</sup>
  - ii) Hershberger<sup>29</sup>
  - iii) Jackson<sup>30</sup>
9. *Leishmania*
  - i) Devault<sup>31</sup>
10. *Pneumocystis*
  - i) Kutty<sup>32</sup>
11. *Salmo* (salmon)
  - i) Ciborowski<sup>33</sup>
12. *Schoenoxiphium* (African plant, sedge family)
  - i) Gehrke<sup>34</sup>
13. *Trypanosoma cruzi*
  - i) Gaunt<sup>35</sup>
14. *Xenorhabdus* (nematode endosymbiont)
  - i) Sergeant<sup>36</sup>
15. *Zea mays* (corn)
  - i) Sharma<sup>37</sup>

### C. Reviews/Other

1. Abecasis<sup>38</sup> [method]
2. Awadalla<sup>39</sup> [review]
3. Hungnes<sup>40</sup> [review]
4. Lam<sup>41</sup> [review]
5. Maydt<sup>42</sup> [method]
6. Parrish<sup>43</sup> [review]
7. Schulz<sup>44</sup> [method]
8. Strimmer<sup>45</sup> [method]
9. Svraka<sup>46</sup> [viral metagenomics]
10. Telenti<sup>47</sup> [methods review]

### D. Viruses

1. dsDNA
  - i) Adenoviridae (Adenovirus)
    - (1) Aoki<sup>48</sup>
    - (2) Darr<sup>49</sup>
    - (3) Ishiko<sup>50</sup>
    - (4) Kaneko<sup>51</sup>
    - (5) Kaneko<sup>52</sup>
    - (6) Lukashev<sup>53</sup>
    - (7) Madisch<sup>54</sup>
    - (8) Mahadevan<sup>55</sup>
    - (9) Maluquer de Motes<sup>56</sup>
    - (10) Robinson<sup>57</sup>
    - (11) Robinson<sup>58</sup>
    - (12) Roy<sup>59</sup>
    - (13) Roy<sup>60</sup>
    - (14) Seto<sup>61</sup>
    - (15) Seto<sup>62</sup>
    - (16) Tong<sup>63</sup>
    - (17) Walsh<sup>64</sup>
    - (18) Walsh<sup>65</sup>
    - (19) Walsh<sup>66</sup>
    - (20) Wevers<sup>67</sup>
    - (21) Yang<sup>68</sup>
    - (22) Zhu<sup>69</sup>
  - ii) Herpesviruses (CMV, HHV-8, HSV1, HPV-2, VZV)
    - (1) Duprez<sup>70</sup>
    - (2) Faure-Della Corte<sup>71</sup>
    - (3) Garrigue<sup>72</sup>
    - (4) Liljeqvist<sup>73</sup>
    - (5) Norberg<sup>74</sup>
    - (6) Norberg<sup>75</sup>
    - (7) Norberg<sup>76</sup>
    - (8) Peters<sup>77</sup>
    - (9) Tyler<sup>78</sup>
    - (10) Zajac<sup>79</sup>
  - iii) Poxviruses
    - (1) Gubser<sup>80</sup>
2. ssDNA
  - i) ChiSCV (provisional)
    - (1) Blinkova<sup>81</sup>
  - ii) Circovirus
    - (1) He<sup>82</sup>
    - (2) Ma<sup>83</sup>
  - iii) Dependovirus (Adeno-associated virus)
    - (1) Chen<sup>84</sup>
    - (2) Gao<sup>85</sup>
    - (3) Gao<sup>86</sup>
    - (4) Li<sup>87</sup>
  - iv) Geminiviridae (Begomovirus, Mastrevirus, Tobacco leaf curl, Tomato leaf curl)
    - (1) Blawid<sup>88</sup>
    - (2) Knierim<sup>89</sup>
    - (3) Kumari<sup>90</sup>
    - (4) Kumari<sup>91</sup>
    - (5) Lozano<sup>92</sup>
    - (6) Schubert<sup>93</sup>
  - v) Papillomavirus
    - (1) Gottschling<sup>94</sup>
    - (2) Rector<sup>95</sup>
  - vi) Parvovirus (Bocavirus, PARV4)

- (1) Arthur<sup>96</sup>
- (2) Cheng<sup>97</sup>
- (3) Cheng<sup>98</sup>
- (4) Fryer<sup>99</sup>
- (5) Kapoor<sup>100</sup>
- (6) Katsoulidou<sup>101</sup>
- (7) Lin<sup>102</sup>
- (8) Panning<sup>103</sup>
- (9) Wang<sup>104</sup>
- (10) Zappa<sup>105</sup>
- vii) Polyomavirus (BK virus)
  - (1) Luo<sup>106</sup>
- 3. dsRNA
  - i) Brnaviridae
    - (1) He<sup>107</sup>
    - (2) Hon<sup>108</sup>
  - ii) Reoviridae
    - (1) Arbovirus
      - (a) He<sup>109</sup>
    - (2) Rotavirus
      - (a) Lamhoujeb<sup>110</sup>
      - (b) Martella<sup>111</sup>
      - (c) Matthijnssens<sup>112</sup>
      - (d) Matthijnssens<sup>113</sup>
      - (e) Parra<sup>114</sup>
      - (f) Phan<sup>115</sup>
      - (g) Phan<sup>116</sup>
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  - i) Alphavirus (Chikungunya)
    - (1) Allison<sup>117</sup>
    - (2) Arankalle<sup>118</sup>
  - ii) Ampelovirus (Plum pox)
    - (1) Capote<sup>119</sup>
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  - iii) *Arteriviridae* (Arterivirus, PRRSV)
    - (1) Chen<sup>122</sup>
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    - (3) Forsberg<sup>124</sup>
    - (4) Li<sup>125</sup>
    - (5) Liu<sup>126</sup>
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    - (1) Chu<sup>127</sup>
    - (2) Guo<sup>128</sup>
    - (3) Guo<sup>129</sup>
    - (4) Jonassen<sup>130</sup>
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    - (7) Pantin-Jackwood<sup>133</sup>
    - (8) Tse<sup>134</sup>
    - (9) Wolfaardt<sup>135</sup>
  - v) Bacteriophage (*Levivirus*)
    - (1) Friedman<sup>136</sup>
  - vi) Calicivirus (norovirus, sapovirus, lagovirus, and vesivirus)
    - (1) Abrantes<sup>137</sup>
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    - (3) Bull<sup>139</sup>
    - (4) Bull<sup>140</sup>
    - (5) Carlsson<sup>141</sup>
    - (6) Chhabra<sup>142</sup>
    - (7) Chhabra<sup>143</sup>
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    - (11) Eden<sup>147</sup>
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    - (13) Forrester<sup>149</sup>
    - (14) Fukuda<sup>150</sup>
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- (18) Hansman<sup>154</sup>
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- (21) Jin<sup>157</sup>
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- (35) Oliver<sup>171</sup>
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- (38) Phan<sup>174</sup>
- (39) Phan<sup>175</sup>
- (40) Phan<sup>176</sup>
- (41) Phan<sup>177</sup>
- (42) Phan<sup>178</sup>
- (43) Rohayem<sup>179</sup>
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- (46) Thackray<sup>182</sup>
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- (50) Yun<sup>186</sup>
- vii) Closterovirus (Citrus tristerza, Tomato chlorosis)
  - (1) Cerni<sup>187</sup>
  - (2) Lozano<sup>188</sup>
- viii) Coronavirus (SARS, avian infectious bronchitis virus, porcine epidemic diarrhea virus, rhinolphus bat, transmissible gastroenteritis virus)
  - (1) Chen<sup>189</sup>
  - (2) Chen<sup>190</sup>
  - (3) Chu<sup>191</sup>
  - (4) DeCaro<sup>192</sup>
  - (5) DeCaro<sup>193</sup>
  - (6) Hon<sup>194</sup>
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  - (8) Lan<sup>196</sup>
  - (9) Lau<sup>197</sup>
  - (10) Lau<sup>198</sup>
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  - (12) Lee<sup>200</sup>
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  - (27) Zhang<sup>215</sup>
  - (28) Zhang<sup>216</sup>
  - (29) Zhang<sup>217</sup>
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  - (1) Flavivirus

- (a) Dengue
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- (d) Tick-borne encephalitis virus
  - (i) Yun<sup>227</sup>
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  - (i) Kuno<sup>228</sup>
  - (ii) Kuno<sup>229</sup>
- (2) Hepacivirus
  - (a) Hepatitis C virus (HCV)
    - (i) Bernardin<sup>230</sup>
    - (ii) Brown<sup>231</sup>
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    - (vii) DiLello<sup>236</sup>
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    - (ix) Gao<sup>238</sup>
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    - (xii) Kalinina<sup>241</sup>
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    - (xiv) Kuntzen<sup>243</sup>
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    - (xvi) Magiorkinis<sup>245</sup>
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  - (a) He<sup>253</sup>
  - (b) Jones<sup>254</sup>
  - (c) Tang<sup>255</sup>
  - (d) Tang<sup>256</sup>
- (4) Unclassified (GBV-C, GBV-D)
  - (a) Epstein<sup>257</sup>
  - (b) Neibecker<sup>258</sup>
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  - (1) James<sup>259</sup>
- xii) *Hepevirus*
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    - (b) van Cuyck<sup>261</sup>
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  - (1) Aphthovirus
    - (a) FMDV
      - (i) Abdul-Hamid<sup>262</sup>
      - (ii) Balinda<sup>263</sup>
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      - (vi) Li<sup>267</sup>
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      - (viii) Rana<sup>269</sup>
      - (ix) Tosh<sup>270</sup>
      - (x) Yang<sup>271</sup>
  - (2) Enterovirus (including echovirus, poliovirus, parechovirus, porcine enterovirus)
    - (a) Al-Hello<sup>272</sup>
    - (b) Al-Sunaidi<sup>273</sup>

- (c) Andersson<sup>274</sup>
- (d) Arita<sup>275</sup>
- (e) Bailly<sup>276</sup>
- (f) Bailly<sup>277</sup>
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- (m) Brown<sup>284</sup>
- (n) Brown<sup>285</sup>
- (o) Chan<sup>286</sup>
- (p) Chen<sup>287</sup>
- (q) Chevaliez<sup>288</sup>
- (r) de Souza Luna<sup>289</sup>
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- (u) Ding<sup>292</sup>
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- (w) Drexler<sup>294</sup>
- (x) Huang<sup>295</sup>
- (y) Huang<sup>296</sup>
- (z) Huang<sup>297</sup>
- (aa) Huang<sup>298</sup>
- (bb) Jegouic<sup>299</sup>
- (cc) Krogstad<sup>300</sup>
- (dd) Kyriakopoulou<sup>301</sup>
- (ee) Kyriakopoulou<sup>302</sup>
- (ff) Kyriakopoulou<sup>303</sup>
- (gg) Kyriakopoulou<sup>304</sup>
- (hh) Li<sup>305</sup>
- (ii) Lindberg<sup>306</sup>
- (jj) Liu<sup>307</sup>
- (kk) Lukashev<sup>308</sup>
- (ll) Lukashev<sup>309</sup>
- (mm) Mirand<sup>310</sup>
- (nn) Norder<sup>311</sup>
- (oo) Oberste<sup>312</sup>
- (pp) Oberste<sup>313</sup>
- (qq) Oberste<sup>314</sup>
- (rr) Paananen<sup>315</sup>
- (ss) Phuektes<sup>316</sup>
- (tt) Sannti<sup>317</sup>
- (uu) Savolainen-Kopra<sup>318</sup>
- (vv) Simonen<sup>319</sup>
- (ww) Smura<sup>320</sup>
- (xx) Smura<sup>321</sup>
- (yy) Smura<sup>322</sup>
- (zz) Tao<sup>323</sup>
- (aaa) van der Sanden<sup>324</sup>
- (bbb) Wakatsuki<sup>325</sup>
- (ccc) Wang<sup>326</sup>
- (ddd) Wang<sup>327</sup>
- (eee) Williams<sup>328</sup>
- (fff) Xu<sup>329</sup>
- (ggg) Yang<sup>330</sup>
- (hhh) Yip<sup>331</sup>
- (iii) Yoke-Fun<sup>332</sup>
- (jjj) Zaharoula<sup>333</sup>
- (kkk) Zhang<sup>334</sup>
- (lll) Zhang<sup>335</sup>
- (mmm) Zhang<sup>336</sup>
- (nnn) Zhang<sup>337</sup>
- (ooo) Zhao<sup>338</sup>
- (ppp) Zoll<sup>339</sup>
- (3) Erbovirus
  - (a) Black<sup>340</sup>
- (4) Iflavirus
  - (a) Moore<sup>341</sup>
- (5) Picornavirus (HAV, cardiovirus, coxsackie, rhinovirus)

- (a) Aguirre<sup>342</sup>
- (b) Belalov<sup>343</sup>
- (c) Blinkova<sup>344</sup>
- (d) Bolanaki<sup>345</sup>
- (e) Buckwalter<sup>346</sup>
- (f) Drexler<sup>347</sup>
- (g) Garcia-Aguirre<sup>348</sup>
- (h) Hales<sup>349</sup>
- (i) Huang<sup>350</sup>
- (j) Hu<sup>351</sup>
- (k) Hu<sup>352</sup>
- (l) Jones<sup>353</sup>
- (m) Liang<sup>354</sup>
- (n) Linsuwanon<sup>355</sup>
- (o) Lipton<sup>356</sup>
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- (r) Ren<sup>359</sup>
- (s) Zoll<sup>339</sup>
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  - (a) Silva<sup>360</sup>
- (7) Potyvirus (cassava brown streak disease-associated virus, papaya ringspot virus, Potato Y virus, soybean mosaic virus, bean common mosaic virus, watermelon mosaic virus)
  - (a) Ali<sup>361</sup>
  - (b) Comes<sup>362</sup>
  - (c) Crescenzi<sup>363</sup>
  - (d) Desbiez<sup>364</sup>
  - (e) Desbiez<sup>365</sup>
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- xiv) *Roniviridae* (okavirus/yellow head virus)
  - (1) Wijegoonawardanelk<sup>382</sup>
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  - (1) Vauloup-Fellous<sup>383</sup>
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  - i) Bunyavirus
    - (1) Bunya other (Guaroa virus, CCHF virus, and Rift Valley fever virus)
      - (a) Bird<sup>384</sup>
      - (b) Briese<sup>385</sup>
      - (c) Deyde<sup>386</sup>
      - (d) Hewson<sup>387</sup>
      - (e) Lukashov<sup>388</sup>
      - (f) Webster<sup>389</sup>
    - (2) Hantavirus
      - (a) Asikainen<sup>390</sup>
      - (b) de Carvalho Nicacio<sup>391</sup>
      - (c) Escutenaire<sup>392</sup>
      - (d) Johansson<sup>393</sup>
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      - (h) Klempa<sup>397</sup>
      - (i) Klempa<sup>398</sup>
      - (j) Klempa<sup>399</sup>
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      - (l) Nemirov<sup>401</sup>
      - (m) Razzauti<sup>402</sup>

- (n) Sironen<sup>403</sup>
- (o) Sironen<sup>404</sup>
- (p) Wang<sup>405</sup>
- (q) Zhang<sup>406</sup>
- ii) *Orthomyxoviridae* (Influenza)
  - (1) Amonsin<sup>407</sup>
  - (2) Boni<sup>408</sup>
  - (3) Goni<sup>409</sup>
  - (4) Goni<sup>410</sup>
  - (5) He<sup>411</sup>
  - (6) He<sup>412</sup>
  - (7) Lam<sup>413</sup>
- iii) *Paramyxoviridae* (parainfluenza, Morbillivirus/PPRV, newcastle disease virus, canine distemper)
  - (1) Bailey<sup>414</sup>
  - (2) Han<sup>415</sup>
  - (3) Han<sup>416</sup>
  - (4) He<sup>417</sup>
  - (5) Rui<sup>418</sup>
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  - (7) Zhang<sup>420</sup>
- iv) *Rhabdoviridae* (Lyssavirus)
  - (1) Tang<sup>421</sup>
- 6. ssRNA-RT
  - i) Orthoretrovirinae
    - (1) Betaretrovirus (Enzootic nasal tumor virus)
      - (a) Walsh<sup>422</sup>
    - (2) Deltaretrovirus (HTLV, STLV)
      - (a) Sintasath<sup>423</sup>
      - (b) Switzer<sup>424</sup>
      - (c) Switzer<sup>425</sup>
      - (d) van Dooren<sup>426</sup>
    - (3) Gammaretrovirus
      - (a) Porcine endogenous retroviruses
        - (i) Mang<sup>427</sup>
        - (ii) Niebert<sup>428</sup>
    - (4) Lentivirus
      - (a) HIV SIV
        - (i) Abecasis<sup>429</sup>
        - (ii) Abecasis<sup>430</sup>
        - (iii) Achkar<sup>431</sup>
        - (iv) Adojaan<sup>432</sup>
        - (v) Aghokeng<sup>433</sup>
        - (vi) Aghokeng<sup>434</sup>
        - (vii) Agnihotri<sup>435</sup>
        - (viii) Agwale<sup>436</sup>
        - (ix) Agwale<sup>437</sup>
        - (x) Ahuka-Mundeke<sup>438</sup>
        - (xi) Ahumada-Ruiz<sup>439</sup>
        - (xii) Ajoge<sup>440</sup>
        - (xiii) Ajoge<sup>441</sup>
        - (xiv) Almeida<sup>442</sup>
        - (xv) Ambrosioni<sup>443</sup>
        - (xvi) Andresen<sup>444</sup>
        - (xvii) Antunes<sup>445</sup>
        - (xviii) Araujo<sup>446</sup>
        - (xix) Aulicino<sup>447</sup>
        - (xx) Aulicino<sup>448</sup>
        - (xxi) Aulicino<sup>449</sup>
        - (xxii) Aulicino<sup>450</sup>
        - (xxiii) Aulicino<sup>451</sup>
        - (xxiv) Aulicino<sup>452</sup>
        - (xxv) Avi<sup>453</sup>
        - (xxvi) Avi<sup>454</sup>
        - (xxvii) Ayele<sup>455</sup>
        - (xxviii) Badreddine<sup>456</sup>
        - (xxix) Baird<sup>457</sup>
        - (xxx) Balakrishnan<sup>458</sup>
        - (xxxi) Baldrich-Rubio<sup>459</sup>
        - (xxxii) Balotta<sup>460</sup>
        - (xxxiii) Bano<sup>461</sup>
        - (xxxiv) Bao<sup>462</sup>



(xxxv)	Barlow <sup>463</sup>
(xxxvi)	Barlow <sup>464</sup>
(xxxvii)	Barreto <sup>465</sup>
(xxxviii)	Barroso <sup>466</sup>
(xxxix)	Bartolo <sup>467</sup>
(xl)	Bartolo <sup>468</sup>
(xli)	Beer <sup>469</sup>
(xlii)	Bezemer <sup>470</sup>
(xliii)	Bhanja <sup>471</sup>
(xliv)	Bhanja <sup>472</sup>
(xlv)	Bhanja <sup>473</sup>
(xlvi)	Bhattacharya <sup>474</sup>
(xlvii)	Bodelle <sup>475</sup>
(xlviii)	Brennan <sup>476</sup>
(xlix)	Brennan <sup>477</sup>
(l)	Brígido <sup>478</sup>
(li)	Brígido <sup>479</sup>
(lii)	Brígido <sup>480</sup>
(liii)	Brindicci <sup>481</sup>
(liv)	Brown <sup>482</sup>
(lv)	Bruselles <sup>483</sup>
(lvi)	Bruzzone <sup>484</sup>
(lvii)	Buzon <sup>485</sup>
(lviii)	Cardoso <sup>486</sup>
(lix)	Cardoso <sup>487</sup>
(lx)	Cardoso <sup>488</sup>
(lxi)	Carmona <sup>489</sup>
(lxii)	Carr <sup>490</sup>
(lxiii)	Carr <sup>491</sup>
(lxiv)	Carrion <sup>492</sup>
(lxv)	Carvalho <sup>493</sup>
(lxvi)	Casado <sup>494</sup>
(lxvii)	Casado <sup>495</sup>
(lxviii)	Casado <sup>496</sup>
(lxix)	Cavaliere <sup>497</sup>
(lxx)	Ceballos <sup>498</sup>
(lxxi)	Chang <sup>499</sup>
(lxxii)	Chen <sup>500</sup>
(lxxiii)	Chen <sup>501</sup>
(lxxiv)	Chin <sup>502</sup>
(lxxv)	Chohan <sup>503</sup>
(lxxvi)	Ciccozzi <sup>504</sup>
(lxxvii)	Ciccozzi <sup>505</sup>
(lxxviii)	Ciccozzi <sup>506</sup>
(lxxix)	Coetzer <sup>507</sup>
(lxxx)	Coetzer <sup>508</sup>
(lxxxii)	Cornelissen <sup>509</sup>
(lxxxiii)	Courgnaud <sup>510</sup>
(lxxxiv)	Courgnaud <sup>511</sup>
(lxxxv)	Costa <sup>512</sup>
(lxxxvi)	Couto-Fernandez <sup>513</sup>
(lxxxvii)	Cuevas <sup>514</sup>
(lxxxviii)	Cuevas <sup>515</sup>
(lxxxix)	D'Arrigo <sup>516</sup>
(xc)	Datta <sup>517</sup>
(xci)	Dazza <sup>518</sup>
(xcii)	De Baar <sup>519</sup>
(xciii)	De Castro <sup>520</sup>
(xciv)	De Sa Filho <sup>521</sup>
(xcv)	De Sa Filho <sup>522</sup>
(xcvi)	De Sa Filho <sup>523</sup>
(xcvii)	De Sa Filho <sup>524</sup>
(xcviii)	De Souza <sup>525</sup>
(xcix)	De Souza <sup>526</sup>
(c)	Delgado <sup>527</sup>
(ci)	Delgado <sup>528</sup>
(cii)	Delgado <sup>529</sup>
(ciii)	Delgado <sup>530</sup>
(civ)	Delviks-Frankenberry <sup>531</sup>
(cv)	Derache <sup>532</sup>
	Dilernia <sup>533</sup>

(cvi) Dilernia<sup>534</sup>  
(cvii) Dilernia<sup>535</sup>  
(cviii) Dilernia<sup>536</sup>  
(cix) Ding<sup>537</sup>  
(cx) Djoko<sup>538</sup>  
(cxi) Djoko<sup>539</sup>  
(cxii) Doyle<sup>540</sup>  
(cxiii) Drexler<sup>541</sup>  
(cxiv) Esbjornsson<sup>542</sup>  
(cxv) Eshleman<sup>543</sup>  
(cxvi) Espinosa<sup>544</sup>  
(cxvii) Eyer-Silva<sup>545</sup>  
(cxviii) Eyer-Silva<sup>546</sup>  
(cxix) Eyzaguirre<sup>547</sup>  
(cxx) Falkensammer<sup>548</sup>  
(cxxi) Fan<sup>549</sup>  
(cxxii) Fang<sup>550</sup>  
(cxxiii) Fang<sup>551</sup>  
(cxxiv) Fernandez-Garcia<sup>552</sup>  
(cxxv) Fernandez-Garcia<sup>553</sup>  
(cxxvi) Foglieni<sup>554</sup>  
(cxxvii) Fokam<sup>555</sup>  
(cxxviii) Fomsgaard<sup>556</sup>  
(cxxix) Fonjongo<sup>557</sup>  
(cxxx) Fontaine<sup>558</sup>  
(cxxxi) Frange<sup>559</sup>  
(cxxxii) Gagliani<sup>560</sup>  
(cxxxiii) Gale<sup>561</sup>  
(cxxxiv) Galimand<sup>562</sup>  
(cxxxv) Galli<sup>563</sup>  
(cxxxvi) Gaschen<sup>564</sup>  
(cxxxvii) Gifford<sup>565</sup>  
(cxxxviii) Gnanakaran<sup>566</sup>  
(cxxxix) Gomez-Carrillo<sup>567</sup>  
(cxl) Gordon<sup>568</sup>  
(cxli) Guan<sup>569</sup>  
(cxlii) Guimaraes<sup>570</sup>  
(cxliii) Guimaraes<sup>571</sup>  
(cxliv) Guimaraes<sup>572</sup>  
(cxlv) Guo<sup>573</sup>  
(cxlvi) Guo<sup>574</sup>  
(cxlvii) Hai-Long<sup>575</sup>  
(cxlviii) Han<sup>576</sup>  
(cxlix) Harris<sup>577</sup>  
(cl) Heeregrave<sup>578</sup>  
(cli) Herring<sup>579</sup>  
(clii) Hirigoyen<sup>580</sup>  
(cliii) Hoelscher<sup>581</sup>  
(cliv) Holguín<sup>582</sup>  
(clv) Holguín<sup>583</sup>  
(clvi) Holguín<sup>584</sup>  
(clvii) Holzmayer<sup>585</sup>  
(clviii) Holzmayer<sup>586</sup>  
(clix) Hu<sup>587</sup>  
(clx) Huang<sup>588</sup>  
(clxi) Huang<sup>589</sup>  
(clxii) Huang<sup>590</sup>  
(clxiii) Huang<sup>591</sup>  
(clxiv) Hunt<sup>592</sup>  
(clxv) Ibe<sup>593</sup>  
(clxvi) Imamichi<sup>594</sup>  
(clxvii) Jadhav<sup>595</sup>  
(clxviii) Jadhav<sup>596</sup>  
(clxix) Janssens<sup>597</sup>  
(clxx) Janssens<sup>598</sup>  
(clxxi) Jeannot<sup>599</sup>  
(clxxii) Jere<sup>600</sup>  
(clxxiii) Jonassen<sup>601</sup>  
(clxxiv) Jones<sup>602</sup>  
(clxxv) Kane<sup>603</sup>  
(clxxvi) Kantor<sup>604</sup>

(clxxvii) Karchava<sup>605</sup>  
(clxxviii) Kebba<sup>606</sup>  
(clxxix) Kemal<sup>607</sup>  
(clxxx) Khoja<sup>608</sup>  
(clxxxi) Kijak<sup>609</sup>  
(clxxxii) Konings<sup>610</sup>  
(clxxxiii) Korber<sup>611</sup>  
(clxxxiv) Koulinska<sup>612</sup>  
(clxxxv) Koulinska<sup>613</sup>  
(clxxxvi) Kousiappa<sup>614</sup>  
(clxxxvii) Kousiappa<sup>615</sup>  
(clxxxviii) Kuiken<sup>616</sup>  
(clxxxix) Kusagawa<sup>617</sup>  
(cxc) Kusagawa<sup>618</sup>  
(cxc i) Laeyendecker<sup>619</sup>  
(cxc ii) Lakhashe<sup>620</sup>  
(cxc iii) Lakhashe<sup>621</sup>  
(cxc iv) Lamers<sup>622</sup>  
(cxc v) Land<sup>623</sup>  
(cxc vi) Lau<sup>624</sup>  
(cxc vii) Lau<sup>625</sup>  
(cxc viii) Laukkanen<sup>626</sup>  
(cxc ix) Leal<sup>627</sup>  
(cc) Lemey<sup>628</sup>  
(cc i) Li<sup>629</sup>  
(cc ii) Li<sup>630</sup>  
(cc iii) Li<sup>631</sup>  
(cc iv) Li<sup>632</sup>  
(cc v) Li<sup>633</sup>  
(cc vi) Liao<sup>634</sup>  
(cc vii) Liégeois<sup>635</sup>  
(cc viii) Liégeois<sup>636</sup>  
(cc ix) Liégeois<sup>637</sup>  
(cc x) Liitsola<sup>638</sup>  
(cc xi) Liitsola<sup>639</sup>  
(cc xii) Lin<sup>295</sup>  
(cc xiii) Locatelli<sup>640</sup>  
(cc xiv) Lole<sup>1</sup>  
(cc xv) Luk<sup>641</sup>  
(cc xvi) Luk<sup>642</sup>  
(cc xvii) Lukashov<sup>643</sup>  
(cc xviii) Machado<sup>644</sup>  
(cc xix) Magiorkinis<sup>645</sup>  
(cc xx) Magiorkinis<sup>646</sup>  
(cc xxi) Magiorkinis<sup>647</sup>  
(cc xxii) Magiorkinis<sup>648</sup>  
(cc xxiii) Malet<sup>649</sup>  
(cc xxiv) Maljkovic<sup>650</sup>  
(cc xxv) Mamadou<sup>651</sup>  
(cc xxvi) Masharsky<sup>652</sup>  
(cc xxvii) Meloni<sup>653</sup>  
(cc xxviii) Meng<sup>654</sup>  
(cc xxix) Meng<sup>655</sup>  
(cc xxx) Mild<sup>656</sup>  
(cc xxxi) Mokili<sup>657</sup>  
(cc xxxii) Monno<sup>658</sup>  
(cc xxxiii) Montavon<sup>659</sup>  
(cc xxxiv) Montavon<sup>660</sup>  
(cc xxxv) Montavon<sup>661</sup>  
(cc xxxvi) Montavon<sup>662</sup>  
(cc xxxvii) Monteiro<sup>663</sup>  
(cc xxxviii) Motomura<sup>664</sup>  
(cc xxxix) Mullick<sup>665</sup>  
(cc xl) Muñoz-Nieto<sup>666</sup>  
(cc xli) Nadai<sup>667</sup>  
(cc xlii) Ndembi<sup>668</sup>  
(cc xliii) Ndembi<sup>669</sup>  
(cc xliv) Neogi<sup>670</sup>  
(cc xlv) Niama<sup>671</sup>  
(cc xlvi) Novelli<sup>672</sup>  
(cc xlvii) Novelli<sup>673</sup>

(ccxlviii) Novitsky<sup>674</sup>  
(ccxlix) Novitsky<sup>675</sup>  
(ccl) Ntemgwa<sup>272</sup>  
(ccli) Ntemgwa<sup>676</sup>  
(cclii) Nyombi<sup>677</sup>  
(ccliii) Oliveira<sup>612,678</sup>  
(ccliv) Op de Coul<sup>679</sup>  
(cclv) Op de Coul<sup>680</sup>  
(cclvi) Pádua<sup>681</sup>  
(cclvii) Palma<sup>682</sup>  
(cclviii) Palma<sup>683</sup>  
(cclix) Pando<sup>684</sup>  
(cclx) Pando<sup>685</sup>  
(cclxi) Pando<sup>686</sup>  
(cclxii) Pando<sup>687</sup>  
(cclxiii) Papa<sup>688</sup>  
(cclxiv) Paraskevis<sup>689</sup>  
(cclxv) Paraskevis<sup>690</sup>  
(cclxvi) Paraskevis<sup>691</sup>  
(cclxvii) Paraskevis<sup>692</sup>  
(cclxviii) Paraskevis<sup>693</sup>  
(cclxix) Parreira<sup>694</sup>  
(cclxx) Parreira<sup>695</sup>  
(cclxxi) Passaes<sup>696</sup>  
(cclxxii) Passaes<sup>697</sup>  
(cclxxiii) Pernas<sup>698</sup>  
(cclxxiv) Perez<sup>699</sup>  
(cclxxv) Perez<sup>700</sup>  
(cclxxvi) Perez<sup>701</sup>  
(cclxxvii) Perez-Alvarez<sup>702</sup>  
(cclxxviii) Perez-Alvarez<sup>703</sup>  
(cclxxix) Perez-Alvarez<sup>704</sup>  
(cclxxx) Persaud<sup>705</sup>  
(cclxxxi) Petroni<sup>706</sup>  
(cclxxxii) Philpott<sup>707</sup>  
(cclxxxiii) Piantadosi<sup>708</sup>  
(cclxxxiv) Pires<sup>709</sup>  
(cclxxxv) Pollakis<sup>710</sup>  
(cclxxxvi) Pollakis<sup>711</sup>  
(cclxxxvii) Posada<sup>712</sup>  
(cclxxxviii) Posada<sup>713</sup>  
(cclxxxix) Powell<sup>714</sup>  
(ccxc) Powell<sup>715</sup>  
(ccxci) Powell<sup>716</sup>  
(ccxcii) Powell<sup>717</sup>  
(ccxciii) Praparanattapan<sup>718</sup>  
(ccxciv) Qiu<sup>719</sup>  
(ccxcv) Quarler<sup>720</sup>  
(ccxcvi) Quesnel-Vallieres<sup>721</sup>  
(ccxcvii) Rainwater<sup>722</sup>  
(ccxcviii) Ramos<sup>723</sup>  
(ccxcix) Razzolini<sup>724</sup>  
(ccc) Resik<sup>725</sup>  
(ccci) Revilla<sup>726</sup>  
(cccii) Rhee<sup>727</sup>  
(ccciii) Rios<sup>728</sup>  
(ccciv) Ristic<sup>729</sup>  
(cccv) Riva<sup>730</sup>  
(cccvi) Riva<sup>731</sup>  
(cccvii) Rodrigues<sup>732</sup>  
(cccviii) Rodrigues<sup>733</sup>  
(cccix) Rousseau<sup>734</sup>  
(cccx) Ruchansky<sup>735</sup>  
(cccxi) Sa-Filho<sup>736</sup>  
(cccxi) Saad<sup>737</sup>  
(cccxi) Saad<sup>738</sup>  
(cccxi) Saad<sup>739</sup>  
(cccxi) Sacktor<sup>740</sup>  
(cccxi) Sahbandar<sup>741</sup>  
(cccxi) Sahbandar<sup>742</sup>  
(cccxi) Salemi<sup>743</sup>

(cccix) Salemi<sup>744</sup>  
(cccxx) Salminen<sup>745</sup>  
(cccxxi) Sanabani<sup>746</sup>  
(cccxxii) Sanabani<sup>747</sup>  
(cccxxiii) Sanabani<sup>748</sup>  
(cccxxiv) Sanabani<sup>749</sup>  
(cccxxv) Sanchez<sup>750</sup>  
(cccxxvi) Santos<sup>751</sup>  
(cccxxvii) Santos-Costa<sup>752</sup>  
(cccxxviii) Schroeder<sup>753</sup>  
(cccxxix) Schultz<sup>754</sup>  
(cccxxx) Segura<sup>755</sup>  
(cccxxxi) Sen<sup>756</sup>  
(cccxxxii) Servais<sup>757</sup>  
(cccxxxiii) Shang<sup>758</sup>  
(cccxxxiv) Shi<sup>759</sup>  
(cccxxxv) Shi<sup>760</sup>  
(cccxxxvi) Sierra<sup>761</sup>  
(cccxxxvii) Sierra<sup>762</sup>  
(cccxxxviii) Snoeck<sup>763</sup>  
(cccxxxix) Snoeck<sup>764</sup>  
(cccl) Soares<sup>765</sup>  
(cccli) Ssemwanga<sup>766</sup>  
(ccclii) Steain<sup>767</sup>  
(cccliii) Steain<sup>768</sup>  
(cccliv) Streeck<sup>769</sup>  
(ccclv) Su<sup>770</sup>  
(ccclvi) Swanson<sup>771</sup>  
(ccclvii) Takahoko<sup>772</sup>  
(ccclviii) Takebe<sup>773</sup>  
(ccclix) Taveira<sup>774</sup>  
(cccl) Tscherning-Casper<sup>775</sup>  
(cccli) Tebit<sup>776</sup>  
(ccclii) Tebit<sup>777</sup>  
(cccliii) Tebit<sup>778</sup>  
(cccliv) Tebit<sup>779</sup>  
(ccclv) Tee<sup>780</sup>  
(ccclvi) Tee<sup>781</sup>  
(ccclvii) Tee<sup>782</sup>  
(ccclviii) Tee<sup>783</sup>  
(ccclix) Teixeira<sup>784</sup>  
(ccclx) Thomson<sup>785</sup>  
(ccclxi) Thomson<sup>786</sup>  
(ccclxii) Thomson<sup>787</sup>  
(ccclxiii) Thomson<sup>788</sup>  
(ccclxiv) Thomson<sup>789</sup>  
(ccclxv) Thomson<sup>790</sup>  
(ccclxvi) Thomson<sup>791</sup>  
(ccclxvii) Thomson<sup>792</sup>  
(ccclxviii) Thomson<sup>793</sup>  
(ccclxix) Toni<sup>794</sup>  
(ccclxx) Torimiro<sup>795</sup>  
(ccclxxi) Tramuto<sup>796</sup>  
(ccclxxii) Triques<sup>797</sup>  
(ccclxxiii) Turk<sup>798</sup>  
(ccclxxiv) Turk<sup>799</sup>  
(ccclxxv) Turk<sup>800</sup>  
(ccclxxvi) Utsumi<sup>801</sup>  
(ccclxxvii) Vallari<sup>802</sup>  
(ccclxxviii) Vallari<sup>803</sup>  
(ccclxxix) van der Hoek<sup>804</sup>  
(ccclxxx) van Harmelen<sup>805</sup>  
(ccclxxxi) van Laethem<sup>806</sup>  
(ccclxxxii) Vázquez de Parga<sup>807</sup>  
(ccclxxxiii) Vazquez-Valls<sup>808</sup>  
(ccclxxxiv) Véras<sup>809</sup>  
(ccclxxxv) Vergne<sup>810</sup>  
(ccclxxxvi) Vergne<sup>811</sup>  
(ccclxxxvii) Vidal<sup>812</sup>  
(ccclxxxviii) Vidal<sup>813</sup>  
(ccclxxxix) Vidal<sup>814</sup>

(cccxc) Vidal<sup>815</sup>  
(cccxc) Vidal<sup>816</sup>  
(cccxcii) Vidal<sup>817</sup>  
(cccxciii) Vidal<sup>818</sup>  
(cccxciv) Vidal<sup>819</sup>  
(cccxcv) Vignoles<sup>820</sup>  
(cccxcvi) Vignoles<sup>821</sup>  
(cccxcvii) Villahermosa<sup>822</sup>  
(cccxcviii) Viñoles<sup>823</sup>  
(cccxcix) von Truchsess<sup>824</sup>  
(cd) Wang<sup>825</sup>  
(cdi) Wang<sup>826</sup>  
(cdii) Wang<sup>827</sup>  
(cdiii) Wang<sup>828</sup>  
(cdiv) Wheeler<sup>829</sup>  
(cdv) Wichukchinda<sup>830</sup>  
(cdvi) Wilbe<sup>831</sup>  
(cdvii) Wilbe<sup>832</sup>  
(cdviii) Wilkinson<sup>833</sup>  
(cdix) Wirachsilp<sup>834</sup>  
(cdx) Womack<sup>835</sup>  
(cdx) Yamaguchi<sup>836</sup>  
(cdxii) Yamaguchi<sup>837</sup>  
(cdxiii) Yamaguchi<sup>838</sup>  
(cdxiv) Yamaguchi<sup>839</sup>  
(cdxv) Yamaguchi<sup>840</sup>  
(cdxvi) Yamaguchi<sup>841</sup>  
(cdxvii) Yamaguchi<sup>842</sup>  
(cdxviii) Yamaguchi<sup>843</sup>  
(cdxix) Yang<sup>844</sup>  
(cdx) Yang<sup>845</sup>  
(cdxxi) Yang<sup>846</sup>  
(cdxii) Yang<sup>847</sup>  
(cdxiii) Yang<sup>848</sup>  
(cdxiv) Ye<sup>849</sup>  
(cdxv) Yerly<sup>850</sup>  
(cdxvi) Yilmaz<sup>851</sup>  
(cdxvii) Yirrell<sup>852</sup>  
(cdxviii) Zarandia<sup>853</sup>  
(cdxix) Zetterberg<sup>854</sup>  
(cdx) Zhang<sup>855</sup>  
(cdxxi) Zhang<sup>856</sup>  
(cdxii) Zhang<sup>857</sup>  
(cdxiii) Zhang<sup>858</sup>  
(cdxiv) Zhang<sup>859</sup>  
(cdxv) Zhang<sup>860</sup>  
(cdxvi) Zhong<sup>861</sup>  
(cdxvii) Zhong<sup>862</sup>  
(cdxviii) zur Megede<sup>863</sup>

(b) Lentivirus other than SIV/HIV (CAEV, FIV, MuLV, MVV, SRLV)

(i) Bruen<sup>864</sup>  
(ii) Clewley<sup>865</sup>  
(iii) Duarte<sup>866</sup>  
(iv) Gjerset<sup>867</sup>  
(v) Gjerset<sup>868</sup>  
(vi) Grego<sup>869</sup>  
(vii) Howard<sup>870</sup>  
(viii) Martins<sup>871</sup>  
(ix) Pisoni<sup>872</sup>  
(x) Reggeti<sup>873</sup>  
(xi) Reina<sup>874</sup>  
(xii) Samman<sup>875</sup>  
(xiii) Steinrigl<sup>876</sup>  
(xiv) Steinrigl<sup>877</sup>

7. dsDNA-RT

- i) Hepadnavirus (hepatitis B virus - HBV, duck hepatitis virus, etc)
- (1) Abdou Chekaraou<sup>878</sup>
  - (2) Ahn<sup>879</sup>
  - (3) Alestig<sup>880</sup>
  - (4) Amini-Bavil-Olyaei<sup>881</sup>
  - (5) Amini-Bavil-Olyaei<sup>882</sup>

- (6) Arankalle<sup>883</sup>
- (7) Audsley<sup>884</sup>
- (8) Banerjee<sup>885</sup>
- (9) Bekondi<sup>886</sup>
- (10) Cavinta<sup>887</sup>
- (11) Chauhan<sup>888</sup>
- (12) Chen<sup>889</sup>
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- (18) Elkady<sup>895</sup>
- (19) Garmiri<sup>896</sup>
- (20) Hannoun<sup>897</sup>
- (21) Hübschen<sup>898</sup>
- (22) Hübschen<sup>899</sup>
- (23) Huy<sup>900</sup>
- (24) Huy<sup>901</sup>
- (25) Juniastruti<sup>902</sup> (first author erroneously parsed in Pubmed)
- (26) Kim<sup>903</sup>
- (27) Kurbanov<sup>904</sup>
- (28) Laoi<sup>905</sup>
- (29) Luo<sup>906</sup>
- (30) Magiorkinis<sup>907</sup>
- (31) Mahgoub<sup>908</sup>
- (32) Makuwa<sup>909</sup>
- (33) Martin<sup>910</sup>
- (34) Meldal<sup>911</sup>
- (35) Mohebbi<sup>912</sup>
- (36) Morozov<sup>913</sup>
- (37) Mugisha<sup>914</sup>
- (38) Mulyanto<sup>915</sup>
- (39) Mulyanto<sup>916</sup>
- (40) Myers<sup>917</sup>
- (41) Nakajima<sup>918</sup>
- (42) Njouom<sup>919</sup>
- (43) Olinger<sup>920</sup>
- (44) Osiowy<sup>921</sup>
- (45) Owiredun<sup>922</sup>
- (46) Phung<sup>923</sup>
- (47) Pourkaim<sup>924</sup>
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- (49) Pourkaim<sup>926</sup>
- (50) Purdy<sup>927</sup>
- (51) Quarleri<sup>928</sup>
- (52) Sa-Nguanmoo<sup>929</sup>
- (53) Simmonds<sup>930</sup>
- (54) Sugauchi<sup>931</sup>
- (55) Suwannakarn<sup>932</sup>
- (56) Tanaka<sup>933</sup>
- (57) Tang<sup>934</sup>
- (58) Tatematsu<sup>935</sup>
- (59) Tran<sup>936</sup>
- (60) Tran<sup>937</sup>
- (61) Trinks<sup>938</sup>
- (62) Vivekanandan<sup>939</sup>
- (63) Yang<sup>940</sup>
- (64) Yang<sup>941</sup>
- (65) Yano<sup>942</sup>
- (66) Yin<sup>943</sup>

#### Reference List

1. Lole KS, Bollinger RC, Paranjape RS, Gadkari D, Kulkarni SS, Novak NG, Ingersoll R, Sheppard HW, Ray SC. Full-length human immunodeficiency virus type 1 genomes from subtype C- infected seroconverters in India, with evidence of intersubtype recombination. *J.Virol.* 1999;73:152-60.
2. Earnhart CG, Marconi RT. OspC Phylogenetic Analyses Support the Feasibility of a Broadly Protective Polyvalent Chimeric Lyme Disease Vaccine. *Clin.Vaccine Immunol.* 2007;14:628-34.

