ISSN 0233-7657. Біополімери і клітина. 2004. Т. 20. № 1-2

Distribution and expression of chicken endogenous retroviruses in the host genome

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The distribution of seven groups of endogenous retroviruses (ALV-related ev loci, HERV-I-related proviruses, EAV-HP, EAV-0, E-33, E-51, ART-CH) in the genome of domestic chicken (Gallus gallus) was studied according to the composition (long-range variation of GC-content) of the host genome. GC-rich proviruses (ev loci, ART-CH and EAV-0) have been localized mainly in GC-richest isochore families H2, H3 and H4, GC-poor HERV-I-related proviruses, E-51 and E-33 localized in GC-poor isochore families L1, L2 and also in H1 (isopycnicity). GC-rich EAV-HP, except expected distribution GC-rich isochores, present also in GC-poor compartments. Investigation of expression by RT-PCR and analysis of EST databases provided a tissue-specific patterns that could change the picture of proviral distribution due to reintegration. Reasons of endogenous retrovirus isopycnicity are likely to be the compositional match between the integrant and the chromosomal region of the host, that led to the stability of integration.

Introduction. Retroviruses are known to integrate as proviruses into the host-cell genome. It is a critical step in the life-cycle of retroviruses, and their replication is not possible without integration [1]. Endogenous retroviruses have integrated into the genome of a germ cell, and they inherit along with the rest of the host genome as Mendelian genes.

A widely accepted view that retroviral integration into the host genome occurs randomly [2] was challenged with the development of methods for the compositional fractionation of vertebrate DNA [3]. This approach led to the discovery of isochores, long (> 300 kb), compositionally homogenous DNA segments [4] and showed that, in the case of stable integration, proviruses of exogenous mammalian retroviruses (bovine leukemia virus, BLV; Rous sarcoma virus, RSV; human T-leukemia virus type I, HTLV-I; human immunodeficienty virus type 1, HIV-1) as well as one endogenous retrovirus (mouse mammary tumor virus, MMTV) located in some regions of the host genome (compartments) and in host genome sequences compositionally matching to the viral sequences (isopycnicity) (reviewed in [5]).

In the case of primary infection, as it has been shown by a mapping of HIV-1 integration sites [6], retroviruses integrate towards gene-rich compartments which is characterized by an open chromatin structure [4].

There is a correlation between the isopycnic localization of provirus and its transcription [7, 8].

Our study on specificity of integration of avian endogenous retroviruses is interesting for several reasons. First of all, compositional organization of the avian genome is different from that of the mammalian one: the isochore pattern of avian genome is characterized by GC-richest isochore H4 [4, 9]. Moreover, endogenous retroviruses exist with the host genome for a long period of time that affect their stucture and, probably, localization in the genome. It is shown that «ancient» endogenous MMTV localized isopycnically while exogenous sequences and recently acquired endogenous MMTV showed a broader distribution

[10]. Similar results has been obtained for *Alu* repeats: the older Alus, the stronger bias of their localization towards GC-rich DNA (isopycnicity) [11].

Three families of chicken (*Gallus gallus*) endogenous retroviruses, different in structure and evolutional age, has been described to date: 1) ALV (avian leukosis virus) — related ev loci; 2) EAV family with subfamilies EAV-HP, EAV-0, E-51, E-33, ART-CH and 3) HERV-I (human endogenous retrovirus type I) — related retroviruses (reviewed in [12, 13]). The EAV family is restricted to all *Gallus* species while evs are specific for domestic chicken and its wild relative red jungle fowl only and therefore is younger than EAV [14].

HERV-I-related retroviruses are known for several classes of vertebrates and are the oldest family of chicken endogenous retroviruses [15].

In the present work we studied a specificity of mentioned above endogenous retrovirus integration in the light of their evolutional age and expression.

Materials and Methods. *DNA, RNA isolation and compositional fractionation.* DNA was isolated from an adult liver and blood (chicken line CB (B12/B12)) after overnight digestion at 55 °C in 500 μl of extraction buffer (10 mM Tris, 400 mM NaCl, 2 mM EDTA, 2 % SDS, Proteinase K) and subsequent extraction by chloroform and precipitation by ethanol. The average size of DNA was 50 kb as determinated by electrophoresis.

Compositional fractionation of DNA by preparative centrifugation in CsCl density gradient and analytical centrifugation were carried out as previously described [16, 17].

Total RNA was prepared from 18-day old embryo fibroblasts and *v-src* induced tumors of chicken line CB (B12/B12) and examined by electrophoresis on formaldehyde-agarose gels.

