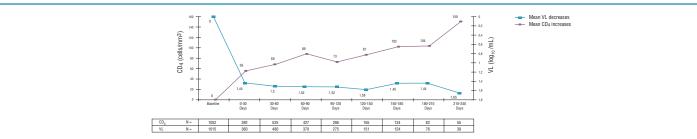
Immuno-Virological Response

Virologic response was defined as HIV RNA below 400 copies/mL and/or a decrease from baseline of at least 1.0 log₁₀ copies/mL. The longitudinal virologic and immunologic on-treatment responses are presented in Figure 10.

Figure 10. CD₄ Increase and Viral Load Decrease



• After the first month of therapy, the mean HIV RNA decrease was -1.44 log₁₀ copies/mL.

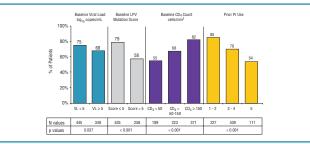
The mean HIV RNA decrease was maintained at Months 3 and 6, with viral load decreases of -1.52 log₁₀ copies/mL and -1.44 log₁₀ copies/mL respectively

The mean CD₄ cell count increase from baseline to month 6 was 104 cells/mm³.

Study of the Virologic Response with Respect to Baseline Characteristics

Virologic response was evaluated with respect to baseline characteristics in a subgroup of patients (n=793) who had a genotype at baseline and at least one HIV RNA measurement after the start of LPV/r-containing regimen; plasma HIV RNA (<5 and ≥5 log₁₀ copies/mL), LPV mutation score (≤5 and >5 mutations), CD₄ count (<50, 50-150, >150 cells/mm³), and prior PI use (1-2, 3-4, 5) (see Figure 11).

Figure 11. Study of the Virologic Response with Respect to **Baseline Characteristics**



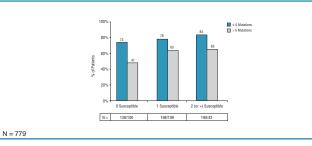
In a univariate analysis, each of these parameters was statistically significantly associated with virologic response.

Virologic Response with Respect to Susceptibility to **Concomitant ARVs and Baseline LPV Mutation Score**

In order to evaluate the virologic response to ARV drugs other than LPV/r: concomitant drugs used in the baseline regimen were classified as susceptible or non-susceptible (i.e., intermediate or resistant)

Virologic response was then evaluated on the basis of the number of ARV drugs used in the baseline regimen to which the virus was susceptible. Results from this analysis are summarized in Figure 12.

Figure 12. Virologic Response with Respect to the Susceptibility to Concomitant ARVs and Baseline LPV Mutation Score



Virologic response was higher in patients with LPV mutation score of 5 or less, compared to those with >5 mutations, and increased with use of other active drugs.

Safety Results

A total of 3819 patients were registered in the ATU through April 2001. During this time period, 356 cases describing 836 adverse events were reported on a voluntary basis. The most frequently reported adverse events were diarrhea (2.67%), nausea (1.20%), rash (0.92%), hyperlipernia (0.89%), abdominal pain (0.86%), vomiting (0.79%), asthenia (0.68%) and fever (0.50%). Adverse events of special interest are presented in Table 4.

Table 4. Adverse Events of Special Interest

Adverse Events of Special Interest	Number of Patients (%)	Comments
Hyperlipemia	36 (0.94%)	8/36 (22%) premature discontinuation
Diabetes	6 (0.16%)	3 considered by the physician to be probably not, or not related to LPV/r, 2 considered by the physician to be possibly or probably related to LPV/r
Pancreatitis	7 (0.18%)	All of these patients had alternative risk factors reported including ddl use (4 patients) or alcohol use (1 patient)
Death	19 (0.50%)	None of the deaths were considered related to drug

CONCLUSIONS

Because of the retrospective and observational aspect of such analysis, data presented here may have some limitations. However, because of the high number of patients treated, the ATU process gives the unique possibility to learn more about antiretroviral drugs in real life conditions.

Virologic response is observed in this cohort in spite of extensive ARV experience and significant level of baseline genotypic resistance, as evidenced by a median of 5 PI mutations.

The significant contribution of LPV/r to the overall response is emphasized by the high level of resistance of concomitant drugs in the LPV/r-containing regimens and by the confirmation of a genotypic breakpoint of five or less mutations for LPV, highly predictive of the extent of virologic response, as described in previous observations

Lower viral load, higher CD₄ cell count and less PI-experience at baseline were other predictive factors of a higher response rate.