3. Hill KK, Smith TJ, Helma CH, Ticknor LO, Foley BT, Svensson RT, Brown JL, Johnson EA, Smith LA, Okinaka RT, Jackson PJ, Marks JD. Genetic diversity among Botulinum Neurotoxin-producing clostridial strains. *J Bacteriol.* 2007;189:818-32.
4. Hill KK, Xie G, Foley BT, Smith TJ, Munk AC, Bruce D, Smith LA, Brettin TS, Detter JC. Recombination and insertion events involving the botulinum neurotoxin complex genes in *Clostridium botulinum* types A, B, E and F and *Clostridium butyricum* type E strains. *BMC.Biol.* 2009;7:66
5. Luquez C, Raphael BH, Maslanka SE. Analysis of neurotoxin gene clusters in *Clostridium botulinum* type Ab strains. *Appl.Environ.Microbiol.* 2009;75:6094-101.
6. Raphael BH, Choudoir MJ, Luquez C, Fernandez R, Maslanka SE. Sequence diversity of genes encoding botulinum neurotoxin type F. *Appl.Environ.Microbiol.* 2010;76:4805-12.
7. Pimenta AL, Racher K, Jamieson L, Blight MA, Holland IB. Mutations in HlyD, part of the type 1 translocator for hemolysin secretion, affect the folding of the secreted toxin. *J.Bacteriol.* 2005;187:7471-80.
8. Oleastro M, Cordeiro R, Menard A, Gomes JP. Allelic diversity among *Helicobacter pylori* outer membrane protein genes homB and homA generated by recombination. *J Bacteriol.* 2010;192:3961-8.
9. Pride DT, Meinersmann RJ, Blaser MJ. Allelic Variation within *Helicobacter pylori* babA and babB. *Infect.Immun.* 2001;69:1160-71.
10. Norberg P, Bergstrom M, Jethava V, Dubhashi D, Hermansson M. The IncP-1 plasmid backbone adapts to different host bacterial species and evolves through homologous recombination. *Nat.Commun.* 2011;2:268
11. Ma L, Jensen JS, Mancuso M, Hamasuna R, Jia Q, McGowin CL, Martin DH. Genetic variation in the complete MgPa operon and its repetitive chromosomal elements in clinical strains of *Mycoplasma genitalium*. *PLoS.ONE.* 2010;5:e15660
12. Sarkar SF, Guttman DS. Evolution of the core genome of *Pseudomonas syringae*, a highly clonal, endemic plant pathogen. *Appl.Environ.Microbiol.* 2004;70:1999-2012.
13. Gaunt MW, Turner SL, Rigottier-Gois L, Lloyd-Macgilp SA, Young JP. Phylogenies of atpD and recA support the small subunit rRNA-based classification of rhizobia. *Int.J.Syst.Evol.Microbiol.* 2001;51:2037-48.
14. Olsen JE, Christensen H, Aarestrup FM. Diversity and evolution of blaZ from *Staphylococcus aureus* and coagulase-negative staphylococci. *J.Antimicrob.Chemother.* 2006;57:450-60.
15. Zhang K, McClure JA, Elsayed S, Conly JM. Novel staphylococcal cassette chromosome mec type, tentatively designated type VIII, harboring class A mec and type 4 ccr gene complexes in a Canadian epidemic strain of methicillin-resistant *Staphylococcus aureus*. *Antimicrob.Agents Chemother.* 2009;53:531-40.
16. Tettelin H, Masignani V, Cieslewicz MJ, Eisen JA, Peterson S, Wessels MR, Paulsen IT, Nelson KE, Margarit I, Read TD, Madoff LC, Wolf AM, Beanan MJ, Brinkac LM, Daugherty SC, DeBoy RT, Durkin AS, Kolonay JF, Madupu R, Lewis MR, Radune D, Fedorova NB, Scanlan D, Khouri H, Mulligan S, Carty HA, Cline RT, Van Aken SE, Gill J, Scarselli M, Mora M, Iacobini ET, Brettoni C, Galli G, Mariani M, Vegni F, Maione D, Rinaudo D, Rappuoli R, Telford JL, Kasper DL, Grandi G, Fraser CM. Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V *Streptococcus agalactiae*. *Proc.Natl.Acad.Sci.U.S.A.* 2002;99:12391-6.
17. Marco A, Marin I. How *Athila* retrotransposons survive in the *Arabidopsis* genome. *BMC Genomics.* 2008;9:219
18. Yang L, Gui JF. Positive Selection on Multiple Antique Allelic Lineages of Transferrin in the Polyploid *Carassius auratus*. *Mol.Biol.Evol.* 2004;
19. Gomes JP, Nunes A, Bruno WJ, Borrego MJ, Florindo C, Dean D. Polymorphisms in the Nine Polymorphic Membrane Proteins of *Chlamydia trachomatis* across All Serovars: Evidence for Serovar Da Recombination and Correlation with Tissue Tropism. *J.Bacteriol.* 2006;188:275-86.
20. Gomes JP, Bruno WJ, Nunes A, Santos N, Florindo C, Borrego MJ, Dean D. Evolution of *Chlamydia trachomatis* diversity occurs by widespread interstrain recombination involving hotspots. *Genome Res.* 2007;17:50-60.
21. Nunes A, Borrego MJ, Nunes B, Florindo C, Gomes JP. Evolutionary dynamics of ompA, the gene encoding the *Chlamydia trachomatis* key antigen. *J.Bacteriol.* 2009;191:7182-92.
22. Nunes A, Nogueira PJ, Borrego MJ, Gomes JP. Adaptive evolution of the *Chlamydia trachomatis* dominant antigen reveals distinct evolutionary scenarios for B- and T-cell epitopes: worldwide survey. *PLoS.ONE.* 2010;5:
23. Somboonna N, Wan R, Ojcius DM, Pettengill MA, Joseph SJ, Chang A, Hsu R, Read TD, Dean D. Hypervirulent *Chlamydia trachomatis* Clinical Strain Is a Recombinant between Lymphogranuloma Venereum (L2) and D Lineages. *MBio.* 2011;2:
24. Zhou L, Yang C, Xiao L. PCR-mediated recombination between *Cryptosporidium* spp. of lizards and snakes. *J.Eukaryot.Microbiol.* 2003;50:563-5.
25. Beszteri B, Acs E, Medlin LK. Ribosomal DNA sequence variation among sympatric strains of the *Cyclotella meneghiniana* complex (Bacillariophyceae) reveals cryptic diversity. *Protist.* 2005;156:317-33.
26. Gaubert P, Begg CM. Re-assessed molecular phylogeny and evolutionary scenario within genets (Carnivora, Viverridae, Genettinae). *Mol.Phylogenet.Evol.* 2007;44:920-7.
27. Janssens TK, Marien J, Cenijn P, Legler J, van Straalen NM, Roelofs D. Recombinational micro-evolution of functionally different metallothionein promoter alleles from *Orchesella cincta*. *BMC Evol.Biol.* 2007;7:88
28. Costas J, Naveira H. Evolutionary history of the human endogenous retrovirus family ERV9. *Mol.Biol.Evol.* 2000;17:320-30.
29. Hershberger KL, Kurian J, Korber BT, Letvin NL. Killer cell immunoglobulin-like receptors (KIR) of the African-origin sabaean monkey: evidence for recombination events in the evolution of KIR. *Eur.J.Immunol.* 2005;35:922-35.



30. Jackson MS, Oliver K, Loveland J, Humphray S, Dunham I, Rocchi M, Viggiano L, Park JP, Hurlles ME, Santibanez-Koref M. Evidence for widespread reticulate evolution within human duplicons. *Am.J.Hum.Genet.* 2005;77:824-40.
31. Devault A, Banuls AL. The promastigote surface antigen gene family of the *Leishmania* parasite: differential evolution by positive selection and recombination. *BMC Evol.Biol.* 2008;8:292
32. Kutty G, Maldarelli F, Achaz G, Kovacs JA. Variation in the major surface glycoprotein genes in *Pneumocystis jirovecii*. *J.Infect.Dis.* 2008;198:741-9.
33. Ciborowski KL, Consuegra S, Garcia dL, Beaumont MA, Wang J, Jordan WC. Rare and fleeting: an example of interspecific recombination in animal mitochondrial DNA. *Biol.Lett.* 2007;3:554-7.
34. Gehrke B, Martin-Bravo S, Muasya M, Luceno M. Monophyly, phylogenetic position and the role of hybridization in *Schoenoxiphium* Nees (Cariceae, Cyperaceae). *Mol.Phylogenet.Evol.* 2010;56:380-92.
35. Gaunt MW, Yeo M, Frame IA, Stothard JR, Carrasco HJ, Taylor MC, Mena SS, Veazey P, Miles GA, Acosta N, de Arias AR, Miles MA. Mechanism of genetic exchange in American trypanosomes. *Nature.* 2003;421:936-9.
36. Sergeant M, Baxter L, Jarrett P, Shaw E, Ousley M, Winstanley C, Morgan JA. Identification, Typing, and Insecticidal Activity of *Xenorhabdus* Isolates from Entomopathogenic Nematodes in United Kingdom Soil and Characterization of the xpt Toxin Loci. *Appl.Environ.Microbiol.* 2006;72:5895-907.
37. Sharma A, Schneider KL, Presting GG. Sustained retrotransposition is mediated by nucleotide deletions and interelement recombinations. *Proc.Natl.Acad.Sci.U.S.A.* 2008;105:15470-4.
38. Abecasis AB, Wang Y, Libin P, Imbrechts S, de OT, Camacho RJ, Vandamme AM. Comparative performance of the REGA subtyping tool version 2 versus version 1. *Infect.Genet.Evol.* 2010;10:380-5.
39. Awadalla P. The evolutionary genomics of pathogen recombination. *Nat.Rev.Genet.* 2003;4:50-60.
40. Hungnes O, Jonassen TO, Jonassen CM, Grinde B. Molecular epidemiology of viral infections. How sequence information helps us understand the evolution and dissemination of viruses. *APMIS.* 2000;108:81-97.
41. Lam TT, Hon CC, Tang JW. Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections. *Crit Rev.Clin.Lab Sci.* 2010;47:5-49.
42. Maydt J, Lengauer T. Recco: recombination analysis using cost optimization. *Bioinformatics.* 2006;22:1064-71.
43. Parrish CR, Holmes EC, Morens DM, Park EC, Burke DS, Calisher CH, Laughlin CA, Saif LJ, Daszak P. Cross-species virus transmission and the emergence of new epidemic diseases. *Microbiol.Mol.Biol.Rev.* 2008;72:457-70.
44. Schultz AK, Zhang M, Bulla I, Leitner T, Korber B, Morgenstern B, Stanke M. jpHMM: improving the reliability of recombination prediction in HIV-1. *Nucleic Acids Res.* 2009;37:W647-W651
45. Strimmer K, Forslund K, Holland B, Moulton V. A novel exploratory method for visual recombination detection. *Genome Biol.* 2003;4:R33
46. Svraka S, Rosario K, Duizer E, van der Avoort H, Breitbart M, Koopmans M. Metagenomic sequencing for virus identification in a public-health setting. *J Gen.Virol.* 2010;91:2846-56.
47. Telenti A. New developments in laboratory monitoring of HIV-1 infection. *Clin.Microbiol.Infect.* 2002;8:137-43.
48. Aoki K, Ishiko H, Konno T, Shimada Y, Hayashi A, Kaneko H, Ohguchi T, Tagawa Y, Ohno S, Yamazaki S. Epidemic keratoconjunctivitis due to the novel hexon-chimeric-intermediate 22,37/H8 human adenovirus. *J.Clin.Microbiol.* 2008;46:3259-69.
49. Darr S, Madisch I, Hofmayer S, Rehren F, Heim A. Phylogeny and primary structure analysis of fiber shafts of all human adenovirus types for rational design of adenoviral gene-therapy vectors. *J.Gen.Virol.* 2009;90:2849-54.
50. Ishiko H, Shimada Y, Konno T, Hayashi A, Ohguchi T, Tagawa Y, Aoki K, Ohno S, Yamazaki S. Novel human adenovirus causing nosocomial epidemic keratoconjunctivitis. *J.Clin.Microbiol.* 2008;46:2002-8.
51. Kaneko H, Aoki K, Ohno S, Ishiko H, Fujimoto T, Kikuchi M, Harada S, Gonzalez G, Koyanagi KO, Watanabe H, Suzutani T. Complete genome analysis of a novel intertypic recombinant human adenovirus causing epidemic keratoconjunctivitis in Japan. *J.Clin.Microbiol.* 2011;49:484-90.
52. Kaneko H, Aoki K, Ishida S, Ohno S, Kitaichi N, Ishiko H, Fujimoto T, Ikeda Y, Nakamura M, Gonzalez G, Koyanagi KO, Watanabe H, Suzutani T. Recombination analysis of intermediate human adenovirus type 53 in Japan by complete genome sequence. *J.Gen.Virol.* 2011;92:1251-9.
53. Lukashev AN, Ivanova OE, Eremeeva TP, Iggo RD. Evidence of frequent recombination among human adenoviruses. *J Gen.Virol.* 2008;89:380-8.
54. Madisch I, Harste G, Pommer H, Heim A. Phylogenetic analysis of the main neutralization and hemagglutination determinants of all human adenovirus prototypes as a basis for molecular classification and taxonomy. *J.Virol.* 2005;79:15265-76.
55. Mahadevan P, Seto J, Tibbetts C, Seto D. Natural variants of human adenovirus type 3 provide evidence for relative genome stability across time and geographic space. *Virology.* 2010;397:113-8.
56. Maluquer de Motes C, Hundesa A, Almeida FC, Bofill-Mas S, Girones R. Isolation of a novel monkey adenovirus reveals a new phylogenetic clade in the evolutionary history of simian adenoviruses. *Virology.* 2011;8:125
57. Robinson CM, Rajaiya J, Walsh MP, Seto D, Dyer DW, Jones MS, Chodosh J. Computational analysis of human adenovirus type 22 provides evidence for recombination among species D human adenoviruses in the penton base gene. *J.Virol.* 2009;83:8980-5.
58. Robinson CM, Singh G, Henquell C, Walsh MP, Peigue-Lafeuille H, Seto D, Jones MS, Dyer DW, Chodosh J. Computational analysis and identification of an emergent human adenovirus pathogen implicated in a respiratory fatality. *Virology.* 2010;

59. Roy S, Clawson DS, Calcedo R, Lebherz C, Sanmiguel J, Wu D, Wilson JM. Use of chimeric adenoviral vectors to assess capsid neutralization determinants. *Virology*. 2005;333:207-14.
60. Roy S, Vandenberghe LH, Kryazhimskiy S, Grant R, Calcedo R, Yuan X, Keough M, Sandhu A, Wang Q, Medina-Jaszek CA, Plotkin JB, Wilson JM. Isolation and characterization of adenoviruses persistently shed from the gastrointestinal tract of non-human primates. *PLoS.Pathog.* 2009;5:e1000503
61. Seto J, Walsh MP, Mahadevan P, Purkayastha A, Clark JM, Tibbetts C, Seto D. Genomic and bioinformatics analyses of HAdV-14p, reference strain of a re-emerging respiratory pathogen and analysis of B1/B2. *Virus Res.* 2009;143:94-105.
62. Seto J, Walsh MP, Metzgar D, Seto D. Computational analysis of adenovirus serotype 5 (HAdV-C5) from an HAdV coinfection shows genome stability after 45 years of circulation. *Virology*. 2010;404:180-6.
63. Tong S, Singh J, Ruone S, Humphrey C, Yip CC, Lau SK, Anderson LJ, Kaur T. Identification of adenoviruses in fecal specimens from wild chimpanzees (*Pan troglodytes schweinfurthii*) in western Tanzania. *Am J Trop.Med.Hyg.* 2010;82:967-70.
64. Walsh MP, Chintakuntlawar A, Robinson CM, Madisch I, Harrach B, Hudson NR, Schnurr D, Heim A, Chodosh J, Seto D, Jones MS. Evidence of molecular evolution driven by recombination events influencing tropism in a novel human adenovirus that causes epidemic keratoconjunctivitis. *PLoS One.* 2009;4:e5635
65. Walsh MP, Seto J, Jones MS, Chodosh J, Xu W, Seto D. Computational analysis identifies human adenovirus type 55 as a re-emergent acute respiratory disease pathogen. *J Clin.Microbiol.* 2010;48:991-3.
66. Walsh MP, Seto J, Tirado D, Chodosh J, Schnurr D, Seto D, Jones MS. Computational analysis of human adenovirus serotype 18. *Virology*. 2010;404:284-92.
67. Wevers D, Leendertz FH, Scuda N, Boesch C, Robbins MM, Head J, Ludwig C, Kuhn J, Ehlers B. A novel adenovirus of Western lowland gorillas (*Gorilla gorilla gorilla*). *Virol.J.* 2010;7:303
68. Yang Z, Zhu Z, Tang L, Wang L, Tan X, Yu P, Zhang Y, Tian X, Wang J, Zhang Y, Li D, Xu W. Genomic analyses of recombinant adenovirus type 11a in China. *J.Clin.Microbiol.* 2009;
69. Zhu Z, Zhang Y, Xu S, Yu P, Tian X, Wang L, Liu Z, Tang L, Mao N, Ji Y, Li C, Yang Z, Wang S, Wang J, Li D, Xu W. Outbreak of acute respiratory disease in China caused by B2 species of adenovirus type 11. *J.Clin.Microbiol.* 2009;47:697-703.
70. Duprez R, Hbid O, Afonso P, Quach H, Belloul L, Fajali N, Ismaili N, Benomar H, Hassane TE, Huerre M, Quintana-Murci L, Gessain A. Molecular epidemiology of the HHV-8 K1 gene from Moroccan patients with Kaposi's sarcoma. *Virology*. 2006;
71. Faure-Della Corte M, Samot J, Garrigue I, Magnin N, Reigadas S, Couzi L, Dromer C, Velly JF, Dechanet-Merville J, Fleury HJ, Lafon ME. Variability and recombination of clinical human cytomegalovirus strains from transplantation recipients. *J Clin.Virol.* 2010;47:161-9.
72. Garrigue I, Faure-Della CM, Magnin N, Recordon-Pinson P, Couzi L, Lebrette ME, Schrive MH, Roncin L, Taupin JL, Dechanet-Merville J, Fleury H, Lafon ME. UL40 human cytomegalovirus variability evolution patterns over time in renal transplant recipients. *Transplantation.* 2008;86:826-35.
73. Liljeqvist JA, Tunback P, Norberg P. Asymptomatically shed recombinant herpes simplex virus type 1 strains detected in saliva. *J.Gen.Virol.* 2009;90:559-66.
74. Norberg P, Bergstrom T, Rekabdar E, Lindh M, Liljeqvist JA. Phylogenetic analysis of clinical herpes simplex virus type 1 isolates identified three genetic groups and recombinant viruses. *J.Virol.* 2004;78:10755-64.
75. Norberg P, Kasubi MJ, Haarr L, Bergstrom T, Liljeqvist JA. Divergence and Recombination of Clinical Herpes Simplex Virus Type 2 Isolates. *J Virol.* 2007;
76. Norberg P, Liljeqvist JA, Bergstrom T, Sammons S, Schmid DS, Loparev VN. Complete-genome phylogenetic approach to varicella-zoster virus evolution: genetic divergence and evidence for recombination. *J Virol.* 2006;80:9569-76.
77. Peters GA, Tyler SD, Grose C, Severini A, Gray MJ, Upton C, Tipples GA. A Full-Genome Phylogenetic Analysis of Varicella-Zoster Virus Reveals a Novel Origin of Replication-Based Genotyping Scheme and Evidence of Recombination between Major Circulating Clades. *J Virol.* 2006;80:9850-60.
78. Tyler SD, Severini A. The complete genome sequence of herpesvirus papio 2 (*Cercopithecine herpesvirus 16*) shows evidence of recombination events among various progenitor herpesviruses. *J.Virol.* 2006;80:1214-21.
79. Medico Zajac MP, Romera SA, Ladelfa MF, Kotsias F, Thiry J, Ziant D, Meurens F, Keil GM, Thiry E, Muyllkens B. Characterization of interspecific recombinants generated from closely related bovine herpesviruses 1 and 5 through multiple PCR sequencing assays. *J.Virol.Methods.* 2009;161:75-83.
80. Gubser C, Hue S, Kellam P, Smith GL. Poxvirus genomes: a phylogenetic analysis. *J.Gen.Virol.* 2004;85:105-17.
81. Blinkova O, Victoria J, Li Y, Keele BF, Sanz C, Ndjanga JB, Peeters M, Travis D, Lonsdorf EV, Wilson ML, Pusey AE, Hahn BH, Delwart EL. Novel circular DNA viruses in stool samples of wild-living chimpanzees. *J.Gen.Virol.* 2010;91:74-86.
82. He CQ, Ding NZ, Fan W, Wu YH, Li JP, Li YL. Identification of chicken anemia virus putative intergenotype recombinants. *Virology*. 2007;366:1-7.
83. Ma CM, Hon CC, Lam TY, Li VY, Wong CK, De Oliveira T, Leung FC. Evidence for recombination in natural populations of porcine circovirus type 2 in Hong Kong and mainland China. *J Gen.Virol.* 2007;88:1733-7.
84. Chen CL, Jensen RL, Schnepf BC, Connell MJ, Shell R, Sferra TJ, Bartlett JS, Clark KR, Johnson PR. Molecular characterization of adeno-associated viruses infecting children. *J.Virol.* 2005;79:14781-92.
85. Gao G, Alvira MR, Somanathan S, Lu Y, Vandenberghe LH, Rux JJ, Calcedo R, Sanmiguel J, Abbas Z, Wilson JM. Adeno-associated viruses undergo substantial evolution in primates during natural infections. *Proc.Natl.Acad.Sci.U.S.A.* 2003;100:6081-6.
86. Gao G, Vandenberghe LH, Alvira MR, Lu Y, Calcedo R, Zhou X, Wilson JM. Clades of adeno-associated viruses are widely disseminated in human tissues. *J.Virol.* 2004;78:6381-8.

87. Li Y, Ge X, Hon CC, Zhang H, Zhou P, Zhang Y, Wu Y, Wang LF, Shi Z. Prevalence and genetic diversity of adeno-associated viruses in bats from China. *J Gen.Virol.* 2010;91:2601-9.
88. Blawid R, Van DT, Maiss E. Transreplication of a Tomato yellow leaf curl Thailand virus DNA-B and replication of a DNAbeta component by Tomato leaf curl Vietnam virus and Tomato yellow leaf curl Vietnam virus. *Virus Res.* 2008;136:107-17.
89. Knierim D, Maiss E. Application of Phi29 DNA polymerase in identification and full-length clone inoculation of tomato yellow leaf curl Thailand virus and tobacco leaf curl Thailand virus. *Arch.Virol.* 2007;152:941-54.
90. Kumari P, Singh AK, Chattopadhyay B, Chakraborty S. Molecular characterization of a new species of Begomovirus and betasatellite causing leaf curl disease of tomato in India. *Virus Res.* 2010;152:19-29.
91. Kumari P, Singh AK, Sharma VK, Chattopadhyay B, Chakraborty S. A novel recombinant tomato-infecting begomovirus capable of transcomplementing heterologous DNA-B components. *Arch.Virol.* 2011;
92. Lozano G, Trenado HP, Valverde RA, Navas-Castillo J. Novel begomovirus species of recombinant nature in sweet potato (*Ipomoea batatas*) and *Ipomoea indica*: taxonomic and phylogenetic implications. *J.Gen.Virol.* 2009;90:2550-62.
93. Schubert J, Habekuss A, Kazmaier K, Jeske H. Surveying cereal-infecting geminiviruses in Germany--diagnostics and direct sequencing using rolling circle amplification. *Virus Res.* 2007;127:61-70.
94. Gottschling M, Bravo IG, Schulz E, Bracho MA, Deaville R, Jepson PD, Bressemer MF, Stockfleth E, Nindl I. Modular organizations of novel cetacean papillomaviruses. *Mol.Phylogenet.Evol.* 2010;
95. Rector A, Stevens H, Lacave G, Lemey P, Mostmans S, Salbany A, Vos M, Van Doorslaer K, Ghim SJ, Rehtanz M, Bossart GD, Jenson AB, Van Ranst M. Genomic characterization of novel dolphin papillomaviruses provides indications for recombination within the Papillomaviridae. *Virology.* 2008;
96. Arthur JL, Higgins GD, Davidson GP, Givney RC, Ratcliff RM. A novel bocavirus associated with acute gastroenteritis in Australian children. *PLoS Pathog.* 2009;5:e1000391
97. Cheng WX, Li JS, Huang CP, Yao DP, Liu N, Cui SX, Jin Y, Duan ZJ. Identification and nearly full-length genome characterization of novel porcine bocaviruses. *PLoS One.* 2010;5:e13583
98. Cheng W, Chen J, Xu Z, Yu J, Huang C, Jin M, Li H, Zhang M, Jin Y, Duan Z. Phylogenetic and Recombination Analysis of human bocavirus 2. *BMC.Infect.Dis.* 2011;11:50
99. Fryer JF, Delwart E, Bernardin F, Tuke PW, Lukashov VV, Baylis SA. Analysis of two human parvovirus PARV4 genotypes identified in human plasma for fractionation. *J Gen.Virol.* 2007;88:2162-7.
100. Kapoor A, Mehta N, Esper F, Poljsak-Prijatelj M, Quan PL, Qaisar N, Delwart E, Lipkin WI. Identification and characterization of a new bocavirus species in gorillas. *PLoS One.* 2010;5:e11948
101. Katsoulidou A, Rokka C, Issaris C, Haida C, Tzannis K, Sypsa V, Detsika M, Paraskevis D, Hatzakis A. Comparative evaluation of the performance of the Abbott RealTime HIV-1 assay for measurement of HIV-1 plasma viral load on genetically diverse samples from Greece. *Virol.J.* 2011;8:10
102. Lin JH, Chiu SC, Lin YC, Chen HL, Lin KH, Shan KH, Wu HS, Liu HF. Clinical and genetic analysis of Human Bocavirus in children with lower respiratory tract infection in Taiwan. *J.Clin.Virol.* 2009;44:219-24.
103. Panning M, Kobbe R, Vollbach S, Drexler JF, Adjei S, Adjei O, Drosten C, May J, Eis-Hubinger AM. Novel human parvovirus 4 genotype 3 in infants, Ghana. *Emerg.Infect.Dis.* 2010;16:1143-6.
104. Wang Y, Gonzalez R, Zhou H, Li J, Li Y, Paranhos-Baccala G, Vernet G, Guo L, Wang J. Detection of human bocavirus 3 in China. *Eur.J.Clin.Microbiol.Infect.Dis.* 2011;
105. Zappa A, Canuti M, Frati E, Pariani E, Perin S, Ruzza ML, Farina C, Podesta A, Zanetti A, Amendola A, Tanzi E. Co-circulation of genetically distinct human metapneumovirus and human bocavirus strains in young children with respiratory tract infections in Italy. *J.Med.Virol.* 2011;83:156-64.
106. Luo C, Bueno M, Kant J, Martinson J, Randhawa P. Genotyping schemes for polyomavirus BK, using gene-specific phylogenetic trees and single nucleotide polymorphism analysis. *J.Virol.* 2009;83:2285-97.
107. He CQ, Ma LY, Wang D, Li GR, Ding NZ. Homologous recombination is apparent in infectious bursal disease virus. *Virology.* 2009;384:51-8.
108. Hon CC, Lam TT, Yip CW, Wong RT, Shi M, Jiang J, Zeng F, Leung FC. Phylogenetic evidence for homologous recombination within the family Birnaviridae. *J.Gen.Virol.* 2008;89:3156-64.
109. He CQ, Ding NZ, He M, Li SN, Wang XM, He HB, Liu XF, Guo HS. Intragenic recombination as a mechanism of genetic diversity in bluetongue virus. *J Virol.* 2010;84:11487-95.
110. Lamhoujeb S, Cook A, Pollari F, Bidawid S, Farber J, Mattison K. Rotaviruses from Canadian farm samples. *Arch.Virol.* 2010;155:1127-37.
111. Martella V, Banyai K, Lorusso E, Decaro N, Bellacicco A, Desario C, Corrente M, Greco G, Moschidou P, Tempesta M, Arista S, Ciarlet M, Lavazza A, Buonavoglia C. Genetic heterogeneity in the VP7 of group C rotaviruses. *Virology.* 2007;367:358-66.
112. Matthijnssens J, Rahman M, Van Ranst M. Two out of the 11 genes of an unusual human G6P[6] rotavirus isolate are of bovine origin. *J.Gen.Virol.* 2008;89:2630-5.
113. Matthijnssens J, Potgieter CA, Ciarlet M, Parreno V, Martella V, Banyai K, Garaicoechea L, Palombo EA, Novo L, Zeller M, Arista S, Gerna G, Rahman M, Van Ranst M. Are Human P[14] Rotavirus Strains the Result of Interspecies Transmissions from sheep or other Ungulates Belonging to the Mammalian Order of Artiodactyla? *J.Virol.* 2009;
114. Parra GI, Bok K, Martinez M, Gomez JA. Evidence of rotavirus intragenic recombination between two sublineages of the same genotype. *J.Gen.Virol.* 2004;85:1713-6.
115. Phan TG, Okitsu S, Maneekarn N, Ushijima H. Evidence of intragenic recombination in g1 rotavirus VP7 genes. *J Virol.* 2007;81:10188-94.
116. Phan TG, Okitsu S, Maneekarn N, Ushijima H. Genetic heterogeneity, evolution and recombination in emerging G9 rotaviruses. *Infect.Genet.Evol.* 2007;7:656-63.
117. Allison AB, Stallknecht DE. Genomic sequencing of Highlands J virus: a comparison to western and eastern equine encephalitis viruses. *Virus Res.* 2009;145:334-40.

118. Arankalle VA, Shrivastava S, Cherian S, Gunjkar RS, Walimbe AM, Jadhav SM, Sudeep AB, Mishra AC. Genetic divergence of Chikungunya viruses in India (1963-2006) with special reference to the 2005-2006 explosive epidemic. *J Gen.Virol.* 2007;88:1967-76.
119. Capote N, Perez-Panades J, Monzo C, Carbonell E, Urbaneja A, Scorza R, Ravelonandro M, Cambra M. Assessment of the diversity and dynamics of Plum pox virus and aphid populations in transgenic European plums under Mediterranean conditions. *Transgenic Res.* 2008;17:367-77.
120. Kajic V, Cerni S, Krajacic M, Mikec I, Skoric D. Molecular typing of Plum Pox virus isolates in Croatia. *J.Plant Pathol.* 2009;90:S1.9-S1.13
121. Maliogka VI, Dovas CI, Katis NI. Evolutionary relationships of virus species belonging to a distinct lineage within the Ampelovirus genus. *Virus Res.* 2008;135:125-35.
122. Chen N, Cao Z, Yu X, Deng X, Zhao T, Wang L, Liu Q, Li X, Tian K. Emergence of novel European genotype porcine reproductive and respiratory syndrome virus in mainland China. *J.Gen.Virol.* 2011;92:880-92.
123. Fang Y, Schneider P, Zhang WP, Faaberg KS, Nelson EA, Rowland RR. Diversity and evolution of a newly emerged North American Type 1 porcine arterivirus: analysis of isolates collected between 1999 and 2004. *Arch.Virol.* 2007;152:1009-17.
124. Forsberg R, Storgaard T, Nielsen HS, Oleksiewicz MB, Cordioli P, Sala G, Hein J, Botner A. The genetic diversity of European type PRRSV is similar to that of the North American type but is geographically skewed within Europe. *Virology.* 2002;299:38-47.
125. Li B, Fang L, Xu Z, Liu S, Gao J, Jiang Y, Chen H, Xiao S. Recombination in vaccine and circulating strains of porcine reproductive and respiratory syndrome viruses. *Emerg.Infect.Dis.* 2009;15:2032-5.
126. Liu D, Zhou R, Zhang J, Zhou L, Jiang Q, Guo X, Ge X, Yang H. Recombination analyses between two strains of porcine reproductive and respiratory syndrome virus in vivo. *Virus Res.* 2011;155:473-86.
127. Chu DK, Chin AW, Smith GJ, Chan KH, Guan Y, Peiris JS, Poon LL. Detection of novel astroviruses in urban brown rats and previously known astroviruses in humans. *J Gen.Virol.* 2010;91:2457-62.
128. Guo L, Gonzalez R, Wang W, Li Y, Paranhos-Baccala G, Vernet G, Wang J. Complete genome sequence of human astrovirus genotype 6. *Virol.J.* 2010;7:29
129. Guo L, Xu X, Song J, Wang W, Wang J, Hung T. Molecular characterization of astrovirus infection in children with diarrhea in Beijing, 2005-2007. *J Med.Virol.* 2010;82:415-23.
130. Jonassen CM, Jonassen TO, Saif YM, Snodgrass DR, Ushijima H, Shimizu M, Grinde B. Comparison of capsid sequences from human and animal astroviruses. *J.Gen.Virol.* 2001;82:1061-7.
131. Lukashov VV, Goudsmit J. Evolutionary relationships among Astroviridae. *J.Gen.Virol.* 2002;83:1397-405.
132. Pantin-Jackwood MJ, Spackman E, Woolcock PR. Phylogenetic analysis of Turkey astroviruses reveals evidence of recombination. *Virus Genes.* 2006;32:187-92.
133. Pantin-Jackwood MJ, Strother KO, Mundt E, Zsak L, Day JM, Spackman E. Molecular characterization of avian astroviruses. *Arch.Virol.* 2010;
134. Tse H, Chan WM, Tsoi HW, Fan RY, Lau CC, Lau SK, Woo PC, Yuen KY. Re-discovery and genomic characterization of bovine astroviruses. *J.Gen.Virol.* 2011;
135. Wolfaardt M, Kiulia NM, Mwenda JM, Taylor MB. Evidence of a recombinant wild type human astrovirus strain from a Kenyan child with gastroenteritis. *J Clin.Microbiol.* 2010;
136. Friedman SD, Genthner FJ, Gentry J, Sobsey MD, Vinje J. Gene Mapping and Phylogenetic Analysis of the Complete Genome from 30 ssRNA Male-Specific Coliphages (Family Leviviridae). *J.Virol.* 2009;
137. Abrantes J, Esteves PJ, van der LW. Evidence for recombination in the major capsid gene VP60 of the rabbit haemorrhagic disease virus (RHDV). *Arch.Virol.* 2008;153:329-35.
138. Ambert-Balay K, Bon F, Le Guyader F, Pothier P, Kohli E. Characterization of new recombinant noroviruses. *J.Clin.Microbiol.* 2005;43:5179-86.
139. Bull RA, Hansman GS, Clancy LE, Tanaka MM, Rawlinson WD, White PA. Norovirus recombination in ORF1/ORF2 overlap. *Emerg.Infect.Dis.* 2005;11:1079-85.
140. Bull RA, Tanaka MM, White PA. Norovirus recombination. *J Gen.Virol.* 2007;88:3347-59.
141. Carlsson B, Lindberg AM, Rodriguez-Diaz J, Hedlund KO, Persson B, Svensson L. Quasispecies dynamics and molecular evolution of human norovirus capsid P region during chronic infection. *J.Gen.Virol.* 2009;90:432-41.
142. Chhabra P, Walimbe AM, Chitambar SD. Molecular characterization of three novel intergenotype norovirus GII recombinant strains from western India. *Virus Res.* 2010;147:242-6.
143. Chhabra P, Walimbe AM, Chitambar SD. Complete genome characterization of Genogroup II norovirus strains from India: Evidence of recombination in ORF2/3 overlap. *Infect.Genet.Evol.* 2010;10:1101-9.
144. Chung JY, Han TH, Park SH, Kim SW, Hwang ES. Detection of GII-4/2006b variant and recombinant noroviruses in children with acute gastroenteritis, South Korea. *J.Med.Virol.* 2010;82:146-52.
145. Coyne KP, Reed FC, Porter CJ, Dawson S, Gaskell RM, Radford AD. Recombination of Feline calicivirus within an endemically infected cat colony. *J.Gen.Virol.* 2006;87:921-6.
146. Dai YC, Hu GF, Zhang XF, Song CL, Xiang WL, Wu XB, Wang LY, Jiang X, Nie J. Molecular epidemiology of norovirus gastroenteritis in children in Jiangmen, China, 2005-2007. *Arch.Virol.* 2011;
147. Eden JS, Bull RA, Tu E, McIver CJ, Lyon MJ, Marshall JA, Smith DW, Musto J, Rawlinson WD, White PA. Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in Australia during 2007 and 2008. *J Clin.Virol.* 2010;49:265-71.
148. Etherington GJ, Dicks J, Roberts IN. Recombination Analysis Tool (RAT): a program for the high-throughput detection of recombination. *Bioinformatics.* 2005;21:278-81.
149. Forrester NL, Moss SR, Turner SL, Schirrmeyer H, Gould EA. Recombination in rabbit haemorrhagic disease virus: possible impact on evolution and epidemiology. *Virology.* 2008;376:390-6.
150. Fukuda S, Sasaki Y, Takao S, Seno M. Recombinant norovirus implicated in gastroenteritis outbreaks in Hiroshima prefecture, Japan. *J Med.Virol.* 2008;80:921-8.

