

Разбор зарубежных статей. Поиск статей, методов работы.



Преподаватель: старший преподаватель
кафедры молекулярной биологии и генетики,
PhD, Смекенов И.Т.

Дисциплина: Рекомбинация ДНК

(Лекция 10)

ЦЕЛЬ ЛЕКЦИИ

Научиться эффективно искать и отбирать релевантные зарубежные статьи по заданной тематике в базах WoS, Scopus и оценивать журналы по Scimago. Освоить стандартизированный разбор методической части статей для воспроизводимости и применения в собственной работе. Сформировать умение критически оценивать качество, валидность и влияние публикаций (библиометрия, цитирование, IF/SJR).

Задачи

- ✓ Сформулировать точный поисковый запрос (ключевые слова, синонимы, булевы операторы).
- ✓ Провести систематический поиск в WoS и Scopus, настроить фильтры по дате, типу статьи, предметной области и языку. Оценить журналы и статьи по метрикам Scimago (SJR), индексам цитирования и х-индексу.
- ✓ Выделить и структурировать методические разделы (протоколы, условия, репликаты, статистика).
- ✓ Провести критическую оценку методов: воспроизводимость, контроль, возможные биас-факторы.
- ✓ Составить сводную таблицу по найденным статьям: цель, методы, ключевые результаты, сильные/слабые стороны.
- ✓ Подготовить рекомендации по адаптации и внедрению лучших методов в собственные исследования.

Ключевые термины

Поиск литературы, PubMed, Web of Science, Scopus, Google Scholar, MeSH, Булевы операторы (AND, OR, NOT), фильтры, DOI, PMID, препринт, рецензирование, раздел методов, воспроизводимость, повторы, элементы управления, протокол, дополнительные данные, PRISMA, систематический обзор, метаанализ, менеджер цитирования, Zotero, Mendeley, EndNote, плагиат, статистическая мощность, проверка размера выборки, рандомизация, ослепление, ARRIVE, CONSORT, открытый доступ, совместное использование данных, принципы FAIR.

- 1) Эффективный разбор статей начинается с хорошо продуманной стратегии поиска: грамотный выбор ключевых слов, использование булевых операторов и фильтров в WoS/Scopus существенно экономит время и повышает качество отбора.
- 2) Scimago (SJR) и сопутствующие метрики помогают отделить журналы с высоким импакт-фактором и релевантностью, но не заменяют критической оценки методологии конкретной статьи.
- 3) Для воспроизводимости исследования ключевыми элементами являются: подробное описание протоколов, концентрации/условий, численность повторов, статистические методы и доступ к сырьевым данным (raw data).
- 4) Критическая оценка методов включает проверку контроля (позитивного/негативного), рандомизации, слепого анализа и оценки источников биасов.
- 5) Систематический разбор статей и сводная таблица по методам позволяют быстро выделять повторяющиеся удачные решения и потенциально проблемные подходы для адаптации в собственной лаборатории.