The overall tolerance to LPV/r-containing regimens was good and adverse events were infrequent and rarely resulted in treatment discontinuation.

A C K N O W L E D G M E N T S

Abbott Laboratories would like to acknowledge all physicians, virologists, and patients who participated in this program

Abbott France would also like to acknowledge people in Abbott Park (Barry Bernstein M.D., Kevin Niemi, Noreen Travers and Eileen Tillmann) who helped in the finalization of this poster.

oster #1926

Pre-registrational Use of ABT-378/r in Heavily-Experienced Patients: The French ATU Program Experience

I. Cohen Codar, F. Boer, R. Terrier, E. Guillevic, D. Pellier, P. NgoVan, JP. Chauvin Abbott Laboratories, Rungis, France

BACKGROUND

Lopinavir/ritonavir (LPV/r, Kaletra[™], formerly known as ABT-378/r), is a recently approved protease inhibitor (PI) for the treatment of HIV-1 infection in the United States and in Europe. Lopinavir, co-formulated with a low dose of ritonavir, takes advantage of the P450 cvtochrome inhibitor properties of ritonavir, Lopinavir is exouisitely sensitive to the pharmacokinetic enhancement of ritonavir, resulting in substantially increased LPV drug exposure. The mean LPV ratio of C_{incuph} (protein binding adjusted) to EC_{sn} (Inhibitory Quotient or IQ) for wild-type virus is >75 at 400/100 mg BID dose. This high IQ potentially contributes to the durability of response by providing superior antiviral activity (Figure 1a, Table 1) and a pharmacologic barrier to the emergence of viral resistance. However, virologic control may be compromised by mutations induced by previous PI therapies. Differences in efficacy may reflect the substantially different inhibitory quotients achieved with LPV/r antiretroviral (ARV) in naïve vs. PI-experienced patients (Figure 1b).

Figure 1a. Phase III ARV-Naïve Patients: HIV RNA < 400 copies/mL (Study 863, ITT: NC=F)

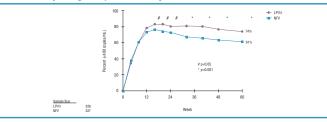


Table 1. Incidence of PI Resistance Through Week 60 (Study 863)

	LPV/r	Nelfinavir
HIV RNA >400 copies/mL	76	119
Genotype available	40	87
Resistance detected in protease	0	31

METHODS

Prior to marketing authorization, a program was developed to provide patients, who were failing currently available therapeutic options, access to potentially life-saving medications. A worldwide expanded access program (EAP) was initially conducted as a clinical trial; however, this EAP was rapidly switched in France through agreement with the Drug Agency to an "ATU" program ("Autorisation Temporaire d'Utilisation", Provisional Authorization for Use) which was conducted from March 2000 to April 2001. Selection criteria of the patient population at study initiation included CD4 <200 cells/mm³ and HIV RNA >4 log₁₀. However, these were progressively removed to authorize the use of LPV/r in a broader PI-experienced population

At baseline demographic data including HIV-RNA, CD, cell count, antiretroviral history and genotype were collected. Follow-up data was provided on a voluntary basis, The overall enrollment in this cohort was 3819 patients. Analysis does not include 193 patients that were previously enrolled in EAP, as well as 179 nominative ATU participants. (Physicians had the possibility to request a "Nominative ATU" for patients who did not fulfill the selection criteria of the ATU, e.g., for children.)

ESULTS

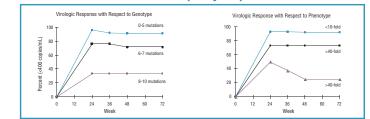
Summary of Demographic and Disease Characteristics

A total of 3447 patients have been in the immuno-virological analysis. The mean baseline HIV RNA and CD₄ cell count for these patients were 4.66 log₁₀ copies/mL and 202 cells/mm³, respectively. Most patients in this cohort had advanced HIV infection; with 51.3% having experienced at least one CDC Class C (AIDS-defining) event. Demographic and disease characteristics are presented in Table 2. Number (N) refers to number of subjects for whom specific data was available. The number (N) of subjects with specific data available has been identified.