151. Han MG, Smiley JR, Thomas C, Saif LJ. Genetic recombination between two genotypes of genogroup III bovine noroviruses (BoNVs) and capsid sequence diversity among BoNVs and Nebraska-like bovine enteric caliciviruses. *J.Clin.Microbiol.* 2004;42:5214-24.
152. Han TH, Kim CH, Chung JY, Park SH, Hwang ES. Emergence of norovirus GII-4/2008 variant and recombinant strains in Seoul, Korea. *Arch.Virol.* 2010;
153. Hansman GS, Doan LT, Kguyen TA, Okitsu S, Katayama K, Ogawa S, Natori K, Takeda N, Kato Y, Nishio O, Noda M, Ushijima H. Detection of norovirus and sapovirus infection among children with gastroenteritis in Ho Chi Minh City, Vietnam. *Arch.Virol.* 2004;149:1673-88.
154. Hansman GS, Takeda N, Oka T, Oseto M, Hedlund K-O, Katayama K. Intergenogroup recombination in sapoviruses. *Emerg.Infect.Dis.* 2005;11:1916-20.
155. Hansman GS, Oka T, Katayama K, Takeda N. Human sapoviruses: genetic diversity, recombination, and classification. *Rev.Med.Virol.* 2007;17:133-41.
156. Hoffmann D, Seebach J, Foley BT, Frosner G, Nadas K, Protzer U, Schatzl HM. Isolated norovirus GII.7 strain within an extended GII.4 outbreak. *J Med.Virol.* 2010;82:1058-64.
157. Jin M, Xie HP, Duan ZJ, Liu N, Zhang Q, Wu BS, Li HY, Cheng WX, Yang SH, Yu JM, Xu ZQ, Cui SX, Zhu L, Tan M, Jiang X, Fang ZY. Emergence of the GII4/2006b variant and recombinant noroviruses in China. *J.Med.Virol.* 2008;80:1997-2004.
158. Kamel AH, Ali MA, El Nady HG, de Rougemont A, Pothier P, Belliot G. Predominance and Circulation of Enteric Viruses in Grand Cairo. *J.Clin.Microbiol.* 2009;
159. Katayama K, Miyoshi T, Uchino K, Oka T, Tanaka T, Takeda N, Hansman GS. Novel recombinant sapovirus. *Emerg.Infect.Dis.* 2004;10:1874-6.
160. Kim M, Lee H, Chang KO, Ko G. Molecular characterization of murine norovirus isolates from South Korea. *Virus Res.* 2010;147:1-6.
161. Martella V, Campolo M, Lorusso E, Cavicchio P, Camero M, Bellacicco AL, Decaro N, Elia G, Greco G, Corrente M, Desario C, Arista S, Banyai K, Koopmans M, Buonavoglia C. Norovirus in captive lion cub (*Panthera leo*). *Emerg.Infect.Dis.* 2007;13:1071-3.
162. Martella V, Lorusso E, Banyai K, Decaro N, Corrente M, Elia G, Cavalli A, Radogna A, Costantini V, Saif LJ, Lavazza A, Di Trani L, Buonavoglia C. Identification of a porcine calicivirus related genetically to human sapoviruses. *J.Clin.Microbiol.* 2008;46:1907-13.
163. Martella V, Lorusso E, Decaro N, Elia G, Radogna A, D'Abramo M, Desario C, Cavalli A, Corrente M, Camero M, Germinario CA, Banyai K, Di Martino B, Marsilio F, Carmichael LE, Buonavoglia C. Detection and molecular characterization of a canine norovirus. *Emerg.Infect.Dis.* 2008;14:1306-8.
164. Martella V, Decaro N, Lorusso E, Radogna A, Moschidou P, Amorisco F, Lucente SM, Desario C, Mari V, Elia G, Banyai K, Carmichael EL, Buonavoglia C. Genetic heterogeneity and recombination in canine noroviruses. *J.Virol.* 2009;
165. Mathijs E, Muylken B, Mauroy A, Ziant D, Delwiche T, Thiry E. Experimental evidence of recombination in murine noroviruses. *J.Gen.Virol.* 2010;91:2723-33.
166. Motomura K, Yokoyama M, Ode H, Nakamura H, Mori H, Kanda T, Oka T, Katayama K, Noda M, Tanaka T, Takeda N, Sato H. Divergent evolution of norovirus GII/4 by genome recombination from May 2006 to February 2009 in Japan. *J Virol.* 2010;84:8085-97.
167. Muller B, Klemm U, Mas MA, Schreier E. Genetic diversity and recombination of murine noroviruses in immunocompromised mice. *Arch.Virol.* 2007;152:1709-19.
168. Nakamura K, Iwai M, Zhang J, Obara M, Horimoto E, Hasegawa S, Kurata T, Takizawa T. Detection of a novel recombinant norovirus from sewage water in toyama prefecture, Japan. *Jpn.J.Infect.Dis.* 2009;62:394-8.
169. Nayak MK, Chatterjee D, Nataraju SM, Pativada M, Mitra U, Chatterjee MK, Saha TK, Sarkar U, Krishnan T. A new variant of Norovirus GII.4/2007 and inter-genotype recombinant strains of NVGII causing acute watery diarrhoea among children in Kolkata, India. *J.Clin.Virol.* 2009;45:223-9.
170. Okada M, Yamashita Y, Oseto M, Shinozaki K. The detection of human sapoviruses with universal and genogroup-specific primers. *Arch.Virol.* 2006;151:2503-9.
171. Oliver SL, Dastjerdi AM, Wong S, El Attar L, Gallimore C, Brown DW, Green J, Bridger JC. Molecular characterization of bovine enteric caliciviruses: a distinct third genogroup of noroviruses (norwalk-like viruses) unlikely to be of risk to humans. *J.Virol.* 2003;77:2789-98.
172. Oliver SL, Brown DW, Green J, Bridger JC. A chimeric bovine enteric calicivirus: evidence for genomic recombination in genogroup III of the Norovirus genus of the Caliciviridae. *Virology.* 2004;326:231-9.
173. Phan TG, Yan H, Li Y, Okitsu S, Muller WE, Ushijima H. Novel recombinant norovirus in China. *Emerg.Infect.Dis.* 2006;12:857-8.
174. Phan TG, Okitsu S, Muller WE, Kohno H, Ushijima H. Novel recombinant sapovirus, Japan. *Emerg.Infect.Dis.* 2006;12:865-7.
175. Phan TG, Trinh QD, Yagyu F, Sugita K, Okitsu S, Muller WE, Ushijima H. Outbreak of sapovirus infection among infants and children with acute gastroenteritis in Osaka City, Japan during 2004-2005. *J.Med.Virol.* 2006;78:839-46.
176. Phan TG, Kuroiwa T, Kaneshi K, Ueda Y, Nakaya S, Nishimura S, Yamamoto A, Sugita K, Nishimura T, Yagyu F, Okitsu S, Muller WE, Maneekarn N, Ushijima H. Changing distribution of norovirus genotypes and genetic analysis of recombinant GIIB among infants and children with diarrhea in Japan. *J.Med.Virol.* 2006;78:971-8.
177. Phan TG, Khamrin P, Quang TD, Dey SK, Takanashi S, Okitsu S, Maneekarn N, Ushijima H. Emergence of intragenotype recombinant sapovirus in Japan. *Infect.Genet.Evol.* 2007;7:542-6.
178. Phan TG, Kaneshi K, Ueda Y, Nakaya S, Nishimura S, Yamamoto A, Sugita K, Takanashi S, Okitsu S, Ushijima H. Genetic heterogeneity, evolution, and recombination in noroviruses. *J.Med.Virol.* 2007;79:1388-400.

179. Rohayem J, Munch J, Rethwilm A. Evidence of recombination in the norovirus capsid gene. *J.Virol.* 2005;79:4977-90.
180. Siebenga JJ, Vennema H, Renckens B, de Bruin E, van d, V, Siezen RJ, Koopmans M. Epochal Evolution of GGII.4 Norovirus Capsid Proteins from 1995 to 2006. *J Virol.* 2007;81:9932-41.
181. Symes SJ, Gunsekere IC, Marshall JA, Wright PJ. Norovirus mixed infection in an oyster-associated outbreak: an opportunity for recombination. *Arch.Virol.* 2007;152:1075-86.
182. Thackray LB, Wobus CE, Chachu KA, Liu B, Alegre ER, Henderson KS, Kelley ST, Virgin HW. Murine noroviruses comprising a single genogroup exhibit biological diversity despite limited sequence divergence. *J Virol.* 2007;
183. Tsugawa T, Numata-Kinoshita K, Honma S, Nakata S, Tatsumi M, Sakai Y, Natori K, Takeda N, Kobayashi S, Tsutsumi H. Virological, Serological, and Clinical Features of an Outbreak of Acute Gastroenteritis Due to Recombinant Genogroup II Norovirus in an Infant Home. *J.Clin.Microbiol.* 2006;44:177-82.
184. Victoria M, Miagostovich MP, Ferreira MS, Vieira CB, Fioretti JM, Leite JP, Colina R, Cristina J. Bayesian coalescent inference reveals high evolutionary rates and expansion of Norovirus populations. *Infect.Genet.Evol.* 2009;9:927-32.
185. Waters A, Coughlan S, Hall WW. Characterisation of a novel recombination event in the norovirus polymerase gene. *Virology.* 2007;363:11-4.
186. Yun SI, Kim JK, Song BH, Jeong AY, Jee YM, Lee CH, Paik SY, Koo Y, Jeon I, Byun SJ, Lee YM. Complete genome sequence and phylogenetic analysis of a recombinant Korean norovirus, CBNU1, recovered from a 2006 outbreak. *Virus Res.* 2010;152:137-52.
187. Cerni S, Ruscic J, Nolasco G, Gatin Z, Krajacic M, Skoric D. Stem pitting and seedling yellows symptoms of Citrus tristeza virus infection may be determined by minor sequence variants. *Virus Genes.* 2008;36:241-9.
188. Lozano G, Grande-Perez A, Navas-Castillo J. Populations of genomic RNAs devoted to the replication or spread of a bipartite plant virus differ in genetic structure. *J.Virol.* 2009;83:12973-83.
189. Chen HW, Huang YP, Wang CH. Identification of Taiwan and China-like recombinant avian infectious bronchitis viruses in Taiwan. *Virus Res.* 2009;
190. Chen HW, Huang YP, Wang CH. Identification of intertypic recombinant infectious bronchitis viruses from slaughtered chickens. *Poult.Sci.* 2010;89:439-46.
191. Chu DK, Peiris JS, Chen H, Guan Y, Poon LL. Genomic characterizations of bat coronaviruses (1A, 1B and HKU8) and evidence for co-infections in Miniopterus bats. *J.Gen.Virol.* 2008;89:1282-7.
192. Decaro N, Martella V, Elia G, Campolo M, Mari V, Desario C, Lucente MS, Lorusso A, Greco G, Corrente M, Tempesta M, Buonavoglia C. Biological and genetic analysis of a bovine-like coronavirus isolated from water buffalo (*Bubalus bubalis*) calves. *Virology.* 2008;370:213-22.
193. Decaro N, Mari V, Campolo M, Lorusso A, Camero M, Elia G, Martella V, Cordioli P, Enjuanes L, Buonavoglia C. Recombinant canine coronaviruses related to transmissible gastroenteritis virus of Swine are circulating in dogs. *J.Virol.* 2009;83:1532-7.
194. Hon CC, Lam TY, Shi ZL, Drummond AJ, Yip CW, Zeng F, Lam PY, Leung FC. Evidence of the recombinant origin of a bat severe acute respiratory syndrome (SARS)-like coronavirus and its implications on the direct ancestor of SARS coronavirus. *J Virol.* 2008;82:1819-26.
195. Lan YC, Liu HF, Shih YP, Yang JY, Chen HY, Chen YM. Phylogenetic analysis and sequence comparisons of structural and non-structural SARS coronavirus proteins in Taiwan. *Infect.Genet.Evol.* 2005;5:261-9.
196. Lan YC, Liu TT, Yang JY, Lee CM, Chen YJ, Chan YJ, Lu JJ, Liu HF, Hsiung CA, Ho MS, Hsiao KJ, Chen HY, Chen YM. Molecular epidemiology of severe acute respiratory syndrome-associated coronavirus infections in Taiwan. *J.Infect.Dis.* 2005;191:1478-89.
197. Lau SK, Woo PC, Li KS, Huang Y, Wang M, Lam CS, Xu H, Guo R, Chan KH, Zheng BJ, Yuen KY. Complete genome sequence of bat coronavirus HKU2 from Chinese horseshoe bats revealed a much smaller spike gene with a different evolutionary lineage from the rest of the genome. *Virology.* 2007;367:428-39.
198. Lau SK, Li KS, Huang Y, Shek CT, Tse H, Wang M, Choi GK, Xu H, Lam CS, Guo R, Chan KH, Zheng BJ, Woo PC, Yuen KY. Eco-epidemiology and complete genome comparison of SARS-related Rhinolophus bat coronavirus in China reveal bats as reservoir for acute, self-limiting infection that allows recombination events. *J.Virol.* 2010;
199. Lau SK, Poon RW, Wong BH, Wang M, Huang Y, Xu H, Guo R, Li KS, Gao K, Chan KH, Zheng BJ, Woo PC, Yuen KY. Coexistence of different genotypes in the same bat and serological characterization of *Rousettus* bat coronavirus HKU9 belonging to a novel Betacoronavirus subgroup. *J Virol.* 2010;84:11385-94.
200. Lee DK, Park CK, Kim SH, Lee C. Heterogeneity in spike protein genes of porcine epidemic diarrhea viruses isolated in Korea. *Virus Res.* 2010;149:175-82.
201. Lim TH, Lee HJ, Lee DH, Lee YN, Park JK, Youn HN, Kim MS, Lee JB, Park SY, Choi IS, Song CS. An emerging recombinant cluster of nephropathogenic strains of avian infectious bronchitis virus in Korea. *Infect.Genet.Evol.* 2011;
202. Mardani K, Noormohammadi AH, Ignjatovic J, Browning GF. Naturally occurring recombination between distant strains of infectious bronchitis virus. *Arch.Virol.* 2010;155:1581-6.
203. McKinley ET, Jackwood MW, Hilt DA, Kissinger JC, Robertson JS, Lemke C, Paterson AH. Attenuated live vaccine usage affects accurate measures of virus diversity and mutation rates in avian coronavirus infectious bronchitis virus. *Virus Res.* 2011;
204. Ntafis V, Mari V, Decaro N, Papanastassopoulou M, Papaioannou N, Mpatziou R, Buonavoglia C, Xylouri E. Isolation, tissue distribution and molecular characterization of two recombinant canine coronavirus strains. *Vet.Microbiol.* 2011;
205. Pyrc K, Dijkman R, Deng L, Jebbink MF, Ross HA, Berkhout B, van der Hoek L. Mosaic structure of human coronavirus NL63, one thousand years of evolution. *J Mol.Biol.* 2006;364:964-73.

206. Rota PA, Oberste MS, Monroe SS, Nix WA, Campagnoli R, Icenogle JP, Penaranda S, Bankamp B, Maher K, Chen MH, Tong S, Tamin A, Lowe L, Frace M, DeRisi JL, Chen Q, Wang D, Erdman DD, Peret TC, Burns C, Ksiazek TG, Rollin PE, Sanchez A, Liffick S, Holloway B, Limor J, McCaustland K, Olsen-Rasmussen M, Fouchier R, Gunther S, Osterhaus AD, Drosten C, Pallansch MA, Anderson LJ, Bellini WJ. Characterization of a novel coronavirus associated with severe acute respiratory syndrome. *Science*. 2003;300:1394-9.
207. Stanhope MJ, Brown JR, Amrine-Madsen H. Evidence from the evolutionary analysis of nucleotide sequences for a recombinant history of SARS-CoV. *Infect.Genet.Evol.* 2004;4:15-9.
208. Stavriniades J, Guttman DS. Mosaic evolution of the severe acute respiratory syndrome coronavirus. *J.Virol.* 2004;78:76-82.
209. van der Hoek L, Pyrc K, Jebbink MF, Vermeulen-Oost W, Berkhout RJ, Wolthers KC, Wertheim-van Dillen PM, Kaandorp J, Spaargaren J, Berkhout B. Identification of a new human coronavirus. *Nat.Med.* 2004;10:368-73.
210. Vijgen L, Keyaerts E, Lemey P, Moes E, Li S, Vandamme AM, Van Ranst M. Circulation of genetically distinct contemporary human coronavirus OC43 strains. *Virology*. 2005;337:85-92.
211. Vijgen L, Keyaerts E, Lemey P, Maes P, Van Reeth K, Nauwynck H, Pensaert M, Van Ranst M. Evolutionary History of the Closely Related Group 2 Coronaviruses: Porcine Hemagglutinating Encephalomyelitis Virus, Bovine Coronavirus, and Human Coronavirus OC43. *J.Virol.* 2006;80:7270-4.
212. Woo PC, Lau SK, Yip CC, Huang Y, Tsoi HW, Chan KH, Yuen KY. Comparative Analysis of 22 Coronavirus HKU1 Genomes Reveals a Novel Genotype and Evidence of Natural Recombination in Coronavirus HKU1. *J.Virol.* 2006;80:7136-45.
213. Yuan J, Hon CC, Li Y, Wang D, Xu G, Zhang H, Zhou P, Poon LL, Lam TT, Leung FC, Shi Z. Intraspecies diversity of SARS-like coronaviruses in *Rhinolophus sinicus* and its implications for the origin of SARS coronaviruses in humans. *J Gen.Virol.* 2010;91:1058-62.
214. Zeng FY, Chan CW, Chan MN, Chen JD, Chow KY, Hon CC, Hui KH, Li J, Li VY, Wang CY, Wang PY, Guan Y, Zheng B, Poon LL, Chan KH, Yuen KY, Peiris JS, Leung FC. The complete genome sequence of severe acute respiratory syndrome coronavirus strain HKU-39849 (HK-39). *Exp.Biol.Med.(Maywood.)*. 2003;228:866-73.
215. Zhang XW, Yap YL, Danchin A. Testing the hypothesis of a recombinant origin of the SARS-associated coronavirus. *Arch.Virol.* 2005;150:1-20.
216. Zhang J, Guy JS, Snijder EJ, Denniston DA, Timoney PJ, Balasuriya UB. Genomic characterization of equine coronavirus. *Virology*. 2007;369:92-104.
217. Zhang CY, Wei JF, He SH. Adaptive evolution of the spike gene of SARS coronavirus: changes in positively selected sites in different epidemic groups. *BMC Microbiol.* 2006;6:88
218. Palacios G, Hui J, Quan PL, Kalkstein A, Honkavuori KS, Bussetti AV, Conlan S, Evans J, Chen YP, vanEngelsdorp D, Efrat H, Pettis J, Cox-Foster D, Holmes EC, Briese T, Lipkin WI. Genetic analysis of Israel acute paralysis virus: distinct clusters are circulating in the United States. *J.Virol.* 2008;82:6209-17.
219. AbuBakar S, Wong PF, Chan YF. Emergence of dengue virus type 4 genotype IIA in Malaysia. *J.Gen.Virol.* 2002;83:2437-42.
220. Barrero PR, Mistchenko AS. Complete genome sequencing of dengue virus type 1 isolated in Buenos Aires, Argentina. *Virus Res.* 2004;101:135-45.
221. Fajardo A, Recarey R, de Mora D, D' Andrea L, Alvarez M, Regato M, Colina R, Khan B, Cristina J. Modeling gene sequence changes over time in type 3 dengue viruses from Ecuador. *Virus Res.* 2009;141:105-9.
222. Ramirez A, Fajardo A, Moros Z, Gerder M, Caraballo G, Camacho D, Comach G, Alarcon V, Zambrano J, Hernandez R, Moratorio G, Cristina J, Liprandi F. Evolution of Dengue Virus type 3 genotype III in Venezuela: diversification, rates and population dynamics. *Virol.J.* 2010;7:329
223. Regato M, Recarey R, Moratorio G, de Mora D, Garcia-Aguirre L, Gonzalez M, Mosquera C, Alava A, Fajardo A, Alvarez M, D' Andrea L, Dubra A, Martinez M, Khan B, Cristina J. Phylogenetic analysis of the NS5 gene of dengue viruses isolated in Ecuador. *Virus Res.* 2008;132:197-200.
224. Tolou HJ, Couissinier-Paris P, Durand JP, Mercier V, de Pina JJ, de Micco P, Billoir F, Charrel RN, de Lamballerie X. Evidence for recombination in natural populations of dengue virus type 1 based on the analysis of complete genome sequences. *J.Gen.Virol.* 2001;82:1283-90.
225. Chuang CK, Chen WJ. Experimental evidence that RNA recombination occurs in the Japanese encephalitis virus. *Virology*. 2009;394:286-97.
226. Santos CL, Sallum MA, Franco HM, Oshiro FM, Rocco IM. Genetic characterization of St. Louis encephalitis virus isolated from human in Sao Paulo, Brazil. *Mem.Inst.Oswaldo Cruz.* 2006;101:57-63.
227. Yun SM, Kim SY, Ju YR, Han MG, Jeong YE, Ryou J. First complete genomic characterization of two tick-borne encephalitis virus isolates obtained from wild rodents in South Korea. *Virus Genes.* 2011;
228. Kuno G, Chang GJ. Characterization of Sepik and Entebbe bat viruses closely related to yellow fever virus. *Am J Trop.Med.Hyg.* 2006;75:1165-70.
229. Kuno G, Chang GJ. Full-length sequencing and genomic characterization of Bagaza, Kedougou, and Zika viruses. *Arch.Virol.* 2007;
230. Bernardin F, Herring B, Page-Shafer K, Kuiken C, Delwart E. Absence of HCV viral recombination following superinfection. *J Viral Hepat.* 2006;13:532-7.
231. Brown RJ, Tarr AW, McClure CP, Juttla VS, Tagiuri N, Irving WL, Ball JK. Cross-genotype characterization of genetic diversity and molecular adaptation in hepatitis C virus envelope glycoprotein genes. *J Gen.Virol.* 2007;88:458-69.
232. Colina R, Casane D, Vasquez S, Garcia-Aguirre L, Chunga A, Romero H, Khan B, Cristina J. Evidence of intratypic recombination in natural populations of hepatitis C virus. *J.Gen.Virol.* 2004;85:31-7.

233. Cristina J, Colina R. Evidence of structural genomic region recombination in Hepatitis C virus. *Viol.J.* 2006;3:53
234. Cristina J. Hepatitis C virus: quasispecies dynamics, viral persistence and antiviral therapy. *Expert Opin.Ther.Patents.* 2007;17:499-510.
235. Di Lello F, Garcia G, Kott V, Sookoian S, Campos R. Diversity of hepatitis C virus genotype 1b in Buenos Aires, Argentina: description of a new cluster associated with response to treatment. *J.Med.Virol.* 2008;80:619-27.
236. Di Lello FA, Pineiro YLF, Munoz G, Campos RH. Diversity of hepatitis B and C viruses in Chile. *J.Med.Virol.* 2009;81:1887-94.
237. Fan X, Lang DM, Xu Y, Lyra AC, Yusim K, Everhart JE, Korber BT, Perelson AS, Di Bisceglie AM. Liver transplantation with hepatitis C virus-infected graft: interaction between donor and recipient viral strains. *Hepatology.* 2003;38:25-33.
238. Gao F, Nainan OV, Khudyakov Y, Li J, Hong Y, Gonzales AC, Spelbring J, Margolis HS. Recombinant hepatitis C virus in experimentally infected chimpanzees. *J Gen.Virol.* 2007;88:143-7.
239. Gupte GM, Ramdasi AY, Kulkarni AS, Arankalle VA. Complete genome sequences of hepatitis C virus subtype 3i and 3a subtype isolates from India. *Indian J Gastroenterol.* 2010;29:101-5.
240. Kalinina O, Norder H, Mukomolov S, Magnius LO. A natural intergenotypic recombinant of hepatitis C virus identified in St. Petersburg. *J.Virol.* 2002;76:4034-43.
241. Kalinina O, Norder H, Magnius LO. Full-length open reading frame of a recombinant hepatitis C virus strain from St Petersburg: proposed mechanism for its formation. *J.Gen.Virol.* 2004;85:1853-7.
242. Koletzki D, Dumont S, Vermeiren H, Peixe P, Nina J, Camacho RJ, Stuyver LJ. Full genome sequence of three isolates of hepatitis C virus subtype 4b from Portugal. *Arch.Virol.* 2009;154:127-32.
243. Kuntzen T, Berical A, Ndjomou J, Bennett P, Schneidewind A, Lennon N, Birren BW, Kuiken C, Henn MR, Simmonds P, Allen TM. A set of reference sequences for the hepatitis C genotypes 4d, 4f, and 4k covering the full open reading frame. *J.Med.Virol.* 2008;80:1370-8.
244. Lee YM, Lin HJ, Chen YJ, Lee CM, Wang SF, Chang KY, Chen TL, Liu HF, Chen YM. Molecular epidemiology of HCV genotypes among injection drug users in Taiwan: Full-length sequences of two new subtype 6w strains and a recombinant form\_2b6w. *J.Med.Virol.* 2010;82:57-68.
245. Magiorikinis G, Magiorikinis E, Paraskevis D, Ho SY, Shapiro B, Pybus OG, Allain JP, Hatzakis A. The global spread of hepatitis C virus 1a and 1b: a phylogenetic and phylogeographic analysis. *PLoS.Med.* 2009;6:e1000198
246. Moreno MP, Casane D, Lopez L, Cristina J. Evidence of recombination in quasispecies populations of a Hepatitis C Virus patient undergoing anti-viral therapy. *Viol.J.* 2006;3:87
247. Noppornpanth S, Lien TX, Poovorawan Y, Smits SL, Osterhaus AD, Haagmans BL. Identification of a naturally occurring recombinant genotype 2/6 hepatitis C virus. *J.Virol.* 2006;80:7569-77.
248. Noppornpanth S, Poovorawan Y, Lien TX, Smits SL, Osterhaus AD, Haagmans BL. Complete genome analysis of hepatitis C virus subtypes 6t and 6u. *J.Gen.Virol.* 2008;89:1276-81.
249. Ross RS, Verbeeck J, Viazov S, Lemey P, Van Ranst M, Roggendorf M. Evidence for a Complex Mosaic Genome Pattern in a Full-length Hepatitis C Virus Sequence. *Evol.Bioinform.Online.* 2008;4:249-54.
250. Shang H, Zhong P, Liu J, Han X, Dai D, Zhang M, Zhao K, Xu R, Yu XF. High prevalence and genetic diversity of HCV among HIV-1 infected people from various high-risk groups in China. *PLoS One.* 2010;5:e10631
251. Sulbaran MZ, Di Lello FA, Sulbaran Y, Cosson C, Loureiro CL, Rangel HR, Cantaloube JF, Campos RH, Moratorio G, Cristina J, Pujol FH. Genetic history of hepatitis C virus in Venezuela: high diversity and long time of evolution of HCV genotype 2. *PLoS.ONE.* 2010;5:e14315
252. Wang XH, Netski DM, Astemborski J, Mehta SH, Torbenson MS, Thomas DL, Ray SC. Progression of fibrosis during chronic hepatitis C is associated with rapid virus evolution. *J Virol.* 2007;81:6513-22.
253. He CQ, Ding NZ, Chen JG, Li YL. Evidence of natural recombination in classical swine fever virus. *Virus Res.* 2007;126:179-85.
254. Jones LR, Weber EL. Homologous recombination in bovine pestiviruses. Phylogenetic and statistic evidence. *Infect.Genet.Evol.* 2004;4:335-43.
255. Tang F, Zhang C. Evidence for positive selection on the E2 gene of bovine viral diarrhoea virus type 1. *Virus Genes.* 2007;35:629-34.
256. Tang F, Pan Z, Zhang C. The selection pressure analysis of classical swine fever virus envelope protein genes Erns and E2. *Virus Res.* 2008;131:132-5.
257. Epstein JH, Quan PL, Briese T, Street C, Jabado O, Conlan S, Ali KS, Verdugo D, Hossain MJ, Hutchison SK, Egholm M, Luby SP, Daszak P, Lipkin WI. Identification of GBV-D, a novel GB-like flavivirus from old world frugivorous bats (*Pteropus giganteus*) in Bangladesh. *PLoS Pathog.* 2010;6:e1000972
258. Neibecker M, Schwarze-Zander C, Rockstroh JK, Spengler U, Blackard JT. Evidence for extensive genotypic diversity and recombination of GB virus C (GBV-C) in Germany. *J.Med.Virol.* 2011;83:685-94.
259. James D, Varga A, Croft H. Analysis of the complete genome of peach chlorotic mottle virus: identification of non-AUG start codons, in vitro coat protein expression, and elucidation of serological cross-reactions. *Arch.Virol.* 2007;152:2207-15.
260. Takahashi M, Nishizawa T, Sato H, Sato Y, Jirintai D, Nagashima S, Okamoto H. Analysis of the full-length genome of a hepatitis E virus isolate obtained from a wild boar in Japan that is classifiable into a novel genotype. *J.Gen.Virol.* 2011;
261. van Cuyck H, Juge F, Roques P. Phylogenetic analysis of the first complete hepatitis E virus (HEV) genome from Africa. *FEMS Immunol.Med.Microbiol.* 2003;39:133-9.
262. Abdul-Hamid NF, Firat-Sarac M, Radford AD, Knowles NJ, King DP. Comparative sequence analysis of representative foot-and-mouth disease virus genomes from Southeast Asia. *Virus Genes.* 2011;



263. Balinda SN, Siegismund HR, Muwanika VB, Sangula AK, Masembe C, Ayebazibwe C, Normann P, Belsham GJ. Phylogenetic analyses of the polyprotein coding sequences of serotype O foot-and-mouth disease viruses in East Africa: evidence for interserotypic recombination. *Virology*. 2010;7:199
264. Carrillo C, Tulman ER, Delhon G, Lu Z, Carreno A, Vagnozzi A, Kutish GF, Rock DL. Comparative genomics of foot-and-mouth disease virus. *J. Virol.* 2005;79:6487-504.
265. Le VP, Nguyen T, Park JH, Kim SM, Ko YJ, Lee HS, Nguyen VC, Mai TD, Do TH, Cho IS, Lee KN. Heterogeneity and genetic variations of serotypes O and Asia 1 foot-and-mouth disease viruses isolated in Vietnam. *Vet. Microbiol.* 2010;145:220-9.
266. Lee KN, Oem JK, Park JH, Kim SM, Lee SY, Tserendorj S, Sodnomdarjaa R, Joo YS, Kim H. Evidence of recombination in a new isolate of foot-and-mouth disease virus serotype Asia 1. *Virus Res.* 2009;139:117-21.
267. Li D, Shang YJ, Liu ZX, Liu XT, Cai XP. Molecular relationships between type Asia 1 new strain from China and type O Panasia strains of foot-and-mouth-disease virus. *Virus Genes.* 2007;35:273-9.
268. Nagendrakumar SB, Madhanmohan M, Rangarajan PN, Srinivasan VA. Genetic analysis of foot-and-mouth disease virus serotype A of Indian origin and detection of positive selection and recombination in leader protease-and capsid-coding regions. *J. Biosci.* 2009;34:85-101.
269. Rana SK, Bagchi T. Partial sequence analysis of VP1 of Indian isolates of foot-and-mouth disease virus type Asia-1. *Virus Genes.* 2008;37:60-8.
270. Tosh C, Hemadri D, Sanyal A. Evidence of recombination in the capsid-coding region of type A foot- and-mouth disease virus. *J. Gen. Virol.* 2002;83:2455-60.
271. Yang X, Zhou YS, Wang HN, Zhang Y, Wei K, Wang T. Isolation, identification and complete genome sequence analysis of a strain of foot-and-mouth disease virus serotype Asia1 from pigs in southwest of China. *Virology*. 2011;8:175
272. Ntemgwa M, Gill MJ, Brenner BG, Moisi D, Wainberg MA. Discrepancies in assignment of subtype/recombinant forms by genotyping programs for HIV type 1 drug resistance testing may falsely predict superinfection. *AIDS Res. Hum. Retroviruses.* 2008;24:995-1002.
273. Al Sunaidi M, Williams CH, Hughes PJ, Schnurr DP, Stanway G. Analysis of a new human parechovirus allows the definition of parechovirus types and the identification of RNA structural domains. *J Virol.* 2007;81:1013-21.
274. Andersson P, Edman K, Lindberg AM. Molecular analysis of the echovirus 18 prototype: evidence of interserotypic recombination with echovirus 9. *Virus Res.* 2002;85:71-83.
275. Arita M, Zhu SL, Yoshida H, Yoneyama T, Miyamura T, Shimizu H. A Sabin 3-derived poliovirus recombinant contained a sequence homologous with indigenous human enterovirus species C in the viral polymerase coding region. *J. Virol.* 2005;79:12650-7.
276. Bailly JL, Cardoso MC, Labbe A, Peigue-Lafeuille H. Isolation and identification of an enterovirus 77 recovered from a refugee child from Kosovo, and characterization of the complete virus genome. *Virus Res.* 2004;99:147-55.
277. Bailly JL, Mirand A, Henquell C, Archimbaud C, Chambon M, Regagnon C, Charbonne F, Peigue-Lafeuille H. Repeated genomic transfers from echovirus 30 to echovirus 6 lineages indicate co-divergence between co-circulating populations of the two human enterovirus serotypes. *Infect. Genet. Evol.* 2010;
278. Baumgarte S, Souza Luna LK, Grywna K, Panning M, Drexler JF, Karsten C, Huppertz HI, Drosten C. Prevalence, types, and RNA concentrations of human parechoviruses, including a sixth parechovirus type, in stool samples from patients with acute enteritis. *J Clin. Microbiol.* 2008;46:242-8.
279. Benschop KS, Schinkel J, Luken ME, van den Broek PJ, Beersma MF, Menelik N, van Eijk HW, Zaaijer HL, VandenBroucke-Grauls CM, Beld MG, Wolthers KC. Fourth human parechovirus serotype. *Emerg. Infect. Dis.* 2006;12:1572-5.
280. Bible JM, Iturriza-Gomara M, Megson B, Brown D, Pantelidis P, Earl P, Bendig J, Tong CY. Molecular epidemiology of human enterovirus 71 in the United Kingdom from 1998 to 2006. *J. Clin. Microbiol.* 2008;46:3192-200.
281. Blomqvist S, Savolainen C, Laine P, Hirttio P, Lamminsalo E, Penttila E, Joks S, Roivainen M, Hovi T. Characterization of a highly evolved vaccine-derived poliovirus type 3 isolated from sewage in Estonia. *J. Virol.* 2004;78:4876-83.
282. Boros A, Pankovics P, Reuter G. Characterization of a novel porcine enterovirus in domestic pig in Hungary. *Infect. Genet. Evol.* 2011;
283. Bouslama L, Nasri D, Chollet L, Belguith K, Bourlet T, Aouni M, Pozzetto B, Pillet S. Natural recombination event within the capsid genomic region leading to a chimeric strain of human enterovirus B. *J Virol.* 2007;81:8944-52.
284. Brown B, Oberste MS, Maher K, Pallansch MA. Complete genomic sequencing shows that polioviruses and members of human enterovirus species C are closely related in the noncapsid coding region. *J. Virol.* 2003;77:8973-84.
285. Brown BA, Maher K, Flemister MR, Naraghi-Arani P, Uddin M, Oberste MS, Pallansch MA. Resolving ambiguities in genetic typing of human enterovirus species C clinical isolates and identification of enterovirus 96, 99 and 102. *J. Gen. Virol.* 2009;90:1713-23.
286. Chan YF, AbuBaker S. Recombinant human enterovirus 71 in hand, foot and mouth disease patients. *Emerg. Infect. Dis.* 2004;10:1468-70.
287. Chen GW, Huang JH, Lo YL, Tsao KC, Chang SC. Mosaic genome structure of echovirus type 30 that circulated in Taiwan in 2001. *Arch. Virol.* 2007;152:1807-17.
288. Chevaliez S, Szendroi A, Caro V, Balanant J, Guillot S, Berencsi G, Delpeyroux F. Molecular comparison of echovirus 11 strains circulating in Europe during an epidemic of multisystem hemorrhagic disease of infants indicates that evolution generally occurs by recombination. *Virology.* 2004;325:56-70.