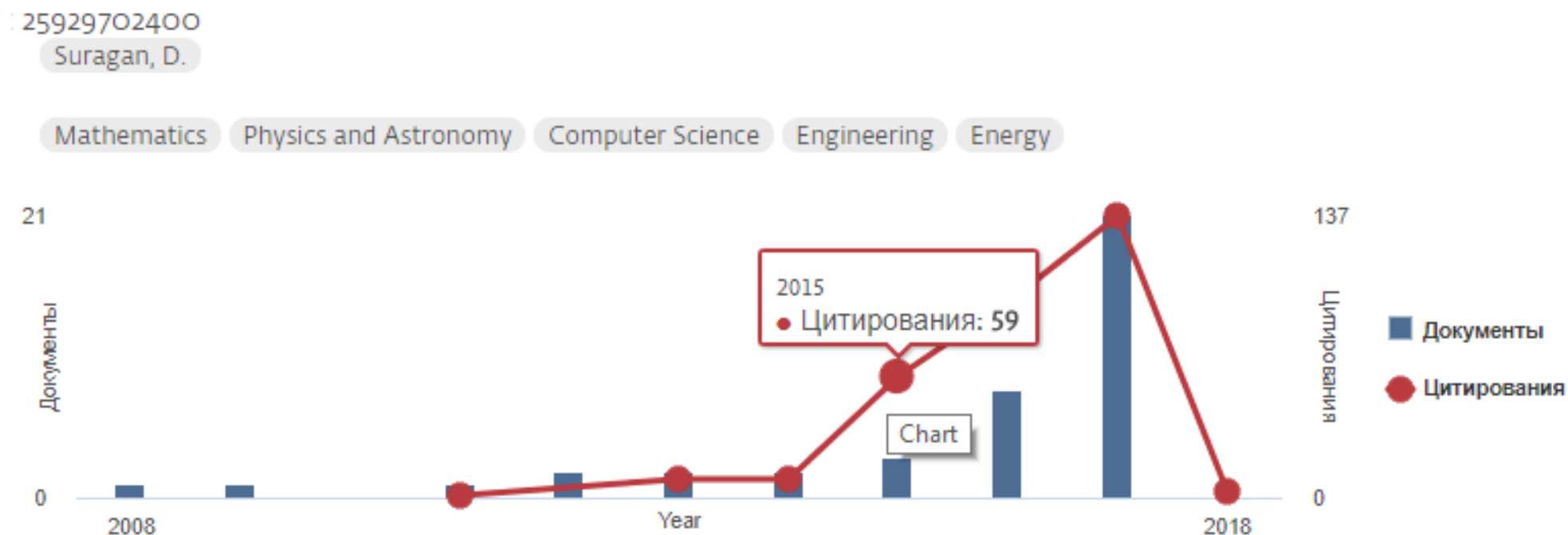
ОСНОВНЫЕ ВОПРОСЫ

- 1) Как правильно составить поисковый запрос для WoS/Scopus, чтобы минимизировать пропуски релевантных статей?
- 2) Как оценивать качество журнала и статьи: какие метрики Scimago/SJR/IF важны и какие ограничения у этих метрик?
- 3) Как оценивать статистическую достоверность результатов и корректность использованных тестов?
- 4) Как выявлять и учитывать возможные источники систематической ошибки и биасов в методах?
- 5) Какие критерии включения/исключения статей использовать при формировании набора для обзора?
- 6) Как оформить таблицу извлечённых данных (какие поля обязательны: авторы, год, цель, образец, методы, условия, n, результаты, замечания)?
- 7) Как осуществлять поиск дополнительных данных (дополнительные файлы, сырьевые данные) и при необходимости — связываться с авторами?
- 8) Какие этические и юридические аспекты учитывать при репликации экспериментальных методов (условия биоэтики, лицензии на протоколы, патенты)?
- 9) Как интегрировать найденные методы в свою лабораторию с учётом оборудования, регламентов безопасности и бюджета?

- **Научная статья (Article)** – опубликованное в научном издании авторское произведение, описывающее результаты промежуточного или законченного оригинального научного исследования (первичная научная статья) или посвященное рассмотрению ранее опубликованных научных статей, связанных общей темой (систематический обзор).



- Публикация в научном журнале позволяет представить и оперативно распространить в научном сообществе результаты исследований.
- Качественная научная статья в авторитетном российском или зарубежном журнале, индексируемом в международных наукометрических базах данных, дает возможность привлечь внимание к исследованию автора и получить высокие показатели цитируемости.



- Целью каждой публикуемой научной статьи является представление оригинальных результатов исследований с использованием материалов и методов, соответствующих определенным областям знания.



Чтобы вызвать интерес к своей работе, ученые должны использовать общепринятые нормы написания статьи. Любой ученый, стремящийся опубликовать свою работу в предполагаемом международном научном журнале, должен учиться использовать эти нормы должным образом.

• **В международном научном сообществе применяется формат научной статьи об оригинальных экспериментальных исследованиях:**

- **Title** – Название;
- **Abstract** – Аннотация;
- **Keywords** – Ключевые слова;
- **Highlights** – Основные положения;
- **Introduction** – Введение;
- **Methods** – Методы;
- **Results** – Результаты;
- **Discussion** – Обсуждение;
- **Conclusion** – Заключение;
- **Funding** – Информация о финансировании;
- **Acknowledgements** – Благодарности;
- **References** – Список литературы.

