Kuidas keskkonnast tekivad geenid?

Aare Abroi
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Metagenomic Analysis of the Viral Communities in Fermented Foods[▽]†

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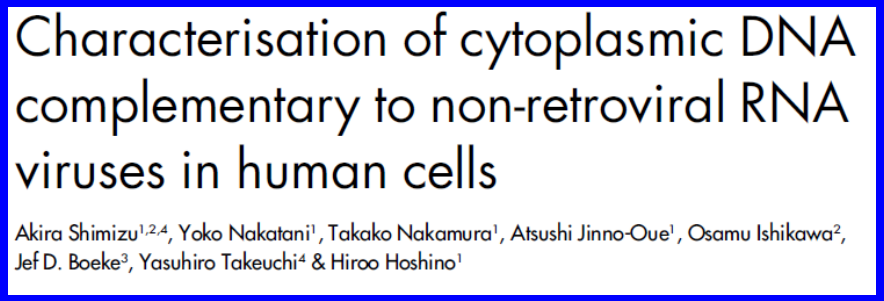
Viruses are recognized as the most abundant biological components on Earth, and they regulate the structure of microbial communities in many environments. In soil and marine environments, microorganism-infecting phages are the most common type of virus. Although several types of bacteriophage have been isolated from fermented foods, little is known about the overall viral assemblages (viromes) of these environments. In this study, metagenomic analyses were performed on the uncultivated viral communities from three fermented foods, fermented shrimp, kimchi, and sauerkraut. Using a high-throughput pyrosequencing technique, a total of 81,831, 70,591 and 69,464 viral sequences were obtained from fermented shrimp, kimchi and sauerkraut, respectively. Moreover, 37 to 50% of these sequences showed no significant hit against sequences in public databases. There were some discrepancies between the prediction of bacteriophages hosts via homology comparison and bacterial distribution, as determined from 16S rRNA gene sequencing. These discrepancies likely reflect the fact that the viral genomes of fermented foods are poorly represented in public databases. Double-stranded DNA viral communities were amplified from fermented foods by using a linker-amplified shotgun library. These communities were dominated by bacteriophages belonging to the viral order *Caudovirales* (i.e., *Myoviridae*, *Podoviridae*, and *Siphoviridae*). This study indicates that fermented foods contain less complex viral communities than many other environmental habitats, such as seawater, human feces, marine sediment, and soil.

Pealkirjas esitatud küsimus on igati õigustatud kui me käsitleme viiruseid osana (elu)keskkonnast.

Kui me käsitleme virosfääri kui geenide ja geneetilise mitmekesisuse ladu, siis ei saa küsimust muidugi niimoodi püstitada.

Ettekanne põhineb valdavalt kahel artiklil:

http://www.ncbi.nlm.nih.gov/pubmed/24875540
http://www.ncbi.nlm.nih.gov/pubmed/24992257



Characterisation of cytoplasmic DNA complementary to non-retroviral RNA viruses in human cells

Akira Shimizu[1,2,4], Yoko Nakatani[1], Takako Nakamura[1], Atsushi Jinno-Oue[1], Osamu Ishikawa[2], Jef D. Boeke[3], Yasuhiro Takeuchi[4] & Hiroo Hoshino[1]

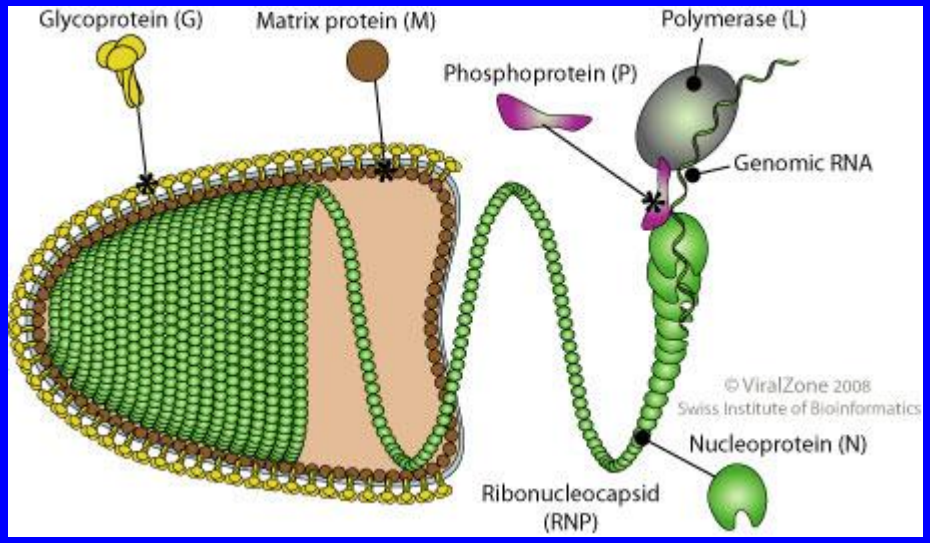
Scientific Reports 2014

Soma-to-Germline Transmission of RNA in Mice Xenografted with Human Tumour Cells: Possible Transport by Exosomes