289. Luna LK, Baumgarte S, Grywna K, Panning M, Drexler JF, Drosten C. Identification of a contemporary human parechovirus type 1 by VIDISCA and characterisation of its full genome. *Virology*. 2008;5:26
290. Dedepisdid E, Kyriakopoulou Z, Pliaka V, Kottaridi C, Bolanaki E, Levidiotou-Stefanou S, Komiotis D, Markoulatos P. A Retrospective characterization of a Vaccine derived Poliovirus type 1 isolated from sewages in Greece. *Appl.Environ.Microbiol.* 2007;
291. Dedepisdid E, Kyriakopoulou Z, Pliaka V, Markoulatos P. Correlation between recombination junctions and RNA secondary structure elements in poliovirus Sabin strains. *Virus Genes.* 2010;41:181-91.
292. Ding NZ, Wang XM, Sun SW, Song Q, Li SN, He CQ. Appearance of mosaic enterovirus 71 in the 2008 outbreak of China. *Virus Res.* 2009;145:157-61.
293. Drexler JF, Grywna K, Stocker A, Almeida PS, Medrado-Ribeiro TC, Eschbach-Bludau M, Petersen N, Costa-Ribeiro-Jr H, Drosten C. Novel human parechovirus from Brazil. *Emerg.Infect.Dis.* 2009;15:310-3.
294. Drexler JF, Grywna K, Lukashev A, Stocker A, Almeida PS, Wieseler J, Ribeiro TC, Petersen N, da Costa RH, Jr., Belalov I, Kummerer BM, Drosten C. Full genome sequence analysis of parechoviruses from Brazil reveals geographical patterns in the evolution of non-structural genes and intratypic recombination in the capsid region. *J.Gen.Virol.* 2011;92:564-71.
295. Lin YT, Lan YC, Chen YJ, Huang YH, Lee CM, Liu TT, Wong WW, Yang JY, Wang CT, Chen YM. Molecular epidemiology of HIV-1 infection and full-length genomic analysis of circulating recombinant form 07\_BC strains from injection drug users in Taiwan. *J Infect.Dis.* 2007;195:1283-93.
296. Huang YP, Lin TL, Kuo CY, Lin MW, Yao CY, Liao HW, Hsu LC, Yang CF, Yang JY, Chen PJ, Wu HS. The circulation of subgenogroups B5 and C5 of enterovirus 71 in Taiwan from 2006 to 2007. *Virus Res.* 2008;137:206-12.
297. Huang SW, Hsu YW, Smith DJ, Kiang D, Tsai HP, Lin KH, Wang SM, Liu CC, Su IJ, Wang JR. Reemergence of enterovirus 71 in 2008 in taiwan: dynamics of genetic and antigenic evolution from 1998 to 2008. *J.Clin.Microbiol.* 2009;47:3653-62.
298. Huang YP, Lin TL, Hsu LC, Chen YJ, Tseng YH, Hsu CC, Fan WB, Yang JY, Chang FY, Wu HS. Genetic diversity and C2-like subgenogroup strains of enterovirus 71, Taiwan, 2008. *Virology*. 2010;7:277
299. Jegouic S, Joffret ML, Blanchard C, Riquet FB, Perret C, Pelletier I, Colbere-Garapin F, Rakoto-Andrianarivelo M, Delpeyroux F. Recombination between polioviruses and co-circulating Coxsackie A viruses: role in the emergence of pathogenic vaccine-derived polioviruses. *PLoS Pathog.* 2009;5:e1000412
300. Krogstad P, Hammon R, Halnon N, Whitton JL. Fatal neonatal myocarditis caused by a recombinant human enterovirus-B variant. *Pediatr.Infect.Dis.J.* 2008;27:668-9.
301. Kyriakopoulou Z, Kottaridi C, Dedepisdid E, Bolanaki E, Levidiotou-Stefanou S, Markoulatos P. Molecular characterization of wild-type polioviruses isolated in Greece during the 1996 outbreak in Albania. *J.Clin.Microbiol.* 2006;44:1150-2.
302. Kyriakopoulou Z, Dedepisdid E, Pliaka V, Tsakogiannis D, Pratti A, Levidiotou-Stefanou S, Markoulatos P. Full-genome sequence analysis of a multirecombinant echovirus 3 strain isolated from sewage in Greece. *J Clin.Microbiol.* 2010;48:1513-9.
303. Kyriakopoulou Z, Dedepisdid E, Pliaka V, Mastorakos P, Stamati A, Pratti A, Levidiotou-Stefanou S, Markoulatos P. Molecular identification and full genome analysis of an echovirus 7 strain isolated from the environment in Greece. *Virus Genes.* 2010;40:183-92.
304. Kyriakopoulou Z, Dedepisdid E, Pliaka V, Tsakogiannis D, Ruether IG, Krikelis A, Markoulatos P. Complete nucleotide sequence analysis of the VP1 genomic region of Echoviruses 6 isolated from sewage in Greece revealed 98% similarity with Echoviruses 6 that were characterized from an aseptic meningitis outbreak 1 year later. *Clin.Microbiol.Infect.* 2010;
305. Li L, Victoria J, Kapoor A, Naeem A, Shaikat S, Sharif S, Alam MM, Angez M, Zaidi SZ, Delwart E. Genomic characterization of novel human parechovirus type. *Emerg.Infect.Dis.* 2009;15:288-91.
306. Lindberg AM, Andersson P, Savolainen C, Mulders MN, Hovi T. Evolution of the genome of Human enterovirus B: incongruence between phylogenies of the VP1 and 3CD regions indicates frequent recombination within the species. *J.Gen.Virol.* 2003;84:1223-35.
307. Liu HM, Zheng DP, Zhang LB, Oberste MS, Kew OM, Pallansch MA. Serial recombination during circulation of type 1 wild-vaccine recombinant polioviruses in China. *J.Virol.* 2003;77:10994-1005.
308. Lukashev AN, Lashkevich VA, Koroleva GA, Ilonen J, Hinkkanen AE. Recombination in uveitis-causing enterovirus strains. *J.Gen.Virol.* 2004;85:463-70.
309. Lukashev AN, Lashkevich VA, Ivanova OE, Koroleva GA, Hinkkanen AE, Ilonen J. Recombination in circulating Human enterovirus B: independent evolution of structural and non-structural genome regions. *J.Gen.Virol.* 2005;86:3281-90.
310. Mirand A, Henquell C, Archimbaud C, Peigue-Lafeuille H, Bailly JL. Emergence of recent echovirus 30 lineages is marked by serial genetic recombination events. *J Gen.Virol.* 2007;88:166-76.
311. Norder H, Bjerregaard L, Magnius LO. Open reading frame sequence of an Asian enterovirus 73 strain reveals that the prototype from California is recombinant. *J.Gen.Virol.* 2002;83:1721-8.
312. Oberste MS, Maher K, Pallansch MA. Evidence for frequent recombination within species human enterovirus B based on complete genomic sequences of all thirty-seven serotypes. *J.Virol.* 2004;78:855-67.
313. Oberste MS, Penaranda S, Maher K, Pallansch MA. Complete genome sequences of all members of the species Human enterovirus A. *J.Gen.Virol.* 2004;85:1597-607.
314. Oberste MS, Maher K, Pallansch MA. Complete genome sequences for nine simian enteroviruses. *J Gen.Virol.* 2007;88:3360-72.
315. Paananen A, Savolainen-Kopra C, Kaijalainen S, Vaarala O, Hovi T, Roivainen M. Genetic and phenotypic diversity of echovirus 30 strains and pathogenesis of type 1 diabetes. *J.Med.Virol.* 2007;79:945-55.
316. Phuektes P, Chua BH, Sanders S, Bek EJ, Kok CC, McMinn PC. Mapping genetic determinants of the cell culture growth phenotype of enterovirus 71. *J.Gen.Virol.* 2011;

317. Santti J, Hyypia T, Kinnunen L, Salminen M. Evidence of recombination among enteroviruses. *J.Virol.* 1999;73:8741-9.
318. Savolainen-Kopra C, Samoilovich E, Kahelin H, Hiekka AK, Hovi T, Roivainen M. Comparison of poliovirus recombinants: accumulation of point mutations provides further advantages. *J.Gen.Virol.* 2009;90:1859-68.
319. Simonen ML, Roivainen M, Iber J, Burns C, Hovi T. Outbreak of poliomyelitis in Finland in 1984-85 - Re-analysis of viral sequences using the current standard approach. *Virus Res.* 2010;147:91-7.
320. Smura TP, Junttila N, Blomqvist S, Norder H, Kaijalainen S, Paananen A, Magnius LO, Hovi T, Roivainen M. Enterovirus 94, a proposed new serotype in human enterovirus species D. *J Gen.Virol.* 2007;88:849-58.
321. Smura T, Blomqvist S, Paananen A, Vuorinen T, Sobotova Z, Bubovica V, Ivanova O, Hovi T, Roivainen M. Enterovirus surveillance reveals proposed new serotypes and provides new insight into enterovirus 5'-untranslated region evolution. *J Gen.Virol.* 2007;88:2520-6.
322. Smura T, Blomqvist S, Hovi T, Roivainen M. The complete genome sequences for a novel enterovirus type, enterovirus 96, reflect multiple recombinations. *Arch.Virol.* 2009;154:1157-61.
323. Tao Z, Cui N, Xu A, Wang H, Song L, Li Y, Liu G, Liu Y, Feng L. Genomic characterization of an enterovirus 97 strain isolated in Shandong, China. *Virus Genes.* 2010;41:158-64.
324. van der Sanden S, van EJ, Martin DP, van der Avoort H, Vennema H, Koopmans M. Detection of Recombination Breakpoints in the Genomes of Human Enterovirus 71 strains isolated in the Netherlands in epidemic and non-epidemic years, 1963-2010. *Infect.Genet.Evol.* 2011;
325. Wakatsuki K, Kawamoto D, Hiwaki H, Watanabe K, Yoshida H. Identification and characterization of two strains of human parechovirus 4 isolated from two clinical cases in Fukuoka City, Japan. *J.Clin.Microbiol.* 2008;46:3144-6.
326. Wang HY, Tsao KC, Hsieh CH, Huang LM, Lin TY, Chen GW, Shih SR, Chang LY. Inferring nonneutral evolution from contrasting patterns of polymorphisms and divergences in different protein coding regions of enterovirus 71 circulating in Taiwan during 1998-2003. *BMC Evol.Biol.* 2010;10:294
327. Wang B, Tian ZJ, Gong DQ, Li DY, Wang Y, Chen JZ, An TQ, Peng JM, Tong GZ. Isolation of serotype 2 porcine teschovirus in China: evidence of natural recombination. *Vet.Microbiol.* 2010;146:138-43.
328. Williams CH, Panayiotou M, Girling GD, Peard CI, Oikarinen S, Hyoty H, Stanway G. Evolution and conservation in human parechovirus genomes. *J.Gen.Virol.* 2009;90:1702-12.
329. Xu A, Tao Z, Wang H, Zhang Y, Song L, Li Y, Liu G, Liu Y, Yang H, Fan Q, Ji F, Zhang Y, Yang J, Feng L, Xu W, Zhao Z. The complete genome analysis of two enterovirus 96 strains isolated in China in 2005 and 2009. *Virus Genes.* 2011;
330. Yang CF, Chen HY, Jorba J, Sun HC, Yang SJ, Lee HC, Huang YC, Lin TY, Chen PJ, Shimizu H, Nishimura Y, Utama A, Pallansch M, Miyamura T, Kew O, Yang JY. Intratypic recombination among lineages of type 1 vaccine-derived poliovirus emerging during chronic infection of an immunodeficient patient. *J.Virol.* 2005;79:12623-34.
331. Yip CC, Lau SK, Zhou B, Zhang MX, Tsoi HW, Chan KH, Chen XC, Woo PC, Yuen KY. Emergence of enterovirus 71 "double-recombinant" strains belonging to a novel genotype D originating from southern China: first evidence for combination of intratypic and intertypic recombination events in EV71. *Arch.Virol.* 2010;155:1413-24.
332. Yoke-Fun C, AbuBakar S. Phylogenetic evidence for inter-typic recombination in the emergence of human enterovirus 71 subgenotypes. *BMC Microbiol.* 2006;6:74
333. Zaharoula K, Evaggelos D, Vaia P, Dimitris T, Anastassia P, Stamatina LS, Panayotis M. Full genome sequence analysis of a multi-recombinant echovirus 3 strain isolated from sewage in Greece. *J Clin.Microbiol.* 2010;
334. Zhang Y, Wang H, Zhu S, Li Y, Song L, Liu Y, Liu G, Nishimura Y, Chen L, Yan D, Wang D, An H, Shimizu H, Xu A, Xu W. Characterization of a rare natural intertypic type 2/type 3 penta-recombinant vaccine-derived poliovirus isolated from a child with acute flaccid paralysis. *J Gen.Virol.* 2010;91:421-9.
335. Zhang Y, Zhu Z, Yang W, Ren J, Tan X, Wang Y, Mao N, Xu S, Zhu S, Cui A, Zhang Y, Yan D, Li Q, Dong X, Zhang J, Zhao Y, Wan J, Feng Z, Sun J, Wang S, Li D, Xu W. An emerging recombinant human enterovirus 71 responsible for the 2008 outbreak of hand foot and mouth disease in Fuyang city of China. *Virol.J.* 2010;7:94
336. Zhang Y, Zhu S, Yan D, Liu G, Bai R, Wang D, Chen L, Zhu H, An H, Kew O, Xu W. Natural type 3/type 2 intertypic vaccine-related poliovirus recombinants with the first crossover sites within the VP1 capsid coding region. *PLoS.ONE.* 2010;5:e15300
337. Zhang Y, Yan D, Zhu S, Wen N, Li L, Wang H, Liu J, Ye X, Ding Z, Wang D, Zhu H, Chen L, Hou X, An H, Liang X, Luo H, Kew O, Xu W. Type 2 vaccine-derived poliovirus from patients with acute flaccid paralysis in china: current immunization strategy effectively prevented its sustained transmission. *J.Infect.Dis.* 2010;202:1780-8.
338. Zhao YN, Perlin DS, Park S, Jiang RJ, Chen L, Chen Y, Gardiner R, Jiang QW. FDJS03 isolates causing an outbreak of aseptic meningitis in China evolved from a distinct echovirus 30 lineage imported from CIS countries. *J Clin.Microbiol.* 2006;
339. Zoll J, Galama JM, van Kuppeveld FJ. Identification of potential recombination break points in human parechoviruses. *J.Virol.* 2009;
340. Black WD, Hartley CA, Ficorilli NP, Studdert MJ. Sequence variation divides Equine rhinitis B virus into three distinct phylogenetic groups that correlate with serotype and acid stability. *J.Gen.Virol.* 2005;86:2323-32.
341. Moore J, Jironkin A, Chandler D, Burroughs N, Evans DJ, Ryabov EV. Recombinants between Deformed wing virus and Varroa destructor virus-1 may prevail in Varroa destructor-infested honeybee colonies. *J.Gen.Virol.* 2011;92:156-61.
342. Aguirre S, Malirat V, Scodeller E, Mattion N. First full-length genomic sequence of a hepatitis A virus isolated in Argentina shows recombination between subgenotypes IA and IB. *Virus Res.* 2010;

343. Belalov IS, Isaeva OV, Lukashev AN. Recombination in hepatitis A virus: evidence for reproductive isolation of genotypes. *J.Gen.Virol.* 2011;92:860-72.
344. Blinkova O, Kapoor A, Victoria J, Naeem A, Shaukat S, Sharif S, Alam MM, Angez M, Zaidi S, Delwart EL. Cardioviruses are genetically diverse and common enteric infections in South Asian children. *J.Virol.* 2009;
345. Bolanaki E, Kottaridi C, Markoulatos P, Margaritis L, Katsorchis T. Evolution of 2B and 2C genomic parts of species B Coxsackie viruses. Phylogenetic study and comparison with other regions. *Virus Genes.* 2006;32:249-59.
346. Buckwalter MR, Nga PT, Gouilh MA, Fiette L, Bureau JF, Laird ME, Buchrieser J, Ozden S, Cheval J, Eloit M, Manuguerra JC, Gessain A, Brey PT, Fontanet A, Albert ML. Identification of a novel neuropathogenic Theiler's murine encephalomyelitis virus. *J.Virol.* 2011;
347. Drexler JF, Baumgarte S, Luna LK, Stocker A, Almeida PS, Ribeiro TC, Petersen N, Herzog P, Pedroso C, Brites C, Ribeiro HC, Jr., Gmyl A, Drosten C, Lukashev A. Genomic features and evolutionary constraints in Saffold-like cardioviruses. *J Gen.Virol.* 2010;91:1418-27.
348. Garcia-Aguirre L, Cristina J. Analysis of the full-length genome of hepatitis A virus isolated in South America: heterogeneity and evolutionary constraints. *Arch.Virol.* 2008;153:1473-8.
349. Hales LM, Knowles NJ, Reddy PS, Xu L, Hay C, Hallenbeck PL. Complete genome sequence analysis of Seneca Valley virus-001, a novel oncolytic picornavirus. *J.Gen.Virol.* 2008;89:1265-75.
350. Huang T, Wang W, Bessaud M, Ren P, Sheng J, Yan H, Zhang J, Lin X, Wang Y, Delpeyroux F, Deubel V. Evidence of recombination and genetic diversity in human rhinoviruses in children with acute respiratory infection. *PLoS.ONE.* 2009;4:e6355
351. Hu YF, Zhao LN, Dong J, Wu ZQ, Du J, Xue Y, Yang F. [Complete genome sequence of Coxsackievirus B5 (CVB5/09) strain isolated in China and its phylogenetic analysis]. *Bing.Du Xue.Bao.* 2010;26:283-9.
352. Hu YF, Yang F, Du J, Dong J, Zhang T, Wu ZQ, Xue Y, Jin Q. Complete Genome Analysis of Coxsackievirus A2, A4, A5, and A10 Strains Isolated from Hand-Foot-and-Mouth Disease Patients in China Revealing Frequent Recombination of Human Enterovirus A. *J.Clin.Microbiol.* 2011;
353. Jones MS, Lukashov VV, Ganac RD, Schnurr DP. Discovery of a novel human picornavirus in a stool sample from a pediatric patient presenting with fever of unknown origin. *J Clin.Microbiol.* 2007;45:2144-50.
354. Liang Z, Kumar AS, Jones MS, Knowles NJ, Lipton HL. Phylogenetic Analysis of the Species Theilovirus: Emerging Murine and Human Pathogens. *J.Virol.* 2008;
355. Linsuwanon P, Payungporn S, Suwannakarn K, Chieochansin T, Theamboonlers A, Poovorawan Y. Complete coding sequence characterization and comparative analysis of the putative novel human rhinovirus (HRV) species C and B. *Viol.J.* 2011;8:5
356. Lipton HL. Human Vilyuisk encephalitis. *Rev.Med.Virol.* 2008;18:347-52.
357. McErlean P, Shackelton LA, Andrews E, Webster DR, Lambert SB, Nissen MD, Sloots TP, Mackay IM. Distinguishing molecular features and clinical characteristics of a putative new rhinovirus species, human rhinovirus C (HRV C). *PLoS.ONE.* 2008;3:e1847
358. Moratorio G, Costa-Mattioli M, Piovani R, Romero H, Musto H, Cristina J. Bayesian coalescent inference of hepatitis A virus populations: evolutionary rates and patterns. *J Gen.Virol.* 2007;88:3039-42.
359. Ren L, Gonzalez R, Xie Z, Xiao Y, Li Y, Liu C, Chen L, Yang Q, Vernet G, Paranhos-Baccala G, Jin Q, Shen K, Wang J. Saffold cardioviruses of 3 lineages in children with respiratory tract infections, Beijing, China. *Emerg.Infect.Dis.* 2010;16:1158-61.
360. Silva TF, Correa RL, Castilho Y, Silvie P, Belot JL, Vaslin MF. Widespread distribution and a new recombinant species of Brazilian virus associated with cotton blue disease. *Viol.J.* 2008;5:123
361. Ali A, Natsuaki T, Okuda S. The complete nucleotide sequence of a pakistani isolate of watermelon mosaic virus provides further insights into the taxonomic status in the bean common mosaic virus subgroup. *Virus Genes.* 2006;32:307-11.
362. Comes S, Fanigliulo A, Pacella R, Parrella G, Crescenzi A. Potato virus Y CFH, a putative recombinant isolate from *Capsicum chinense* cv. Habanero. *Commun.Agric.Appl.Biol.Sci.* 2006;71:1251-6.
363. Crescenzi A, Fanigliulo A, Comes S. Characterization of the Potato Y Virus isolate PVY-LF02 inducing necrosis in tomato. *Acta Horticulturae.* 2005;695:331-8.
364. Desbiez C, Lecoq H. The nucleotide sequence of Watermelon mosaic virus (WMV, Potyvirus) reveals interspecific recombination between two related potyviruses in the 5' part of the genome. *Arch.Virol.* 2004;149:1619-32.
365. Desbiez C, Joannon B, Wipf-Scheibel C, Chandeysson C, Lecoq H. Recombination in natural populations of watermelon mosaic virus: new agronomic threat or damp squib? *J.Gen.Virol.* 2011;
366. Fanigliulo A, Comes S, Pacella R, Harrach B, Martin DP, Crescenzi A. Characterisation of Potato virus Y nnp strain inducing veinal necrosis in pepper: a naturally occurring recombinant strain of PVY. *Arch.Virol.* 2005;150:709-20.
367. Fernandez-Rodriguez T, Rubio L, Carballo O, Marys E. Genetic variation of papaya ringspot virus in Venezuela. *Arch.Virol.* 2008;153:343-9.
368. Gagarinova AG, Babu M, Stromvik MV, Wang A. Recombination analysis of Soybean mosaic virus sequences reveals evidence of RNA recombination between distinct pathotypes. *Viol.J.* 2008;5:143
369. Gagarinova AG, Babu M, Poysa V, Hill JH, Wang A. Identification and molecular characterization of two naturally occurring Soybean mosaic virus isolates that are closely related but differ in their ability to overcome Rsv4 resistance. *Virus Res.* 2008;138:50-6.
370. Gibbs A, Ohshima K. Potyviruses and the digital revolution. *Annu.Rev.Phytopathol.* 2010;48:205-23.
371. Hu X, He C, Xiao Y, Xiong X, Nie X. Molecular characterization and detection of recombinant isolates of potato virus Y from China. *Arch.Virol.* 2009;154:1303-12.
372. Hu X, Nie X, He C, Xiong X. Differential pathogenicity of two different recombinant PVYNTN isolates in *Physalis floridana* is likely determined by the coat protein gene. *Viol.J.* 2011;8:207

373. Kogovsek P, Gow L, Pompe-Novak M, Gruden K, Foster GD, Boonham N, Ravnikar M. Single-step RT real-time PCR for sensitive detection and discrimination of Potato virus Y isolates. *J.Virol.Methods*. 2008;149:1-11.
374. Margaritopoulos JT, Dovas CI, Gounaris J, Skouras PJ, Kanavaki OM, Katis NI, Tsitsipis JA. Molecular analysis of the coat protein of Potato virus Y isolates in Greece suggests multiple introduction from different genetic pools. *J Phytopathol*. 2010;158:73-80.
375. Mbanzibwa DR, Tian YP, Tugume AK, Patil BL, Yadav JS, Bagewadi B, Abarshi MM, Alicai T, Changadeya W, Mkumbira J, Muli MB, Mukasa SB, Tairo F, Baguma Y, Kyamanywa S, Kullaya A, Maruthi MN, Fauquet CM, Valkonen JP. Evolution of cassava brown streak disease-associated viruses. *J.Gen.Virol*. 2011;92:974-87.
376. Myrta A, Varga A, James D. The complete genome sequence of an El Amar isolate of plum pox virus (PPV) and its phylogenetic relationship to other PPV strains. *Arch.Virol*. 2006;
377. Schubert J, Fomitcheva V, Sztangret-Wisniewska J. Differentiation of Potato virus Y strains using improved sets of diagnostic PCR-primers. *J.Virol.Methods*. 2007;140:66-74.
378. Untiveros M, Quispe D, Kreuze J. Analysis of complete genomic sequences of isolates of the Sweet potato feathery mottle virus strains C and EA: molecular evidence for two distinct potyvirus species and two P1 protein domains. *Arch.Virol*. 2010;155:2059-63.
379. Visser JC, Bellstedt DU. An assessment of molecular variability and recombination patterns in South African isolates of Potato virus Y. *Arch.Virol*. 2009;154:1891-900.
380. Yamasaki S, Sakai J, Fuji S, Kamisoyama S, Emoto K, Ohshima K, Hanada K. Comparisons among isolates of Sweet potato feathery mottle virus using complete genomic RNA sequences. *Arch.Virol*. 2010;155:795-800.
381. Yang Y, Gong J, Li H, Li C, Wang D, Li K, Zhi H. Identification of a novel Soybean mosaic virus isolate in China that contains a unique 5' terminus sharing high sequence homology with Bean common mosaic virus. *Virus Res*. 2011;
382. Wijegoonawardane PK, Sittidilokratna N, Petchampai N, Cowley JA, Gudkovs N, Walker PJ. Homologous genetic recombination in the yellow head complex of nidoviruses infecting *Penaeus monodon* shrimp. *Virology*. 2009;390:79-88.
383. Vauloup-Fellous C, Hubschen JM, Abernathy ES, Icenogle J, Gaidot N, Dubreuil P, Parent-du-Chatelet I, Grangeot-Keros L, Muller CP. Phylogenetic analysis of rubella viruses involved in congenital rubella infections in France between 1995 and 2009. *J Clin.Microbiol*. 2010;
384. Bird BH, Khristova ML, Rollin PE, Ksiazek TG, Nichol ST. Complete genome analysis of 33 ecologically and biologically diverse Rift Valley fever virus strains reveals widespread virus movement and low genetic diversity due to recent common ancestry. *J Virol*. 2006;
385. Briese T, Rambaut A, Lipkin WI. Analysis of the medium (M) segment sequence of Guaroa virus and its comparison to other orthobunyaviruses. *J.Gen.Virol*. 2004;85:3071-7.
386. Deyde VM, Khristova ML, Rollin PE, Ksiazek TG, Nichol ST. Crimean-Congo hemorrhagic fever virus genomics and global diversity. *J Virol*. 2006;80:8834-42.
387. Hewson R, Gmyl A, Gmyl L, Smirnova SE, Karganova G, Jamil B, Hasan R, Chamberlain J, Clegg C. Evidence of segment reassortment in Crimean-Congo haemorrhagic fever virus. *J.Gen.Virol*. 2004;85:3059-70.
388. Lukashev AN. Evidence for recombination in Crimean-Congo hemorrhagic fever virus. *J.Gen.Virol*. 2005;86:2333-8.
389. Webster CG, Reitz SR, Perry KL, Adkins S. A natural M RNA reassortant arising from two species of plant- and insect-infecting bunyaviruses and comparison of its sequence and biological properties to parental species. *Virology*. 2011;413:216-25.
390. Asikainen K, Hanninen T, Henttonen H, Niemimaa J, Laakkonen J, Andersen HK, Bille N, Leirs H, Vaeheri A, Plyusnin A. Molecular evolution of puumala hantavirus in Fennoscandia: phylogenetic analysis of strains from two recolonization routes, Karelia and Denmark. *J.Gen.Virol*. 2000;81:2833-41.
391. de Carvalho Nicacio C, Gonzalez Della Valle M, Padula P, Bjorling E, Plyusnin A, Lundkvist A. Cross-protection against challenge with Puumala virus after immunization with nucleocapsid proteins from different hantaviruses. *J.Virol*. 2002;76:6669-77.
392. Escutenaire S, Chalon P, Heyman P, van der Auwera G, van der Groen G, Verhagen R, Thomas I, Karelle-Bui L, Vaeheri A, Pastoret PP, Plyusnin A. Genetic characterization of Puumala hantavirus strains from Belgium: evidence for a distinct phylogenetic lineage. *Virus Res*. 2001;74:1-15.
393. Johansson P, Olsson M, Lindgren L, Ahlm C, Elgh F, Holmstrom A, Bucht G. Complete gene sequence of a human Puumala hantavirus isolate, Puumala Umea/01: sequence comparison and characterisation of encoded gene products. *Virus Res*. 2004;105:147-55.
394. Johansson P, Olsson GE, Low HT, Bucht G, Ahlm C, Juto P, Elgh F. Puumala hantavirus genetic variability in an endemic region (Northern Sweden). *Infect.Genet.Evol*. 2008;8:286-96.
395. Johansson P, Yap G, Low HT, Siew CC, Kek R, Ng LC, Bucht G. Molecular characterization of two hantavirus strains from different *rattus* species in Singapore. *Virol.J*. 2010;7:15
396. Kirsanovs S, Klempa B, Franke R, Lee MH, Schonrich G, Rang A, Kruger DH. Genetic reassortment between high-virulent and low-virulent Dobrava-Belgrade virus strains. *Virus Genes*. 2010;41:319-28.
397. Klempa B, Tkachenko EA, Dzagurova TK, Yunicheva YV, Morozov VG, Okulova NM, Slyusareva GP, Smirnov A, Kruger DH. Hemorrhagic fever with renal syndrome caused by 2 lineages of dobrava hantavirus, Russia. *Emerg.Infect.Dis*. 2008;14:617-25.
398. Klempa B, Schmidt HA, Ulrich R, Kaluz S, Labuda M, Meisel H, Hjelle B, Kruger DH. Genetic interaction between distinct Dobrava hantavirus subtypes in *Apodemus agrarius* and *A. flavicollis* in nature. *J.Virol*. 2003;77:804-9.

399. Klempa B, Stanko M, Labuda M, Ulrich R, Meisel H, Kruger DH. Central European Dobrava Hantavirus Isolate from a Striped Field Mouse (*Apodemus agrarius*). *J.Clin.Microbiol.* 2005;43:2756-63.
400. Lindkvist M, Lahti K, Lilliehook B, Holmstrom A, Ahlm C, Bucht G. Cross-reactive immune responses in mice after genetic vaccination with cDNA encoding hantavirus nucleocapsid proteins. *Vaccine.* 2007;25:1690-9.
401. Nemirov K, Leirs H, Lundkvist A, Olsson GE. Puumala hantavirus and *Myodes glareolus* in northern Europe: no evidence of co-divergence between genetic lineages of virus and host. *J Gen.Virol.* 2010;91:1262-74.
402. Razzauti M, Plyusnina A, Henttonen H, Plyusnin A. Accumulation of point mutations and reassortment of genomic RNA segments are involved in the microevolution of Puumala hantavirus in a bank vole (*Myodes glareolus*) population. *J.Gen.Virol.* 2008;89:1649-60.
403. Sironen T, Vaheri A, Plyusnin A. Molecular evolution of Puumala hantavirus. *J.Virol.* 2001;75:11803-10.
404. Sironen T, Vaheri A, Plyusnin A. Phylogenetic evidence for the distinction of Saaremaa and Dobrava hantaviruses. *Virolog.J.* 2005;2:90
405. Wang H, Alminaitte A, Vaheri A, Plyusnin A. Interaction between hantaviral nucleocapsid protein and the cytoplasmic tail of surface glycoprotein Gn. *Virus Res.* 2010;151:205-12.
406. Zhang Y, Zhang H, Dong X, Yuan J, Zhang H, Yang X, Zhou P, Ge X, Li Y, Wang LF, Shi Z. Hantavirus outbreak associated with laboratory rats in Yunnan, China. *Infect.Genet.Evol.* 2010;10:638-44.
407. Amonsin A, Lapkuntod J, Suwannakarn K, Kitikoon P, Suradhat S, Tantilertcharoen R, Boonyapisitsopa S, Bunpapong N, Wongphatcharachai M, Wisedchanwet T, Theamboonlers A, Poovorawan Y, Sasipreeyajan J, Thanawongnuwech R. Genetic characterization of 2008 reassortant influenza A virus (H5N1), Thailand. *Virolog.J.* 2010;7:233
408. Boni MF, de Jong MD, van Doorn HR, Holmes EC. Guidelines for identifying homologous recombination events in influenza A virus. *PLoS One.* 2010;5:e10434
409. Goni N, Fajardo A, Moratorio G, Colina R, Cristina J. Modeling gene sequences over time in 2009 H1N1 influenza A virus populations. *Virolog.J.* 2009;6:215
410. Goni N, Moratorio G, Ramas V, Coppola L, Chiparelli H, Cristina J. Phylogenetic analysis of pandemic 2009 influenza A virus circulating in the South American region: genetic relationships and vaccine strain match. *Arch.Virol.* 2011;156:87-94.
411. He CQ, Han GZ, Wang D, Liu W, Li GR, Liu XP, Ding NZ. Homologous recombination evidence in human and swine influenza A viruses. *Virology.* 2008;380:12-20.
412. He CQ, Xie ZX, Han GZ, Dong JB, Wang D, Liu JB, Ma LY, Tang XF, Liu XP, Pang YS, Li GR. Homologous recombination as an evolutionary force in the avian influenza A virus. *Mol.Biol.Evol.* 2009;26:177-87.
413. Lam TT, Hon CC, Pybus OG, Kosakovsky Pond SL, Wong RT, Yip CW, Zeng F, Leung FC. Evolutionary and transmission dynamics of reassortant H5N1 influenza virus in Indonesia. *PLoS Pathog.* 2008;4:e1000130
414. Bailey D, Banyard A, Dash P, Ozkul A, Barrett T. Full genome sequence of peste des petits ruminants virus, a member of the Morbillivirus genus. *Virus Res.* 2005;110:119-24.
415. Han GZ, Liu XP, Li SS. Cross-species recombination in the haemagglutinin gene of canine distemper virus. *Virus Res.* 2008;136:198-201.
416. Han GZ, He CQ, Ding NZ, Ma LY. Identification of a natural multi-recombinant of Newcastle disease virus. *Virology.* 2008;371:54-60.
417. He CQ, Ding NZ, Han GZ, Liu W. Natural recombination between Newcastle disease virus vaccine strains and circulating viruses. *J Virol.* 2008;
418. Rui Z, Juan P, Jingliang S, Jixun Z, Xiaoting W, Shouping Z, Xiaojiao L, Guozhong Z. Phylogenetic characterization of Newcastle disease virus isolated in the mainland of China during 2001-2009. *Vet.Microbiol.* 2009;
419. Yang HT, Jiang Q, Zhou X, Bai MQ, Si HL, Wang XJ, Lu Y, Zhao H, He HB, He CQ. Identification of a natural human serotype 3 parainfluenza virus. *Virolog.J.* 2011;8:58
420. Zhang R, Wang X, Su J, Zhao J, Zhang G. Isolation and analysis of two naturally-occurring multi-recombination Newcastle disease viruses in China. *Virus Res.* 2010;151:45-53.
421. Tang K, Wu X. Computational analysis suggests that lyssavirus glycoprotein gene plays a minor role in viral adaptation. *Int.J.Evol.Biol.* 2011;2011:143498
422. Walsh SR, Linnerth-Petrik NM, Laporte AN, Menzies PI, Foster RA, Wootton SK. Full-length genome sequence analysis of enzootic nasal tumor virus reveals an unusually high degree of genetic stability. *Virus Res.* 2010;151:74-87.
423. Sintasath DM, Wolfe ND, Zheng HQ, LeBreton M, Peeters M, Tamoufe U, Djoko CF, Dikko JL, Mpoudi-Ngole E, Heneine W, Switzer WM. Genetic characterization of the complete genome of a highly divergent simian T-lymphotropic virus (STLV) type 3 from a wild *Cercopithecus mona* monkey. *Retrovirology.* 2009;6:97
424. Switzer WM, Qari SH, Wolfe ND, Burke DS, Folks TM, Heneine W. Ancient origin and molecular features of the novel human T-lymphotropic virus type 3 revealed by complete genome analysis. *J.Virol.* 2006;80:7427-38.
425. Switzer WM, Salemi M, Qari SH, Jia H, Gray RR, Katzourakis A, Marriott SJ, Pryor KN, Wolfe ND, Burke DS, Folks TM, Heneine W. Ancient, independent evolution and distinct molecular features of the novel human T-lymphotropic virus type 4. *Retrovirology.* 2009;6:9
426. Van Dooren S, Shanmugam V, Bhullar V, Parekh B, Vandamme AM, Heneine W, Switzer WM. Identification in gelada baboons (*Theropithecus gelada*) of a distinct simian T-cell lymphotropic virus type 3 with a broad range of Western blot reactivity. *J.Gen.Virol.* 2004;85:507-19.
427. Mang R. Endogenous retroviruses and xenotransplantation. *Veterinary Sciences Tomorrow.* 2001;

428. Niebert M, Tonjes RR. Evolutionary spread and recombination of porcine endogenous retroviruses in the suiformes. *J.Virol.* 2005;79:649-54.
429. Abecasis A, Paraskevis D, Epalanga M, Fonseca M, Burity F, Bartolomeu J, Carvalho AP, Gomes P, Vandamme AM, Camacho R. HIV-1 genetic variants circulation in the North of Angola. *Infect.Genet.Evol.* 2005;5:231-7.
430. Abecasis AB, Lemey P, Vidal N, De Oliveira T, Peeters M, Camacho R, Shapiro B, Rambaut A, Vandamme AM. Recombination confounds the early evolutionary history of human immunodeficiency virus type 1: subtype G is a circulating recombinant form. *J Virol.* 2007;81:8543-51.
431. Achkar JM, Burda ST, Konings FA, Urbanski MM, Williams CA, Seifen D, Kahirimbanyi MN, Vogler M, Parta M, Lupatkin HC, Zolla-Pazner S, Nyambi PN. Infection With HIV Type 1 Group M Non-B Subtypes in Individuals Living in New York City. *J.Acquir.Immune.Defic.Syndr.* 2004;36:835-44.
432. Adojaan M, Kivisild T, Mannik A, Krispin T, Ustina V, Zilmer K, Liebert E, Jaroslavtsev N, Priimagi L, Tefanova V, Schmidt J, Krohn K, Villems R, Salminen M, Ustav M. Predominance of a rare type of HIV-1 in Estonia. *J.Acquir.Immune.Defic.Syndr.* 2005;39:598-605.
433. Aghokeng AF, Ayouba A, Ahuka S, Liegeois F, Mbala P, Muyembe JJ, Mpoudi-Ngole E, Delaporte E, Peeters M. Genetic diversity of simian lentivirus in wild De Brazza's monkeys (*Cercopithecus neglectus*) in Equatorial Africa. *J Gen.Virol.* 2010;91:1810-6.
434. Aghokeng AF, Mpoudi-Ngole E, Chia JE, Edoul EM, Delaporte E, Peeters M. High failure rate of ViroSeq™ HIV-1 Genotyping System for drug resistance testing in Cameroon, a context of broad HIV-1 genetic diversity. *J.Clin.Microbiol.* 2011;
435. Agnihotri KD, Tripathy SP, Jere AP, Kale SM, Paranjape RS. Molecular analysis of gp41 sequences of HIV type 1 subtype C from India. *J.Acquir.Immune.Defic.Syndr.* 2006;41:345-51.
436. Agwale SM, Zeh C, Robbins KE, Odama L, Saekhou A, Edubio A, Njoku M, Sani-Gwarzo N, Gboun MS, Gao F, Reitz M, Hone D, Pieniazek D, Wambebe C, Kalish ML. Molecular surveillance of HIV-1 field strains in Nigeria in preparation for vaccine trials(1). *Vaccine.* 2002;20:2131-9.
437. Agwale SM, Zeh C, Paxinos E, Odama L, Pieniazek D, Wambebe C, Kalish ML, Ziermann R. Genotypic and phenotypic analyses of human immunodeficiency virus type 1 in antiretroviral drug-naive Nigerian patients. *AIDS Res.Hum.Retroviruses.* 2006;22:22-6.
438. Ahuka-Mundeke S, Liegeois F, Ayouba A, Foupouapouognini Y, Nerrienet E, Delaporte E, Peeters M. Full-length genome sequence of a simian immunodeficiency virus (SIV) infecting a captive agile mangabey (*Cercocebus agilis*) is closely related to SIVrcm infecting wild red-capped mangabeys (*Cercocebus torquatus*) in Cameroon. *J Gen.Virol.* 2010;91:2959-64.
439. Ahumada-Ruiz S, Flores-Figueroa D, Toala-Gonzalez I, Thomson MM. Analysis of HIV-1 pol sequences from Panama: identification of phylogenetic clusters within subtype B and detection of antiretroviral drug resistance mutations. *Infect.Genet.Evol.* 2009;9:933-40.
440. Ajoge HO, Gordon ML, Ibrahim S, Shittu OS, Ndung'u T, Olonitola SO. Drug resistance pattern of HIV-1 isolates sampled in 2007 from therapy-naive pregnant women in North-Central Nigeria. *AIDS Res.Hum.Retroviruses.* 2011;
441. Ajoge HO, Gordon ML, de OT, Green TN, Ibrahim S, Shittu OS, Olonitola SO, Ahmad AA, Ndung'u T. Genetic characteristics, coreceptor usage potential and evolution of Nigerian HIV-1 subtype G and CRF02\_AG isolates. *PLoS.ONE.* 2011;6:e17865
442. Almeida FJ, Berezin EN, Rodrigues R, Safadi MA, Arnoni MV, Oliveira C, Brigido LF. Diversity and prevalence of antiretroviral genotypic resistance mutations among HIV-1-infected children. *J.Pediatr.(Rio J.).* 2009;85:104-9.
443. Ambrosioni J, Andreani G, Acuipl C, Barral R, Rabinovich R, Martinez PL. Comparative reactivity of serum samples from Argentinean HIV-infected patients with V3 peptides from subtype B or BF recombinants. *Arch.Virol.* 2010;155:2029-34.
444. Andresen BS, Vinner L, Tang S, Bragstad K, Kronborg G, Gerstoft J, Corbet S, Fomsgaard A. Characterization of near full-length genomes of HIV type 1 strains in Denmark: basis for a universal therapeutic vaccine. *AIDS Res.Hum.Retroviruses.* 2007;23:1442-8.
445. Antunes R, Figueiredo S, Bartolo I, Pinheiro M, Rosado L, Soares I, Lourenco H, Taveira N. Evaluation of the Clinical Sensitivities of Three Viral Load Assays with Plasma Samples from a Pediatric Population Predominantly Infected with Human Immunodeficiency Virus Type 1 Subtype G and BG Recombinant Forms. *J.Clin.Microbiol.* 2003;41:3361-7.
446. Araujo AF, Brites C, Monteiro-Cunha J, Santos LA, Galvao-Castro B, Alcantara LC. Lower prevalence of human immunodeficiency virus type 1 Brazilian subtype B found in northeastern Brazil with slower progression to AIDS. *AIDS Res.Hum.Retroviruses.* 2010;26:1249-54.
447. Aulicino PC, Kopka J, Mangano AM, Rocco C, Iacono M, Bologna R, Sen L. Circulation of novel HIV type 1 A, B/C, and F subtypes in Argentina. *AIDS Res.Hum.Retroviruses.* 2005;21:158-64.
448. Aulicino PC, Kopka J, Rocco C, Mangano A, Sen L. Sequence analysis of a South American HIV type 1 BC recombinant. *AIDS Res.Hum.Retroviruses.* 2005;21:894-6.
449. Aulicino PC, Holmes EC, Rocco C, Mangano A, Sen L. Extremely rapid spread of human immunodeficiency virus type 1 BF recombinants in Argentina. *J Virol.* 2007;81:427-9.
450. Aulicino PC, Bello G, Rocco C, Romero H, Mangano A, Morgado MG, Sen L. Description of the first full-length HIV type 1 subtype F1 strain in Argentina: implications for the origin and dispersion of this subtype in South America. *AIDS Res.Hum.Retroviruses.* 2007;23:1176-82.
451. Aulicino PC, Rocco CA, Mecikovsky D, Bologna R, Mangano A, Sen L. HIV type-1 genotypic resistance profiles in vertically infected patients from Argentina reveal an association between K103N+L100I and L74V mutations. *Antivir.Ther.* 2010;15:641-50.
452. Aulicino PC, Bello G, Guimaraes ML, Ruchansky D, Rocco C, Mangano A, Morgado MG, Sen L. Longitudinal analysis of HIV-1 BF1 recombinant strains in vertically infected children from Argentina reveals