Probes and hybridization. Determination of proviruses in DNA fractions was studied by hybridizations with three types of probes: 1) long probes (from 100 bp) known from literature data or obtained using PCR primers designed by program Primer3 (www-genome.wi.mit.edu/cgi-bin/primer); 2) oligonucleotide probes designed by Primer3; 3) genome of Rous sarcoma virus without src gene and 3'LTR [18] (table 1).

PCR conditions for primers ART.1, ART.2, PRO, JO, E51.1, E51.2 and H3, H4 have been previously described in papers referenced in table 1. PCR for primers designed by program Primer3 was carried out in a 50 μl volume containing 300 ng of genomic DNA, 200 μM dNTP, 0,2 mM of each primer and 2 units of Taq polymerase («Roche», France). DNA was denatured at 94 °C for 3 min and subjected to 30 cycles consisting of 1 min at 94 °C, 40 s at 56 °C, 40 s at 72 °C with the final extension of 7 min at 72 °C.

PCR products were cloned using TA-cloning kit («Promega», USA) and sequenced.

For hybridization, DNA was denaturated in 0,4 M NaOH and loaded (50 ng from each fraction) on «Hybond N+» membrane («Amersham», Great Britain). Hybridizations were carried out in Rapid-hyb solution («Amersham») in conditions recommended by manufacturer.

The hybridization, signals were evaluated with a PhosphorImager. The Gaussian curves of proviral distribution were obtained using a program IgorPro (from Wave Metrics Inc., USA).

RT-PCR. Reverse transcription was carried out using kit Roche and according to the protocol of manufacturer with 2 μg of RNA, 20 U AMV-reverse transcriptase and other necessary ingredients, at 42 °C for 1 h. PCR has been performed in 50 μl reaction mixture in the presence of 3 μl of cDNA, 2 U of Taq DNA polymerase («Sigma», USA), and various primers (ART.1, ART.2; H3, H4; E33.up, E33.down; E51.up, E51.down; PRO, JO (see table 1); evFLR3, evFLF3; EAV0-pol.1, EAV0-pol.2.

Primers evFLF3 (gtatatcaccgcgctgttggactct) and evFLR3 (gtcatcccttggggcaagacct) capable of amplifying *gag-pol* genes of ev-1 are from [22]; EAV0-pol.1 (cgggtgactgggaaattaga) and EAV0-pol.2 (tttcgcacatg-aagaacagc) were designed for *pol* gene of EAV-0 using program Primer3. PCR conditions for EAV0-pol.1 and EAV0-pol.2 were the same as for other primers designed by Primer3.

To verify RT-PCR products, Southern blot hybridization (with the same probes amplified from genomic DNA) in stringent conditions has been performed. In the case of ev-1, probe evgag-pol.1P (taacgc-aattagtggaaaaagaat) [22] were used.

EST databases analysis. Three chicken EST databases: 1) bursal library from Department of Cellular Immunology, Heinrich-Pette-Institute (Germany) [23, 24] at http://swallow.gsf.de/dt40Est.html;

2) BBSRC libraries [25] at http://www.chick.umist.ac.uk;

3) Delaware Biotechnology Institute database [26] at http://www.chickest.udel.edu were used for analysis of expression of chicken endogenous retroviruses.

Table 1
Probes for hybridization and PCR primers used for the detection of chicken endogenous retroviruses

Retrovirus	Probes and PCR primers (5'—3')	Specificity	Reference
ev loci	RSV (7030 bp)	ev loci	[18]
ART-CH	ART.1-ART.2* (922 bp)	ART-CH (sequence between LTRs)	[19]
	ART.1 tggataaaagaggcctgaa		
	ART.2 gttggcttcggtctgccaacg		
EAV-0	EAV0.1-EAV0.2 (135 bp)	EAV-0 (LTR)	Program Primer3
	EAV0.1 gggatgtaacgtgtcaggct		
	EAV0.2 atgatgagcggtaaaatggc		
HERV-I-related	PRO-JO (856 bp)	HERV-I-related (pol)	[20]
	PRO gt t/g tti g/t ti ga t/c aci ggi g/t c		
	JO ati agi a g/t a/g tc a/g tci ac a/g ta		
E-51	1) E51.up-E51.down (235 bp)	E-51 (env)	Primer3
	E51.up ttctctgggaggtccatgtt		
	E51.down tgccaacctttctatctgggg		
	2) E51LTR atcagctaattggtccagtgagcgcagaggc	E-51, E-33 (LTRs)	Primer3
E-33	1) E33.1-E33.2 (205 bp)	E-33, E-51, ART-CH (LTRs)	Primer3
	E-33.1 gctgccgagaaaacaagaaa		
	E-33.2 gccaaatgactgcaaacgta		
	2) E33LTR gaggaagcaactaaataaggcacgatgttatcagt	E-33, E-51, ART-CH (LTRs)	Primer3
EAV-HP	1) H3-H4 (548 bp)	EAV-HP, E-51 (env)	[21]
	H3 aacaacaccgatttagccagc		
	H4 caacacctctggctgttccc		
	2) HP.up-HP.down (160 bp)	EAV-HP (LTR)	Primer3
	HP.up tgtgttgtaggcgtagcgag		
	HP.down gtgaggcaaatggcgtttat		
	3) HPLTR gaggaaacacttgtatttaaacacgtagcc	EAV-HP (LTR)	Primer3