- Данный формат основан на простой логике: в каждом разделе статьи содержится ответ на определенный вопрос.
- «Какой проблеме посвящено исследование?» – отвечает раздел «Введение».
- «Как изучалась проблема?» – ответ дан в разделе «Методы».
- «Каковы основные находки или открытия?» – ответ можно найти в разделе «Результаты».
- «Что означают полученные результаты?» – отвечает раздел «Обсуждение».



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1 CA - A Cancer Journal for Clinicians	journal	72.576 Q1	144	45	127	3078	20088	103	206.85	68.40	

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1	journal	72.576 Q1	144	45	127	3078	20088	103	206.85	68.40	
2	journal	48.894 Q1	134	3	12	559	1043	12	86.00	186.33	

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1 Nature Methods	journal	21.178 Q1	257	354	946	6282	13444	545	23.03	17.75	
		14.568	99	365	1083	5858	12450	612	16.91	16.05	

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1 Nature Methods	journal	21.178 Q1	257	354	946	6282	13444	545	23.03	17.75	🇬🇧
		14.568	99	365	1083	5858	12450	612	16.91	16.05	🇬🇧

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1 Nature Methods	journal	21.178 Q1	257	354	946	6282	13444	545	23.03	17.75	
2 Nature Biotechnology	journal	14.568 Q1	399	365	1083	5858	12450	612	16.91	16.05	
3 Nano Today	journal	6.236 Q1	119	52	164	8226	2421	137	16.19	158.19	
4 Ageing Research Reviews	journal	4.125 Q1	98	72	255	12419	2483	248	10.34	172.49	
5 BMC Biology 	journal	3.628 Q1	90	151	369	8248	1845	310	6.45	54.62	
6 Small	journal	3.549 Q1	195	1063	2156	64207	21160	2090	10.17	60.40	
7 Trends in Biotechnology	journal	3.482 Q1	195	150	335	8974	3393	273	11.41	59.83	

BMC Biology

Country	United Kingdom -  SJR Ranking of United Kingdom	90 H Index
Subject Area and Category	Agricultural and Biological Sciences Agricultural and Biological Sciences (miscellaneous) Ecology, Evolution, Behavior and Systematics Plant Science Biochemistry, Genetics and Molecular Biology Biochemistry, Genetics and Molecular Biology (miscellaneous) Biotechnology Cell Biology Developmental Biology Physiology Structural Biology	
Publisher	BioMed Central	
Publication type	Journals	
ISSN	17417007	
Coverage	2003-ongoing	
Scope	BMC Biology - the flagship biology journal of the BMC series - publishes research and methodology articles of special importance and broad interest in any area of biology and biomedical sciences. BMC Biology (ISSN 1741-7007) is covered by PubMed, MEDLINE, BIOSIS,	

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BMC Biology



Научный журнал

Переведено с английского языка. - BMC Biology - это онлайн-научный журнал открытого доступа, в котором публикуются оригинальные рецензируемые исследования во всех областях биологии, а также статьи с отзывами и комментариями. Публикация была основана в 2003 году.

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Редактор: [Mirna Kvaĳo](#)

Научная дисциплина: [Биология](#)

Похожие запросы: [Cell](#), [PLOS One](#), [ЕЩЁ](#)

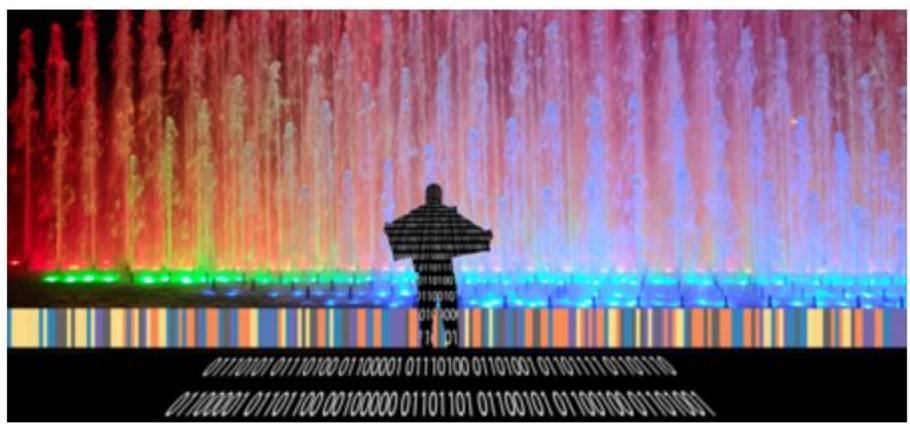
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impact on peer
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As a result of the significant disruption that is being caused by the COVID-19 pandemic we are very