- a decrease in CRF12\_BF pol gene mosaic patterns and high diversity of BF unique recombinant forms. *Infect.Genet.Evol.* 2011;11:349-57.
453. Avi R, Huik K, Sadam M, Karki T, Krispin T, Ainsalu K, Paap P, Schmidt J, Nikitina N, Lutsar I. Characterization of integrase region polymorphisms in HIV type 1 CRF06\_cpx viruses in treatment-naive patients in Estonia. *AIDS Res.Hum.Retroviruses.* 2010;26:1109-13.
454. Avi R, Huik K, Pauskar M, Ustina V, Karki T, Krispin T, Ainsalu K, Paap P, Schmidt J, Nikitina N, Lutsar I. Emerging transmitted drug resistance in treatment-naive human immunodeficiency virus-1 CRF06\_cpx-infected patients in Estonia. *Scand.J Infect.Dis.* 2010;
455. Ayele W, Pollakis G, Abebe A, Fisseha B, Tegbaru B, Tesfaye G, Mengistu Y, Wolday D, van Gemen B, Goudsmit J, Dorigo-Zetsma W, De Baar MP. Development of a nucleic acid sequence-based amplification assay that uses gag-based molecular beacons to distinguish between human immunodeficiency virus type 1 subtype C and C' infections in Ethiopia. *J.Clin.Microbiol.* 2004;42:1534-41.
456. Badreddine S, Smith K, van Zyl H, Bodelle P, Yamaguchi J, Swanson P, Devare SG, Brennan CA. Identification and characterization of HIV type 1 subtypes present in the Kingdom of Saudi Arabia: high level of genetic diversity found. *AIDS Res.Hum.Retroviruses.* 2007;23:667-74.
457. Baird HA, Galetto R, Gao Y, Simon-Loriere E, Abreha M, Archer J, Fan J, Robertson DL, Arts EJ, Negrone M. Sequence determinants of breakpoint location during HIV-1 intersubtype recombination. *Nucleic Acids Res.* 2006;34:5203-16.
458. Balakrishnan P, Kumarasamy N, Kantor R, Solomon S, Vidya S, Mayer KH, Newstein M, Thyagarajan SP, Katzenstein D, Ramratnam B. HIV type 1 genotypic variation in an antiretroviral treatment-naive population in southern India. *AIDS Res.Hum.Retroviruses.* 2005;21:301-5.
459. Baldrich-Rubio E, Anagonou S, Stirrups K, Lafia E, Candotti D, Lee H, Allain JP. A complex human immunodeficiency virus type 1 A/G/J recombinant virus isolated from a seronegative patient with AIDS from Benin, West Africa. *J.Gen.Virol.* 2001;82:1095-106.
460. Balotta C, Facchi G, Violin M, Van Dooren S, Cozzi-Lepri A, Forbici F, Bertoli A, Riva C, Senese D, Caramello P, Carnevale G, Rizzardini G, Cremonini L, Monno L, Rezza G, Perno CF, Ippolito G, d'Arminio-Monforte A, Vandamme AM, Moroni M. Increasing prevalence of non-clade B HIV-1 strains in heterosexual men and women, as monitored by analysis of reverse transcriptase and protease sequences. *J.Acquir.Immune.Defic.Sydr.* 2001;27:499-505.
461. Bano AS, Sood V, Neogi U, Goel N, Kuttiat VS, Wanchu A, Banerjee AC. Genetic and functional characterization of human immunodeficiency virus type 1 VprC variants from north India: presence of unique recombinants with mosaic genomes from B, C and D subtypes within the open reading frame of Vpr. *J.Gen.Virol.* 2009;90:2768-76.
462. Bao L, Vidal N, Fang H, Deng W, Chen S, Guo W, Qin C, Peeters M, Delaporte E, Andrieu JM, Lu W. Molecular tracing of sexual HIV Type 1 transmission in the southwest border of China. *AIDS Res.Hum.Retroviruses.* 2008;24:733-42.
463. Barlow KL, Tatt ID, Cane PA, Pillay D, Clewley JP. Recombinant strains of HIV type 1 in the United Kingdom. *AIDS Res.Hum.Retroviruses.* 2001;17:467-74.
464. Barlow KL, Ajao AO, Clewley JP. Characterization of a Novel Simian Immunodeficiency Virus (SIVmonNG1) Genome Sequence from a Mona Monkey (*Cercopithecus mona*). *J.Virol.* 2003;77:6879-88.
465. Barreto CC, Nishyia A, Araujo LV, Ferreira JE, Busch MP, Sabino EC. Trends in antiretroviral drug resistance and clade distributions among HIV-1--infected blood donors in Sao Paulo, Brazil. *J.Acquir.Immune.Defic.Sydr.* 2006;41:338-41.
466. Barroso H, Taveira N. Evidence for negative selective pressure in HIV-2 evolution in vivo. *Infect.Genet.Evol.* 2005;5:239-46.
467. Bartolo I, Rocha C, Bartolomeu J, Gama A, Marcelino R, Fonseca M, Mendes A, Epalanga M, Silva PC, Taveira N. Highly divergent subtypes and new recombinant forms prevail in the HIV/AIDS epidemic in Angola: New insights into the origins of the AIDS pandemic. *Infect.Genet.Evol.* 2008;
468. Bartolo I, Casanovas J, Bastos R, Rocha C, Abecasis AB, Folgosa E, Mondlane J, Manuel R, Taveira N. HIV-1 genetic diversity and transmitted drug resistance in health care settings in Maputo, Mozambique. *J.Acquir.Immune Defic.Sydr.* 2009;51:323-31.
469. Beer BE, Foley BT, Kuiken CL, Toozee Z, Goeken RM, Brown CR, Hu J, St Claire M, Korber BT, Hirsch VM. Characterization of novel simian immunodeficiency viruses from red-capped mangabeys from Nigeria (SIVrcmNG409 and -NG411). *J.Virol.* 2001;75:12014-27.
470. Bezemer D, Jurriaans S, Prins M, van der Hoek L, Prins JM, de Wolf F, Berkhout B, Coutinho R, Back NK. Declining trend in transmission of drug-resistant HIV-1 in Amsterdam. *AIDS.* 2004;18:1571-7.
471. Bhanja P, Mandal DK, Jana S, Bhattacharya SK, Chakrabarti S. Detection and characterization of HIV type 2 in Calcutta, India. *AIDS Res.Hum.Retroviruses.* 2004;20:101-4.
472. Bhanja P, Sengupta S, Singh NY, Sarkar K, Bhattacharya SK, Chakrabarti S. Determination of Gag and Env subtypes of HIV-1 detected among injecting drug users (IDUs) in Manipur, India: Evidence for intersubtype recombination. *Virus Res.* 2005;
473. Bhanja P, Sengupta S, Banerjee D, Sarkar K, Jana S, Chakrabarti S. Detection of intersubtype recombinants with respect to env and nef genes of HIV-1 among female sex workers in Calcutta, India. *Virus Res.* 2007;
474. Bhattacharya T, Daniels M, Heckerman D, Foley B, Frahm N, Kadie C, Carlson J, Yusim K, McMahon B, Gaschen B, Mallal S, Mullins JI, Nickle DC, Herbeck J, Rousseau C, Learn GH, Miura T, Brander C, Walker B, Korber B. Founder effects in the assessment of HIV polymorphisms and HLA allele associations. *Science.* 2007;315:1583-6.
475. Bodelle P, Vallari A, Coffey R, McArthur CP, Beyeme M, Devare SG, Schochetman G, Brennan CA. Identification and Genomic Sequence of an HIV Type 1 Group N Isolate from Cameroon. *AIDS Research and Human Retroviruses.* 2004;20:902-8.



476. Brennan CA, Brites C, Bodelle P, Golden A, Hackett J, Jr., Holzmayer V, Swanson P, Vallari A, Yamaguchi J, Devare S, Pedroso C, Ramos A, Badaro R. HIV-1 strains identified in Brazilian blood donors: significant prevalence of B/F1 recombinants. *AIDS Res.Hum.Retroviruses*. 2007;23:1434-41.
477. Brennan CA, Bodelle P, Coffey R, Devare SG, Golden A, Hackett J, Jr., Harris B, Holzmayer V, Luk KC, Schochetman G, Swanson P, Yamaguchi J, Vallari A, Ndembi N, Ngansop C, Makamche F, Mbanya D, Gurtler LG, Zekeng L, Kaptue L. The prevalence of diverse HIV-1 strains was stable in Cameroonian blood donors from 1996 to 2004. *J.Acquir.Immune.Defic.Sydr*. 2008;49:432-9.
478. Brigido LF, Franco HM, Custodio RM, Oliveira CA, JL PF, Eira M, Bergel F, Araujo F, Carvalheiro JR, Rodrigues R. Short Communication: Molecular Characteristics of HIV Type 1 Circulating in Sao Paulo, Brazil. *AIDS Res.Hum.Retroviruses*. 2005;21:673-82.
479. Brigido LF, Nunes CC, Oliveira CM, Knoll RK, Ferreira JL, Freitas CA, Alves MA, Dias C, Rodrigues R. HIV type 1 subtype C and CRF01\_AG recombinants prevail at the cities with the highest AIDS prevalence rate in Brazil. *AIDS Res.Hum.Retroviruses*. 2007;23:1579-86.
480. Brigido LF, Ferreira JL, Almeida VC, Rocha SQ, Ragazzo TG, Estevam DL, Rodrigues R. Southern Brazil HIV type 1 C expansion into the state of Sao Paulo, Brazil. *AIDS Res.Hum.Retroviruses*. 2011;27:339-44.
481. Brindicci G, Punzi G, Lagioia A, Lo CS, Ladisa N, Di Nicuolo G, Saracino A, Angarano G, Monno L. Difficulties in classifying a/g recombinants: methodological problems or genetic variability? *AIDS Res.Hum.Retroviruses*. 2007;23:840-6.
482. Brown RJ, Peters PJ, Caron C, Gonzalez-Perez MP, Stones L, Ankghuambom C, Pondei K, McClure CP, Alemnji G, Taylor S, Sharp PM, Clapham PR, Ball JK. Inter-compartment recombination of HIV-1 contributes to env intra-host diversity and modulates viral tropism and sensitivity to entry inhibitors. *J.Virol*. 2011;
483. Bruselles A, Rozera G, Bartolini B, Prosperi M, Del NF, Narciso P, Capobianchi MR, Abbate I. Use of massive parallel pyrosequencing for near full-length characterization of a unique HIV Type 1 BF recombinant associated with a fatal primary infection. *AIDS Res.Hum.Retroviruses*. 2009;25:937-42.
484. Bruzzone B, Ventura A, Bisio F, Mboundou FA, Miguel LM, Saladini F, Zazzi M, Icardi G, De MA, Viscoli C. Impact of extensive HIV-1 variability on molecular diagnosis in the Congo basin. *J Clin.Virol*. 2010;47:372-5.
485. Buzon MJ, Wrin T, Codoner FM, Dalmau J, Phung P, Bonjoch A, Coakley E, Clotet B, Martinez-Picado J. Combined antiretroviral therapy and immune pressure lead to in vivo HIV-1 recombination with ancestral viral genomes. *J.Acquir.Immune.Defic.Sydr*. 2011;
486. Cardoso LP, Queiroz BB, Stefani MM. HIV-1 pol phylogenetic diversity and antiretroviral resistance mutations in treatment naive patients from Central West Brazil. *J.Clin.Virol*. 2009;46:134-9.
487. Cardoso LP, Stefani MM. High level of multidrug resistance mutations in HIV type 1 pol gene and resistance-associated mutations to enfuvirtide (T-20) among antiretroviral-experienced patients from central Brazil. *AIDS Res.Hum.Retroviruses*. 2009;25:943-50.
488. Cardoso LP, Pereira GA, Viegas AA, Schmaltz LE, Stefani MM. HIV-1 primary and secondary antiretroviral drug resistance and genetic diversity among pregnant women from central Brazil. *J Med.Virol*. 2010;82:351-7.
489. Carmona R, Perez-Alvarez L, Munoz M, Casado G, Delgado E, Sierra M, Thomson M, Vega Y, Vazquez dP, Contreras G, Medrano L, Najera R. Natural resistance-associated mutations to Enfuvirtide (T20) and polymorphisms in the gp41 region of different HIV-1 genetic forms from T20 naive patients. *J.Clin.Virol*. 2005;32:248-53.
490. Carr JK, Nadai Y, Eyzaguirre L, Saad MD, Khakimov MM, Yakubov SK, Bix DL, Graham RR, Wolfe ND, Earhart KC, Sanchez JL. Outbreak of a West African recombinant of HIV-1 in Tashkent, Uzbekistan. *J.Acquir.Immune.Defic.Sydr*. 2005;39:570-5.
491. Carr JK, Wolfe ND, Torimiro JN, Tamoufe U, Mpoudi-Ngole E, Eyzaguirre L, Bix DL, McCutchan FE, Burke DS. HIV-1 recombinants with multiple parental strains in low-prevalence, remote regions of Cameroon: evolutionary relics? *Retrovirology*. 2010;7:39
492. Carrion G, Eyzaguirre L, Montano SM, Laguna-Torres V, Serra M, Aguayo N, Avila MM, Ruchansky D, Pando MA, Vinales J, Perez J, Barboza A, Chauca G, Romero A, Galeano A, Blair PJ, Weissenbacher M, Bix DL, Sanchez JL, Olson JG, Carr JK. Documentation of Subtype C HIV Type 1 Strains in Argentina, Paraguay, and Uruguay. *AIDS Research and Human Retroviruses*. 2004;20:1022-5.
493. Carvalho BC, Cardoso LP, Damasceno S, de Araujo Stefani MM. Moderate Prevalence of Transmitted Drug Resistance and Interiorization of HIV Type 1 Subtype C in the Inland North State of Tocantins, Brazil. *AIDS Res.Hum.Retroviruses*. 2011;
494. Casado C, Garcia S, Rodriguez C, del Romero J, Bello G, Lopez-Galindez C. Different evolutionary patterns are found within human immunodeficiency virus type 1-infected patients. *J.Gen.Virol*. 2001;82:2495-508.
495. Casado G, Thomson MM, Delgado E, Sierra M, Vazquez-de Parga E, Perez-Alvarez L, Ocampo A, Najera R. Near full-length genome characterization of an HIV type 1 CRF05\_DF virus from Spain. *AIDS Res.Hum.Retroviruses*. 2003;19:719-25.
496. Casado G, Thomson MM, Sierra M, Najera R. Identification of a Novel HIV-1 Circulating ADG Intersubtype Recombinant Form (CRF19\_cpx) in Cuba. *J.Acquir.Immune.Defic.Sydr*. 2005;40:532-7.
497. Cavalieri E, Florido C, Leal E, Machado DM, Camargo M, Diaz RS, Janini LM. Intra-host and inter-host variability of the HIV type 1 nef gene in Brazilian children. *AIDS Res.Hum.Retroviruses*. 2009;25:1129-40.
498. Ceballos A, Andreani G, Ripamonti C, Dilermia D, Mendez R, Rabinovich RD, Cardenas PC, Zala C, Cahn P, Scarlatti G, Peralta LM. Lack of viral selection in human immunodeficiency virus type 1 mother-to-child transmission with primary infection during late pregnancy and/or breastfeeding. *J.Gen.Virol*. 2008;89:2773-82.

499. Chang SY, Sheng WH, Lee CN, Sun HY, Kao CL, Chang SF, Liu WC, Yang JY, Wong WW, Hung CC, Chang SC. Molecular epidemiology of HIV type 1 subtypes in Taiwan: outbreak of HIV type 1 CRF07\_BC infection in intravenous drug users. *AIDS Res.Hum.Retroviruses*. 2006;22:1055-66.
500. Chen JH, Wong KH, Chen Z, Chan K, Lam HY, To SW, Cheng VC, Yuen KY, Yam WC. Increased genetic diversity of HIV-1 circulating in Hong Kong. *PLoS One*. 2010;5:e12198
501. Chen L, Yang S, Li J, Li J, Liu Y, Wang Z, Yang B, Li T, Li H, Bao Z, Zhuang D, Liu S, Li L. Near full-length genomic characterization of a novel HIV-1 CRF07\_BC/CRF08\_BC recombinant strain from Yunnan, China. *AIDS Res.Hum.Retroviruses*. 2010;
502. Chin MP, Ristic N. Genetic analysis of a UNAIDS HIV type 1 from Brazil revealed an unexpected recombination pattern. *AIDS Res.Hum.Retroviruses*. 2010;26:1261-3.
503. Chohan B, Lavreys L, Rainwater SM, Overbaugh J. Evidence for frequent reinfection with human immunodeficiency virus type 1 of a different subtype. *J.Virol*. 2005;79:10701-8.
504. Ciccozzi M, Gori C, Boros S, Ruiz-Alvarez MJ, Harxhi A, Dervishi M, Qyra S, Schinaia N, D'Arrigo R, Ceccherini-Silberstein F, Bino S, Perno CF, Rezza G. Molecular diversity of HIV in Albania. *J.Infect.Dis*. 2005;192:475-9.
505. Ciccozzi M, Lo PA, Cenci A, Staltari O, Butto S, Equestre M, Ciccaglione A, Caroleo B, Rezza G, Guadagnino V. May Phylogenetic Analysis Support Epidemiological Investigation in Identifying the Source of HIV Infection? *AIDS Res.Hum.Retroviruses*. 2010;
506. Ciccozzi M, Vujosevic D, Lo PA, Mugosa B, Vratnica Z, Lai A, Lausevic D, Draskovic N, Marjanovic A, Cella E, Santoro MM, Alteri C, Fabeni L, Ciotti M, Zehender G. Genetic Diversity of HIV-1 in Montenegro. *AIDS Res.Hum.Retroviruses*. 2010;
507. Coetzer M, Cilliers T, Papathanasopoulos M, Ramjee G, Karim SA, Williamson C, Morris L. Longitudinal analysis of HIV type 1 subtype C envelope sequences from South Africa. *AIDS Res.Hum.Retroviruses*. 2007;23:316-21.
508. Coetzer M, Nedellec R, Cilliers T, Meyers T, Morris L, Mosier DE. Extreme genetic divergence is required for coreceptor switching in HIV-1 subtype C. *J.Acquir.Immune.Defic.Syndr*. 2011;56:9-15.
509. Cornelissen M, van Den BR, Zorgdrager F, Goudsmit J. Spread of distinct human immunodeficiency virus type 1 AG recombinant lineages in Africa. *J.Gen.Virol*. 2000;81:515-23.
510. Courgnaud V, Salemi M, Pourrut X, Mpoudi-Ngole E, Abela B, Auzel P, Bibollet-Ruche F, Hahn B, Vandamme AM, Delaporte E, Peeters M. Characterization of a Novel Simian Immunodeficiency Virus with a vpu Gene from Greater Spot-Nosed Monkeys (*Cercopithecus nictitans*) Provides New Insights into Simian/Human Immunodeficiency Virus Phylogeny. *J.Virol*. 2002;76:8298-309.
511. Courgnaud V, Abela B, Pourrut X, Mpoudi-Ngole E, Loul S, Delaporte E, Peeters M. Identification of a new simian immunodeficiency virus lineage with a vpu gene present among different cercopithecus monkeys (*C. mona*, *C. cephus*, and *C. nictitans*) from Cameroon. *J.Virol*. 2003;77:12523-34.
512. Costa LJ, Mayer AJ, Busch MP, Diaz RS. Evidence for Selection of more Adapted Human Immunodeficiency Virus Type 1 Recombinant Strains in a Dually Infected Transfusion Recipient. *Virus Genes*. 2004;28:259-72.
513. Couto-Fernandez JC, Silva-de-Jesus C, Veloso VG, Rachid M, Gracie RS, Chequer-Fernandez SL, Oliveira SM, Arakaki-Sanchez D, Chequer PJ, Morgado MG. Human immunodeficiency virus type 1 (HIV-1) genotyping in Rio de Janeiro, Brazil: assessing subtype and drug-resistance associated mutations in HIV-1 infected individuals failing highly active antiretroviral therapy. *Mem.Inst.Oswaldo Cruz*. 2005;100:73-8.
514. Cuevas MT, Ruibal I, Villahermosa ML, Diaz H, Delgado E, Parga EV, Perez-Alvarez L, De Armas MB, Cuevas L, Medrano L, Noa E, Osmanov S, Najera R, Thomson MM. High HIV-1 genetic diversity in Cuba. *AIDS*. 2002;16:1643-53.
515. Cuevas MT, Fernandez-Garcia A, Pinilla M, Garcia-Alvarez V, Thomson M, Delgado E, Gonzalez-Galeano M, Miralles C, Serrano-Bengoechea E, Ojea de CR, Lopez-Alvarez MJ, Lezaun MJ, Sanchez-Garcia AM, Sanchez-Martinez M, Munoz-Nieto M, Perez-Alvarez L. Short communication: Biological and genetic characterization of HIV type 1 subtype B and nonsubtype B transmitted viruses: usefulness for vaccine candidate assessment. *AIDS Res.Hum.Retroviruses*. 2010;26:1019-25.
516. D'Arrigo R, Ciccozzi M, Gori C, Montieri S, Aquaro S, Bellagamba R, Boumris E, Di Perri G, Pizzi D, Antinori A, Rezza G, Perno CF. gp41 sequence variability in HIV type 1 non-B subtypes infected patients undergoing enfuvirtide pressure. *AIDS Res.Hum.Retroviruses*. 2007;23:1296-302.
517. Datta S, Banerjee A, Chandra PK, Mahapatra PK, Chakrabarti S, Chakravarty R. Drug trafficking routes and hepatitis B in injection drug users, Manipur, India. *Emerg.Infect.Dis*. 2006;12:1954-7.
518. Dazza MC, Ekwalinga M, Nende M, Shamamba KB, Bitshi P, Paraskevis D, Saragosti S. Characterization of a Novel vpu-Harboring Simian Immunodeficiency Virus from a Dent's Mona Monkey (*Cercopithecus mona denti*). *J.Virol*. 2005;79:8560-71.
519. De Baar MP, Abebe A, Kliphuis A, Tesfaye G, Goudsmit J, Pollakis G. HIV type 1 C and C' subclusters based on long terminal repeat sequences in the Ethiopian type 1 subtype C epidemic. *AIDS Res.Hum.Retroviruses*. 2003;19:917-22.
520. de Castro CA, Grinsztejn B, Veloso VG, Bastos FI, Pilotto JH, Morgado MG. Prevalence, estimated HIV-1 incidence and viral diversity among people seeking voluntary counseling and testing services in Rio de Janeiro, Brazil. *BMC.Infect.Dis*. 2010;10:224
521. de Sa Filho DJ, Sanabani S, Diaz RS, Munerato P, Brunstein A, Fusuma E, Sabino EC, Janini LM. Analysis of full-length human immunodeficiency virus type 1 genome reveals a variable spectrum of subtypes B and f recombinants in Sao Paulo, Brazil. *AIDS Res.Hum.Retroviruses*. 2005;21:145-51.
522. de Sa Filho DJ, Sucupira MC, Casiero MM, Sabino EC, Diaz RS, Janini LM. Identification of two HIV type 1 circulating recombinant forms in Brazil. *AIDS Res.Hum.Retroviruses*. 2006;22:1-13.

523. Sa-Filho DJ, Da Silva SM, Candido V, Gagliani LH, Cavaliere E, Diaz RS, Caseiro MM. HIV Type 1 pol Gene Diversity and Antiretroviral Drug Resistance Mutations in Santos, Brazil. *AIDS Res.Hum.Retroviruses*. 2008;
524. de Sa-Filho DJ, Ambar RF, Duarte NB, Matias RB, Candido V, Gagliani LH, Caseiro MM. HIV type 1 diversity from newly diagnosed patients in Santos metropolitan area/Brazil. *AIDS Res.Hum.Retroviruses*. 2009;25:925-9.
525. de Silva TI, Turner R, Hue S, Trikha R, van TC, Onyango C, Jaye A, Foley B, Whittle H, Rowland-Jones SL, Cotten M. HIV-1 subtype distribution in the Gambia and the significant presence of CRF49\_cpx, a novel circulating recombinant form. *Retrovirology*. 2010;7:82
526. de Souza AC, de Oliveira CM, Rodrigues CL, Silva SA, Levi JE. Short communication: Molecular characterization of HIV type 1 BF pol recombinants from Sao Paulo, Brazil. *AIDS Res.Hum.Retroviruses*. 2008;24:1521-5.
527. Delgado E, Leon-Ponte M, Villahermosa ML, Cuevas MT, Deibis L, Echeverria G, Thomson MM, Perez-Alvarez L, Osmanov S, Najera R. Analysis of HIV type 1 protease and reverse transcriptase sequences from Venezuela for drug resistance-associated mutations and subtype classification: a UNAIDS study. *AIDS Res.Hum.Retroviruses*. 2001;17:753-8.
528. Delgado E, Thomson MM, Villahermosa ML, Sierra M, Ocampo A, Miralles C, Rodriguez-Perez R, Diz-Aren J, Ojea-de Castro R, Losada E, Cuevas MT, Vazquez-de Parga E, Carmona R, Perez-Alvarez L, Medrano L, Cuevas L, Taboada JA, Najera R. Identification of a newly characterized HIV-1 BG intersubtype circulating recombinant form in Galicia, Spain, which exhibits a pseudotype-like virion structure. *J.Acquir.Immune.Defic.Syndr*. 2002;29:536-43.
529. Delgado E, Ampofo WK, Sierra M, Torpey K, Perez-Alvarez L, Bonney EY, Mukadi YD, Lartey M, Nyarko C, Amenyah RN, Thomson M, Najera R. High prevalence of unique recombinant forms of HIV-1 in Ghana: molecular epidemiology from an antiretroviral resistance study. *J.Acquir.Immune.Defic.Syndr*. 2008;48:599-606.
530. Delgado E, Rios M, Fernandez J, Perez-Alvarez L, Najera R, Thomson MM. Identification of a new HIV type 1 BF intersubtype circulating recombinant form (CRF44\_BF) in Chile. *AIDS Res.Hum.Retroviruses*. 2010;26:821-6.
531. Delviks-Frankenberry KA, Nikolenko GN, Maldarelli F, Hase S, Takebe Y, Pathak VK. Subtype-specific differences in the human immunodeficiency virus type 1 reverse transcriptase connection subdomain of CRF01\_AE are associated with higher levels of resistance to 3'-azido-3'-deoxythymidine. *J.Virol*. 2009;83:8502-13.
532. Derache A, Maiga AI, Traore O, Akonde A, Cisse M, Jarrousse B, Koita V, Diarra B, Carcelain G, Barin F, Pizzocolo C, Pizarro L, Katlama C, Calvez V, Marcelin AG. Evolution of genetic diversity and drug resistance mutations in HIV-1 among untreated patients from Mali between 2005 and 2006. *J.Antimicrob.Chemother*. 2008;
533. Dileria DA, Lourtau L, Gomez AM, Ebenrstejin J, Toibaro JJ, Bautista CT, Marone R, Carobene M, Pampuro S, Gomez-Carrillo M, Losso MH, Salomon H. Drug-resistance surveillance among newly HIV-1 diagnosed individuals in Buenos Aires, Argentina. *AIDS*. 2007;21:1355-60.
534. Dileria DA, Gomez AM, Lourtau L, Marone R, Losso MH, Salomon H, Gomez-Carrillo M. HIV type 1 genetic diversity surveillance among newly diagnosed individuals from 2003 to 2005 in Buenos Aires, Argentina. *AIDS Res.Hum.Retroviruses*. 2007;23:1201-7.
535. Dileria DA, Jones L, Rodriguez S, Turk G, Rubio AE, Pampuro S, Gomez-Carrillo M, Bautista C, Deluchi G, Benetucci J, Lasala MB, Lourtau L, Losso MH, Perez H, Cahn P, Salomon H. HLA-driven convergence of HIV-1 viral subtypes B and F toward the adaptation to immune responses in human populations. *PLoS.ONE*. 2008;3:e3429
536. Dileria DA, Jones LR, Pando MA, Rabinovich RD, Damilano GD, Turk G, Rubio AE, Pampuro S, Gomez-Carrillo M, Salomon H. Analysis of HIV Type 1 BF Recombinant Sequences from South America Dates the Origin of CRF12\_BF to a Recombination Event in the 1970s. *AIDS Res.Hum.Retroviruses*. 2011;27:569-78.
537. Ding N, Guo D, Zhang C. Reidentification of the recombination map of CRF03\_AB: evidence for a new additional mosaic a subtype segment. *AIDS Res.Hum.Retroviruses*. 2008;24:1337-9.
538. Djoko CF, Rimoin AW, Vidal N, Tamoufe U, Wolfe ND, Butel C, LeBreton M, Tshala FM, Kayembe PK, Muyembe JJ, Edidi-Basepeo S, Pike BL, Fair JN, Mbacham WF, Saylor KE, Mpoudi-Ngole E, Delaporte E, Grillo M, Peeters M. High HIV Type 1 Group M pol Diversity and Low Rate of Antiretroviral Resistance Mutations Among the Uniformed Services in Kinshasa, DRC. *AIDS Res.Hum.Retroviruses*. 2010;
539. Djoko CF, Wolfe ND, Vidal N, Tamoufe U, Montavon C, LeBreton M, Pike BL, Fair J, Mbacham WF, Benito A, Rimoin AW, Saylor K, Mpoudi-Ngole E, Grillo MP, Peeters M. HIV type 1 pol gene diversity and genotypic antiretroviral drug resistance mutations in Malabo, Equatorial Guinea. *AIDS Res.Hum.Retroviruses*. 2010;26:1027-31.
540. Doyle T, Garcia-Diaz AM, Ambrose J, Strang A, Cambiano V, Johnson M, Geretti AM. Detecting HIV-1 superinfection by pol gene population sequencing among untreated HIV-1-infected men who experience sudden rises in plasma HIV-1 RNA load. *AIDS*. 2011;25:542-4.
541. Drexler JF, Souza Luna LK, Pedroso C, Pedral-Sampaio DB, Queiroz AT, Brites C, Netto EM, Drosten C. Rates of and reasons for failure of commercial human immunodeficiency virus type 1 viral load assays in Brazil. *J Clin.Microbiol*. 2007;45:2061-3.
542. Esbjornsson J, Mild M, Mansson F, Norrgren H, Medstrand P. HIV-1 Molecular Epidemiology in Guinea-Bissau, West Africa: Origin, Demography and Migrations. *PLoS.ONE*. 2011;6:e17025
543. Eshleman SH, Gonzales MJ, Becker-Pergola G, Cunningham SC, Guay LA, Jackson JB, Shafer RW. Identification of Ugandan HIV type 1 variants with unique patterns of recombination in pol involving subtypes A and D. *AIDS Res.Hum.Retroviruses*. 2002;18:507-11.