*Probes were designated by the names of PCR primers used for their preparation.

GeneBank accession numbers. The sequences described here have been obtained from the GeneBank/EMBL/DDLB databases as follows: ev-1 (AY-013303), ART-CH (L25262), EAV-HP (AJ238124), EAV-HP *pol* gene (AJ292967), EAV-0 (X59844, M31063), E-51 (M95189), E-33 (M95190), chicken HERV-I-related endogenous retrovirus (AY182230).

Results and Discussion. *Compositional analysis of chicken endogenous retroviruses.* Compositionally retroviruses belong in two classes: GC-poor class and GC-rich class [27, 28]. As it is shown in table 2, four chicken endogenous retroviruses — ev loci, ART-CH, EAV-HP and EAV-0 are GC-rich and therefore belong to the first class. Other three groups, thought the whole genomic structure is not identified, appear to be GC-poor.

Interestingly, GC-level of *gag*, *pol* and *env* genes are close to those of a whole genome. In contrast, LTRs are GC-poor even in GC-rich retroviruses (except EAV-HP); this fact is known for avian retroviruses only [27]. Therefore low GC-level of E-33 LTR may not indicate that E-33 belong to GC-poor class. However, since it demonstrates high percent similarity to E-51 [13], we can assume that E-33 is GC-poor.

E-51 and HERV-I-related retroviruses have GC-poor *env* and *pol* genes correspondingly. The later has been estimated on the basis of sequencing of HERV-I-related fragment from CB (B12/B12) chicken genome [29]. GC-poorness of this group was confirmed by compositional analysis of HERV-I present in human endogenous retrovirus database — http://herv.im-

Table 2
GC-content of chicken endogenous retroviruses

Retrovirus	GC content of				
	full provirus	LTR	*gag*	*pol*	*env*
ev-1	52.5	44.5	56.6	53.4	48.2
ART-CH	51.4	49.0	52.0[1]	—	—
EAV-HP	53.1	53.2	56.1	52.9	47.1
EAV-0	52.8	49.8	56.8[2]	53.7[2]	48.3
E-51	NI	46.0	NI	NI	46.1
E-33	NI	45.0	NI	NI	NI
HERV-I-related	NI	NI	NI	42.3	NI

NI — not identified; [1]GC-content of sequence between LTRs which contains part of *gag*; [2]sequences available from BBSRC EST clones.

g.cas.cz/ [30] and HERV-I-related retroviruses sequenced from genomes of other vertebrates [15]. Their GC-content range from 42 to 45 % GC.

The localization of chicken endogenous retroviruses in the host genome. e v l o c i. Using PCR assay [31] we have found out that genomic DNA of CB (B12/B12) chicken contain three ALV-related proviruses (ev loci): ev-1, ev-7 and ev-10 [32]. The probe for their detection on compositional DNA fractions (RSV genome without *src* gene and 3'LTR) is capable to hybridize with all of them. Two different hybridizations showed almost similar results: ev loci were centered in GC-rich fractions with peak at 55 % GC and 57 % GC (fig. 1) that corresponds to the border between isochore families H3 and H4. It matches very well high GC-level of ALV-related proviruses (table 2) and indicates isopycnic localization.

R e t r o t r a n s p o s o n A R T-C H. The hybridization with specific probe ART.1-ART.2 demonstrates three peaks of ART-CH localization: at 55 % GC, 59 % GC and 64 % GC (fig. 1) and indicates that GC-rich ART-CH distributed mainly in GC-richest isochores H3 and H4.

E A V-0. There is a peak of EAV-0 distribution obtained with LTR specific probe: at 48 % GC (isochore H2) (fig. 1), which matches GC-content of the complete provirus (52.8 % GC).

H E R V-I-r e l a t e d r e t r o v i r u s e s. GC-poor proviral sequences were centered at 42 % GC and 49 % GC (fig. 2). Interestingly, the first peak exactly matches GC-level of hybridization probe (42.3 % GC) which represents parts of *pro* and *pol* genes. Peak corresponds to GC-poor isochore L2 and to the H2. It is possible that the second peak is due to the retroviral reintegration.