Cristina Cossetti[1], Luana Lugini[2], Letizia Astrologo[3], Isabella Saggio[3], Stefano Fais[2], Corrado Spadafora[1]*

PlosOne 2014

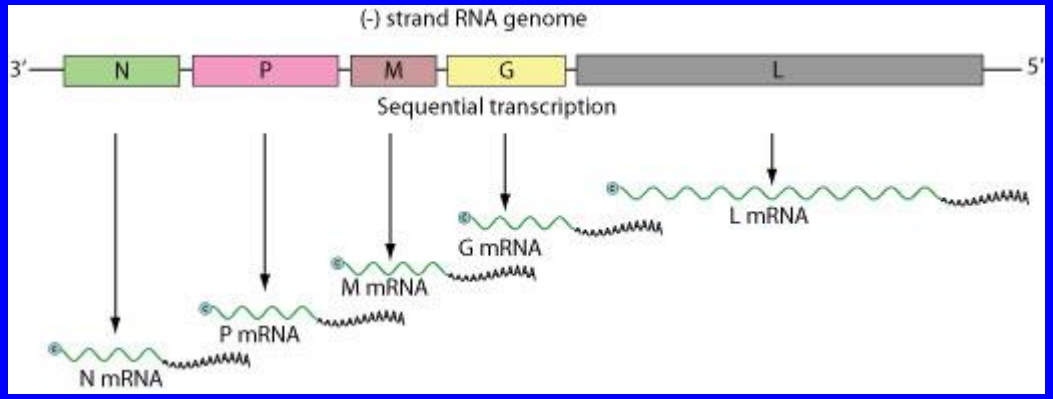
Kas RNA viirustest tehakse DNA-d?



Vesicular stomatitis virus

-ssRNA virus

Cytoplasmic replication without DNA intermediate



Close relative of Rabies virus

Negative-stranded RNA linear genome, about 11-15 kb in size. Encodes for 5 to six proteins.