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Hospitable publishing process. *BMC Biology* offers rapid evaluation and clear and continuous communication on the progress of your manuscript. Upon submission, our [in-house editors](#) work with an [Editorial Board](#) of leading international experts and carefully selected reviewers to ensure a high quality and constructive editorial and peer review process.

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Announcement: COVID-19 and impact on peer review

As a result of the significant disruption that is being caused by the COVID-19 pandemic we are very aware that many researchers will have difficulty in meeting the timelines associated with our peer review process during normal times. Please do let us know if you need additional time. Our systems will continue to remind you of the original timelines but we intend to be highly flexible at this time.

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Portable peer review. To reduce time spent on serial submissions and iterative reviewing, *BMC Biology* offers to consider manuscripts on the basis of reviews received at other journals. We also support transfers of reviews obtained at *BMC Biology* to other journals, including those outside of BMC and Springer Nature. Learn more from our [portable reviews page](#) and [Editorial](#).

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This section provides general style and formatting information only. Formatting guidelines for specific article types can be found below.

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Multiple links between 5-methylcytosine content of mRNA and translation



Ulrike Schumann^{1†}, He-Na Zhang^{2†}, Tennille Sibbritt¹, Anyu Pan¹, Attila Horvath¹, Simon Gross¹, Susan J. Clark^{3,4}, Li Yang^{2,5} and Thomas Preiss^{1,6*}

Abstract

Background: 5-Methylcytosine (m^5C) is a prevalent base modification in tRNA and rRNA but it also occurs more broadly in the transcriptome, including in mRNA, where it serves incompletely understood molecular functions. In pursuit of potential links of m^5C with mRNA translation, we performed polysome profiling of human HeLa cell lysates and subjected RNA from resultant fractions to efficient bisulfite conversion followed by RNA sequencing (bsRNA-seq). Bioinformatic filters for rigorous site calling were devised to reduce technical noise.

Results: We obtained ~ 1000 candidate m^5C sites in the wider transcriptome, most of which were found in mRNA. Multiple novel sites were validated by amplicon-specific bsRNA-seq in independent samples of either human HeLa, LNCaP and PrEC cells. Furthermore, RNAi-mediated depletion of either the NSUN2 or TRDMT1 m^5C :RNA methyltransferases showed a clear dependence on NSUN2 for the majority of tested sites in both mRNAs and noncoding RNAs. Candidate m^5C sites in mRNAs are enriched in 5'UTRs and near start codons and are embedded in a local context reminiscent of the NSUN2-dependent m^5C sites found in the variable loop of tRNA. Analysing mRNA sites across the polysome profile revealed that modification levels, at bulk and for many individual sites, were inversely correlated with ribosome association.

Conclusions: Our findings emphasise the major role of NSUN2 in placing the m^5C mark transcriptome-wide. We further present evidence that substantiates a functional interdependence of cytosine methylation level with mRNA translation. Additionally, we identify several compelling candidate sites for future mechanistic analysis.

Keywords: Epitranscriptome, RNA methylation, 5-Methylcytosine, NSUN2, TRDMT1, Bisulfite conversion, Bisulfite RNA-seq, RNA stability, mRNA translation, Polysome

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Current approaches to vaccine preparation

[Jiang-Jian Liu](#) and [Arnost Cepica](#)[Copyright and License information](#) [Disclaimer](#)**This article has been corrected.** See [Can Vet J](#). 1990 May; 31(5): 327.This article has been [cited by](#) other articles in PMC.