E-51. GC-poor E-51 (46 % GC) shows peaks of distribution at 46—47 % GC as it is demonstrated by hybridization with probes E51.up-E51.down and E51LTR (fig. 2). Therefore, we define the localization of E-51 in isochore H1 as isopycnic.

E-33. We used two probes with different specificity to detect E-33 LTR in DNA from liver because E-33 genes has not been sequenced yet.

Probes E33LTR and E33.1-E33.2 reveal three peaks: at 39 % GC, 47 % GC and 55—56 % GC (fig. 3). Since probes are not specific to E-33 and could detect also ART-CH and E-51 (table 1), it is possible to assume that 47 % GC peak corresponds to E-51 and 55—56 % GC peak — to ART-CH. Therefore GC-poor peak at 39 % GC, which belong to the border of isochores L1 and L2, is a real place of E-33 localization.

E A V-H P. GC-rich provirus EAV-HP (53.1 %) is present both in GC-rich and GC-poor isochores (fig. 4).

Hybridization on liver DNA demonstrates three peaks of proviral distribution: peak in GC-rich part (57—58 % GC) (border of isohores H3 and H4) which matches GC level of full retrovirus (53.1 %), and two other peaks located at the border of isochores L1 and L2 (39—40 % GC) and H1-H2 (47—48 % GC).

All peaks of EAV-HP proviral sequences distribution in DNA from blood cells were slightly shifted towards GC-poor part: they were observed at

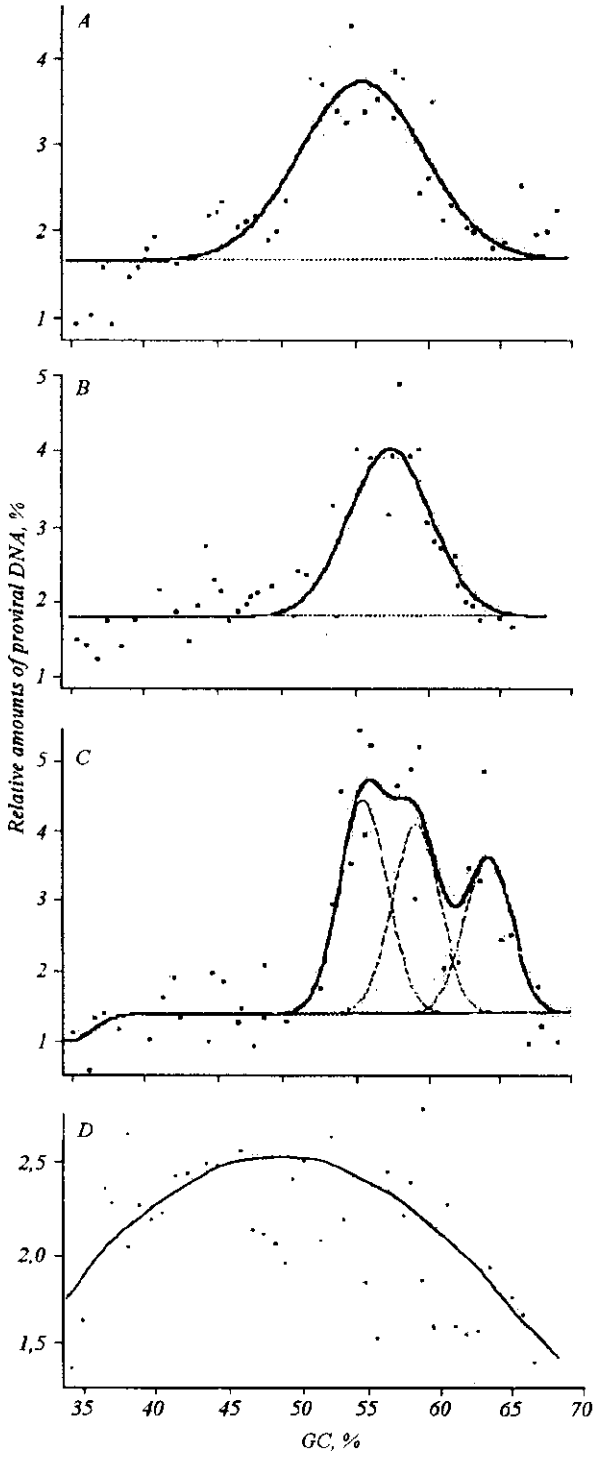

Fig. 1. Distribution of ALV-related proviruses (*A*, *B*), retrotransposon ART-CH (*C*) and retrovirus EAV-0 (*D*) in the chicken DNA from blood