RNA viiruse RNA-ga komplementaarne DNA on detekteeritav rakkudes

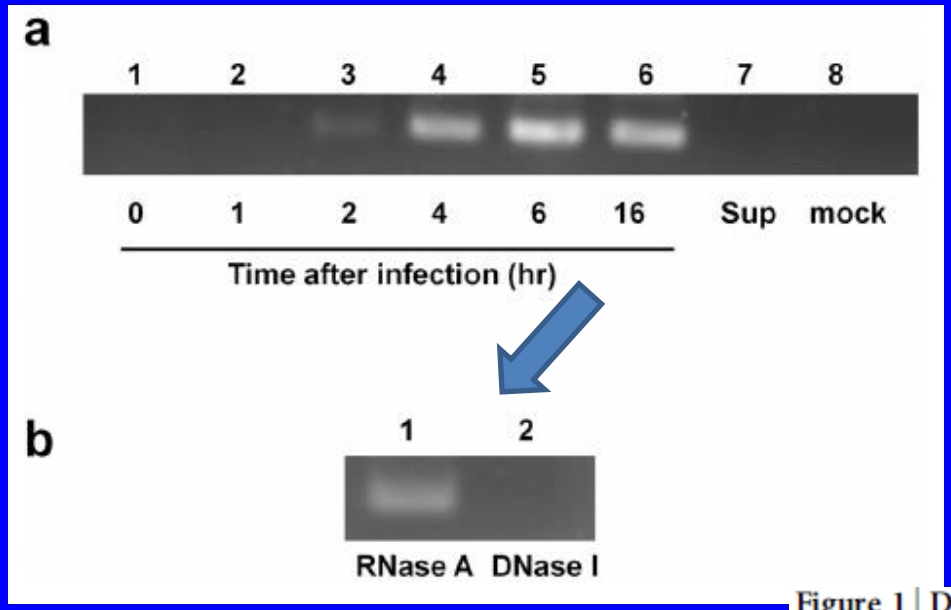