Table 2. Summary of Demographic and Disease Characteristics

Gender		CD ₄ Cell Count (cells/mm³)	
Male	79.5%	<50	21.4%
Age (N = 1805)		[50 – 150] [150 – 300]	24.5% 30.0%
Mean	42 years	≥300 Mean	24.1% 202
Median	40 years	Median	165
CDC Classification (N = 3279)		Standard Deviation Minimum	178
Asymptomatic (Stage A)	16.8%	Maximum	1193
Symptomatic (Stage B) AIDS – Indicator (Stage C)	31.9% 51.3%	HIV RNA (log ₁₀ copies/mL)	
HIV Diagnosis Date (N = 2753)		<5 log ₁₀ copies/mL	60.9%
<1990	40.8%	≥5 log ₁₀ copies/mL Mean	39.1% 4.66
1990 – 1995 ≥1995	41.4% 17.8%	Median	4.78
21355	17.076	Standard Deviation Minimum	0.92 0.70
N = 3447		Maximum	7.05

Figure 1b. Kaletra + EFV/NRTIs in Multiple PI-Experienced, NNRTI-Naïve Patients (Study 957)



Response to therapy in Study 957 was associated with the number of baseline mutations and baseline phenotype. Patients with less than five mutations or <10-fold phenotypic change in susceptibility had a better virologic response as compared to patients with more mutations (six or more) or greater phenotypic change in susceptibility (≥10-fold).

Antiretroviral Experience

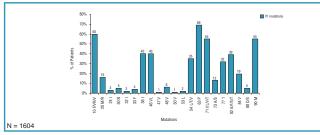
Information on pre-study antiretroviral therapy is available on 3412 ATU participants and is described in Figures 2 and 3.

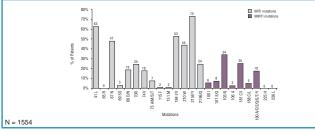
Figure 2. Number of Previous Antiretroviral Drugs per Class Figure 3. Previous Antiretroviral Drugs PI NRTI NNRTE

The majority of patients were previously treated with at least 3 PIs (62%), 5 NRTIs (59%), and 1 NNRTI (75%). Treatment experience with individual antiretrovirals is provided in Figure 3.

Baseline Genotype

HIV RNA sequences, obtained in this heavily-ARV experienced patient population according to the French guidelines (Rapport Delfraissy 2000), were provided for a subset of enrolled patients (Figures 4a and 4b). Figure 4a. Baseline Prevalence of PI Mutations Figure 4b. Baseline Prevalence of NRTI and NNRTI Mutations

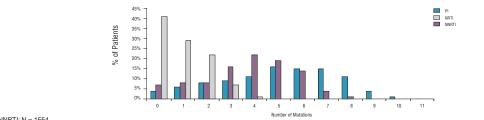




The prevalence of multiple baseline PI mutations associated with cross resistance to the PI class was high (Figure 4a). The most common PI mutations occurred at positions 63, 10, 71 and 90.

Most of the patients had thymidine NRTI (41, 67, 210, 215) and lamivudine (184) resistance mutations. For NNRTIs, a large proportion of patients had at least one mutation that confers cross resistance to all NNRTIs currently available for therapeutic use (101, 103, 181, 190).

Figure 5. Baseline Number of PI, NRTI and NNRTI Mutations



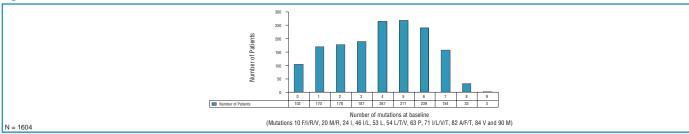
PI: N = 1604, NRTI and NNRTI: N = 1554

As presented in Figure 5, the number of PI-associated mutations within this population ranged from 0 to 11, with a median of 5 mutations. The median number of NRTI and NNRTI mutations was 4 and 1, respectively.

LPV Mutation Score

The LPV mutation score is the number of protease specific mutations identified out of 11 protease mutations previously described to be associated with reduced susceptibility to lopinavir (amino acids 10, 20, 24, 46, 53, 54, 63, 71, 82, 84 and 90).

Figure 6. Baseline LPV Mutation Score



• Within this population, the baseline LPV mutation score ranged from 0 to 9 (Figure 6), with a median of 4 mutations.

• Forty-eight percent of the patients (777/1604) had a baseline LPV mutation score of 4-6.

Concomitant Antiretroviral Therapy

Information concerning concomitant ARVs used in the LPV/r-containing regimens for the study population is provided in Figure 7.

Figure 7. Description of LPV/r-Containing Regimens



The majority of patients (58%) received two additional ARVs, which in most cases consisted of two NRTIs. A sizeable group of patients (30%) received three additional drugs, consisting mainly of either three NRTIs or two NRTIs plus one NNRTI. Nine percent (9%) of patients received more than three concomitant ARVs. Concomitant use of another PI was infrequent in this study population.