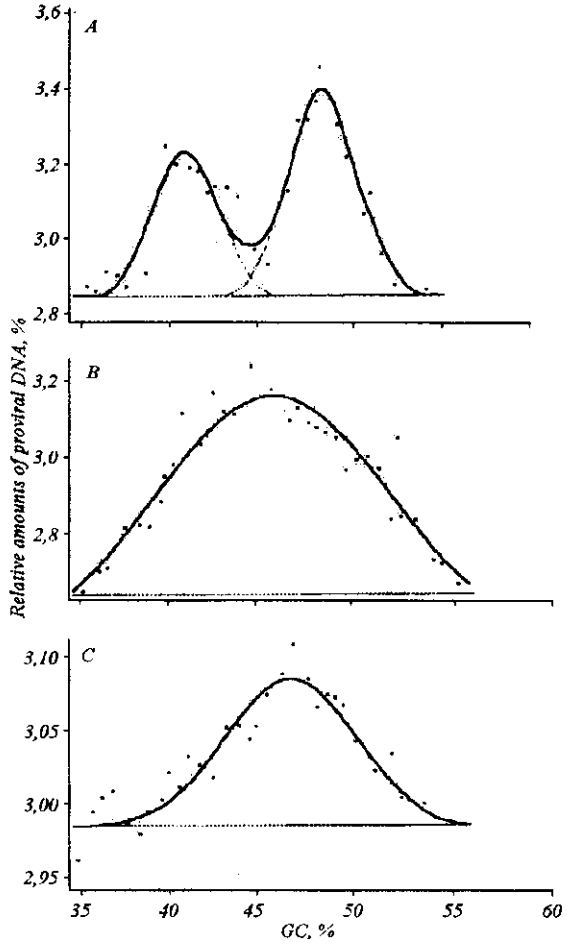

Fig. 2. Distribution of HERV-I-related proviruses (*A*) and retrovirus E-51 (*B*, *C*) in chicken DNA from blood: *B* — hybridization with probe E51.up-E51.down; *C* — hybridization with probe E51LTR

37—38 % GC (isochore family L1), 45 % GC (L2) and 53 % GC (H3).

It should be mentioned that such shift could be due to the different specificity of hybridization probes used in both cases: probe used to determine EAV-HP sequences in DNA from blood cells could also reveal E-51 sequences.

Expression of chicken endogenous retroviruses. RT-PCR and subsequent hybridization demonstrated expression of five chicken endogenous retroviruses (E-51, E-33, EAV-0, EAV-HP, HERV-I-related) in embryonic fibroblasts and *v-src* induced tumors (fig. 5). The sizes of hybridization bands were identical in both cases. We did not find out expression of ev-1 and ART-CH in these tissues. Others ALV-related retroviruses present in the genome of CB (B12/B12) chicken — ev-7 and ev-10 were not studied for expression since their sequences are not known.

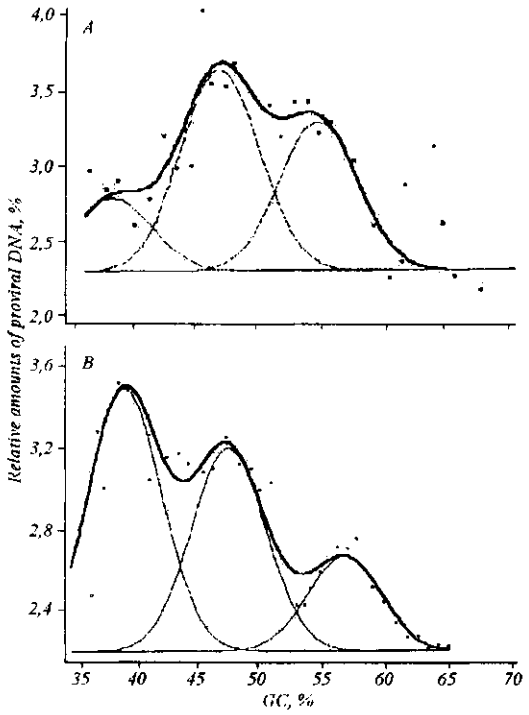

Fig. 3. Hybridization of E-33 with probes E33LTR (*A*) and E33.1-E33.2 (*B*) on the chicken DNA from liver

Expression in other tissues was studied by analysis of EST databases. In total, proviral sequences were found in 21 tissues and cell types (table 3). HERV-I-related proviruses and E-33 seem not express in tissues present in databases. However expression of E-33 remain to be obscure, because only LTR (the only sequenced part) has been used for searching EST clones. Retroviral transcripts were not found in muscle tissue and macrophage cells.

