co-infection ($P = 0.014$), and high height ($P = 0.009$). An association was found between low homocysteine serum level and the following variables: high prothrombin time ($P = 0.027$), and presence of monoclonal gammopathy ($P = 0.019$).

Conclusion: Associations were found between high homocysteine serum level and high creatinine, and between low homocysteine serum level and high prothrombin time and presence of monoclonal gammopathy.

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Control of HIV-infection with Visits Scheduled Every Four or Every Six Months. A Comparative Randomized Study

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Background: Guidelines generally recommend scheduling visits for monitoring HIV infection every 3–4 months. But those repetitive controls are many times unrewarding and suppose an inconvenience for patients. Studies are needed to determine the most efficient scheduling of those visits.

Methods: Randomized prospective study, carried out in the HIV clinic of the University General Hospital of Castellon, Spain. Control of HIV-infection, in terms of virologic and immunologic response, and adherence to visits, is compared in patients who are scheduled to visits every four versus every 6 months, throughout one year. Patients are included if (1) they are taking antiretroviral therapies of those recommended by guidelines, (2) they have had undetectable HIV-RNA for at least the last two controls, and (3) they give informed consent.

Results: We include 62 patients. Table shows the most relevant results. An intention-to-treat analysis is carried out. Comparisons are made with nonparametric tests. Values are medians, if not otherwise specified.

Conclusions: Visits scheduled every 6 months, instead of every 4 months, do not seem to jeopardize adequate control of HIV infection.

	Every 4 months	Every 6 months	*P*
Number of patients	32	30	–
Gender male, %	78	67	0.312
Age, years	43	41	0.757
Baseline CD4 cell count, per mm^3	465		0.111
Variation of CD4 cell count after 1 year of follow-up, per mm^3	8	−6	0.479
HIV-RNA undetectable after 1 year of follow-up, %	66	80	0.345
Adherence to scheduled visits, %	88	97	0.070

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European Virus Archive

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The EVA consortium is dedicated to the provision of unique collections of high quality and authenticated virus strains through its virtual bio-resource centre, for fundamental and applied research. The core of the European Viral Archives, is composed by the following participants:

No.	Participant organisation name	Short name	Country
1.	Institut de Recherche pour le Développement	IRD	France
2.	Veterinary Laboratories Agency	VLA	UK
3.	Bernhard-Nocht-Institut für Tropenmedizin	BNI	Germany
4.	Universitaetsklinikum Bonn	UKB	Germany
5.	Health Protection Agency	HPA	UK
6.	Université de Genève	UNIGE	Switzerland
7.	Univerza v Ljubljani	UL	Slovenia
8.	Institute of Virology, Slovak Academy of Sciences	IVSAS	Slovakja
9.	Université de la Méditerranée	UNIVMED	France

The nine member laboratories within the EVA consortium will merge their specialised collections to create a catalogue advertising these viruses through a web portal. EVA provides the catalogue to our customer and the strains are supplied, to EVA specifications, by the respective member laboratory remain the property of the originator. Using standardised procedures for virus production, preservation, qualification, and storage procedures, users will be assured of a consistent level of service, irrespective of the lab supplying the virus. All viruses supplied will meet EVA's standard specification on quality and authentication. The EVA consortium is committed to continuous improvement and development within the field of scientific and medical research. This is evident from our objectives, which include:

- The development of optimized methods for the characterization and conservation of viruses within the EVA collection,
- The development of protocols and facilities for the preservation and long term storage of virus,
- The derivation and development of virus products for diagnosis, identification and antiviral therapy.

The EVA consortium quality policy is based on the following principles, in accordance with the recommendations of the EVA Scientific Advisory Board:

- A unique collection of a wide range of viruses within an international network,
- Comprehensively identified virus strains,
- Standardised quality of virus strain and service level to users,
- Assured bio-security of originating laboratories, users and the general public.

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HLA-C-35C/T Variant: Genetic Association to HIV-1 Disease Progression and Functional Links

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Genomic studies on HIV-1 have identified host determinants influencing viral replication and infection. A greater understanding of their functional effect may provide alternatives to slow disease progression and improve the response to antiretroviral treatment. A variant 35 kb upstream of the *HLA-C* gene (−35 C/T) has been implicated as a major determinant in early phase and late outcomes of HIV infection, influencing steady-state viral load and time to death. The protective −35CC genotype has been associated with