Abstract

Numerous conventional vaccines for animal use are currently available, and many of these vaccines have been instrumental in the control of infectious diseases of major economic importance. A vaccine has even been instrumental in global eradication of smallpox, an important human disease. However, many of the current vaccines are deficient in efficiency, potency, or safety. It has been recognized that the conventional methodologies are a limitation to further vaccine development. Introduction of monoclonal antibodies, recombinant DNA, and protein engineering techniques has facilitated a rather rapid increase in the knowledge of pathogenetic mechanisms, as well as of protective antigens at the molecular level. This

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Ruitenberg EJ¹.

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Abstract

A historical review on the preparation and use of vaccines is presented. The example of smallpox vaccination in man is interesting, as it affords an insight into the development of the principle of vaccination, the improvement of the vaccine and the eradication of the disease. Moreover, the various stages of vaccinology were described. Initially, vaccines were prepared on the basis of the attenuated or inactivated pathogens. After the introduction of animal cell culture techniques among others it became possible to realise an amplification of the preparation of virus vaccines. Since the introduction of recent biotechnological methods, including monoclonal antibodies and recombinant DNA technology, the development and preparation of well characterised and purified vaccines became possible. Immunology, including the development of adjuvants and the immunogenetic aspects, is essential in the further development of vaccines. Furthermore, it should be stressed that in using vaccines, the control aspects of the new generation of vaccines including the application of so-called Good Manufacturing Practice (GMP), directives for their preparation should be strictly adhered to.

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Methods Of Vaccine Production

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[Vaccine production](#) methods have varied greatly over the years and are best discussed according to a parallel chronological and sophistication approach.

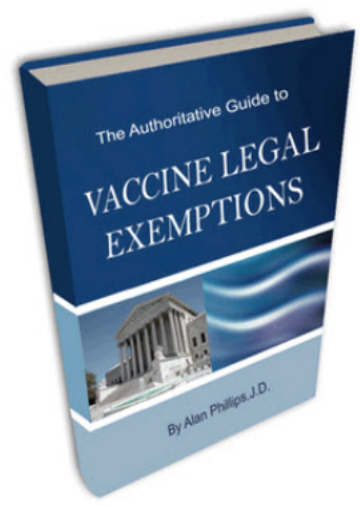
Killed (Inactivated) Pathogen

In this method, the normal pathogen is treated with a strong, denaturing disinfectant like formaldehyde or phenol. The process denatures the proteins and [carbohydrates](#) that are essential for the organism to live and infect a host, but if treated properly, the surface antigens are left intact. The process must be done carefully to control the unwinding of proteins or carbohydrates by denaturation, because the preparation must be recognized as the original antigen. The main problems with killed pathogen [vaccines](#) are the following: (a) if the vaccine is not inactivated totally, disease can result; (b) if the preparation is overtreated, vaccine failure usually results because of denaturation; (c) the production laboratory must grow the pathogen in large quantities to be commercially useful, putting laboratory technicians at risk; and (d) the patient may experience abnormal and harmful responses, such as fever, convulsions, and death. These vaccines typically are viewed as "dirty" vaccines, and some, like the pertussis vaccine, have been associated with problems serious enough to warrant their temporary removal from the market.

Live/Attenuated Pathogens

The word attenuated for our purposes simply means "low virulence." The true

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REVIEW ARTICLE

Front. Immunol., 19 September 2018 | <https://doi.org/10.3389/fimmu.2018.01963>

New Vaccine Technologies to Combat Outbreak Situations

 **Susanne Rauch***,  **Edith Jasny**,  **Kim E. Schmidt** and  **Benjamin Petsch**

CureVac AG, Tuebingen, Germany

Ever since the development of the first vaccine more than 200 years ago, vaccinations have greatly decreased the burden of infectious diseases worldwide, famously leading to the eradication of small pox and allowing the restriction of diseases such as polio, tetanus, diphtheria, and measles. A multitude of research efforts focuses on the improvement of established and the discovery of new vaccines such as the HPV (human papilloma virus) vaccine in 2006. However, radical changes in the density, age distribution and traveling habits of the population worldwide as well as the changing climate favor the