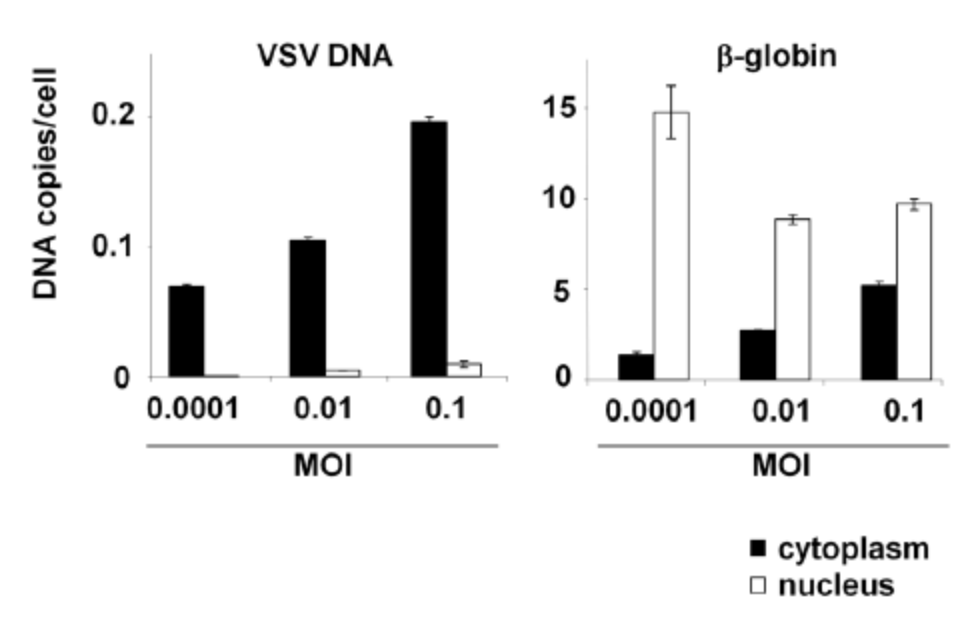
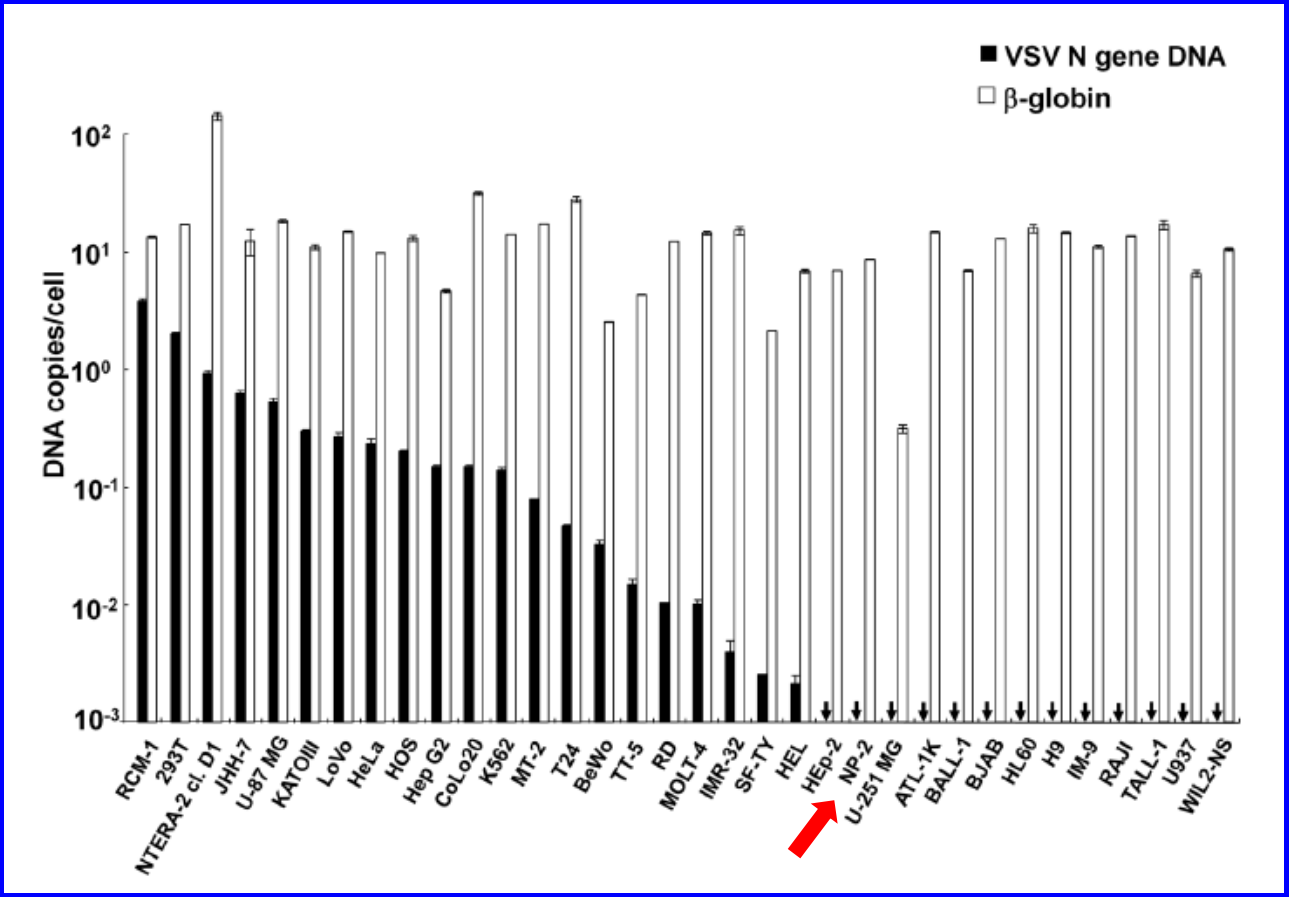