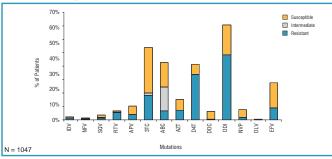
resistant and susceptible. These criteria are summarized in Table 3.

Table 3. AC11 Interpretation of Genotype

Pls	Resistance		
IDV	M46I/L		
	V82A/F/S/T		
	184V		
	L90M + ≥2 mutations including: K20M/R, L24I, V32I, M36I, I54V, A71V/T, G73S		
SQV	G48V		
	184V		
	L90M		
NFV	D30N		
	184V N88S/D		
	L90M		
RTV	V82A/F/S/T		
RIV	184V		
APV (1)	150V		
	≥4 mutations including: L10I, V32I, M46I/L, I47V, I54L/M/V,		
	G73S, V82A/F/I/T/S, I84V, L90M		
LPV/r (1)`	≥8 mutations including: L10F/I/R/V, K20M/R, L24I, M46I/L, I50V, ,		
	F53L, I54L/T/V, L63P, A71/L/V/T, V82A/F/T, I84V, L90M		
NRTIS	Resistance		
AZT	T215Y/F		
	≥3 mutations including: M41L, D67N, K70R, L210W, K219Q/E Q151M		
070	Insertion at codon 69		
3TC	M184V/I		
441 (4)	Insertion at codon 69		
ddl (1)	L74V ≥3 TAMs dont T215Y/F		
	25 TAMIS UDIT 12151/P		
	Insertion at codon 69		
ddC (2)	T69D/N/S		
uuu (2)	Q151M		
	Insertion at codon 69		
d4T	V75M/S/A/T		
	T215Y/F		
	≥3 mutations including: M41L, D67N, K70R, L210W, K219Q/E		
	Q151M		
	Insertion at codon 69		
ABC (1)	≥6 mutations including: M41L, K65R, D67N, K70R, L74V,		
	Y115F, M184V/I, L210W, T215Y/F, 219Q/E		
	Q151M		
	Insertion at codon 69		
TDF (1)	Insertion at codon 69		
NRTIS	Resistance		
EFV	L100I		
	K101E		
	K103N		
	Y181C/I		
	Y188C/L		
	G190A/C/E/Q/S/T/V		
	P225H		
NVP	L100I		
	K101E		
	K103N		
	V106A		
	Y181C/I		
	Y188C/H/L G190A/C/E/Q/S/T/V		
DLV	1 1001		
DLV	L1001 K101E		
	K101E K103N		
	V106A		
	V100A Y181C		
	Y188C/L		
	G190E		
	P236L		

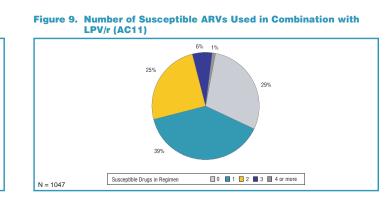
As presented in Figures 8 and 9, high levels of resistance to concomitant ARVs were observed, indicating that a large majority of patients did not receive multiple active drugs as part of their LPV/r-based regimen

Figure 8. Concomitant Antiretroviral Drugs and Resistance Interpretation Based on AC11 Criteria



Using the algorithm of genotypic resistance defined by the French authorities (AC11, October 2001), the drug susceptibility of ARVs used in the baseline regimen was classified as resistant, suspected

	Suspected Resistance
	L90M
/A, V771	
	V82A/F/S/T + ≥2 mutations including: I54V/L, A71V/T, G73S, V77I
	V82A/F/S/T + ≥2 mutations including: M36I, M46I/L, A71V/T, V771
	L90M + ≥2 mutations including: K20M/R, V32I, L33F, M36I, M46I/L,
	154L/V, A71V/T, V771
	6 or 7 mutations including: L10F/I/R/V, K20M/R, L24I, M46I/L, I50V, F53L,
	I54L/T/V, L63P, A711/L/V/T, V82A/F/T, I84V, L90M
	Suspected Resistance
	Q151M
	K65R
	K65R
	Nort
	4 or 5 mutations including: M41L, K65R, D67N, K70R, L74V, Y115F,
	M184V/I, L210W, T215Y/F, 219Q/E
	K65R
	≥4 TAMs including T215Y/F
	Suspected Resistance
TDF: tenofovir.	



01K-036-1029-6