544. Espinosa A, Vignoles M, Carrillo MG, Sheppard H, Donovan R, Peralta LM, Rossi D, Radulich G, Salomon H, Weissenbacher M. Intersubtype BF Recombinants of HIV-1 in a Population of Injecting Drug Users in Argentina. *J.Acquir.Immune.Defic.Syndr.* 2004;36:630-6.
545. Eyer-Silva WA, Morgado MG. Molecular epidemiology of HIV-1 infection in a small Brazilian county: usefulness of envelope and polymerase sequences to epidemiologic studies. *J.Acquir.Immune.Defic.Syndr.* 2006;41:664-70.
546. Eyer-Silva WA, Couto-Fernandez JC, Morgado MG. Molecular epidemiology of HIV type 1 in inner Rio De Janeiro State, Brazil. *AIDS Res.Hum.Retroviruses.* 2007;23:303-8.
547. Eyzaguirre LM, Erasilova IB, Nadai Y, Saad MD, Kovtunen NG, Gomatos PJ, Zeman VV, Botros BA, Sanchez JL, Birx DL, Earhart KC, Carr JK. Genetic characterization of HIV-1 strains circulating in Kazakhstan. *J Acquir.Immune.Defic.Syndr.* 2007;46:19-23.
548. Falkensammer B, Doerler M, Kessler HH, Puchhammer-Stoeckl E, Parson W, Duftner C, Dierich MP, Stoiber H. Subtype and genotypic resistance analysis of HIV-1 infected patients in Austria. *Wien.Klin.Wochenschr.* 2007;119:181-5.
549. Fan J, Negroni M, Robertson DL. The distribution of HIV-1 recombination breakpoints. *Infect.Genet.Evol.* 2007;
550. Fang G, Weiser B, Kuiken C, Philpott SM, Rowland-Jones S, Plummer F, Kimani J, Shi B, Kaul R, Bwayo J, Anzala O, Burger H. Recombination following superinfection by HIV-1. *AIDS.* 2004;18:153-9.
551. Fang Z, Xing H, Meng Z, Hong K, Liao L, He X, Shao Y. Genetic characterization analysis of the tat exon-1 region of HIV type 1 CRF07\_BC strains in China. *AIDS Res.Hum.Retroviruses.* 2010;26:359-63.
552. Fernandez-Garcia A, Cuevas MT, Munoz-Nieto M, Ocampo A, Pinilla M, Garcia V, Serrano-Bengoechea E, Lezaun MJ, Delgado E, Thomson M, Gonzalez-Galeano M, Contreras G, Najera R, Perez-Alvarez L. Development of a panel of well-characterized human immunodeficiency virus type 1 isolates from newly diagnosed patients including acute and recent infections. *AIDS Res.Hum.Retroviruses.* 2009;25:93-102.
553. Fernandez-Garcia A, Perez-Alvarez L, Cuevas MT, Delgado E, Munoz-Nieto M, Cilla G, Iribarren JA, Pinilla M, Ocampo A, Miralles C, Perez-Castro S, Gonzalez-Galeano M, de Castro RO, Trigo M, Garcia V, Sanchez AM, Thomson MM. Identification of a new HIV type 1 circulating BF intersubtype recombinant form (CRF47\_BF) in Spain. *AIDS Res.Hum.Retroviruses.* 2010;26:827-32.
554. Foglieni B, Candotti D, Guarnori I, Raffaele L, Berzuini A, Spreafico M, Orani A, Rossotti R, Rossi D, Allain JP, Prati D. A cluster of human immunodeficiency virus Type 1 recombinant form escaping detection by commercial genomic amplification assays. *Transfusion.* 2011;51:719-30.
555. Fokam J, Salpini R, Santoro MM, Cento V, D'Arrigo R, Gori C, Perno CF, Colizzi V, Nanfack A, Gwom LC, Cappelli G, Takou D. Performance evaluation of an in-house human immunodeficiency virus type-1 protease-reverse transcriptase genotyping assay in Cameroon. *Arch.Virol.* 2011;
556. Fomsgaard A, Vinner L, Therrien D, Jorgensen LB, Nielsen C, Mathiesen L, Pedersen C, Corbet S. Full-length characterization of A1/D intersubtype recombinant genomes from a therapy-induced HIV type 1 controller during acute infection and his noncontrolling partner. *AIDS Res.Hum.Retroviruses.* 2008;24:463-72.
557. Fonjungo PN, Mpoudi EN, Torimiro JN, Alemnji GA, Eno LT, Lyonga EJ, Nkengasong JN, Lal RB, Rayfield M, Kalish ML, Folks TM, Pieniazek D. Human immunodeficiency virus type 1 group m protease in cameroon: genetic diversity and protease inhibitor mutational features. *J.Clin.Microbiol.* 2002;40:837-45.
558. Fontaine E, Riva C, Peeters M, Schmit JC, Delaporte E, Van Laethem K, Van Vaerenbergh K, Snoeck J, Van Wijngaerden E, De Clercq E, Van Ranst M, Vandamme AM. Evaluation of two commercial kits for the detection of genotypic drug resistance on a panel of HIV type 1 subtypes A through J. *J.Acquir.Immune.Defic.Syndr.* 2001;28:254-8.
559. Frange P, Galimand J, Vidal N, Goujard C, Deveau C, Souala F, Peeters M, Meyer L, Rouzioux C, Chaix ML. New and old complex recombinant HIV-1 strains among patients with primary infection in 1996-2006 in France: the French ANRS CO06 primo cohort study. *Retrovirology.* 2008;5:69
560. Gagliani LH, Alkmim Maia WT, Sa-Filho D, Janini LM, Sucupira MC, Caseiro MM, Diaz RS. The Association Between Primary Antiretroviral Resistance and HAART Virologic Failure in a Developing Set. *AIDS Res.Hum.Retroviruses.* 2010;
561. Gale CV, Yirrell DL, Campbell E, Van der PL, Grosskurth H, Kaleebu P. Genotypic variation in the pol gene of HIV type 1 in an antiretroviral treatment-naive population in rural southwestern Uganda. *AIDS Res.Hum.Retroviruses.* 2006;22:985-92.
562. Galimand J, Frange P, Rouzioux C, Deveau C, Avettand-Fenoel V, Ghosn J, Lascoux C, Goujard C, Meyer L, Chaix ML. Short communication: evidence of HIV type 1 complex and second generation recombinant strains among patients infected in 1997-2007 in France: ANRS CO06 PRIMO Cohort. *AIDS Res.Hum.Retroviruses.* 2010;26:645-51.
563. Galli A, Lai A, Corvasce S, Saladini F, Riva C, Deho L, Caramma I, Franzetti M, Romano L, Galli M, Zazzi M, Balotta C. Recombination analysis and structure prediction show correlation between breakpoint clusters and RNA hairpins in the pol gene of human immunodeficiency virus type 1 unique recombinant forms. *J.Gen.Virol.* 2008;89:3119-25.
564. Gaschen B, Taylor J, Yusim K, Foley B, Gao F, Lang D, Novitsky V, Haynes B, Hahn BH, Bhattacharya T, Korber B. Diversity considerations in HIV-1 vaccine selection. *Science.* 2002;296:2354-60.
565. Gifford R, De Oliveira T, Rambaut A, Myers RE, Gale CV, Dunn D, Shafer R, Vandamme AM, Kellam P, Pillay D. Assessment of automated genotyping protocols as tools for surveillance of HIV-1 genetic diversity. *AIDS.* 2006;20:1521-9.
566. Gnanakaran S, Daniels MG, Bhattacharya T, Lapedes AS, Sethi A, Li M, Tang H, Greene K, Gao H, Haynes BF, Cohen MS, Shaw GM, Seaman MS, Kumar A, Gao F, Montefiori DC, Korber B. Genetic signatures in the envelope glycoproteins of HIV-1 that associate with broadly neutralizing antibodies. *PLoS.Comput.Biol.* 2010;6:e1000955

567. Gomez-Carrillo M, Quarleri JF, Rubio AE, Carobene MG, Dilernia D, Carr JK, Salomon H. Drug Resistance Testing Provides Evidence of the Globalization of HIV Type 1: A New Circulating Recombinant Form. *AIDS Research and Human Retroviruses*. 2004;20:885-8.
568. Gordon M, De Oliveira T, Bishop K, Coovadia HM, Madurai L, Engelbrecht S, Janse VR, Mosam A, Smith A, Cassol S. Molecular Characteristics of Human Immunodeficiency Virus Type 1 Subtype C Viruses from KwaZulu-Natal, South Africa: Implications for Vaccine and Antiretroviral Control Strategies. *J.Virol*. 2003;77:2587-99.
569. Guan Q, Wei M, Huang HL, Xing H, Hong KX, Ma PF, Liang H, Si XF, Hei FX, Zhang ZR, Shao YM. [Sequence analysis of gag-pol gene of HIV-1 B/C recombinant viruses in China]. *Zhonghua Yi.Xue.Za Zhi*. 2004;84:387-91.
570. Guimaraes ML, dos Santos MA, Loureiro R, Galvao-Castro B, Morgado MG. High frequency of recombinant genomes in HIV type 1 samples from Brazilian southeastern and southern regions. *AIDS Res.Hum.Retroviruses*. 2002;18:1261-9.
571. Guimaraes ML, Eyer-Silva WA, Couto-Fernandez JC, Morgado MG. Identification of two new CRF\_BF in Rio de Janeiro State, Brazil. *AIDS*. 2008;22:433-5.
572. Guimaraes ML, Couto-Fernandez JC, Eyer-Silva WA, Teixeira SL, Chequer-Fernandez SL, Morgado MG. Analysis of HIV-1 BF pr/rt recombinant strains from Rio de Janeiro/Brazil reveals multiple unrelated mosaic structures. *Infect.Genet.Evol*. 2010;10:1094-100.
573. Guo H, Guo D, Wei JF, Yang H, Huan X, Tsui SK, Yang R, Zhang C. First detection of a novel HIV Type 1 CRF01\_AE/07\_BC recombinant among an epidemiologically linked cohort of IDUs in Jiangsu, China. *AIDS Res.Hum.Retroviruses*. 2009;25:463-7.
574. Guo D, Ding N, Xu Y, Guo H, Wei JF, Wang JH, He G, Yang R, Zhang C. Near full-length genome characterization of an HIV-1 CRF01\_AE strain in Jiangsu, China: evidence of two independent introductions from Fujian. *AIDS Res.Hum.Retroviruses*. 2009;25:619-23.
575. Hai-Long H, Jian Z, Ping-Ping Y, Liang C, Xun L, Shan ZZ, Yan-Sheng Y. Genetic characterization of CRF01\_AE full-length human immunodeficiency virus type 1 sequences from Fujian, China. *AIDS Res.Hum.Retroviruses*. 2007;23:569-74.
576. Han X, Zhang M, Dai D, Wang Y, Zhang Z, Liu J, Geng W, Jiang Y, Takebe Y, Shang H. Genotypic resistance mutations to antiretroviral drugs in treatment-naive HIV/AIDS patients living in Liaoning Province, China: baseline prevalence and subtype-specific difference. *AIDS Res.Hum.Retroviruses*. 2007;23:357-64.
577. Harris B, Truchsess IV, Schatzl HM, Devare SG, Hackett J. Genomic Characterization of a Novel HIV Type 1 B/G Intersubtype Recombinant Strain from an Injecting Drug User in Germany. *AIDS Res.Hum.Retroviruses*. 2005;21:654-60.
578. Heeregrave EJ, Ampofo WK, Tetteh JK, Ofori M, Ofori SB, Shah AS, Pollakis G, Paxton WA. Generation of HIV-1 primary isolates representative of plasma variants using the U87.CD4 cell line. *J Virol.Methods*. 2010;169:341-50.
579. Herring BL, Cunningham AL, Dwyer DE. Potential Drug Resistance Polymorphisms in the Integrase Gene of HIV Type 1 Subtype A. *AIDS Research and Human Retroviruses*. 2004;20:1010-4.
580. Hirigoyen DL, Cartwright CP. Use of sequence data generated in the Bayer Tru Gene genotyping assay to recognize and characterize non-subtype-b human immunodeficiency virus type 1 strains. *J.Clin.Microbiol*. 2005;43:5263-71.
581. Hoelscher M, Kim B, Maboko L, Mhalu F, von Sonnenburg F, Bix DL, McCutchan FE. High proportion of unrelated HIV-1 intersubtype recombinants in the Mbeya region of southwest Tanzania. *AIDS*. 2001;15:1461-70.
582. Holguin A, Alvarez A, Soriano V. HIV-1 subtype J recombinant viruses in Spain. *AIDS Res.Hum.Retroviruses*. 2002;18:523-9.
583. Holguin A, Alvarez A, Soriano V. Heterogeneous nature of HIV-1 recombinants spreading in Spain. *J.Med.Virol*. 2005;75:374-80.
584. Holguin A, Erazo K, Escobar G, de MM, Yebra G, Martin L, Jovel LE, Castaneda L, Perez E. Drug Resistance Prevalence in Human Immunodeficiency Virus Type 1 Infected Pediatric Populations in Honduras and El Salvador During 1989-2009. *Pediatr.Infect.Dis.J*. 2011;30:e82-e87
585. Holzmayer V, Zekeng L, Kaptue L, Gurtler L, Devare SG, Hackett J, Jr. Near-full-length genomic sequence of a human immunodeficiency type 1 subtype G strain from Cameroon. *AIDS Res.Hum.Retroviruses*. 2005;21:414-9.
586. Holzmayer V, Aitken C, Skinner C, Ryall L, Devare SG, Hackett J, Jr. Characterization of genetically diverse HIV type 1 from a London cohort: near full-length genomic analysis of a subtype H strain. *AIDS Res.Hum.Retroviruses*. 2009;25:721-6.
587. Hu J, Switzer WM, Foley BT, Robertson DL, Goeken RM, Korber BT, Hirsch VM, Beer BE. Characterization and Comparison of Recombinant Simian Immunodeficiency Virus from Drill (*Mandrillus leucophaeus*) and Mandrill (*Mandrillus sphinx*) Isolates. *J.Virol*. 2003;77:4867-80.
588. Huang DD, Giesler TA, Bremer JW. Sequence characterization of the protease and partial reverse transcriptase proteins of the NED panel, an international HIV type 1 subtype reference and standards panel. *AIDS Res.Hum.Retroviruses*. 2003;19:321-8.
589. Huang W, Eshleman SH, Toma J, Fransen S, Stawiski E, Paxinos EE, Whitcomb JM, Young AM, Donnell D, Mmiro F, Musoke P, Guay LA, Jackson JB, Parkin NT, Petropoulos CJ. Coreceptor tropism in human immunodeficiency virus type 1 subtype D: high prevalence of CXCR4 tropism and heterogeneous composition of viral populations. *J Virol*. 2007;81:7885-93.
590. Huang HL, Yan PP, Zheng J, Wu SL, Cheng G, Lin X, Zheng WX, Xie MR, Zhang JM, Yan YS. Genetic characterization of three CRF01\_AE full-length HIV type 1 sequences from Fujian Province, China. *Chin Med.J.(Engl.)*. 2006;119:1622-8.

591. Huang DD, Foley BT, Tolzmann CA, Ouma A, Bremer JW. Complex mosaic composition of near full-length genomes of two NED (NIH-ENVA-DOD) subtype panel HIV type 1 strains, BCF-Dioum and BCF-Kita, originating from the Democratic Republic of Congo (DRC). *AIDS Res.Hum.Retroviruses*. 2009;25:1039-43.
592. Hunt GM, Papathanasopoulos MA, Gray GE, Tiemessen CT. Characterisation of near-full length genome sequences of three South African human immunodeficiency virus type 1 subtype C isolates. *Virus Genes*. 2003;26:49-56.
593. Ibe S, Yokomaku Y, Shiino T, Tanaka R, Hattori J, Fujisaki S, Iwatani Y, Mamiya N, Utsumi M, Kato S, Hamaguchi M, Sugiura W. HIV-2 CRF01\_AB: first circulating recombinant form of HIV-2. *J Acquir.Immune Defic.Syindr*. 2010;54:241-7.
594. Imamichi H, Koita O, Dabitaio D, Dao S, Ibrah M, Sogoba D, Dewar RL, Berg SC, Jiang MK, Parta M, Washington JA, Polis MA, Lane HC, Tounkara A. Identification and characterization of CRF02\_AG, CRF06\_cpx, and CRF09\_cpx recombinant subtypes in Mali, West Africa. *AIDS Res.Hum.Retroviruses*. 2009;25:45-55.
595. Jadhav S, Tripathy S, Kulkarni S, Agnihotri K, Risbud A, Paranjape R. Molecular phylogenetics of nearly full-length HIV type 2 envelope gene sequences from West India. *AIDS Res.Hum.Retroviruses*. 2009;25:115-21.
596. Jadhav SD, Tripathy SP, Kulkarni SS, Chaturbhuj DN, Ghare R, Bhattacharya J, Paranjape RS. Genetic conservation in gp36 transmembrane sequences of Indian HIV-2 isolates. *AIDS Res.Hum.Retroviruses*. 2011;
597. Janssens W, Laukkanen T, Salminen MO, Carr JK, Auwera Gvd, Heyndrickx L, Groen Gvd, McCutchan FE. HIV-1 subtype H near-full length genome reference strains and analysis of subtype-H-containing inter-subtype recombinants. *AIDS*. 2000;14:1533-43.
598. Janssens W, Salminen MO, Laukkanen T, Heyndrickx L, Auwera Gvd, Colebunders R, McCutchan FE, Groen Gvd. Near full-length genome analysis of HIV type 1 CRF02.AG subtype C and CRF02.AG subtype G recombinants. *AIDS Res.Hum.Retroviruses*. 2000;16:1183-9.
599. Jeannot AC, Reigadas S, Schrive MH, Pinson P, Fleury HJ. Pol bootscanning analysis of HIV type 1 can exhibit unexpected recombinations. *AIDS Res.Hum.Retroviruses*. 2009;25:713-6.
600. Jere A, Tripathy S, Agnihotri K, Jadhav S, Paranjape R. Genetic analysis of Indian HIV-1 nef: subtyping, variability and implications. *Microbes.Infect*. 2004;6:279-89.
601. Jonassen TO, Grinde B, Asjo B, Hasle G, Hungnes O. Intersubtype recombinant HIV type 1 involving HIV-MAL-like and subtype H-like sequence in four Norwegian cases. *AIDS Res.Hum.Retroviruses*. 2000;16:49-58.
602. Jones LR, Dileria DA, Manrique JM, Moretti F, Salomon H, Gomez-Carrillo M. In-depth analysis of the origins of HIV type 1 subtype C in South America. *AIDS Res.Hum.Retroviruses*. 2009;25:951-9.
603. Kane CT, Montavon C, Toure MA, Faye MA, Ndiaye AG, Diallo AG, Ndoeye I, Liegeois F, Delaporte E, Mboup S, Peeters M. Full-length genome sequencing of HIV type 1 group O viruses isolated from a heterosexual transmission cluster in Senegal. *AIDS Res.Hum.Retroviruses*. 2001;17:1211-6.
604. Kantor R, Katzenstein DA, Efron B, Carvalho AP, Wynhoven B, Cane P, Clarke J, Sirivichayakul S, Soares MA, Snoeck J, Pillay C, Rudich H, Rodrigues R, Holguin A, Ariyoshi K, Bouzas MB, Cahn P, Sugiura W, Soriano V, Brigido LF, Grossman Z, Morris L, Vandamme AM, Tanuri A, Phanuphak P, Weber JN, Pillay D, Harrigan PR, Camacho R, Schapiro JM, Shafer RW. Impact of HIV-1 subtype and antiretroviral therapy on protease and reverse transcriptase genotype: results of a global collaboration. *PLoS Med*. 2005;2:e112
605. Karchava M, Pulver W, Smith L, Philpott S, Sullivan TJ, Wethers J, Parker MM. Prevalence of drug-resistance mutations and non-subtype B strains among HIV-infected infants from New York State. *J Acquir.Immune.Defic.Syindr*. 2006;42:614-9.
606. Kebba A, Kaleebu P, Serwanga J, Rowland S, Yirell D, Downing R, Gilmour J, Imami N, Gotch F, Whitworth J. HIV type 1 antigen-responsive CD4+ T-lymphocytes in exposed yet HIV Type 1 seronegative Ugandans. *AIDS Res.Hum.Retroviruses*. 2004;20:67-75.
607. Kemal KS, Foley B, Burger H, Anastos K, Minkoff H, Kitchen C, Philpott SM, Gao W, Robison E, Holman S, Dehner C, Beck S, Meyer WA, III, Landay A, Kovacs A, Bremer J, Weiser B. HIV-1 in genital tract and plasma of women: compartmentalization of viral sequences, coreceptor usage, and glycosylation. *Proc.Natl.Acad.Sci.U.S.A*. 2003;100:12972-7.
608. Khoja S, Ojwang P, Khan S, Okinda N, Harania R, Ali S. Genetic analysis of HIV-1 subtypes in Nairobi, Kenya. *PLoS.ONE*. 2008;3:e3191
609. Kijak GH, Rubio AE, Quarleri JF, Salomon H. HIV type 1 genetic diversity is a major obstacle for antiretroviral drug resistance hybridization-based assays. *AIDS Res.Hum.Retroviruses*. 2001;17:1415-21.
610. Konings FAJ, Nyambi PN. V118I Substitution in the Reverse Transcriptase Gene of HIV Type 1 CRF02\_AG Strains Infecting Drug-Naive Individuals in Cameroon. *AIDS Research and Human Retroviruses*. 2004;20:673-8.
611. Korber BT, Kuiken C. The HIV Databases: History, Design, and Function. In: Leitner T, ed. *The molecular epidemiology of human viruses*. Norwell, Mass: Kluwer Academic Publishers; 2002:58
612. Koulinska IN, Msamanga G, Mwakagile D, Essex M, Renjifo B. Common Genetic Arrangements among Human Immunodeficiency Virus Type 1 Subtype A and D Recombinant Genomes Vertically Transmitted in Tanzania. *AIDS Res.Hum.Retroviruses*. 2002;18:947-56.
613. Koulinska IN, Chaplin B, Mwakagile D, Essex M, Renjifo B. Hypermutation of HIV type 1 genomes isolated from infants soon after vertical infection. *AIDS Res.Hum.Retroviruses*. 2003;19:1115-23.
614. Kousiappa I, van de Vijver DA, Kostrikis LG. Near full-length genetic analysis of HIV sequences derived from cyprus: evidence of a highly polyphyletic and evolving infection. *AIDS Res.Hum.Retroviruses*. 2009;25:727-40.
615. Kousiappa I, Achilleos C, Hezka J, Lazarou Y, Othonos K, Demetriades I, Kostrikis LG. Molecular Characterization of HIV Type 1 Strains from Newly Diagnosed Patients in Cyprus (2007-2009) Recovers

- Multiple Clades Including Unique Recombinant Strains and Lack of Transmitted Drug Resistance. *AIDS Res.Hum.Retroviruses*. 2011;
616. Kuiken C, Leitner T. HIV-1 Subtyping. In: Rodrigo AG, Learn GH, eds. *Computational and evolutionary analysis of HIV molecular sequences*. Boston, MA: Kluwer Academic Publishers; 2001:44-6.
617. Kusagawa S, Takebe Y, Yang R, Motomura K, Ampofo W, Brandful J, Koyanagi Y, Yamamoto N, Sata T, Ishikawa K, Nagai Y, Tatsumi M. Isolation and characterization of a full-length molecular DNA clone of Ghanaian HIV type 1 intersubtype A/G recombinant CRF02\_AG, which is replication competent in a restricted host range. *AIDS Res.Hum.Retroviruses*. 2001;17:649-55.
618. Kusagawa S, Sato H, Tomita Y, Tatsumi M, Kato K, Motomura K, Yang R, Takebe Y. Isolation and characterization of replication-competent molecular DNA clones of HIV type 1 CRF01\_AE with different coreceptor usages. *AIDS Res.Hum.Retroviruses*. 2002;18:115-22.
619. Laeyendecker O, Zhang GW, Quinn TC, Garten R, Ray SC, Lai S, Liu W, Chen J, Yu XF. Molecular epidemiology of HIV-1 subtypes in southern China. *J.Acquir.Immune.Defic.Syndr*. 2005;38:356-62.
620. Lakhshashe S, Tripathy S, Paranjape R, Bhattacharya J. Evidence of a Novel B/C Recombinant Exhibiting Unique Breakpoints of Near Full-Length HIV Type 1 Genome from Northeastern India. *AIDS Res.Hum.Retroviruses*. 2008;24:229-34.
621. Lakhshashe S, Tripathy S, Paranjape R, Bhattacharya J. Characterization of B/C recombinants of near full-length HIV type 1 from northeastern India with mosaics identical to ARE195FL but with a different ancestral origin. *AIDS Res.Hum.Retroviruses*. 2008;24:92-9.
622. Lamers SL, Salemi M, Galligan DC, De Oliveira T, Fogel GB, Granier SC, Zhao L, Brown JN, Morris A, Masliah E, McGrath MS. Extensive HIV-1 intra-host recombination is common in tissues with abnormal histopathology. *PLoS One*. 2009;4:e5065
623. Land AM, Ball TB, Luo M, Rutherford J, Sarna C, Wachih C, Kimani J, Plummer FA. Full-length HIV type 1 proviral sequencing of 10 highly exposed women from Nairobi, Kenya reveals a high proportion of intersubtype recombinants. *AIDS Res.Hum.Retroviruses*. 2008;24:865-72.
624. Lau KA, Wang B, Kamarulzaman A, Peng NK, Saksena NK. Near Full-Length Sequence Analysis of a Unique CRF01\_AE/B Recombinant from Kuala Lumpur, Malaysia. *AIDS Res.Hum.Retroviruses*. 2007;23:1139-45.
625. Lau KA, Wang B, Kamarulzaman A, Ngk KP, Saksena NK. Continuous crossover(s) events of HIV-1 CRF01\_AE and B subtype strains in Malaysia: evidence of rapid and extensive HIV-1 evolution in the region. *Curr.HIV.Res*. 2008;6:108-16.
626. Laukkanen T, Carr JK, Janssens W, Liitsola K, Gotte D, McCutchan FE, Op dC, Cornelissen M, Heyndrickx L, van der Groen G, Salminen MO. Virtually full-length subtype F and F/D recombinant HIV-1 from Africa and South America. *Virology*. 2000;269:95-104.
627. Leal E, Villanova FE. Diversity of HIV-1 subtype B: implications to the origin of BF recombinants. *PLoS One*. 2010;5:e11833
628. Lemey P, Derdelinckx I, Rambaut A, Van Laethem K, Dumont S, Vermeulen S, Van Wijngaerden E, Vandamme AM. Molecular footprint of drug-selective pressure in a human immunodeficiency virus transmission chain. *J.Virol*. 2005;79:11981-9.
629. Li XJ, Kusagawa S, Xia X, Yang C, Wang Q, Yokota Y, Hoshina Y, Onogi T, Nohtomi K, Imamura Y, Shiino T, Yang R, Yamamoto N, Ben K, Takebe Y. Molecular epidemiology of the heterosexual HIV-1 transmission in Kunming, Yunnan Province of China suggests origin from the local IDU epidemic. *AIDS Res.Hum.Retroviruses*. 2005;21:977-80.
630. Li L, Chen L, Yang S, Liu Y, Li J, Wang Z, Yang B, Li H, Bao Z, Zhuang D, Liu S, Li J. Near Full-Length Sequence Analysis of a Novel HIV-1 C/CRF01\_AE Recombinant Variant from Yunnan, China. *AIDS Res.Hum.Retroviruses*. 2010;26:1255-9.
631. Li L, Chen L, Yang S, Liu Y, Li H, Bao Z, Wang Z, Zhuang D, Liu S, Li J. Near full-length genomic characterization of a novel HIV type 1 subtype B/C recombinant strain from Yunnan, China. *AIDS Res.Hum.Retroviruses*. 2010;26:711-6.
632. Li L, Liang S, Chen L, Liu W, Li H, Liu Y, Bao Z, Wang Z, Zhuang D, Liu S, Li J. Genetic characterization of 13 subtype CRF01\_AE near full-length genomes in Guangxi, China. *AIDS Res.Hum.Retroviruses*. 2010;26:699-704.
633. Li Y, Tee KK, Liao H, Hase S, Uenishi R, Li XJ, Tsuchiura T, Yang R, Govindasamy S, Yong YK, Tan HY, Pybus OG, Kamarulzaman A, Takebe Y. Identification of a novel second-generation circulating recombinant form (CRF48\_01B) in Malaysia: a descendant of the previously identified CRF33\_01B. *J Acquir.Immune Defic.Syndr*. 2010;54:129-36.
634. Liao L, Xing H, Li X, Ruan Y, Zhang Y, Qin G, Shao Y. Genotypic Analysis of the Protease and Reverse Transcriptase of HIV Type 1 Isolates from Recently Infected Injecting Drug Users in Western China. *AIDS Res.Hum.Retroviruses*. 2007;23:1062-5.
635. Liegeois F, Courgnaud V, Switzer WM, Murphy HW, Loul S, Aghokeng A, Pourrut X, Mpoudi-Ngole E, Delaporte E, Peeters M. Molecular characterization of a novel simian immunodeficiency virus lineage (SIVtal) from northern talapoin (Miopithecus ogouensis). *Virology*. 2006;
636. Liegeois F, Lafay B, Formenty P, Locatelli S, Courgnaud V, Delaporte E, Peeters M. Full-length genome characterization of a novel simian immunodeficiency virus lineage (SIVolc) from olive Colobus (*Procolobus verus*) and new SIVwrcPbb strains from Western Red Colobus (*Piliocolobus badius badius*) from the Tai Forest in Ivory Coast. *J.Virol*. 2009;83:428-39.
637. Liegeois F, Butel C, Ondeme AM, Verrier D, Motsch P, Gonzalez JP, Peeters M, Rouet F, Onanga R. Full-length genome sequence of a simian immunodeficiency virus (SIVsunK08) from a wild captured sun-tailed monkey (*Cercopithecus solatus*) in Gabon provides evidence for a species specific monophyletic SIVsun lineage. *AIDS Res.Hum.Retroviruses*. 2011;

638. Liitsola K, Holm K, Bobkov A, Pokrovsky V, Smolskaya T, Leinikki P, Osmanov S, Salminen M. An AB recombinant and its parental HIV type 1 strains in the area of the former Soviet Union: low requirements for sequence identity in recombination. *UNAIDS Virus Isolation Network. AIDS Res.Hum.Retroviruses.* 2000;16:1047-53.
639. Liitsola K, Holmstrom P, Laukkanen T, Brummer-Korvenkontio H, Leinikki P, Salminen MO. Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data. *Scand.J.Infect.Dis.* 2000;32:475-80.
640. Locatelli S, Lafay B, Liegeois F, Ting N, Delaporte E, Peeters M. Full molecular characterization of a simian immunodeficiency virus, SIVwrcpbt from Temminck's red colobus (*Ptilocolobus badius temminckii*) from Abuko Nature Reserve, The Gambia. *Virology.* 2008;376:90-100.
641. Luk KC, Holzmayer V, Yamaguchi J, Swanson P, Brennan CA, Ngansop C, Mbanya D, Gayum H, Djuidje MN, Ndemi N, Kamdem D, Kaptue L, Gurtler L, Devare SG, Hackett J. Near full-length genome characterization of three additional HIV type 1 CRF13\_cpx strains from Cameroon. *AIDS Res.Hum.Retroviruses.* 2007;23:297-302.
642. Luk KC, Holzmayer V, Ndemi N, Swanson P, Brennan CA, Ngansop C, Mbanya D, Kaptue L, Gurtler L, Devare SG, Hackett J. Near full-length genome characterization of an HIV type 1 CRF25\_cpx strain from Cameroon. *AIDS Res.Hum.Retroviruses.* 2008;24:1309-14.
643. Lukashov VV, Goudsmit J. Evolutionary relationships among parvoviruses: virus-host coevolution among autonomous primate parvoviruses and links between adeno- associated and avian parvoviruses. *J.Virol.* 2001;75:2729-40.
644. Machado ES, Lambert JS, Watson DC, Afonso AO, da Cunha SM, Nogueira SA, Caride E, Oliveira RH, Sill AM, DeVico A, Tanuri A. Genotypic resistance and HIV-1 subtype in Brazilian children on dual and triple combination therapy. *J.Clin.Virol.* 2004;30:24-31.
645. Magiorkinis G, Paraskevis D, Magiorkinis E, Vandamme AM, Hatzakis A. Reanalysis of the HIV-1 circulating recombinant form A/E (CRF01\_AE): evidence of A/E/G recombination. *J.Acquir.Immune.Defic.Syndr.* 2002;30:124-9.
646. Magiorkinis E, Paraskevis D, Magiorkinis G, Chryssou S, Chini M, Lazanas M, Papparizos V, Saroglou G, Antoniadou A, Giamarellou E, Karafoulidou A, Hatzakis A. Mutations associated with genotypic resistance to antiretroviral therapy in treatment naive HIV-1 infected patients in Greece. *Virus Res.* 2002;85:109-15.
647. Magiorkinis G, Paraskevis D, Vandamme AM, Magiorkinis E, Sypsa V, Hatzakis A. In vivo characteristics of human immunodeficiency virus type 1 intersubtype recombination: determination of hot spots and correlation with sequence similarity. *J.Gen.Virol.* 2003;84:2715-22.
648. Magiorkinis G, Paraskevis D, Magiorkinis E, Vandamme AM, Hatzakis A. Re-analysis of 34 full-length HIV-1 intersubtype recombinant sequences. *Infect.Genet.Evol.* 2005;5:225-9.
649. Malet I, Soulie C, Tchertanov L, Derache A, Amellal B, Traore O, Simon A, Katlama C, Mouscadet JF, Calvez V, Marcelin AG. Structural effects of amino acid variations between B and CRF02-AG HIV-1 integrases. *J.Med.Virol.* 2008;80:754-61.
650. Maljkovic I, Wilbe K, Solver E, Alaeus A, Leitner T. Limited transmission of drug-resistant HIV type 1 in 100 Swedish newly detected and drug-naive patients infected with subtypes A, B, C, D, G, U, and CRF01\_AE. *AIDS Res.Hum.Retroviruses.* 2003;19:989-97.
651. Mamadou S, Vidal N, Montavon C, Ben A, Djibo A, Rabiou S, Soga G, Delaporte E, Mboup S, Peeters M. Emergence of complex and diverse CRF02-AG/CRF06-cpx recombinant HIV type 1 strains in Niger, West Africa. *AIDS Res.Hum.Retroviruses.* 2003;19:77-82.
652. Masharsky AE, Klimov NA, Kozlov AP. Molecular cloning and analysis of full-length genome of HIV type 1 strains prevalent in countries of the former Soviet Union. *AIDS Res.Hum.Retroviruses.* 2003;19:933-9.
653. Meloni ST, Kim B, Sankale JL, Hamel DJ, Tovanabuttra S, Mboup S, McCutchan FE, Kanki PJ. Distinct human immunodeficiency virus type 1 subtype a virus circulating in west Africa: sub-subtype a3. *J.Virol.* 2004;78:12438-45.
654. Meng Z, Xing H, He X, Ma L, Xu W, Shao Y. Genetic characterization of three newly isolated CRF07\_BC near full-length genomes in China. *AIDS Res.Hum.Retroviruses.* 2007;23:1049-54.
655. Meng Z, He X, Xing H, Xin R, Sun J, Yi F, Ma L, Shao Y. Construction and characterization of an infectious molecular clone of HIV type 1 CRF07\_BC. *AIDS Res.Hum.Retroviruses.* 2008;24:259-64.
656. Mild M, Esbjornsson J, Fenyo EM, Medstrand P. Frequent inpatient recombination between HIV-1 R5 and X4 envelopes: Implications for coreceptor switch. *J Virol.* 2007;
657. Mokili JL, Rogers M, Carr JK, Simmonds P, Bopopi JM, Foley BT, Korber BT, Birx DL, McCutchan FE. Identification of a novel clade of human immunodeficiency virus type 1 in Democratic Republic of Congo. *AIDS Res.Hum.Retroviruses.* 2002;18:817-23.
658. Monno L, Brindicci G, Lo CS, Punzi G, Scarabaggio T, Riva C, Di Bari C, Pierotti P, Saracino A, Lagioia A, Mazzotta F, Balotta C, Angarano G. HIV-1 subtypes and circulating recombinant forms (CRFs) from HIV-1 infected patients residing in two regions of central and southern Italy. *J.Med.Virol.* 2005;75:483-90.
659. Montavon C, Bibollet-Ruche F, Robertson D, Koumare B, Mulanga C, Esu-Williams E, Toure C, Mboup S, Saman E, Delaporte E, Peeters M. The identification of a complex A/G/I/J recombinant HIV type 1 virus in various West African countries. *AIDS Res.Hum.Retroviruses.* 1999;15:1707-12.
660. Montavon C, Toure-Kane C, Liegeois F, Mpoudi E, Bourgeois A, Vergne L, Perret JL, Boumah A, Saman E, Mboup S, Delaporte E, Peeters M. Most env and gag subtype A HIV-1 viruses circulating in West and West Central Africa are similar to the prototype AG recombinant virus IBNG. *J.Acquir.Immune.Defic.Syndr.* 2000;23:363-74.
661. Montavon C, Toure-Kane C, Nkengasong JN, Vergne L, Hertogs K, Mboup S, Delaporte E, Peeters M. CRF06-cpx: a new circulating recombinant form of HIV-1 in West Africa involving subtypes A, G, K, and J. *J.Acquir.Immune.Defic.Syndr.* 2002;29:522-30.



662. Montavon C, Vergne L, Bourgeois A, Mpoudi-Ngole E, Malonga-Mouellet G, Butel C, Toure-Kane C, Delaporte E, Peeters M. Identification of a new circulating recombinant form of HIV type 1, CRF11-cpx, involving subtypes A, G, J, and CRF01-AE, in Central Africa. *AIDS Res.Hum.Retroviruses*. 2002;18:231-6.
663. Monteiro JP, Araujo AF, Santos ED, Galvao-Castro B, Alcantara LC. Lack of high-level resistance mutations in HIV-1 BF recombinant strains circulating in northeast Brazil. *AIDS Res.Hum.Retroviruses*. 2010;
664. Motomura K, Kusagawa S, Kato K, Nohtomi K, Lwin HH, Tun KM, Thwe M, Oo KY, Lwin S, Kyaw O, Zaw M, Nagai Y, Takebe Y. Emergence of new forms of human immunodeficiency virus type 1 intersubtype recombinants in central Myanmar. *AIDS Res.Hum.Retroviruses*. 2000;16:1831-43.
665. Mullick R, Sengupta S, Sarkar K, Chakrabarti S. Molecular characterization of tat gene and long terminal repeat region of human immunodeficiency virus type-1 detected among the injecting drug users (IDUs) of Manipur, India: identification of BC recombinants. *Virus Res*. 2010;147:195-201.
666. Munoz-Nieto M, Perez-Alvarez L, Thomson M, Garcia V, Ocampo A, Casado G, Delgado E, Miralles C, de Parga EV, Sierra M, Contreras G, Najera R. HIV type 1 intersubtype recombinants during the evolution of a dual infection with subtypes B and G. *AIDS Res.Hum.Retroviruses*. 2008;24:337-43.
667. Nadai Y, Eyzaguirre LM, Sill A, Cleghorn F, Nolte C, Charurat M, Collado-Chastel S, Jack N, Bartholomew C, Pape JW, Figueroa P, Blattner WA, Carr JK. HIV-1 epidemic in the Caribbean is dominated by subtype B. *PLoS.ONE*. 2009;4:e4814
668. Ndembi N, Abraha A, Pilch H, Ichimura H, Mbanya D, Kaptue L, Salata R, Arts EJ. Molecular Characterization of HIV-1 and HIV-2 in Yaounde, Cameroon: Evidence of Major Drug Resistance Mutations in Newly Diagnosed non-B Infected Patients. *J Clin.Microbiol*. 2007;
669. Ndembi N, Lyagoba F, Nanteza B, Kushemerwa G, Serwanga J, Katongole-Mbidde E, Grosskurth H, Kaleebu P. Transmitted antiretroviral drug resistance surveillance among newly HIV type 1-diagnosed women attending an antenatal clinic in Entebbe, Uganda. *AIDS Res.Hum.Retroviruses*. 2008;24:889-95.
670. Neogi U, Sood V, Goel N, Wanchu A, Banerjee AC. Novel HIV-1 long terminal repeat (LTR) sequences of subtype B and mosaic intersubtype B/C recombinants in North India. *Arch.Virol*. 2008;153:1961-6.
671. Niama FR, Vidal N, Bazepo SE, Mpoudi E, Toure-Kane C, Parra HJ, Delaporte E, Peeters M. CRF45\_AKU, a circulating recombinant from Central Africa, is probably the common ancestor of HIV type 1 MAL and HIV type 1 NOGIL. *AIDS Res.Hum.Retroviruses*. 2009;25:1345-53.
672. Novelli P, Vella C, Oxford J, Daniels RS. Construction and biological characterization of an infectious molecular clone of HIV type 1GB8. *AIDS Res.Hum.Retroviruses*. 2000;16:1175-8.
673. Novelli P, Vella C, Oxford J, Daniels RS. Construction and characterization of a full-length HIV-1(92UG001) subtype D infectious molecular clone. *AIDS Res.Hum.Retroviruses*. 2002;18:85-8.
674. Novitsky VA, Gaolekwe S, McLane MF, Ndung'u TP, Foley BT, Vannberg F, Marlink R, Essex M. HIV type 1 A/J recombinant with a pronounced pol gene mosaicism. *AIDS Res.Hum.Retroviruses*. 2000;16:1015-20.
675. Novitsky V, Lagakos S, Herzig M, Bonney C, Kebaabetswe L, Rossen Khan R, Nkwe D, Margolin L, Musonda R, Moyo S, Woldegabriel E, van Widenfelt E, Makhema J, Essex M. Evolution of proviral gp120 over the first year of HIV-1 subtype C infection. *Virology*. 2009;383:47-59.
676. Ntemgwa M, Toni TD, Brenner BG, Routy JP, Moisi D, Oliveira M, Wainberg MA. Near full-length genomic analysis of a novel subtype A1/C recombinant HIV type 1 isolate from Canada. *AIDS Res.Hum.Retroviruses*. 2008;24:655-9.
677. Nyombi BM, Kristiansen KI, Bjune G, Muller F, Holm-Hansen C. Diversity of human immunodeficiency virus type 1 subtypes in Kagera and Kilimanjaro regions, Tanzania. *AIDS Res.Hum.Retroviruses*. 2008;24:761-9.
678. Oliveira AC, Martins AN, Pires AF, Arruda MB, Tanuri A, Pereira HS, Brindeiro RM. Enfuvirtide (T-20) resistance-related mutations in HIV type 1 subtypes B, C, and F isolates from Brazilian patients failing HAART. *AIDS Res.Hum.Retroviruses*. 2009;25:193-8.
679. Op de Coul E, van der Schoot A, Goudsmit J, van den Burg R, Janssens W, Heyndrickx L, van der Groen G, Cornelissen M. Independent introduction of transmissible F/D recombinant HIV-1 from Africa into Belgium and The Netherlands. *Virology*. 2000;270:267-77.
680. Op de Coul EL, Coutinho RA, van der Schoot A, van Doornum GJ, Lukashov VV, Goudsmit J, Cornelissen M. The impact of immigration on env HIV-1 subtype distribution among heterosexuals in the Netherlands: influx of subtype B and non-B strains. *AIDS*. 2001;15:2277-86.
681. Padua E, Parreira R, Tendeiro R, Nunes B, Castela J, Soares I, Mouzinho A, Reis E, Paixao MT. Potential impact of viral load and genetic makeup of HIV type 1 on mother-to-child transmission: characterization of env-C2V3C3 and nef sequences. *AIDS Res.Hum.Retroviruses*. 2009;25:1171-7.
682. Palma AC, Araujo F, Duque V, Borges F, Paixao MT, Camacho R. Molecular epidemiology and prevalence of drug resistance-associated mutations in newly diagnosed HIV-1 patients in Portugal. *Infect.Genet.Evol*. 2007;7:391-8.
683. Palma AC, Abecasis AB, Vercauteren J, Carvalho AP, Cabanas J, Vandamme AM, Camacho RJ. Effect of human immunodeficiency virus type 1 protease inhibitor therapy and subtype on development of resistance in subtypes B and G. *Infect.Genet.Evol*. 2010;10:373-9.
684. Pando MA, Eyzaguirre LM, Carrion G, Montano SM, Sanchez JL, Carr JK, Avila MM. High genetic variability of HIV-1 in female sex workers from Argentina. *Retrovirology*. 2007;4:58
685. Pando MA, Eyzaguirre LM, Segura M, Bautista CT, Marone R, Ceballos A, Montano SM, Sanchez JL, Weissenbacher M, Avila MM, Carr JK. First report of an HIV-1 triple recombinant of subtypes B, C and F in Buenos Aires, Argentina. *Retrovirology*. 2006;3:59
686. Pando MA, De Salvo C, Bautista CT, Eyzaguirre L, Carrion G, Feola M, Lado I, Hoffman M, Biglione MM, Carr JK, Montano SM, Sanchez JL, Weissenbacher M, Avila MM. Human immunodeficiency virus and tuberculosis in Argentina: prevalence, genotypes and risk factors. *J Med.Microbiol*. 2008;57:190-7.