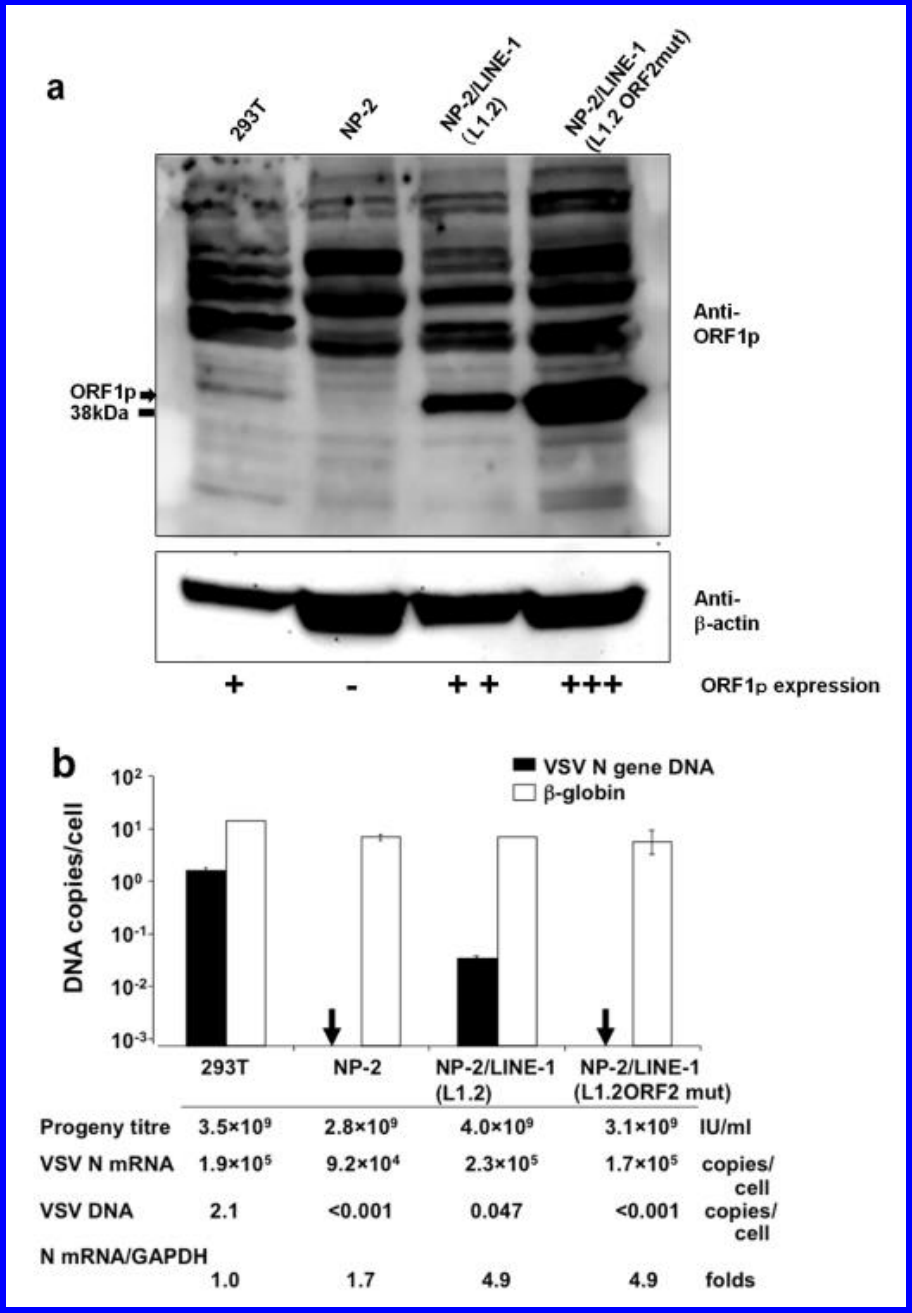
Figure 1 | Detection of VSV DNA in 293T human cells. (a) DNA was extracted from 293T cells at 0, 1, 2, 4, 6, or 16 hr after infection with VSV at an MOI of 0.1 and subjected to PCR amplification for the VSV N gene using the N478-F/N681-R primer pair. The VSV inoculum (Sup) (lane 7) and mock-infected samples (lane 8) were included as controls. The samples prepared 1 hr after inoculation (lane 2) or VSV Sup did not produce VSV DNA. The DNA sequence of the PCR product obtained from the cells harvested at 16 hr post-infection (lane 6) was verified to be the expected VSV N amplicon. (b) DNA samples were harvested at 16 hr post-infection and were treated with RNase A or DNase I and subsequently used for PCR. The VSV DNA was not detected after DNase I treatment (lane 2). All samples used in Figures 1a and 1b were prepared in a single experiment, and cropped gel images are shown.