Both in liver and blood cells, which we used for localization of proviruses, expression was observed. In liver, EAV-HP, HERV-I-related proviruses, E-33 and E-51 were not express. In blood cells, such as B-cells, T-cells, intestinal lymphocytes and in lymphoid tissue EAV-0, E-33 and HERV-I-related sequences were not found.

Besides tissue-specificity of expression, the presentation of different retroviral genes in EST databases is non-uniform. ev loci expressed mainly in pancreas and heart; truncated *pol*-transcripts are present in a minor quantity. ART-CH transcripts include the whole length of retrotransposon; they were found in adult cerebrum and 16-day embryo brain thought brain expression has not been iden-

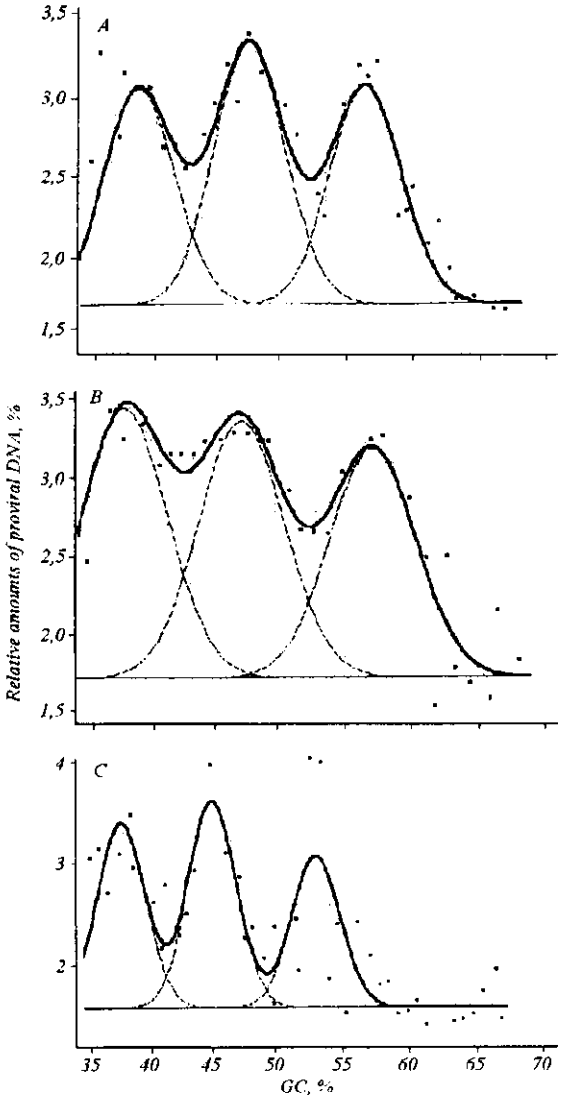

Fig. 4. Hybridization of provirus EAV-HP with probes HPLTR (*A*), HP.up-HP.down (*B*) and H3-H4 (*C*) on the chicken DNA from liver (*A*, *B*) and blood (*C*)

tified before [19]. The majority of EAV-0 transcripts were *env*-specific; there were also *pol*-sequences, which had not been found in other retroviruses, and *gag*-sequences not known before. EAV-HP expressed mainly in pancreas as *env*-specific transcripts which have been observed more frequent then *gag*-specific transcripts.

The localization of seven groups of chicken endogenous retroviruses in compositional fractions as well as correlation between the isochore localization and their transcription have been studied.

The proviral distribution seems to be compartmentalized and isopycnic: GC-rich ev loci, ART-CH

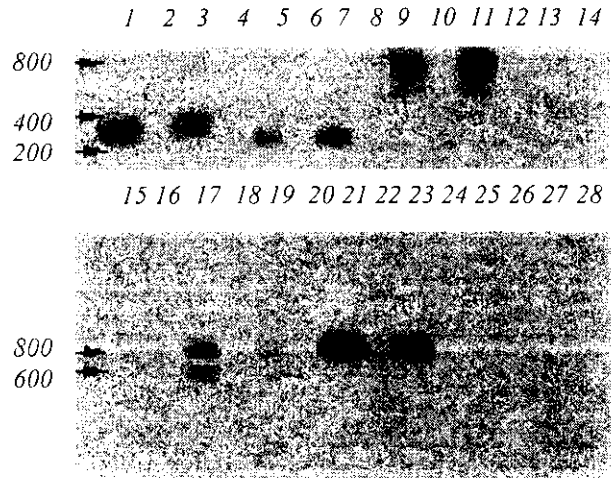

Fig. 5. Hybridization of RT-PCR products of chicken endogenous retroviruses: *1—4* — EAV-0; *5—8* — E-51; *9—12* — EAV-HP; *13—16* — ev-1; *17—20* — HERV-I-related proviruses; *21—24* — E-33; *25—28* — ART-CH. Uneven digits: RT-PCR on RNA from fibroblasts and from tumor; even digits: control (without reverse transcriptase)