687. Pando MA, Gomez-Carrillo M, Vignoles M, Rubio AE, dos Ramos Farias MS, Vila M, Rossi D, Ralon G, Marone R, Reynaga E, Sosa J, Torres O, Maestri M, Avila MM, Salomon H. Incidence of HIV type 1 infection, antiretroviral drug resistance, and molecular characterization in newly diagnosed individuals in Argentina: A Global Fund Project. *AIDS Res.Hum.Retroviruses*. 2011;27:17-23.
688. Papa A, Papadimitriou E, Papoutsis A, Kiosses V, Antoniadis A. HIV-1 subtypes and circulating recombinant forms (CRFs) in Northern Greece. *Virus Res*. 2002;85:85-93.
689. Paraskevis D, Magiorkinis E, Magiorkinis G, Anastassopoulou C, Lazanas M, Chrysos G, Vandamme AM, Hatzakis A. Molecular characterization of a complex, recombinant human immunodeficiency virus type 1 (HIV-1) isolate (A/G/J/K/?): evidence to support the existence of a novel HIV-1 subtype. *J.Gen.Virol*. 2001;82:2509-14.
690. Paraskevis D, Magiorkinis M, Vandamme AM, Kostrikis LG, Hatzakis A. Re-analysis of human immunodeficiency virus type 1 isolates from Cyprus and Greece, initially designated 'subtype I', reveals a unique complex A/G/H/K/? mosaic pattern. *J.Gen.Virol*. 2001;82:575-80.
691. Paraskevis D, Lemey P, Salemi M, Suchard M, Van De PY, Vandamme AM. Analysis of the Evolutionary Relationships of HIV-1 and SIVcpz Sequences Using Bayesian Inference: Implications for the Origin of HIV-1. *Mol.Biol.Evol*. 2003;20:1986-96.
692. Paraskevis D, Deforche K, Abecasis A, Camacho R, Vandamme AM. Analysis of complex HIV-1 intersubtype recombinants using a Bayesian scanning method. *Infect.Genet.Evol*. 2005;5:219-24.
693. Paraskevis D, Magiorkinis E, Katsoulidou A, Hatzitheodorou E, Antoniadou A, Papadopoulos A, Poulakou G, Pappazios V, Botsi C, Stavrianeas N, Lelekis M, Chini M, Gargalianos P, Magafas N, Lazanas M, Chryssos G, Petrikkos G, Panos G, Kordossis T, Theodoridou M, Sypsa V, Hatzakis A. Prevalence of resistance-associated mutations in newly diagnosed HIV-1 patients in Greece. *Virus Res*. 2005;112:115-22.
694. Parreira R, Padua E, Piedade J, Venenno T, Paixao MT, Esteves A. Genetic analysis of human immunodeficiency virus type 1 nef in Portugal: Subtyping, identification of mosaic genes, and amino acid sequence variability. *J.Med.Virol*. 2005;77:8-16.
695. Parreira R, Piedade J, Domingues A, Lobao D, Santos M, Venenno T, Baptista JL, Mussa SA, Barreto AT, Baptista AJ, Esteves A. Genetic characterization of human immunodeficiency virus type 1 from Beira, Mozambique. *Microbes.Infect*. 2006;
696. Passaes CP, Bello G, Lorete RS, Matos Almeida SE, Junqueira DM, Veloso VG, Morgado MG, Guimaraes ML. Genetic characterization of HIV-1 BC recombinants and evolutionary history of the CRF31\_BC in Southern Brazil. *Infect.Genet.Evol*. 2009;9:474-82.
697. Passaes CP, Guimaraes ML, Bello G, Morgado MG. Near full-length genome characterization of HIV type 1 unique BC recombinant forms from Southern Brazil. *AIDS Res.Hum.Retroviruses*. 2009;25:1339-44.
698. Pernas M, Casado C, Fuentes R, Perez-Elias MJ, Lopez-Galindez C. A dual superinfection and recombination within HIV-1 subtype B 12 years after primo-infection. *J Acquir.Immune.Defic.Syndr*. 2006;42:12-8.
699. Perez L, Thomson MM, Bleda MJ, Aragones C, Gonzalez Z, Perez J, Sierra M, Casado G, Delgado E, Najera R. HIV Type 1 molecular epidemiology in Cuba: high genetic diversity, frequent mosaicism, and recent expansion of BG intersubtype recombinant forms. *AIDS Res.Hum.Retroviruses*. 2006;22:724-33.
700. Perez L, Alvarez LP, Carmona R, Aragones C, Delgado E, Thomson MM, Gonzalez Z, Contreras G, Perez J, Najera R. Genotypic resistance to antiretroviral drugs in patients infected with several HIV type 1 genetic forms in Cuba. *AIDS Res.Hum.Retroviruses*. 2007;23:407-14.
701. Perez H, Vignoles M, Laufer N, Gomez A, Coll P, Lotner J, Rolon M, Salomon H, Cahn P. Low rate of emergence of nevirapine and lamivudine resistance after post-partum interruption of a triple-drug regimen. *Antivir.Ther*. 2008;13:135-9.
702. Perez-Alvarez L, Thomson MM, Villahermosa ML, de Parga EV, Rodriguez A, Cuevas MT, Delgado E, Manjon N, Miralles C, Medrano L, Taboada JA, Najera R. HIV-1 subtype G and BG recombinant viruses in Spanish natives: evidence of characteristic mutations in reverse transcriptase and protease. *AIDS*. 2001;15:1907-10.
703. Perez-Alvarez L, Cuevas MT, Villahermosa ML, Pedreira JD, Manjon N, Herrero I, Lopez-Calvo S, Delgado E, de Parga EV, Medrano L, Thomson MM, Taboada JA, Najera R. Prevalence of drug resistance mutations in B, non-B subtypes, and recombinant forms of human immunodeficiency virus type 1 in infected individuals in Spain (Galicia). *J.Hum.Virol*. 2001;4:35-8.
704. Perez-Alvarez L, Munoz M, Delgado E, Miralles C, Ocampo A, Garcia V, Thomson M, Contreras G, Najera R. Isolation and biological characterization of HIV-1 BG intersubtype recombinants and other genetic forms circulating in Galicia, Spain. *J.Med.Virol*. 2006;78:1520-8.
705. Persaud D, Palumbo P, Ziemniak C, Chen J, Ray SC, Hughes M, Havens P, Purswani M, Gaur AH, Chadwick EG. Early archiving and predominance of nonnucleoside reverse transcriptase inhibitor-resistant HIV-1 among recently infected infants born in the United States. *J.Infect.Dis*. 2007;195:1402-10.
706. Petroni A, Deluchi G, Pryluka D, Rotryng F, Bortolozzi R, Lopardo G, Bouzas MB, Zapiola I, Garone D, Rodriguez C, Chioconi E, Lazaro ME, Murano F, Maranzana A, Oliva SM, Aparicio M, Beltran M, Benetucci JA. Update on primary HIV-1 resistance in Argentina: emergence of mutations conferring high-level resistance to nonnucleoside reverse transcriptase inhibitors in drug-naive patients. *J Acquir.Immune.Defic.Syndr*. 2006;42:506-10.
707. Philpott S, Burger H, Tsoukas C, Foley B, Anastos K, Kitchen C, Weiser B. Human immunodeficiency virus type 1 genomic RNA sequences in the female genital tract and blood: compartmentalization and intrapatient recombination. *J.Virol*. 2005;79:353-63.
708. Piantadosi A, Chohan B, Chohan V, McClelland RS, Overbaugh J. Chronic HIV-1 infection frequently fails to protect against superinfection. *PLoS Pathog*. 2007;3:e177

709. Pires IL, Soares MA, Speranza FA, Ishii SK, Vieira MC, Gouvea MI, Guimaraes MA, de Oliveira FE, Magnanini MM, Brindeiro RM, Tanuri A. Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health service of Rio de Janeiro, Brazil. *J.Clin.Microbiol.* 2004;42:426-30.
710. Pollakis G, Abebe A, Kliphuis A, De Wit TF, Fisseha B, Tegbaru B, Tesfaye G, Negassa H, Mengistu Y, Fontanet AL, Cornelissen M, Goudsmit J. Recombination of HIV type 1C (C/C") in Ethiopia: possible link of EthHIV-1C' to subtype C sequences from the high-prevalence epidemics in India and Southern Africa. *AIDS Res.Hum.Retroviruses.* 2003;19:999-1008.
711. Pollakis G, Abebe A, Kliphuis A, Chalaby MI, Bakker M, Mengistu Y, Brouwer M, Goudsmit J, Schuitemaker H, Paxton WA. Phenotypic and genotypic comparisons of CCR5- and CXCR4-tropic human immunodeficiency virus type 1 biological clones isolated from subtype C-infected individuals. *J.Virol.* 2004;78:2841-52.
712. Posada D, Crandall KA. Evaluation of methods for detecting recombination from DNA sequences: computer simulations. *Proc.Natl.Acad.Sci.U.S.A.* 2001;98:13757-62.
713. Posada D. Evaluation of methods for detecting recombination from DNA sequences: empirical data. *Mol.Biol.Evol.* 2002;19:708-17.
714. Powell RL, Zhao J, Konings FA, Tang S, Nanfack A, Burda S, Urbanski MM, Saa DR, Hewlett I, Nyambi PN. Identification of a novel circulating recombinant form (CRF) 36\_cpx in Cameroon that combines two CRFs (01\_AE and 02\_AG) with ancestral lineages of subtypes A and G. *AIDS Res.Hum.Retroviruses.* 2007;23:1008-19.
715. Powell RL, Zhao J, Konings FA, Tang S, Ewane L, Burda S, Urbanski MM, Saa DR, Hewlett I, Nyambi PN. Circulating recombinant form (CRF) 37\_cpx: an old strain in Cameroon composed of diverse, genetically distant lineages of subtypes A and G. *AIDS Res.Hum.Retroviruses.* 2007;23:923-33.
716. Powell RL, Konings FA, Nanfack A, Burda S, Urbanski MM, Saa D, Nyambi PN. Quasispecies analysis of novel HIV-1 recombinants of subtypes A and G reveals no similarity to the mosaic structure of CRF02\_AG. *J.Med.Virol.* 2007;79:1270-85.
717. Powell RL, Lezeau L, Kinge T, Nyambi PN. Longitudinal quasispecies analysis of viral variants in HIV type 1 dually infected individuals highlights the importance of sequence identity in viral recombination. *AIDS Res.Hum.Retroviruses.* 2010;26:253-64.
718. Praparattanapan J, Tragoolpua Y, Pathom-Aree W, Kotarathitithum W, Chaiwarith R, Nuntachit N, Sirisanthana T, Supparatpinyo K. Current Molecular Epidemiology and Recombination of HIV Type 1 Subtypes in Northern Thailand. *AIDS Res.Hum.Retroviruses.* 2011;
719. Qiu Z, Xing H, Wei M, Duan Y, Zhao Q, Xu J, Shao Y. Characterization of five nearly full-length genomes of early HIV type 1 strains in Ruili city: implications for the genesis of CRF07\_BC and CRF08\_BC circulating in China. *AIDS Res.Hum.Retroviruses.* 2005;21:1051-6.
720. Quarleri JF, Rubio A, Carobene M, Turk G, Vignoles M, Harrigan RP, Montaner JSG, Salomon H, Gomez-Carrillo M. HIV Type 1 BF Recombinant Strains Exhibit Different pol Gene Mosaic Patterns: Descriptive Analysis from 284 Patients under Treatment Failure. *AIDS Research and Human Retroviruses.* 2004;20:1100-7.
721. Quesnel-Vallieres M, Kouzayha I, Tran E, Barry I, Lasgi C, Merindol N, Monteil V, Ransy DG, Boucher M, Lapointe N, Soudeyns H. Novel HIV-1 recombinant forms in antenatal cohort, Montreal, Quebec, Canada. *Emerg.Infect.Dis.* 2011;17:271-4.
722. Rainwater S, DeVange S, Sagar M, Ndinya-Achola J, Mandaliya K, Kreiss JK, Overbaugh J. No evidence for rapid subtype C spread within an epidemic in which multiple subtypes and intersubtype recombinants circulate. *AIDS Res.Hum.Retroviruses.* 2005;21:1060-5.
723. Ramos A, Nguyen L, Hu DJ, Vanichseni S, Choopanya K, Young NL, Tappero JW, Mastro TD, Folks TM, Subbarao S. New HIV Type 1 CRF01\_AE/B Recombinants Displaying Unique Distribution of Breakpoints from Incident Infections among Injecting Drug Users in Thailand. *AIDS Res.Hum.Retroviruses.* 2003;19:667-74.
724. Razzolini F, Vicenti I, Saladini F, Micheli V, Romano L, Cargnel A, Zazzi M. Natural variability in the HR-1 and HR-2 domains of HIV type 1 gp41 from different clades circulating in Italy. *AIDS Res.Hum.Retroviruses.* 2007;23:558-63.
725. Resik S, Lemey P, Ping LH, Kouri V, Joanes J, Perez J, Vandamme AM, Swanstrom R. Limitations to contact tracing and phylogenetic analysis in establishing HIV type 1 transmission networks in Cuba. *AIDS Res.Hum.Retroviruses.* 2007;23:347-56.
726. Revilla A, Delgado E, Christian EC, Dalrymple J, Vega Y, Carrera C, Gonzalez-Galeano M, Ocampo A, de Castro RO, Lezaun MJ, Rodriguez R, Marino A, Ordóñez P, Cilla G, Cisterna R, Santamaria JM, Prieto S, Rakhmanova A, Vinogradova A, Rios M, Perez-Alvarez L, Najera R, Montefiori DC, Seaman MS, Thomson MM. Construction and Phenotypic Characterization of HIV Type 1 Functional Envelope Clones of Subtypes G and F. *AIDS Res.Hum.Retroviruses.* 2011;
727. Rhee SY, Kantor R, Katzenstein DA, Camacho R, Morris L, Sirivichayakul S, Jorgensen L, Brigido LF, Schapiro JM, Shafer RW. HIV-1 pol mutation frequency by subtype and treatment experience: extension of the HIVseq program to seven non-B subtypes. *AIDS.* 2006;20:643-51.
728. Rios M, Delgado E, Perez-Alvarez L, Fernandez J, Galvez P, de Parga EV, Yung V, Thomson MM, Najera R. Antiretroviral drug resistance and phylogenetic diversity of HIV-1 in Chile. *J Med.Virol.* 2007;79:647-56.
729. Ristic N, Zukurov J, Alkmim W, Diaz RS, Janini LM, Chin MP. Analysis of the origin and evolutionary history of HIV-1 CRF28\_BF and CRF29\_BF reveals a decreasing prevalence in the AIDS epidemic of Brazil. *PLoS.ONE.* 2011;6:e17485
730. Riva C, Romano L, Saladini F, Lai A, Carr JK, Francisci D, Balotta C, Zazzi M. Identification of a possible ancestor of the subtype A1 HIV Type 1 variant circulating in the former Soviet Union. *AIDS Res.Hum.Retroviruses.* 2008;24:1319-25.

731. Riva C, Lai A, Caramma I, Corvasce S, Violin M, Deho L, Prati F, Rossi C, Colombo MC, Capetti A, Franzetti M, Rossini V, Tambussi G, Ciccozzi M, Suligoi B, Mussini C, Rezza G, Balotta C. Transmitted HIV Type 1 drug resistance and Non-B subtypes prevalence among seroconverters and newly diagnosed patients from 1992 to 2005 in Italy. *AIDS Res.Hum.Retroviruses*. 2010;26:41-9.
732. Rodrigues R, Scherer LC, Oliveira CM, Franco HM, Sperhackle RD, Ferreira JL, Castro SM, Stella IM, Brigido LF. Low prevalence of primary antiretroviral resistance mutations and predominance of HIV-1 clade C at polymerase gene in newly diagnosed individuals from south Brazil. *Virus Res*. 2006;116:201-7.
733. Rodrigues R, Manenti S, Romao PR, de Paula Ferreira JL, Batista JP, Siqueira AF, de Macedo Brigido LF. Young pregnant women living with HIV/AIDS in Criciuma, Southern Brazil, are infected almost exclusively with HIV type 1 clade C. *AIDS Res.Hum.Retroviruses*. 2010;26:351-7.
734. Rousseau CM, Learn GH, Bhattacharya T, Nickle DC, Heckerman D, Chetty S, Brander C, Goulder PJ, Walker BD, Kiepiela P, Korber BT, Mullins JI. Extensive intrasubtype recombination in South African human immunodeficiency virus type 1 subtype C infections. *J Virol*. 2007;81:4492-500.
735. Ruchansky D, Casado C, Russi JC, Arbiza JR, Lopez-Galindez C. Identification of a new HIV Type 1 circulating recombinant form (CRF38\_BF1) in Uruguay. *AIDS Res.Hum.Retroviruses*. 2009;25:351-6.
736. Sa-Filho D, Kallas EG, Sanabani S, Sabino E, Sucupira MC, Sanchez-Rosa AC, Tescarollo G, Tomiyama H, Bassichetto K, Janini LM, Diaz RS. Characterization of the full-length human immunodeficiency virus-1 genome from recently infected subjects in Brazil. *AIDS Res.Hum.Retroviruses*. 2007;23:1087-94.
737. Saad MD, Al Jaufy A, Grahan RR, Nadai Y, Earhart KC, Sanchez JL, Carr JK. HIV Type 1 Strains Common in Europe, Africa, and Asia Cocirculate in Yemen. *AIDS Res.Hum.Retroviruses*. 2005;21:644-8.
738. Saad MD, Shcherbinskaya AM, Nadai Y, Kruglov YV, Antonenko SV, Lyullchuk MG, Kravchenko ON, Earhart KC, Sanchez JL, Bix DL, Carr JK. Molecular epidemiology of HIV Type 1 in Ukraine: birthplace of an epidemic. *AIDS Res.Hum.Retroviruses*. 2006;22:709-14.
739. Saad MD, Aliev Q, Botros BA, Carr JK, Gomatos PJ, Nadai Y, Michael AA, Nasibov Z, Sanchez JL, Brix DI, Earhart KC. Genetic forms of HIV Type 1 in the former Soviet Union dominate the epidemic in Azerbaijan. *AIDS Res.Hum.Retroviruses*. 2006;22:796-800.
740. Sacktor N, Nakasujja N, Skolasky RL, Rezapour M, Robertson K, Musisi S, Katabira E, Ronald A, Clifford DB, Laeyendecker O, Quinn TC. HIV subtype D is associated with dementia, compared with subtype A, in immunosuppressed individuals at risk of cognitive impairment in Kampala, Uganda. *Clin.Infect.Dis*. 2009;49:780-6.
741. Sahbandar IN, Takahashi K, Djoerban Z, Firmansyah I, Naganawa S, Motomura K, Sato H, Kitamura K, Pohan HT, Sato S. Current HIV type 1 molecular epidemiology profile and identification of unique recombinant forms in Jakarta, Indonesia. *AIDS Res.Hum.Retroviruses*. 2009;25:637-46.
742. Sahbandar IN, Takahashi K, Motomura K, Djoerban Z, Firmansyah I, Kitamura K, Sato H, Pohan HT, Sato S. The Indonesian Variants of CRF33\_01B: Near-Full Length Sequence Analysis. *AIDS Res.Hum.Retroviruses*. 2010;
743. Salemi M, De Oliveira T, Courgnaud V, Moulton V, Holland B, Cassol S, Switzer WM, Vandamme AM. Mosaic genomes of the six major primate lentivirus lineages revealed by phylogenetic analyses. *J.Virol*. 2003;77:7202-13.
744. Salemi M, Gray RR, Goodenow MM. An exploratory algorithm to identify intra-host recombinant viral sequences. *Mol.Phylogenet.Evol*. 2008;49:618-28.
745. Salminen M. Detecting recombination in viral sequences. In: Salemi M, Vandamme AM, eds. *The phylogenetic handbook: A practical approach to DNA and protein phylogeny*. Cambridge, U.K: Cambridge University Press; 2003:348-77.
746. Sanabani S, Neto WK, Sa Filho DJ, Diaz RS, Munerato P, Janini LM, Sabino EC. Full-length genome analysis of human immunodeficiency virus type 1 subtype C in Brazil. *AIDS Res.Hum.Retroviruses*. 2006;22:171-6.
747. Sanabani S, Kleine NW, Kalmar EM, Diaz RS, Janini LM, Sabino EC. Analysis of the near full length genomes of HIV-1 subtypes B, F and BF recombinant from a cohort of 14 patients in Sao Paulo, Brazil. *Infect.Genet.Evol*. 2006;6:368-77.
748. Sanabani SS, Pastena ER, Kleine NW, Barreto CC, Ferrari KT, Kalmar EM, Ferreira S, Sabino EC. Near full-length genome analysis of low prevalent human immunodeficiency virus type 1 subclade F1 in Sao Paulo, Brazil. *Viol.J*. 2009;6:78
749. Sanabani SS, Pastena ER, Neto WK, Martinez VP, Sabino EC. Characterization and frequency of a newly identified HIV-1 BF1 intersubtype circulating recombinant form in Sao Paulo, Brazil. *Viol.J*. 2010;7:74
750. Sanchez GI, Bautista CT, Eyzaguirre L, Carrion G, Arias S, Sateren WB, Negrete M, Montano SM, Sanchez JL, Carr JK. Molecular epidemiology of human immunodeficiency virus-infected individuals in Medellin, Colombia. *Am.J.Trop.Med.Hyg*. 2006;74:674-7.
751. Santos AF, Sousa TM, Soares EA, Sanabani S, Martinez AM, Sprinz E, Silveira J, Sabino EC, Tanuri A, Soares MA. Characterization of a new circulating recombinant form comprising HIV-1 subtypes C and B in southern Brazil. *AIDS*. 2006;20:2011-9.
752. Santos-Costa Q, Parreira R, Moniz-Pereira J, Azevedo-Pereira JM. Molecular characterization of the env gene of two CCR5/CXCR4-independent human immunodeficiency 2 primary isolates. *J.Med.Virol*. 2009;81:1869-81.
753. Schroeder TL, Burger H, Weiser B, Bengualid V, Kimani J, Anzala AO, Parker MM, Lamson D, Philpott SM. Characterization of intersubtype recombinant HIV type 1 genomes using a nonradioactive heteroduplex tracking assay. *AIDS Res.Hum.Retroviruses*. 2005;21:314-8.
754. Schultz AK, Zhang M, Leitner T, Kuiken C, Korber B, Morgenstern B, Stanke M. A jumping profile Hidden Markov Model and applications to recombination sites in HIV and HCV genomes. *BMC.Bioinformatics*. 2006;7:265

755. Segura M, Estani SS, Marone R, Bautista CT, Pando MA, Eyzaguirre L, Sanchez JL, Carr JK, Montano SM, Weissenbacher M, Avila MM. Buenos Aires cohort of men who have sex with men: prevalence, incidence, risk factors, and molecular genotyping of HIV type 1. *AIDS Res.Hum.Retroviruses*. 2007;23:1322-9.
756. Sen S, Tripathy SP, Chimanpure VM, Patil AA, Bagul RD, Paranjape RS. Human immunodeficiency virus type 1 drug resistance mutations in peripheral blood mononuclear cell proviral DNA among antiretroviral treatment-naive and treatment-experienced patients from Pune, India. *AIDS Res.Hum.Retroviruses*. 2007;23:489-97.
757. Servais J, Lambert C, Karita E, Vanhove D, Fischer A, Baurith T, Schmit JC, Schneider F, Hemmer R, Arendt V. HIV Type 1 pol Gene Diversity and Archived Nevirapine Resistance Mutation in Pregnant Women in Rwanda. *AIDS Research and Human Retroviruses*. 2004;20:279-83.
758. Shang H, Han X, Shi X, Zuo T, Goldin M, Chen D, Han B, Sun W, Wu H, Wang X, Zhang L. Genetic and neutralization sensitivity of diverse HIV-1 ENV clones from chronically infected patients in China. *J.Biol.Chem*. 2011;
759. Shi B, Philpott SM, Weiser B, Kuiken C, Brunner C, Fang G, Fowke KR, Plummer FA, Rowland-Jones S, Bwayo J, Anzala AO, Kimani J, Kaul R, Burger A. Construction of an Infectious HIV Type 1 Molecular Clone from an African Patient with a Subtype D/C Recombinant Virus. *AIDS Research and Human Retroviruses*. 2004;20:1015-8.
760. Shi B, Kitchen C, Weiser B, Mayers D, Foley B, Kemal K, Anastos K, Suchard M, Parker M, Brunner C, Burger H. Evolution and recombination of genes encoding HIV-1 drug resistance and tropism during antiretroviral therapy. *Virology*. 2010;404:5-20.
761. Sierra M, Thomson MM, Rios M, Casado G, Castro RO, Delgado E, Echevarria G, Munoz M, Colomina J, Carmona R, Vega Y, Parga EV, Medrano L, Perez-Alvarez L, Contreras G, Najera R. The analysis of near full-length genome sequences of human immunodeficiency virus type 1 BF intersubtype recombinant viruses from Chile, Venezuela and Spain reveals their relationship to diverse lineages of recombinant viruses related to CRF12\_BF. *Infect.Genet.Evol*. 2005;5:209-17.
762. Sierra M, Thomson MM, Posada D, Perez L, Aragonés C, Gonzalez Z, Perez J, Casado G, Najera R. Identification of 3 phylogenetically related HIV-1 BG intersubtype circulating recombinant forms in Cuba. *J Acquir.Immune.Defic.Syindr*. 2007;45:151-60.
763. Snoeck J, Van Dooren S, Van Laethem K, Derdelinckx I, Van Wijngaerden E, De Clercq E, Vandamme AM. Prevalence and origin of HIV-1 group M subtypes among patients attending a Belgian hospital in 1999. *Virus Res*. 2002;85:95-107.
764. Snoeck J, Van Laethem K, Hermans P, Van Wijngaerden E, Derdelinckx I, Schrooten Y, van de Vijver DA, De Wit S, Clumeck N, Vandamme AM. Rising prevalence of HIV-1 non-B subtypes in Belgium: 1983-2001. *J.Acquir.Immune.Defic.Syindr*. 2004;35:279-85.
765. Soares MA, De Oliveira T, Brindeiro RM, Diaz RS, Sabino EC, Brigido L, Pires IL, Morgado MG, Dantas MC, Barreira D, Teixeira PR, Cassol S, Tanuri A. A specific subtype C of human immunodeficiency virus type 1 circulates in Brazil. *AIDS*. 2003;17:11-21.
766. Ssemwanga D, Lyagoba F, Ndembi N, Mayanja BN, Larke N, Wang S, Baalwa J, Williamson C, Grosskurth H, Kaleebu P. Multiple HIV-1 infections with evidence of recombination in heterosexual partnerships in a low risk Rural Clinical Cohort in Uganda. *Virology*. 2011;411:113-31.
767. Steain MC, Wang B, Yang C, Shi YP, Nahlen B, Lal RB, Saksena NK. HIV Type 1 Sequence Diversity and Dual Infections in Kenya. *AIDS Res.Hum.Retroviruses*. 2005;21:882-5.
768. Steain MC, Wang B, Saksena NK. Analysis of HIV-1 sequences vertically transmitted to infants in Kisumu, Kenya. *J.Clin.Virol*. 2006;36:298-302.
769. Streeck H, Li B, Poon AF, Schneidewind A, Gladden AD, Power KA, Daskalakis D, Bazner S, Zuniga R, Brander C, Rosenberg ES, Frost SD, Altfeld M, Allen TM. Immune-driven recombination and loss of control after HIV superinfection. *J.Exp.Med*. 2008;205:1789-96.
770. Su B, Liu L, Wang F, Gui X, Zhao M, Tien P, Zhang L, Chen Z. HIV-1 subtype B' dictates the AIDS epidemic among paid blood donors in the Henan and Hubei provinces of China. *AIDS*. 2003;17:2515-20.
771. Swanson P, Devare SG, Hackett J, Jr. Full-length sequence analysis of HIV-1 isolate CM237: a CRF01\_AE/B intersubtype recombinant from Thailand. *AIDS Res.Hum.Retroviruses*. 2003;19:707-12.
772. Takahoko M, Tobiume M, Ishikawa K, Ampofo W, Yamamoto N, Matsuda M, Tatsumi M. Infectious DNA clone of HIV type 1 A/G recombinant (CRF02\_AG) replicable in peripheral blood mononuclear cells. *AIDS Res.Hum.Retroviruses*. 2001;17:1083-7.
773. Takebe Y, Motomura K, Tatsumi M, Lwin HH, Zaw M, Kusagawa S. High prevalence of diverse forms of HIV-1 intersubtype recombinants in Central Myanmar: geographical hot spot of extensive recombination. *AIDS*. 2003;17:2077-87.
774. Taveira N, Bartolo I, Antunes R, Figueiredo S, Lourenco H, Camacho R, Bezerra V, Pinheiro M, Goncalo J, Barroso H, Moniz-Pereira J. Identification of a new B/G recombinant human immunodeficiency virus type 1 in Portugal. *AidsPortugal*. 2001;[accessed 18 April 2005 at <http://www.aidsportugal.com/article.php?sid=598>]
775. Tscherning-Casper C, Dolcini G, Mauclere P, Fenyo EM, Barre-Sinoussi F, Albert J, Menu E. Evidence of the existence of a new circulating recombinant form of HIV type 1 subtype A/J in Cameroon. The European Network on the Study of In Utero Transmission of HIV-1. *AIDS Res.Hum.Retroviruses*. 2000;16:1313-8.
776. Tebit DM, Zekeng L, Kaptue L, Salminen M, Krausslich HG, Herchenroder O. Genotypic and phenotypic analysis of HIV type 1 primary isolates from western Cameroon. *AIDS Res.Hum.Retroviruses*. 2002;18:39-48.
777. Tebit DM, Zekeng L, Kaptue L, Krausslich HG, Herchenroder O. Construction and characterisation of a full-length infectious molecular clone from a fast replicating, X4-tropic HIV-1 CRF02.AG primary isolate. *Virology*. 2003;313:645-52.

778. Tebit DM, Zekeng L, Kaptue L, Gurtler L, Fackler OT, Keppler OT, Herchenroder O, Krausslich HG. Construction and characterization of an HIV-1 group O infectious molecular clone and analysis of vpr- and nef-negative derivatives. *Virology*. 2004;326:329-39.
779. Tebit DM, Sangare L, Tiba F, Saydou Y, Makamte A, Somlare H, Bado G, Kouldiaty BG, Zabsonre I, Yameogo SL, Sathiandee K, Drabo JY, Krausslich HG. Analysis of the diversity of the HIV-1 pol gene and drug resistance associated changes among drug-naive patients in Burkina Faso. *J.Med.Virol*. 2009;81:1691-701.
780. Tee KK, Pon CK, Kamarulzaman A, Ng KP. Emergence of HIV-1 CRF01\_AE/B unique recombinant forms in Kuala Lumpur, Malaysia. *AIDS*. 2005;19:119-26.
781. Tee KK, Saw TL, Pon CK, Kamarulzaman A, Ng KP. The evolving molecular epidemiology of HIV type 1 among injecting drug users (IDUs) in Malaysia. *AIDS Res.Hum.Retroviruses*. 2005;21:1046-50.
782. Tee KK, Li XJ, Nohtomi K, Ng KP, Kamarulzaman A, Takebe Y. Identification of a novel circulating recombinant form (CRF33\_01B) disseminating widely among various risk populations in Kuala Lumpur, Malaysia. *J.Acquir.Immune Defic.Syndr*. 2006;43:523-9.
783. Tee KK, Kusagawa S, Li XJ, Onogi N, Isogai M, Hase S, Uenishi R, Liao H, Kamarulzaman A, Takebe Y. Isolation and characterization of a replication-competent molecular clone of an HIV-1 circulating recombinant form (CRF33\_01B). *PLoS.ONE*. 2009;4:e6666
784. Teixeira C, de Sa-Filho D, Alkmim W, Janini LM, Diaz RS, Komninakis S. Short communication: high polymorphism rates in the HR1 and HR2 gp41 and presence of primary resistance-related mutations in HIV type 1 circulating in Brazil: possible impact on enfuvirtide efficacy. *AIDS Res.Hum.Retroviruses*. 2010;26:307-11.
785. Thomson MM, Villahermosa ML, Vazquez-de-Parga E, Cuevas MT, Delgado E, Manjon N, Medrano L, Perez-Alvarez L, Contreras G, Carrillo MG, Salomon H, Najera R. Widespread circulation of a B/F intersubtype recombinant form among HIV-1-infected individuals in Buenos Aires, Argentina. *AIDS*. 2000;14:897-9.
786. Thomson MM, Delgado E, Manjon N, Ocampo A, Villahermosa ML, Marino A, Herrero I, Cuevas MT, Vazquez-de Parga E, Perez-Alvarez L, Medrano L, Taboada JA, Najera R. HIV-1 genetic diversity in Galicia Spain: BG intersubtype recombinant viruses circulating among injecting drug users. *AIDS*. 2001;15:509-16.
787. Thomson MM, Delgado E, Herrero I, Villahermosa ML, Vazquez-de Parga E, Cuevas MT, Carmona R, Medrano L, Perez-Alvarez L, Cuevas L, Najera R. Diversity of mosaic structures and common ancestry of human immunodeficiency virus type 1 BF intersubtype recombinant viruses from Argentina revealed by analysis of near full-length genome sequences. *J.Gen.Virol*. 2002;83:107-19.
788. Thomson MM, Perez-Alvarez L, Najera R. Molecular epidemiology of HIV-1 genetic forms and its significance for vaccine development and therapy. *Lancet Infect.Dis*. 2002;2:461-71.
789. Thomson MM, Sierra M, Tanuri A, May S, Casado G, Manjon N, Najera R. Analysis of Near Full-Length Genome Sequences of HIV Type 1 BF Intersubtype Recombinant Viruses from Brazil Reveals Their Independent Origins and Their Lack of Relationship to CRF12\_BF. *AIDS Research and Human Retroviruses*. 2004;20:1126-33.
790. Thomson MM, Casado G, Posada D, Sierra M, Najera R. Identification of a novel HIV-1 complex circulating recombinant form (CRF18\_cpx) of Central African origin in Cuba. *AIDS*. 2005;19:1155-63.
791. Thomson MM, de Parga EV, Vinogradova A, Sierra M, Yakovlev A, Rakhmanova A, Delgado E, Casado G, Munoz M, Carmona R, Vega Y, Perez-Alvarez L, Contreras G, Medrano L, Osmanov S, Najera R. New insights into the origin of the HIV type 1 subtype A epidemic in former soviet union's countries derived from sequence analyses of preepidemically transmitted viruses. *AIDS Res.Hum.Retroviruses*. 2007;23:1599-604.
792. Thomson MM, Vinogradova A, Delgado E, Rakhmanova A, Yakovlev A, Cuevas MT, Munoz M, Pinilla M, Vega Y, Perez-Alvarez L, Osmanov S, Najera R. Molecular epidemiology of HIV-1 in St Petersburg, Russia: predominance of subtype A, former Soviet Union variant, and identification of intrasubtype subclusters. *J.Acquir.Immune Defic.Syndr*. 2009;51:332-9.
793. Thomson MM, Fernandez-Garcia A. Phylogenetic structure in African HIV-1 subtype C revealed by selective sequential pruning. *Virology*. 2011;
794. Toni T, Adje-Toure C, Vidal N, Minga A, Huet C, Borger MY, Recordon-Pinson P, Masquelier B, Nolan M, Nkengasong J, Fleury HJ, Delaporte E, Peeters M. Presence of CRF09\_cpx and Complex CRF02\_AG/CRF09\_cpx Recombinant HIV Type 1 Strains in Cote d'Ivoire, West Africa. *AIDS Res.Hum.Retroviruses*. 2005;21:667-72.
795. Torimiro JN, D'Arrigo R, Takou D, Nanfack A, Pizzi D, Ngong I, Carr JK, Joseph FP, Perno CF, Cappelli G. Human immunodeficiency virus type 1 intersubtype recombinants predominate in the AIDS epidemic in Cameroon. *New Microbiol*. 2009;32:325-31.
796. Tramuto F, Bonura F, Perna AM, Mancuso S, Firenze A, Romano N, Vitale F. Genetic Diversity of HIV-1 Non-B Strains in Sicily: Evidence of Intersubtype Recombinants by Sequence Analysis of gag, pol, and env Genes. *AIDS Res.Hum.Retroviruses*. 2007;23:1131-8.
797. Triques K, Bourgeois A, Vidal N, Mpoudi-Ngole E, Mulanga-Kabeya C, Nzilambi N, Torimiro N, Saman E, Delaporte E, Peeters M. Near-full-length genome sequencing of divergent African HIV type 1 subtype F viruses leads to the identification of a new HIV type 1 subtype designated K. *AIDS Res.Hum.Retroviruses*. 2000;16:139-51.
798. Turk G, Carobene M, Monczor A, Rubio AE, Gomez-Carrillo M, Salomon H. Higher transactivation activity associated with LTR and Tat elements from HIV-1 BF intersubtype recombinant variants. *Retrovirology*. 2006;3:14
799. Turk G, Gherardi MM, Laufer N, Saracco M, Luzzi R, Cox JH, Cahn P, Salomon H. Magnitude, breadth and function profile of T-cell responses during HIV primary infection with B and BF viral variants. *J Virol*. 2008;

800. Turk G, Gundlach S, Carobene M, Schindler M, Salomon H, Benaroch P. Single Nef proteins from HIV type 1 subtypes C and F fail to upregulate invariant chain cell surface expression but are active for other functions. *AIDS Res.Hum.Retroviruses*. 2009;25:285-96.
801. Utsumi T, Lusida MI, Yano Y, Nugrahaputra VE, Amin M, Juniastuti, Soetjipto, Hayashi Y, Hotta H. Complete genome sequence and phylogenetic relatedness of hepatitis B virus isolates in Papua, Indonesia. *J.Clin.Microbiol*. 2009;47:1842-7.
802. Vallari A, Bodelle P, Ngansop C, Makamche F, Ndembi N, Mbanya D, Kaptue L, Gurtler LG, McArthur CP, Devare SG, Brennan CA. Four new HIV-1 group N isolates from Cameroon: Prevalence continues to be low. *AIDS Res.Hum.Retroviruses*. 2010;26:109-15.
803. Vallari A, Holzmayer V, Harris B, Yamaguchi J, Ngansop C, Makamche F, Mbanya D, Kaptue L, Ndembi N, Gurtler L, Devare S, Brennan CA. Confirmation of Putative HIV-1 Group P in Cameroon. *J Virol*. 2010;
804. van der Hoek L, Pollakis G, Lukashov VV, Jebbink MF, Jeeninga RE, Bakker M, Dukers N, Jurriaans S, Paxton WA, Back NK, Berkhout B. Characterization of an HIV-1 group M variant that is distinct from the known subtypes. *AIDS Res.Hum.Retroviruses*. 2007;23:466-70.
805. van Harmelen J, Williamson C, Kim B, Morris L, Carr J, Karim SS, McCutchan F. Characterization of full-length HIV type 1 subtype C sequences from South Africa. *AIDS Res.Hum.Retroviruses*. 2001;17:1527-31.
806. Van Laethem K, Schrooten Y, Lemey P, Van Wijngaerden E, De Wit S, Van Ranst M, Vandamme AM. A genotypic resistance assay for the detection of drug resistance in the human immunodeficiency virus type 1 envelope gene. *J.Virol.Methods*. 2005;123:25-34.
807. Vazquez dP, Rakhmanova A, Perez-Alvarez L, Vinogradova A, Delgado E, Thomson MM, Casado G, Sierra M, Munoz M, Carmona R, Vega Y, Contreras G, Medrano L, Osmanov S, Najera R. Analysis of drug resistance-associated mutations in treatment-naive individuals infected with different genetic forms of HIV-1 circulating in countries of the former Soviet Union. *J.Med.Virol*. 2005;77:337-44.
808. Vazquez-Valls E, Escoto-Delgadillo M, Lopez-Marquez FC, Castellero-Manzano M, Echeagaray-Guerrero E, Bitzer-Quintero OK, Kobayashi-Gutierrez A, Torres-Mendoza BM. Molecular epidemiology of HIV type 1 in Mexico: emergence of BG and BF intersubtype recombinants. *AIDS Res.Hum.Retroviruses*. 2010;26:777-81.
809. Veras NM, Veras VS, Ramalho ED, Kyaw C, Silva RR, Brigido MM, Martins CR. HIV type 1 genetic variability in central Brazil. *AIDS Res.Hum.Retroviruses*. 2007;23:1481-90.
810. Vergne L, Peeters M, Mpoudi-Ngole E, Bourgeois A, Liegeois F, Toure-Kane C, Mboup S, Mulanga-Kabeya C, Saman E, Jourdan J, Reynes J, Delaporte E. Genetic diversity of protease and reverse transcriptase sequences in non-subtype-B human immunodeficiency virus type 1 strains: evidence of many minor drug resistance mutations in treatment-naive patients. *J.Clin.Microbiol*. 2000;38:3919-25.
811. Vergne L, Malonga-Mouellet G, Mistoul I, Mavoungou R, Mansaray H, Peeters M, Delaporte E. Resistance to antiretroviral treatment in Gabon: need for implementation of guidelines on antiretroviral therapy use and HIV-1 drug resistance monitoring in developing countries. *J.Acquir.Immune.Defic.Syndr*. 2002;29:165-8.
812. Vidal N, Mulanga-Kabeya C, Nzilambi N, Delaporte E, Peeters M. Identification of a complex env subtype E HIV type 1 virus from the Democratic Republic of Congo, recombinant with A, G, H, J, K, and unknown subtypes. *AIDS Res.Hum.Retroviruses*. 2000;16:2059-64.
813. Vidal N, Peeters M, Mulanga-Kabeya C, Nzilambi N, Robertson D, Ilunga W, Sema H, Tshimanga K, Bongo B, Delaporte E. Unprecedented degree of human immunodeficiency virus type 1 (HIV-1) group M genetic diversity in the Democratic Republic of Congo suggests that the HIV-1 pandemic originated in Central Africa. *J.Virol*. 2000;74:10498-507.
814. Vidal N, Koyalta D, Richard V, Lechiche C, Ndinaromtan T, Djimasngar A, Delaporte E, Peeters M. High genetic diversity of HIV-1 strains in Chad, West Central Africa. *J.Acquir.Immune.Defic.Syndr*. 2003;33:239-46.
815. Vidal N, Mulanga C, Bazepeo SE, Lepira F, Delaporte E, Peeters M. Identification and molecular characterization of subsubtype A4 in central Africa. *AIDS Res.Hum.Retroviruses*. 2006;22:182-7.
816. Vidal N, Mulanga C, Bazepeo SE, Mwamba JK, Tshimpaka J, Kashi M, Mama N, Valea D, Delaporte E, Lepira F, Peeters M. HIV type 1 pol gene diversity and antiretroviral drug resistance mutations in the Democratic Republic of Congo (DRC). *AIDS Res.Hum.Retroviruses*. 2006;22:202-6.
817. Vidal N, Niyongabo T, Nduwimana J, Butel C, Ndayiragije A, Wakana J, Nduwimana M, Delaporte E, Peeters M. HIV type 1 diversity and antiretroviral drug resistance mutations in Burundi. *AIDS Res.Hum.Retroviruses*. 2007;23:175-80.
818. Vidal N, Frange P, Chaix ML, Mulanga C, Lepira F, Bazepeo SE, Goujard C, Meyer L, Rouzioux C, Delaporte E, Peeters M. Characterization of an old complex circulating recombinant form, CRF27\_cpx, originating from the Democratic Republic of Congo (DRC) and circulating in France. *AIDS Res.Hum.Retroviruses*. 2008;24:315-21.
819. Vidal N, Bazepeo SE, Mulanga C, Delaporte E, Peeters M. Genetic characterization of eight full-length HIV type 1 genomes from the Democratic Republic of Congo (DRC) reveal a new subsubtype, A5, in the A radiation that predominates in the recombinant structure of CRF26\_A5U. *AIDS Res.Hum.Retroviruses*. 2009;25:823-32.
820. Vignoles M, Barboni G, Agosti MR, Quarleri J, Garcia MK, Giraudi V, Ayala SG, Salomon H. High frequency of primary mutations associated with antiretroviral drug resistance in recently diagnosed HIV-infected children. *Antivir.Ther*. 2007;12:1133-7.
821. Vignoles M, Barboni G, Agosti MR, Quarleri J, Garcia MK, Ayala SG, Salomon H. Evaluation of minority populations of HIV type-1 with K103N and M184V drug resistance mutations among children in Argentina. *Antivir.Ther*. 2009;14:1175-81.
822. Villahermosa ML, Perez-Alvarez L, Carmona R, Cuevas MT, Thomson MM, Medrano L, Vazquez dP, Delgado E, Pedreira JD, Najera R. Primary resistance mutations to fusion inhibitors and polymorphisms in gp41 sequences of HIV-1 non-B subtypes and recombinants. *AIDS*. 2003;17:1083-6.