RNA viirusega komplementaarne DNA on ennekõige tsütoplasmas.



RNA viirusega komplementaarset DNA tekib paljudes, kuid mitte kõikides rakkudes



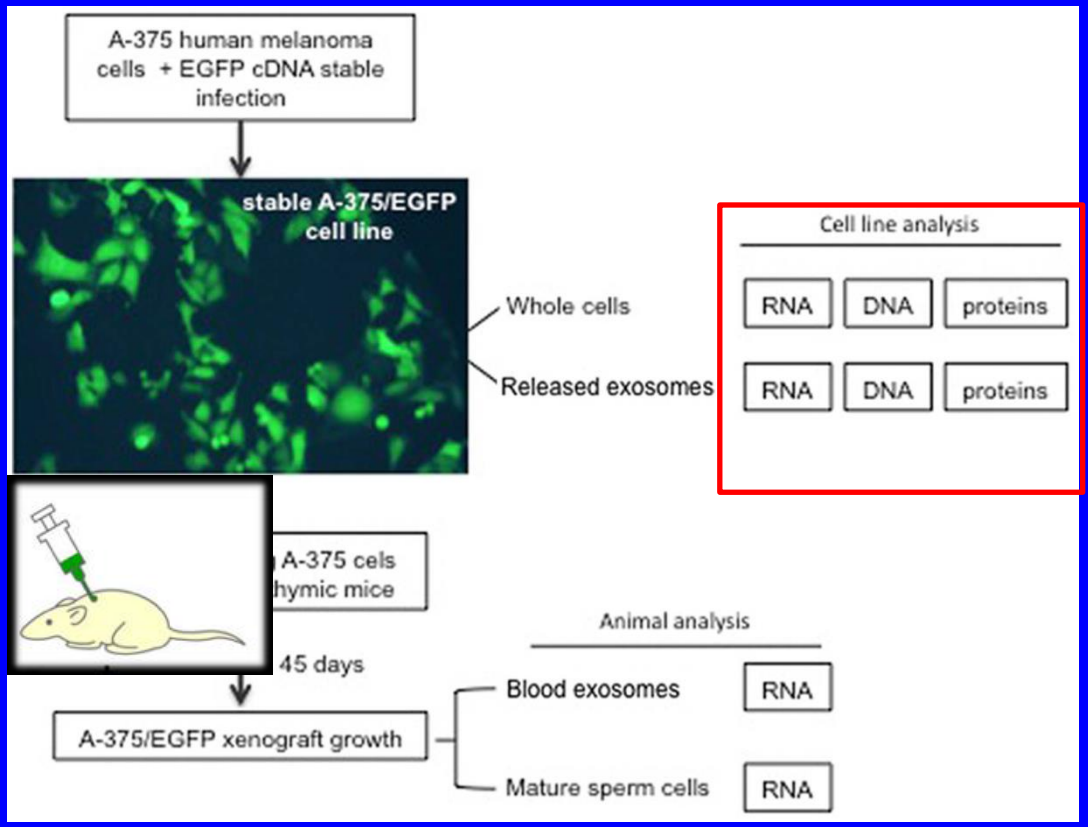


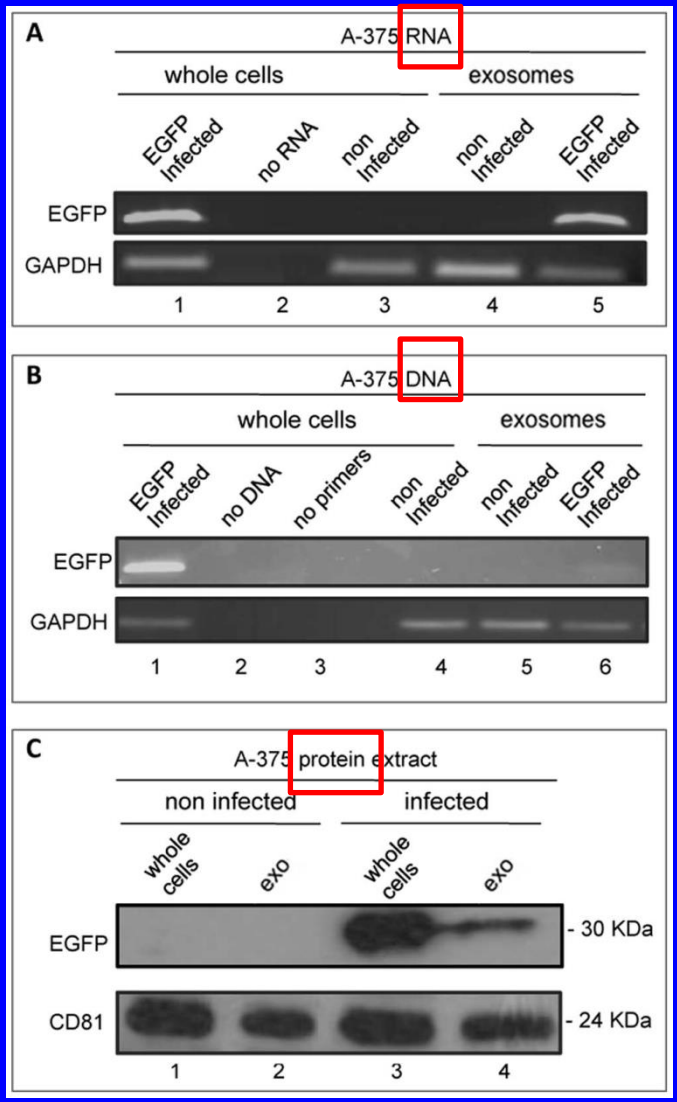
Pöördtranskriptaase aktiivsuse viimine rakkudesse (LINE-1) viib viirusega komplementaarse DNA tekkeni

RNA viirustest (keskkonnast) võib saada DNA (geen), aga kuidas ta genoomi saab või kinnistub, eriti läbi idutee paljunevate organismide puhul?

