tained (85.7%) were receiving regimens that con-

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multivariate analysis by logistic regression
revealed that sex, age, and duration of treat-
ment were not significant factors influencing plasma virus load. Only dis-

ease stage and drug adherence level were
found to be significant factors (P < .005
and P < .003, respectively). We found that
patients with partial adherence (i.e., grades
B to D) were 4 times more likely to have a
detectable virus load than were patients
with grade A adherence (adjusted OR,
4.22; 95% CI, 1.75–12.33).

Like Duong et al. [1], we found that
self-reported adherence was indepen-
dently associated with antiretroviral effi-
cacy, in terms of good virus suppression.
However, instead of using a score derived
from 4 questions [1], we used an adher-
ence level that was calculated from the ab-
solute number of missed doses and
checked by use of the grading table. The
sensitivity and positive predictive value of
our method were slightly higher than those
of the adherence score used by
Duong et al. [1], and the specificity
and negative predictive value were lower.
The high positive predictive value of our
method suggests that a single assessment
of longer-term adherence (i.e., 4–6 weeks)
worked.

Continual monitoring and reinforce-
ment of patients’ adherence to therapy has
clearly become one of the most crucial
elements in the success of HIV man-
gement [2]. To date, all methods that have
been developed to measure levels of drug
adherence have had limitations [3]. The
self-report approach has significantly pre-
dicted virological treatment failure in
HIV-infected patients [4]. Conceivably,
as-
essment of drug adherence using meth-
ods other than self-report may not be fea-
sible in most clinical settings. This would
definitely be true for developing countries,
where access to combination antiretroviral
treatment has been increasingly necessary
[5]. We have developed a user-friendly
tool to assess and grade self-reported anti-
retroviral drug adherence among HIV-
infected patients. The grading table that
we have designed is simple, standardized,
fast, and cost-free. Its application may aid
the use of antiretroviral therapy in devel-
oping countries.

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Interleukin-1 Receptor
Antagonist Gene
Polymorphism and Cancer

Srr—We read with great interest the re-
view article by Witkin et al. [1] about
the influence of IL-1 receptor antagonist (IL-
1RA) gene polymorphism on disease.
IL-1RA is an anti-inflammatory cytokine that
binds specifically to the IL-1 receptor [2].
Its expression has been found in associa-
tion with several types of tumors, such as
diabetic cancer [3], bronchogenic car-
cinoma [4], glioblastoma [5], and gastric

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cervical carcinoma [6]. We would like to add some interesting details concerning the connection between IL-1RA gene polymorphism and cancer.

Witkin et al. [1] mentioned that the concentration of IL-1RA in the serum of patients with gynecologic cancers is elevated in comparison with that in patients with benign diseases and with that in healthy women. This observation is based on an article by Fujiwaki et al. [7]. It should be noted that only 15 patients with solid tumors were enrolled in that study: 7 patients with cervical cancer, 6 with endometrial cancer, and only 2 with ovarian cancer.

It is known that gene polymorphisms can cause changes in the expression of proteins [8]. Therefore, a polymorphism in the IL-1RA gene may have a substantial impact on the IL-1 cytokine system. For instance, the study of Unfried et al. [9] demonstrated a significant association between the allele 2 polymorphism of the IL-1RA gene and recurrent idiopathic miscarriage. Furthermore, El-Omar et al. [10] and Machado et al. [11] have observed an association between IL-1RA and gastric cancer.

Because few data are available on the connection between IL-1RA and cervical cancer, we conducted a prospective case-control study to investigate the relationship between polymorphisms in the gene encoding for the IL-1RA and the clinical characteristics of patients with cervical cancer. Blood samples were analyzed, and DNA was extracted. The genomic DNA fragments were amplified by PCR.

One hundred thirteen women with cervical cancer and 107 female control subjects with benign disorders were enrolled. Because germline mutations do not fluctuate with age, the age of control subjects was not specified; however, only women $>47$ years old were included in the control group. The median age of the patients with cervical cancer was 46 years (range, 25–80 years). Of the 220 women included in our study, 58.4% were in stage T1 or T2, and 41.6% were in stage T3 or T4. The frequency of the IL-1RA 1/2 genotype in the study group was statistically significantly different from that in the control group with respect to allele 2 heterozygosity (24.8% vs. 13.1%, respectively; $P = .04$).

No statistically significant differences were observed between the frequency of the IL-1RA 1/3 genotype among patients with cervical cancer and the frequency in the control group (4.4% vs. 3.7%) or in the frequencies of the homozygous allele 2. Only 1 woman with cervical cancer was identified as homozygous for allele 3, and an additional 9 patients were identified as homozygous for allele 2. In the control group, 3 women were heterozygous for allele 2/3. No statistically significant correlations were observed between IL-1RA 1/2 polymorphism and tumor stage ($P = .5$), grade of tumor differentiation ($P = .4$), recurrence status ($P = .5$), and age at treatment ($P = .5$).

These data support the claim that allele 2 of the gene encoding for IL-1RA plays a role as a genetic determinant of whether an individual will develop cancer with solid tumors. Further prospective studies are warranted to clarify the role of the IL-1RA gene in the pathophysiology of cancer.

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Clinical Infectious Diseases 2002; 34:1535–6
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Interleukin-1 Receptor Antagonist Gene Polymorphism, Infectious Burden, and Coronary Artery Disease

Sr—We read with great interest the review by Witkin et al. [1], which reported that persons who are homozygous for allele 2 of the IL-1 receptor antagonist (IL-1RA) gene have a more prolonged and more severe proinflammatory immune response than do persons with other IL-1RA genotypes. Thus, being homozygous for allele 2 of the IL-1RA gene might be detrimental for subjects with chronic inflammatory conditions and might also be associated with coronary artery disease (CAD).

There is increasing evidence that inflammation and, possibly, infection play an important role in atherogenesis [2–4]. The hypothesis that infectious agents may