and EAV-0 have been found mainly in GC-richest isochores H2, H3 and H4 approximately matching the viral genome in base composition. GC-poor HERV-I-related proviruses, E-51 and probably E-33 localized in GC-poor isochore families L1, L2 and in lowest GC-rich H1. GC-rich EAV-HP, except expected peak in GC-rich isochores, has also peaks in GC-poor compartments.

The main thing we can conclude from study of expression of chicken endogenous retroviruses is that expression is tissue-specific. For instance, EAV-HP, unlike other proviruses, has high level of expression in pancreas but was not expressed in liver. ART-CH and ev-1 transcribes in almost all tissues studied except embryonal fibroblasts. In contrast, embryo fibroblasts is the only cell type where the expression of HERV-I-related proviruses have been found.

Different level of expression may affect the picture of proviral localization, since after transcription retrovirus may integrate in new sites of the host genome. Deleted proviruses with inactive *pol* gene use reverse transcriptase of a helper virus [19, 33]. Analysis of EST databases showed that considerable amount of *pol*-transcripts belongs to EAV-0, which, along with structurally complete ev loci, may be the main provider of reverse transcriptase in the chicken genome. Indeed, as it has been demonstrated by Weissnahr et al. [34], EAV-0 is able to produce virus-like particles with an active reverse transcriptase. Taking into account tissue-specific expression and possibility of reintegration, it is not surprisingly that picture of proviral localization may be different in different tissues even for one retrovirus.

An obvious possibility for compartmentilized, isopycnic integration of retroviral sequences, which lack oncogenes, is that this is the result of selection for certain integration sites, the activation of an oncogene providing a replicative advantage to the infected cell [5]. However, since endogenous retroviruses, unlike exogenous ones, do not activate oncogenes and appear do not have any function at all (see [13] for review), the host cell cannot obtain any advantages from their integration. In this case, reasons of compartmentalization can be comparable to that of interspersed repeats, another permanent component of the genome. Olofson and Bernardi [35] demonstrated that the base composition of CR1 (48 % GC), which is an ancient class of non-LTR retrotransposons from the chicken genome, matches that of isochore H1, mainly harboring it. As in the case of mammalian Alus, LINES and chicken CR1, factors of endogenous retrovirus isopycnicity are likely to be the compositional match between the integrant and the chromosomal region of the host, and the degree of interference of the integrated sequences with the function of neighboring genes [28].

Another question then concerns the reasons of EAV-HP non-isopycnic localization. In general, proviral localization not in isopycnic chromosomal environment, known for exogenous retroviruses activating oncogenes, suggests that selection for a replicative advantage can override isopycnic integration. Examples of such integration has been found in the case of MMTV activating *Wnt/int* oncogene (reviewed in [5]).

Preferential expression of EAV-HP in pancreas resembles tissue-specific, hormone-dependent and developmentally regulated manner known for MMTV [10]. In addition, GC-poor isochores, where EAV-HP was also found, contain more tissue-specific and developmentally-regulated genes then the GC-rich ones [4].

Thus EAV-HP may have an unknown function associated with genes located in GC-poor isochore families. It is known that some human endogenous retroviruses have developmental functions [36].

We can partially confirm the finding known for MMTV and Alus: «the older retroelement, the stron-

Table 3
Expression of chicken endogenous retroviruses in different tissues (on the basis of EST databases analysis)

Tissue[1]	Retrovirus				
	ev-1	ART-CH	EAV-0	EAV-HP	E-51
1. Adult pancreas	+			+	
2. Adult heart	+	+	+	+	
3. Adult liver	+	+	+		
4. Adult cerebrum	+	+			+
5. Adult cerebellum	+			+	
6. Adult brain-other parts	+			+	+
7. 16-day embryo brain	+	+			
8. Adult small intestine	+			+	
9. Adult kidny and adrenal	+	+	+	+	
10. Ovary	+	+	+	+	+
11. Chondrocytes		+			+
12. Embryonal stage 10	+	+	+	+	
13. Embryonal stage 20-21	+	+	+	+	
14. Embryonal stage 22	+	+	+	+	
15. Embryonal stage 36	+	+	+	+	+
16. Fat	+	+	+	+	
17. Splenic T-cell	+				
18. Lymphoid tissue[2]	+				
19. Pituitary tissue[3]	+				
20. Intestinal lymphocytes		+		+	
21. Bursa				+	+