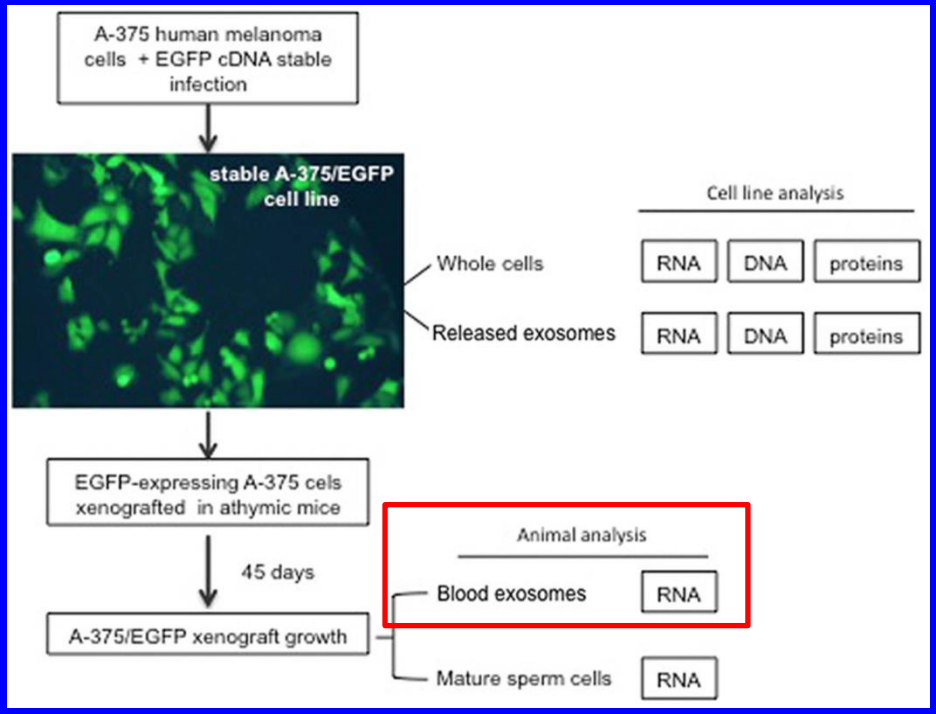
A growing body of data now supports the view that genetic information can be transmitted via non-Mendelian transgenerational inheritance, a phenomenon in which traits unlinked to chromosomal genes are transmitted to the progeny, generating persistent phenotypes.

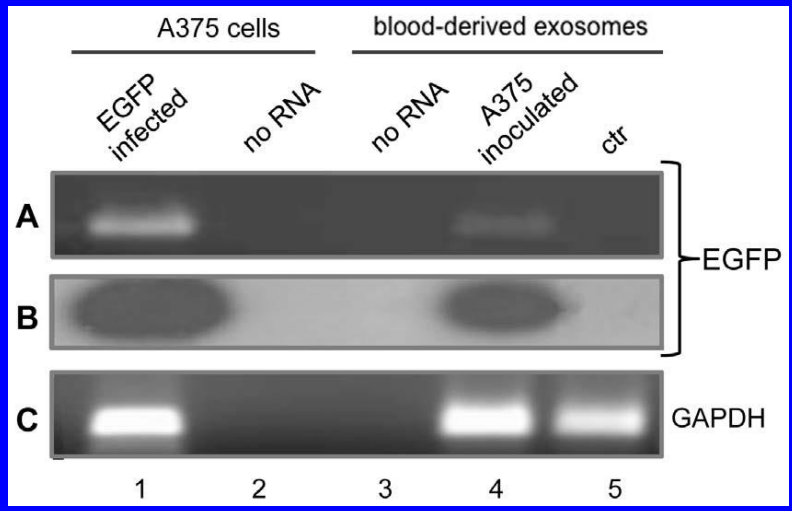
EGFP-d ekspresseeriva rakuliini eksosoomid sisaldavad EGFP RNAd



