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My laboratory research focuses on understanding HIV-drug-resistance (DR) and persistence of infection despite antiretroviral therapy (ART). To study DR mutations my group adapted an oligonucleotide ligation assay (OLA) to detect single-base changes conferring DR; optimized OLA to all prevalent subtypes; and validated OLA quantification of mutant by “next generation sequencing” (NGS). Our trials of OLA testing at codons 65, 103, 181, 184, 190 pre-ART of 1,228 Kenyans initiating non-nucleoside reverse transcriptase inhibitor-based ART show that: (1) NGS (pyrosequencing for 2006 study and Illumina from 2010 and 2014 studies) confirms all OLA detected DR constituting >5% of an individual’s pre-ART quasispecies; (2) M184V was rarely and K65R was never detected as the sole pre-ART mutant codon; (3) DR at ≥1 OLA codon predicts virologic failure (VF; ≥400c/mL) with NVP- (p<0.0001) and EFV-ART (p<0.0030) compared to wild-type codons; (4) Detection of DR at multiple codons confers a high risk of VF to NVP- (p<0.0001) and EFV-ART (p<0.0027), while K103N alone predicted VF to NVP- (p<0.0001) but not to EFV-ART (p=0.4109). (5) Prediction of VF by mutant load (% mutant x VL) was similar to risk by mutant%. These data are likely relevant to assessing risk of VF from WHO DR surveillance.