823. Vinales J, Serra M, Russi JC, Ruchansky D, Sosa-Estani S, Montano SM, Carrion G, Eyzaguirre LM, Carr JK, Olson JG, Bautista CT, Sanchez JL, Weissenbacher M. Seroincidence and phylogeny of human immunodeficiency virus infections in a cohort of commercial sex workers in Montevideo, Uruguay. *Am.J.Trop.Med.Hyg.* 2005;72:495-500.
824. von Truchsess I, Harris B, Schatzl HM, Hackett J, Jr. The first B/G intersubtype recombinant form of human immunodeficiency virus type 1 (HIV-1) identified in Germany was undetected or underquantitated by some commercial viral load assays. *J.Med.Virol.* 2006;78:311-7.
825. Wang Z, Liu Z, Zeng G, Wen S, Qi Y, Ma S, Naoumov NV, Hou J. A new intertype recombinant between genotypes C and D of hepatitis B virus identified in China. *J.Gen.Virol.* 2005;86:985-90.
826. Wang B, Lau KA, Ong LY, Shah M, Steain MC, Foley B, Dwyer DE, Chew CB, Kamarulzaman A, Ng KP, Saksena NK. Complex patterns of the HIV-1 epidemic in Kuala Lumpur, Malaysia: Evidence for expansion of circulating recombinant form CRF33\_01B and detection of multiple other recombinants. *Virology.* 2007;367:288-97.
827. Wang H, Zhuang K, Liu L, Tang Z, Tang J, Tien P, Zhang L, Chen Z. Acute infection of Chinese macaques by a CCR5-tropic SHIV carrying a primary HIV-1 subtype B' envelope. *J Acquir.Immune Defic.Syindr.* 2010;53:285-91.
828. Wang W, Xu J, Jiang S, Yang K, Meng Z, Ma Y, Li M, Zhang X, Shao Y, Zhang F, Zhang X. The Dynamic Face of HIV-1 Subtypes Among Men who Have Sex with Men in Beijing, China. *Curr.HIV.Res.* 2011;9:136-9.
829. Wheeler WH, Ziebell RA, Zabina H, Pieniazek D, Prejean J, Bodnar UR, Mahle KC, Heneine W, Johnson JA, Hall HI. Prevalence of transmitted drug resistance associated mutations and HIV-1 subtypes in new HIV-1 diagnoses, U.S.-2006. *AIDS.* 2010;24:1203-12.
830. Wichukchinda N, Shiino T, Srisawat J, Rojanawiwat A, Pathipvanich P, Sawanpanyalert P, Ariyoshi K, Auwanit W. Heterosexual Transmission of Novel CRF01\_AE and Subtype B Recombinant Forms of HIV Type 1 in Northern Thailand. *AIDS Res.Hum.Retroviruses.* 2005;21:734-8.
831. Wilbe K, Casper C, Albert J, Leitner T. Identification of two CRF11-cpx genomes and two preliminary representatives of a new circulating recombinant form (CRF13-cpx) of HIV type 1 in Cameroon. *AIDS Res.Hum.Retroviruses.* 2002;18:849-56.
832. Wilbe K, Salminen M, Laukkanen T, McCutchan F, Ray SC, Albert J, Leitner T. Characterization of novel recombinant HIV-1 genomes using the branching index. *Virology.* 2003;316:116-25.
833. Wilkinson E, Engelbrecht S. Molecular characterization of non-subtype C and recombinant HIV-1 viruses from Cape Town, South Africa. *Infect.Genet.Evol.* 2009;9:840-6.
834. Wirachsilp P, Kantakamalakul W, Foongladda S, Chuenchitra T, Kohriangudom S, Athipanyasilp N, Tanprasertsuk S, Gasitrong M, Suthent R. Surveillance of subtype and genetic variation of the circulating strains of HIV-1 in Thailand. *Southeast Asian J.Trop.Med.Public Health.* 2007;38:814-27.
835. Womack C, Roth W, Newman C, Rissing JP, Lovell R, Haburchak D, Essex M, Bond VC. Identification of non-B human immunodeficiency virus type 1 subtypes in rural Georgia. *J.Infect.Dis.* 2001;183:138-42.
836. Yamaguchi J, Vallari AS, Swanson P, Bodelle P, Kaptue L, Ngansop C, Zekeng L, Gurtler LG, Devare SG, Brennan CA. Evaluation of HIV type 1 group O isolates: identification of five phylogenetic clusters. *AIDS Res.Hum.Retroviruses.* 2002;18:269-82.
837. Yamaguchi J, Bodelle P, Kaptue L, Zekeng L, Gurtler LG, Devare SG, Brennan CA. Near full-length genomes of 15 HIV type 1 group O isolates. *AIDS Res.Hum.Retroviruses.* 2003;19:979-88.
838. Yamaguchi J, Bodelle P, Vallari AS, Coffey R, McArthur CP, Schochetman G, Devare SG, Brennan CA. HIV Infections in Northwestern Cameroon: Identification of HIV Type 1 Group O and Dual HIV Type 1 Group M and Group O Infections. *AIDS Research and Human Retroviruses.* 2004;20:944-57.
839. Yamaguchi J, Coffey R, Vallari A, Ngansop C, Mbanya D, Ndembi N, Kaptue L, Gurtler LG, Bodelle P, Schochetman G, Devare SG, Brennan CA. Identification of HIV type 1 group N infections in a husband and wife in Cameroon: viral genome sequences provide evidence for horizontal transmission. *AIDS Res.Hum.Retroviruses.* 2006;22:83-92.
840. Yamaguchi J, Vallari A, Ndembi N, Coffey R, Ngansop C, Mbanya D, Kaptue L, Gurtler LG, Devare SG, Brennan CA. HIV type 2 intergroup recombinant identified in Cameroon. *AIDS Res.Hum.Retroviruses.* 2008;24:86-91.
841. Yamaguchi J, Badreddine S, Swanson P, Bodelle P, Devare SG, Brennan CA. Identification of new CRF43\_02G and CRF25\_cpx in Saudi Arabia based on full genome sequence analysis of six HIV type 1 isolates. *AIDS Res.Hum.Retroviruses.* 2008;24:1327-35.
842. Yamaguchi J, Ndembi N, Ngansop C, Mbanya D, Kaptue L, Gurtler LG, Devare SG, Brennan CA. HIV type 1 group M subtype G in Cameroon: five genome sequences. *AIDS Res.Hum.Retroviruses.* 2009;25:469-73.
843. Yamaguchi J, Vallari A, Ngansop C, Makamche F, Ndembi N, Mbanya D, Kaptue L, Gurtler LG, Devare SG, Brennan CA. Near full-length sequence of HIV type 1 subtype J strain 04CMU11421 from Cameroon. *AIDS Res.Hum.Retroviruses.* 2010;26:693-7.
844. Yang R, Xia X, Kusagawa S, Zhang C, Ben K, Takebe Y. On-going generation of multiple forms of HIV-1 intersubtype recombinants in the Yunnan Province of China. *AIDS.* 2002;16:1401-7.
845. Yang R, Kusagawa S, Zhang C, Xia X, Ben K, Takebe Y. Identification and characterization of a new class of human immunodeficiency virus type 1 recombinants comprised of two circulating recombinant forms, CRF07\_BC and CRF08\_BC, in China. *J.Virol.* 2003;77:685-95.
846. Yang C, Li M, Newman RD, Shi YP, Ayisi J, van Eijk AM, Otieno J, Misore AO, Steketee RW, Nahlen BL, Lal RB. Genetic diversity of HIV-1 in western Kenya: subtype-specific differences in mother-to-child transmission. *AIDS.* 2003;17:1667-74.



847. Yang C, Li M, Shi YP, Winter J, van Eijk AM, Ayisi J, Hu DJ, Steketee R, Nahlen BL, Lal RB. Genetic diversity and high proportion of intersubtype recombinants among HIV type 1-infected pregnant women in Kisumu, western Kenya. *AIDS Res.Hum.Retroviruses*. 2004;20:565-74.
848. Yang C, Li M, Mokili JL, Winter J, Lubaki NM, Mwandagarirwa KM, Kasali MJ, Losoma AJ, Quinn TC, Bollinger RC, Lal RB. Genetic Diversification and Recombination of HIV Type 1 Group M in Kinshasa, Democratic Republic of Congo. *AIDS Res.Hum.Retroviruses*. 2005;21:661-6.
849. Ye JR, Xin RL, Bai LS, Lu HY, Yu SQ, Zeng Y. Sequence analysis of the gag-pol gene of human immunodeficiency virus type 1 of intersubtype (B/C) recombinant strain in Beijing, China. *AIDS Res.Hum.Retroviruses*. 2011;27:331-7.
850. Yerly S, Vora S, Rizzardi P, Chave JP, Vernazza PL, Flepp M, Telenti A, Battegay M, Veuthey AL, Bru JP, Rickenbach M, Hirschel B, Perrin L. Acute HIV infection: impact on the spread of HIV and transmission of drug resistance. *AIDS*. 2001;15:2287-92.
851. Yilmaz G, Midilli K, Turkoglu S, Bayraktaroglu Z, Kuskucu AM, Ozkan E, Atasever L, Calangu S, Altas K. Genetic subtypes of human immunodeficiency virus type 1 (HIV-1) in Istanbul, Turkey. *Int.J.Infect.Dis*. 2006;10:286-90.
852. Yirell DL, Kaleebu P, Morgan D, Watera C, Magambo B, Lyagoba F, Whitworth J. Inter- and intra-genic intersubtype HIV-1 recombination in rural and semi-urban Uganda. *AIDS*. 2002;16:279-86.
853. Zarandia M, Tsertsvadze T, Carr JK, Nadai Y, Sanchez JL, Nelson AK. HIV-1 genetic diversity and genotypic drug susceptibility in the Republic of Georgia. *AIDS Res.Hum.Retroviruses*. 2006;22:470-6.
854. Zetterberg V, Ustina V, Zilmer K, Liitsola K, Kalikova N, Sevastianova K, Brummer-Korvenkontio H, Leinikki P, Salminen MO. Two Viral Strains and a Possible Novel Recombinant Are Responsible for the Explosive Injecting Drug Use-Associated HIV Type 1 Epidemic in Estonia. *AIDS Research and Human Retroviruses*. 2004;20:1148-56.
855. Zhang M, Wilbe K, Wolfe ND, Gaschen B, Carr JK, Leitner T. HIV type 1 CRF13<sub>cpx</sub> revisited: identification of a new sequence from Cameroon and signal for subs subtype J2. *AIDS Res.Hum.Retroviruses*. 2005;21:955-60.
856. Zhang M, Schultz AK, Calef C, Kuiken C, Leitner T, Korber B, Morgenstern B, Stanke M. jpHMM at GOBICS: a web server to detect genomic recombinations in HIV-1. *Nucleic Acids Res*. 2006;34:W463-W465
857. Zhang C, Ding N, Wei JF. Different sliding window sizes and inappropriate subtype references result in discordant mosaic maps and breakpoint locations of HIV-1 CRFs. *Infect.Genet.Evol*. 2008;
858. Zhang Y, Lu L, Ba L, Liu L, Yang L, Jia M, Wang H, Fang Q, Shi Y, Yan W, Chang G, Zhang L, Ho DD, Chen Z. Dominance of HIV-1 subtype CRF01<sub>AE</sub> in sexually acquired cases leads to a new epidemic in Yunnan province of China. *PLoS Med*. 2006;3:e443
859. Zhang CY, Wei JF, He SH. The key role for local base order in the generation of multiple forms of China HIV-1 B/C intersubtype recombinants. *BMC Evol.Biol*. 2005;5:53
860. Zhang K, Hawken M, Rana F, Welte FJ, Gartner S, Goldsmith MA, Power C. Human immunodeficiency virus type 1 clade A and D neurotropism: molecular evolution, recombination, and coreceptor use. *Virology*. 2001;283:19-30.
861. Zhong P, Kang L, Pan Q, Konings F, Burda S, Ma L, Xue Y, Zheng X, Jin Z, Nyambi P. Identification and distribution of HIV type 1 genetic diversity and protease inhibitor resistance-associated mutations in Shanghai, P. R. China. *J.Acquir.Immune.Defic.Syndr*. 2003;34:91-101.
862. Zhong P, Pan Q, Ning Z, Xue Y, Gong J, Zhen X, Zhou L, Sheng F, Zhang W, Gai J, Cheng H, Yue Q, Xing H, Zhuang M, Lu W, Shao Y, Kang L. Genetic diversity and drug resistance of human immunodeficiency virus type 1 (HIV-1) strains circulating in Shanghai. *AIDS Res.Hum.Retroviruses*. 2007;23:847-56.
863. zur Megede J, Engelbrecht S, De Oliveira T, Cassol S, Scriba TJ, van Rensburg EJ, Barnett SW. Novel evolutionary analyses of full-length HIV type 1 subtype C molecular clones from Cape Town, South Africa. *AIDS Res.Hum.Retroviruses*. 2002;18:1327-32.
864. Bruen TC, Poss M. Recombination in feline immunodeficiency virus genomes from naturally infected cougars. *Virology*. 2007;364:362-70.
865. Clewley JP. Enigmas and paradoxes: the genetic diversity and prevalence of the primate lentiviruses. *Curr.HIV Res*. 2004;2:113-25.
866. Duarte A, Tavares L. Phylogenetic analysis of Portuguese Feline Immunodeficiency Virus sequences reveals high genetic diversity. *Vet.Microbiol*. 2006;114:25-33.
867. Gjerset B, Storset AK, Rimstad E. Genetic diversity of small-ruminant lentiviruses: characterization of Norwegian isolates of Caprine arthritis encephalitis virus. *J.Gen.Virol*. 2006;87:573-80.
868. Gjerset B, Jonassen CM, Rimstad E. Natural transmission and comparative analysis of small ruminant lentiviruses in the Norwegian sheep and goat populations. *Virus Res*. 2007;125:153-61.
869. Grego E, Bertolotti L, Quasso A, Profiti M, Lacerenza D, Muz D, Rosati S. Genetic characterization of small ruminant lentivirus in Italian mixed flocks: evidence for a novel genotype circulating in a local goat population. *J Gen.Virol*. 2007;88:3423-7.
870. Howard TM, Sheng Z, Wang M, Wu Y, Rasheed S. Molecular and phylogenetic analyses of a new amphotropic murine leukemia virus (MuLV-1313). *Virol.J*. 2006;3:101
871. Martins AN, Medeiros SO, Simonetti JP, Schatzmayr HG, Tanuri A, Brindeiro RM. Phylogenetic and genetic analysis of Feline Immunodeficiency Virus gag, pol and env genes from domestic cats under NRTI treatment or treatment-naive circulating in Rio de Janeiro, Brazil. *J.Virol*. 2008;
872. Pisoni G, Bertoni G, Puricelli M, Maccalli M, Moroni P. Demonstration of coinfection with and recombination by caprine arthritis-encephalitis virus and maedi-visna virus in naturally infected goats. *J Virol*. 2007;81:4948-55.
873. Reggeti F, Bienzle D. Feline immunodeficiency virus subtypes A, B and C and intersubtype recombinants in Ontario, Canada. *J.Gen.Virol*. 2004;85:1843-52.

874. Reina R, Grego E, Bertolotti L, De Meneghi D, Rosati S. Genome analysis of small-ruminant lentivirus genotype E: a caprine lentivirus with natural deletions of the dUTPase subunit, vpr-like accessory gene, and 70-base-pair repeat of the U3 region. *J.Virol.* 2009;83:1152-5.
875. Samman A, McMonagle EL, Logan N, Willett BJ, Biek R, Hosie MJ. Phylogenetic characterisation of naturally occurring feline immunodeficiency virus in the United Kingdom. *Vet.Microbiol.* 2011;
876. Steinrigl A, Klein D. Phylogenetic analysis of feline immunodeficiency virus in Central Europe: a prerequisite for vaccination and molecular diagnostics. *J.Gen.Virol.* 2003;84:1301-7.
877. Steinrigl A, Ertl R, Langbein I, Klein D. Phylogenetic analysis suggests independent introduction of feline immunodeficiency virus clades A and B to Central Europe and identifies diverse variants of clade B. *Vet.Immunol.Immunopathol.* 2009;
878. Abdou CM, Brichtler S, Mansour W, Le GF, Garba A, Deny P, Gordien E. A novel hepatitis B virus (HBV) subgenotype D (D8) strain, resulting from recombination between genotypes D and E, is circulating in Niger along with HBV/E strains. *J Gen.Virol.* 2010;91:1609-20.
879. Ahn SH, Yuen L, Han KH, Littlejohn M, Chang HY, Damerow H, Ayres A, Heo J, Locarnini S, Revill PA. Molecular and clinical characteristics of hepatitis B virus in Korea. *J Med.Virol.* 2010;82:1126-34.
880. Alestig E, Hannoun C, Horal P, Lindh M. Phylogenetic origin of hepatitis B virus strains with precore C-1858 variant. *J.Clin.Microbiol.* 2001;39:3200-3.
881. Amini-Bavil-Olyae S, Sarrami-Forooshani R, Mahboudi F, Sabahi F, Adeli A, Noorinayer B, Azizi M, Reza ZM. Genotype characterization and phylogenetic analysis of hepatitis B virus isolates from Iranian patients. *J.Med.Virol.* 2005;75:227-34.
882. Amini-Bavil-Olyae S, Sarrami-Forooshani R, Adeli A, Sabahi F, Abachi M, Azizi M, Mahboudi F. Complete genomic sequence and phylogenetic relatedness of hepatitis B virus isolates from Iran. *J.Med.Virol.* 2005;76:318-26.
883. Arankalle VA, Gandhe SS, Borkakoty BJ, Walimbe AM, Biswas D, Mahanta J. A novel HBV recombinant (genotype I) similar to Vietnam/Laos in a primitive tribe in eastern India. *J Viral Hepat.* 2010;17:501-10.
884. Audsley J, Littlejohn M, Yuen L, Sasadeusz J, Ayres A, Desmond C, Spelman T, Lau G, Matthews GV, Avihingsanon A, Seaberg E, Philp F, Saulynas M, Ruxrungtham K, Dore GJ, Locarnini SA, Thio CL, Lewin SR, Revill PA. HBV mutations in untreated HIV-HBV co-infection using genomic length sequencing. *Virology.* 2010;405:539-47.
885. Banerjee A, Kurbanov F, Datta S, Chandra PK, Tanaka Y, Mizokami M, Chakravarty R. Phylogenetic relatedness and genetic diversity of hepatitis B virus isolates in Eastern India. *J.Med.Virol.* 2006;78:1164-74.
886. Bekondi C, Olinger CM, Boua N, Talarmin A, Muller CP, Le Faou A, Venard V. Central African Republic is part of the West-African hepatitis B virus genotype E crescent. *J.Clin.Virol.* 2007;40:31-7.
887. Cavinta L, Sun J, May A, Yin J, von Meltzer M, Radtke M, Barzaga NG, Cao G, Schaefer S. A new isolate of hepatitis B virus from the Philippines possibly representing a new subgenotype C6. *J.Med.Virol.* 2009;81:983-7.
888. Chauhan R, Kazim SN, Kumar M, Bhattacharjee J, Krishnamoorthy N, Sarin SK. Identification and characterization of genotype A and D recombinant hepatitis B virus from Indian chronic HBV isolates. *World J.Gastroenterol.* 2008;14:6228-36.
889. Chen BF, Kao JH, Liu CJ, Chen DS, Chen PJ. Genotypic dominance and novel recombinations in HBV genotype B and C co-infected intravenous drug users. *J.Med.Virol.* 2004;73:13-22.
890. Chen BF, Liu CJ, Jow GM, Chen PJ, Kao JH, Chen DS. Evolution of Hepatitis B virus in an acute hepatitis B patient co-infected with genotypes B and C. *J.Gen.Virol.* 2006;87:39-49.
891. Chen BF, Chen PJ, Jow GM, Sablon E, Liu CJ, Chen DS, Kao JH. High prevalence of mixed genotype infections in hepatitis B virus infected intravenous drug users. *J.Med.Virol.* 2004;74:536-42.
892. Chen BF, Liu CJ, Jow GM, Chen PJ, Kao JH, Chen DS. High prevalence and mapping of pre-S deletion in hepatitis B virus carriers with progressive liver diseases. *Gastroenterology.* 2006;130:1153-68.
893. Chen J, Huang A, Xu L, Chen D, Yu H, Zhu Z, Huang Z, Yang Z, Chen L, Tan T. Identification of recombinant intermediates of hepatitis B virus between genotype B and C in vitro. *Zhong.Nan.Da.Xue.Xue.Bao.Yi.Xue.Ban.* 2011;36:101-8.
894. Cui C, Shi J, Hui L, Xi H, Zhuoma, Quni, Tsedan, Hu G. The dominant hepatitis B virus genotype identified in Tibet is a C/D hybrid. *J.Gen.Virol.* 2002;83:2773-7.
895. Elkady A, Tanaka Y, Kurbanov F, Oynsuren T, Mizokami M. Virological and clinical implication of core promoter C1752/V1753 and T1764/G1766 mutations in hepatitis B virus genotype D infection in Mongolia. *J.Gastroenterol.Hepatol.* 2008;23:474-81.
896. Garmiri P, Loua A, Haba N, Candotti D, Allain JP. Deletions and recombinations in the core region of hepatitis B virus genotype E strains from asymptomatic blood donors in Guinea, west Africa. *J.Gen.Virol.* 2009;90:2442-51.
897. Hannoun C, Norder H, Lindh M. An aberrant genotype revealed in recombinant hepatitis B virus strains from Vietnam. *J.Gen.Virol.* 2000;81:2267-72.
898. Hubschen JM, Andernach IE, Muller CP. Hepatitis B virus genotype E variability in Africa. *J.Clin.Virol.* 2008;43:376-80.
899. Hubschen JM, Mbah PO, Forbi JC, Otegbayo JA, Olinger CM, Charpentier E, Muller CP. Detection of a new subgenotype of hepatitis B virus genotype A in Cameroon but not in neighbouring Nigeria. *Clin.Microbiol.Infect.* 2011;17:88-94.
900. Huy TT, Ushijima H, Quang VX, Win KM, Luengrojanakul P, Kikuchi K, Sata T, Abe K. Genotype C of hepatitis B virus can be classified into at least two subgroups. *J.Gen.Virol.* 2004;85:283-92.
901. Huy TT, Sall AA, Reynes JM, Abe K. Complete genomic sequence and phylogenetic relatedness of hepatitis B virus isolates in Cambodia. *Virus Genes.* 2008;36:299-305.

902. Juniastuti, Utsumi T, Nugrahaputra VE, Amin M, Hayashi Y, Hotta H, Lusida MI. Another novel subgenotype of hepatitis B virus genotype C from papuans of Highland origin. *J.Med.Virol.* 2011;83:225-34.
903. Kim MC, Kwon YK, Joh SJ, Kim SJ, Tolf C, Kim JH, Sung HW, Lindberg AM, Kwon JH. Recent Korean isolates of duck hepatitis virus reveal the presence of a new geno- and serotype when compared to duck hepatitis virus type 1 type strains. *Arch.Virol.* 2007;152:2059-72.
904. Kurbanov F, Tanaka Y, Fujiwara K, Sugauchi F, Mbanya D, Zekeng L, Ndemi N, Ngansop C, Kaptue L, Miura T, Ido E, Hayami M, Ichimura H, Mizokami M. A new subtype (subgenotype) Ac (A3) of hepatitis B virus and recombination between genotypes A and E in Cameroon. *J.Gen.Virol.* 2005;86:2047-56.
905. Laoi BN, Crowley B. Molecular characterization of hepatitis B virus (HBV) isolates, including identification of a novel recombinant, in patients with acute HBV infection attending an Irish hospital. *J.Med.Virol.* 2008;80:1554-64.
906. Luo K, Liu Z, He H, Peng J, Liang W, Dai W, Hou J. The putative recombination of hepatitis B virus genotype B with pre-c/c region of genotype C. *Virus Genes.* 2004;29:31-41.
907. Magiorikinis EN, Magiorikinis GN, Paraskevis DN, Hatzakis AE. Re-analysis of a human hepatitis B virus (HBV) isolate from an East African wild born Pan troglodytes schweinfurthii: evidence for interspecies recombination between HBV infecting chimpanzee and human. *Gene.* 2005;349:165-71.
908. Mahgoub S, Candotti D, Elekiaby M, Allain JP. Hepatitis B virus (HBV) infection and recombination between HBV genotypes D and E in asymptomatic blood donors from Khartoum, Sudan. *J Clin.Microbiol.* 2010;
909. Makuwa M, Souquiere S, Telfer P, Apetrei C, Vray M, Bedjabaga I, Mouinga-Ondeme A, Onanga R, Marx PA, Kazanji M, Roques P, Simon F. Identification of hepatitis B virus subgenotype A3 in rural Gabon. *J.Med.Virol.* 2006;78:1175-84.
910. Martin CM, Welge JA, Blackard JT. Hepatitis B virus (HBV) X gene diversity and evidence of recombination in HBV/HIV co-infected persons. *J.Med.Virol.* 2011;83:1142-50.
911. Meldal BH, Moula NM, Barnes IH, Boukef K, Allain JP. A novel hepatitis B virus subgenotype, D7, in Tunisian blood donors. *J.Gen.Virol.* 2009;90:1622-8.
912. Mohebbi SR, Amini-Bavil-Olyae S, Zali N, Noorinayer B, Derakhshan F, Chiani M, Rostami NM, Antikchi MH, Sabahi F, Zali MR. Molecular epidemiology of hepatitis B virus in Iran. *Clin.Microbiol.Infect.* 2008;14:858-66.
913. Morozov V, Pisareva M, Groudinin M. Homologous recombination between different genotypes of hepatitis B virus. *Gene.* 2000;260:55-65.
914. Mugisha L, Kaiser M, Ellerbrok H, Pauli G, Opuda-Asibo J, Joseph OO, Leendertz FH. The "original" hepatitis B virus of Eastern chimpanzees (*Pan troglodytes schweinfurthii*). *Virus Res.* 2011;155:372-5.
915. Mulyanto, Depamede SN, Surayah K, Tjahyono AA, Jirintai, Nagashima S, Takahashi M, Okamoto H. Identification and characterization of novel hepatitis B virus subgenotype C10 in Nusa Tenggara, Indonesia. *Arch.Virol.* 2010;155:705-15.
916. Mulyanto, Depamede SN, Wahyono A, Jirintai, Nagashima S, Takahashi M, Okamoto H. Analysis of the full-length genomes of novel hepatitis B virus subgenotypes C11 and C12 in Papua, Indonesia. *J.Med.Virol.* 2011;83:54-64.
917. Myers R, Clark C, Khan A, Kellam P, Tedder R. Genotyping Hepatitis B virus from whole- and sub-genomic fragments using position-specific scoring matrices in HBV STAR. *J.Gen.Virol.* 2006;87:1459-64.
918. Nakajima A, Usui M, Huy TT, Hlaing NK, Masaki N, Sata T, Abe K. Full-length sequence of hepatitis B virus belonging to genotype h identified in a Japanese patient with chronic hepatitis. *Jpn.J.Infect.Dis.* 2005;58:244-6.
919. Njouom R, Mba SA, Nerrienet E, Foupouapouognigni Y, Rousset D. Detection and characterization of hepatitis B virus strains from wild-caught gorillas and chimpanzees in Cameroon, Central Africa. *Infect.Genet.Evol.* 2010;
920. Olinger CM, Jutavijittum P, Hubschen JM, Yousukh A, Samounry B, Thammavong T, Toriyama K, Muller CP. Possible new hepatitis B virus genotype, southeast Asia. *Emerg.Infect.Dis.* 2008;14:1777-80.
921. Osiowy C, Gordon D, Borlang J, Giles E, Villeneuve JP. Hepatitis B virus genotype G epidemiology and co-infection with genotype A in Canada. *J.Gen.Virol.* 2008;89:3009-15.
922. Owiredu WK, Kramvis A, Kew MC. Hepatitis B virus DNA in serum of healthy black African adults positive for hepatitis B surface antibody alone: possible association with recombination between genotypes A and D. *J.Med.Virol.* 2001;64:441-54.
923. Phung TB, Alestig E, Nguyen TL, Hannoun C, Lindh M. Genotype X/C recombinant (putative genotype I) of hepatitis B virus is rare in Hanoi, Vietnam--genotypes B4 and C1 predominate. *J Med.Virol.* 2010;82:1327-33.
924. Pourkarim MR, Verbeeck J, Rahman M, Amini-Bavil-Olyae S, Forier AM, Lemey P, Maes P, Van RM. Phylogenetic analysis of hepatitis B virus full-length genomes reveals evidence for a large nosocomial outbreak in Belgium. *J.Clin.Virol.* 2009;46:61-8.
925. Pourkarim MR, Lemey P, Amini-Bavil-Olyae S, Maes P, Van RM. Novel hepatitis B virus subgenotype A6 in African-Belgian patients. *J.Clin.Virol.* 2009;
926. Pourkarim MR, Amini-Bavil-Olyae S, Verbeeck J, Lemey P, Zeller M, Rahman M, Maes P, Nevens F, Van RM. Molecular evolutionary analysis and mutational pattern of full-length genomes of hepatitis B virus isolated from Belgian patients with different clinical manifestations. *J.Med.Virol.* 2010;82:379-89.
927. Purdy MA, Gonzales AC, Dimitrova Z, Khudyakov Y. Supragenotypic groups of the hepatitis B virus genome. *J.Gen.Virol.* 2008;89:1179-83.
928. Quarleri J, Moretti F, Bouzas MB, Laufer N, Carrillo MG, Giuliano SF, Perez H, Cahn P, Salomon H. Hepatitis B virus genotype distribution and its lamivudine-resistant mutants in HIV-coinfected patients with chronic and occult hepatitis B. *AIDS Res.Hum.Retroviruses.* 2007;23:525-31.

929. Sa-Nguanmoo P, Tangkijvanich P, Thawornsuk N, Vichaiwattana P, Prianantathavorn K, Theamboonlers A, Tanaka Y, Poovorawan Y. Molecular epidemiological study of hepatitis B virus among migrant workers from Cambodia, Laos, and Myanmar to Thailand. *J Med.Virol.* 2010;82:1341-9.
930. Simmonds P, Midgley S. Recombination in the genesis and evolution of hepatitis B virus genotypes. *J.Virol.* 2005;79:15467-76.
931. Sugauchi F, Orito E, Ichida T, Kato H, Sakugawa H, Kakumu S, Ishida T, Chutaputti A, Lai CL, Ueda R, Miyakawa Y, Mizokami M. Hepatitis B virus of genotype B with or without recombination with genotype C over the precore region plus the core gene. *J.Virol.* 2002;76:5985-92.
932. Suwannakarn K, Tangkijvanich P, Theamboonlers A, Abe K, Poovorawan Y. A novel recombinant of Hepatitis B virus genotypes G and C isolated from a Thai patient with hepatocellular carcinoma. *J.Gen.Virol.* 2005;86:3027-30.
933. Tanaka Y, Sanchez LV, Sugiyama M, Sakamoto T, Kurbanov F, Tatematsu K, Roman S, Takahashi S, Shirai T, Panduro A, Mizokami M. Characteristics of hepatitis B virus genotype G coinfecting with genotype H in chimeric mice carrying human hepatocytes. *Virology.* 2008;376:408-15.
934. Tang YZ, Liu L, Pan MM, Wang YM, Deng GH. Evolutionary pattern of full hepatitis B virus genome during sequential nucleos(t)ide analog therapy. *Antiviral Res.* 2011;90:116-25.
935. Tatematsu K, Tanaka Y, Kurbanov F, Sugauchi F, Mano S, Maeshiro T, Nakayoshi T, Wakuta M, Miyakawa Y, Mizokami M. A Genetic Variant of Hepatitis B Virus Divergent from Known Human and Ape Genotypes Isolated from a Japanese Patient and Provisionally Assigned to New Genotype J. *J.Virol.* 2009;
936. Tran HT, Ushijima H, Ngoc TT, Ha ID, Hayashi S, Sata T, Abe K. Recombination of genotypes B and C in hepatitis B virus isolated from a Vietnamese patient with fulminant hepatitis. *Jpn.J.Infect.Dis.* 2003;56:35-7.
937. Tran TT, Trinh TN, Abe K. New complex recombinant genotype of hepatitis B virus identified in Vietnam. *J.Virol.* 2008;82:5657-63.
938. Trinks J, Cuestas ML, Tanaka Y, Mathet VL, Minassian ML, Rivero CW, Benetucci JA, Gimenez ED, Segura M, Bobillo MC, Corach D, Ghiringhelli PD, Sanchez DO, Avila MM, Peralta LA, Kurbanov F, Weissenbacher MC, Simmonds P, Mizokami M, Oubina JR. Two simultaneous hepatitis B virus epidemics among injecting drug users and men who have sex with men in Buenos Aires, Argentina: characterization of the first D/A recombinant from the American continent. *J.Viral Hepat.* 2008;15:827-38.
939. Vivekanandan P, Singh OV. Molecular methods in the diagnosis and management of chronic hepatitis B. *Expert Rev.Mol.Diagn.* 2010;10:921-35.
940. Yang J, Xing K, Deng R, Wang J, Wang X. Identification of Hepatitis B virus putative intergenotype recombinants by using fragment typing. *J.Gen.Virol.* 2006;87:2203-15.
941. Yang J, Xi Q, Deng R, Wang J, Hou J, Wang X. Identification of interspecies recombination among hepadnaviruses infecting cross-species hosts. *J Med.Virol.* 2007;79:1750-41.
942. Yano Y, Truong BX, Seo Y, Kato H, Miki A, Tanaka Y, Mizokami M, Kagawa A, Miyazaki H, Kasuga M, Azuma T, Hayashi Y. Japanese case of hepatitis B virus genotypes C/D hybrid. *Hepatol.Res.* 2007;
943. Yin J, Zhang H, He Y, Xie J, Liu S, Chang W, Tan X, Gu C, Lu W, Wang H, Bi S, Cui F, Liang X, Schaefer S, Cao G. Distribution and hepatocellular carcinoma-related viral properties of hepatitis B virus genotypes in Mainland China: a community-based study. *Cancer Epidemiol.Biomarkers Prev.* 2010;19:777-86.