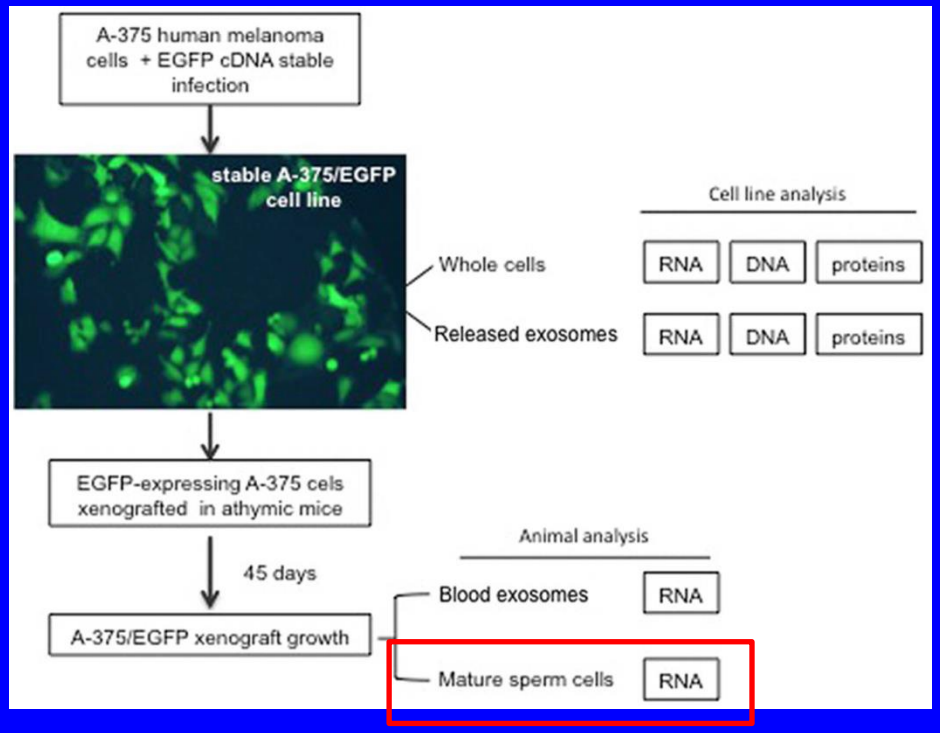


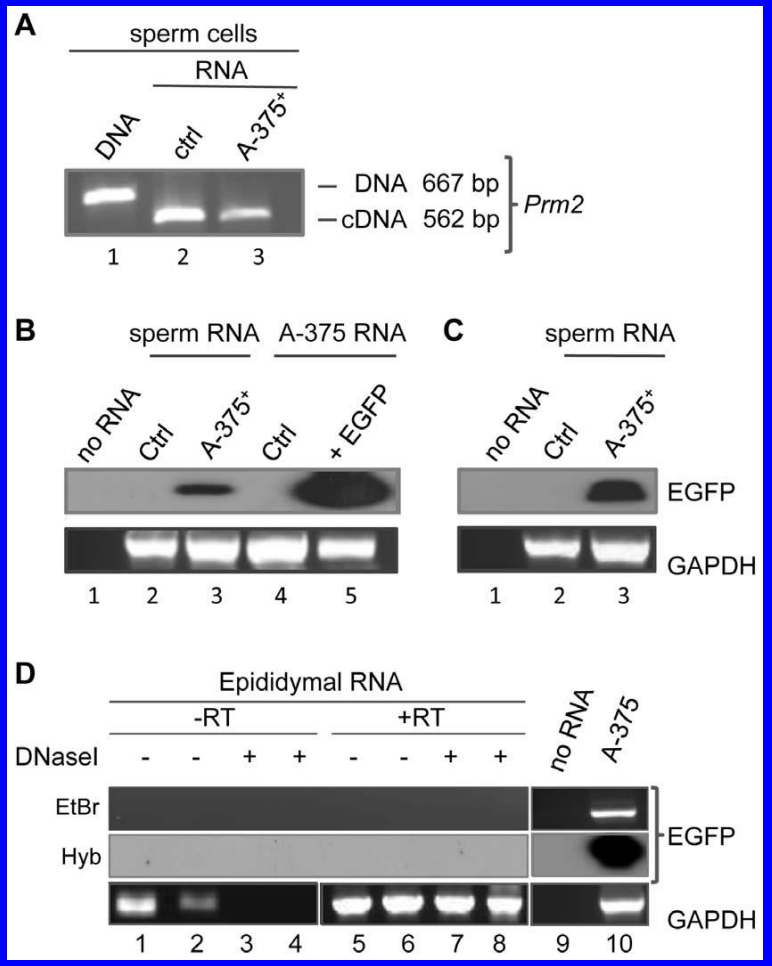
Ksenograftiga organismi eksosoomid sisaldavad EGFP RNA-d





Ksenograftiga organismi spermatosoidid sisaldavad EGFP RNA-d





In conclusion, this work reveals that a flow of information can be transferred from the soma to the germline, escaping the principle of the Weismann barrier which postulates that somatically acquired genetic variations cannot be transferred to the germline.

Samasugune geeni-voog saab rakenduda ka viiruste nukleiinhappele.

Kui pruunisilmsetel vanematel on sinisilmne laps siis tuleb vaid õige viirus üles leida ☺.

Embrüogeneesis on retroelemendid aktiivsed.

Ja lõpetuseks törts bioinformaatika juttu ka.

Kui organismides tõepoolest hulbib ringi igatsugu „genoomi-välist“ DNA-d ja RNA-d, kas NGS andmetest on võimalik see nukleiinhape üles leida ja annoteerida?

Ning eristada seda tehnoloogilisest saastusest?