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RNA Vaccines

Description

mRNA is an intermediate carrier of genetic information used as template for endogenous protein production in the vaccinated subject. Two major types of RNA have been utilized as prophylactic vaccines against pathogens that cause infectious diseases:

- 1) Non-replicating mRNA
- 2) Self-amplifying mRNA

Non-replicating mRNA contains the sequence of the antigen of choice flanked by 5' and 3' untranslated regions (UTRs). The advantages of using non-replicating mRNA vaccines compared to self-amplifying mRNA are rooted in the simplicity of the construct, the small size of the RNA, and the absence of any additional encoded proteins that could induce unintended immune responses (105). The design of optimized, efficiently translated mRNA for use as a vaccine has been reviewed previously (105–107). Briefly, conventional non-replicating mRNA is obtained by *in vitro* transcription of a cDNA template, typically plasmid DNA (pDNA) produced in *E. coli*. The pDNA template is linearized using restriction enzymes and is transcribed *in vitro* into mRNA in a mixture containing recombinant phage DNA-dependent RNA polymerase (typically derived from T7 or T3 or Sp6 phage) and nucleoside triphosphates (NTPs) (108). Upon purification, usually via FPLC or HPLC to remove any remaining product related impurities such as reaction components (i.e., enzymes, free NTPs, residual pDNA) or abortive transcriptional byproducts, a pure single mRNA product is obtained (109). Notably, purification of *in vitro* transcribed mRNA seems to be crucial for the amount of immunogen produced in target cells as demonstrated by up to 1,000-fold increased protein production in primary human DCs transfected with HPLC purified compared to unpurified mRNA (110). The *in vitro* transcribed mRNA product contains a protein-encoding open reading frame (ORF) flanked by elements essential for the function of mature eukaryotic mRNA: a cap structure, joined to the 5' and a poly(A) tail at the 3' end, as well as 5' and a 3' untranslated regions (UTR) (111–113). The 5' cap is vital for the creation of stable mature mRNA and increases protein translation via binding to eukaryotic translation initiation factor 4E (111, 114). The 5' cap can be added either during the transcription by inclusion of a cap analog or anti-reverse cap (ARCA) in the reaction (115), or subsequently, using the vaccinia virus capping complex (116). The UTRs, which can be of eukaryotic or viral origin, increase the half-life, and stability of the mRNA, resulting in higher expression of the protein (117–120). The poly A tail of an optimal length is an essential regulatory element to enhance translation and can be either encoded into the DNA template or alternatively added enzymatically post transcription (111, 121, 122). The sequence of the ORF can be optimized using either enrichment of the GC content (123, 124) or enhancement of open reading frames (125) for enhanced expression and stability.

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Kemal KS¹, Reinis M, Weiser B, Burger H.

Author information

Abstract

HIV-1 in plasma represents the viral quasispecies replicating in the patient at any given time. Studies of HIV-1 viral RNA from plasma or other body fluids therefore reflect the virus present in real time. To obtain near full-length genomic sequences derived from virion RNA it is first necessary to carefully isolate and amplify the RNA. The procedure described below, involves viral RNA extraction, reverse transcription (RT) of the extracted RNA to produce cDNA copies, and PCR amplification of long HIV-1 gene fragments using site-specific, overlapping primers. The primers are based on subtype B HIV-1 strains, and plasma specimens are used in the procedures. However, the protocol can easily be adapted to other HIV-1 subtypes by modifying the primers to match the subtype of interest.

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Methods for Viral RNA Isolation and PCR Amplification for Sequencing of Near Full-Length HIV-1 Genomes

Kimdar Sherefa Kemal, Milan Reinis, Barbara Weiser, and Harold Burger

Abstract

HIV-1 in plasma represents the viral quasispecies replicating in the patient at any given time. Studies of HIV-1 viral RNA from plasma or other body fluids therefore reflect the virus present in real time. To obtain near full-length genomic sequences derived from virion RNA it is first necessary to carefully isolate and amplify the RNA.

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Key words: HIV-1, HIV-1 viral RNA, HIV-1 primers, Long RT-PCR amplification of HIV-1.

1. Introduction

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