[1]Tissues 1—15 are from BBSRC database; 16—19 are from University of Delaware database; 20 is from GeneBank (accession numbers: CD734212; CD737734; CD739800); 21 is from Heinrich-Pette-Institute (Germany); [2]Lymphoid tissue contains mixture of thymus, bursa, spleen, peripheral blood lymphocytes and bone marrow; [3]pituitary tissue contains mixture of pituitary gland, hypothalamus and pineal gland; + — retroviral sequences were found.

ger bias of its localization towards isopycnic regions» [10, 11]: ev loci (52.5 % GC) centered at 55—57 % GC in the chicken genome (isochores H3-H4) whereas related to them exogenous RSV (54 % GC) has peak of distribution in hamster genome at 50 % GC (isochore H2) [7]. In contrast, proviruses older that ev loci (EAV-0, E-51, E-33, EAV-HP and especially HERV-I-related retroviruses, which seem to be the most ancient family) localized in GC-poorer regions mainly matching their composition.

Thus the results present here shows three variants of chicken endogenous retrovirus localization: 1) GC-rich proviruses (ev loci, ART-CH, EAV-0) localized in GC-rich isochores; 2) GC-poor proviruses (HERV-I-related, E-51, E-33) localized in GC-poor isochores; 3) GC-rich EAV-HP localize both in GC-rich and GC-poor isochores. These findings suggest the stability of integration in compositionally matching environment or, in the case of EAV-HP, may be due to the interference with neighboring genes.

Acknowledgements. This research was supported by a NATO grant (LST.CLG9/6685). We thank M. Costantini, G. Bucciarelli, G. Wronka and L. Tsyba for assistance with the preparation of gradients, Dr J. Heinar and V. Stepanets for providing RNA and DNA.

Л. Г. Борисенко, А. В. Риндич, Дж. Бернарді

Розподіл та експресія ендогенних ретровірусів курки у геномі хазяїна

Резюме

Розподіл семи груп ендогенних ретровірусів (ALV-родинні, HERV-I-родинні, EAV-HP, EAV-0, E-33, E-51, ART-CH) у геномі курки досліджували у зв'язку з композиційним складом

(варіюванням GC-вмісту) геному хазяїна. GC-багаті ретровіруси (ALV-родинні, ART-CH та EAV-0) локалізовані, головним чином, в GC-найбагатших родинах ізохор H2, H3 і H4, GC-бідні HERV-I-родинні провіруси, E-51 та E-33 локалізовані в GC-бідних родинах ізохор L1, L2, а також в H1 (ізопікнічність). GC-багатий ретровірус EAV-HP, окрім очікуваної наявності в GC-багатих ізохорах, присутній також в GC-бідних компартментах. Дослідження експресії шляхом RT-PCR, а також аналіз баз даних EST свідчать, що експресія ендогенних ретровірусів курки може бути тканиноспецифічною. Це, в свою чергу, може впливати на картину провірусної локалізації внаслідок реінтеграції. Причиною ізопікнічної локалізації ендогенних ретровірусів є композиційна відповідність між інтегрованою послідовністю та хромосомною ділянкою хазяїна, що забезпечує стабільність інтеграції.

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Распределение и экспрессия эндогенных ретровирусов курицы в геноме хозяина

Резюме

Распределение семи групп эндогенных ретровирусов (ALV-родственные, HERV-I-родственные, EAV-HP, EAV-0, E-33, E-51, ART-CH) в геноме курицы исследовали в связи с композиционным составом (варьированием GC-содержания) генома хозяина. GC-богатые ретровирусы (ALV-родственные, ART-CH и EAV-0) локализованы, главным образом, в наиболее GC-богатых семействах изохор H2, H3 и H4, GC-бедные HERV-I-родственные провирусы, E-51 и E-33 локализованы в GC-бедных семействах изохор L1, L2, а также в H1 (изопикничность). GC-богатый ретровирус EAV-HP, кроме ожидаемого наличия в GC-богатых изохорах, присутствует также в GC-бедных компартментах. Исследование экспрессии с помощью RT-PCR, а также анализ баз данных EST свидетельствуют о том, что экспрессия эндогенных ретровирусув курицы может быть тканеспецифичной. Это, в свою очередь, может влиять на картину провирусной локализации вследствие реинтеграции. Причиной изопикничной локализации эндогенных ретровирусов является композиционное соответствие между интегрированной последовательностью и хромосомным участком хозяина, что обеспечивает стабильность интеграции.

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УДК 577.21:578.26
Надійшла до редакції 14.11.03