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KEMENTERIAN KESEHATAN REPUBLIK INDONESIA

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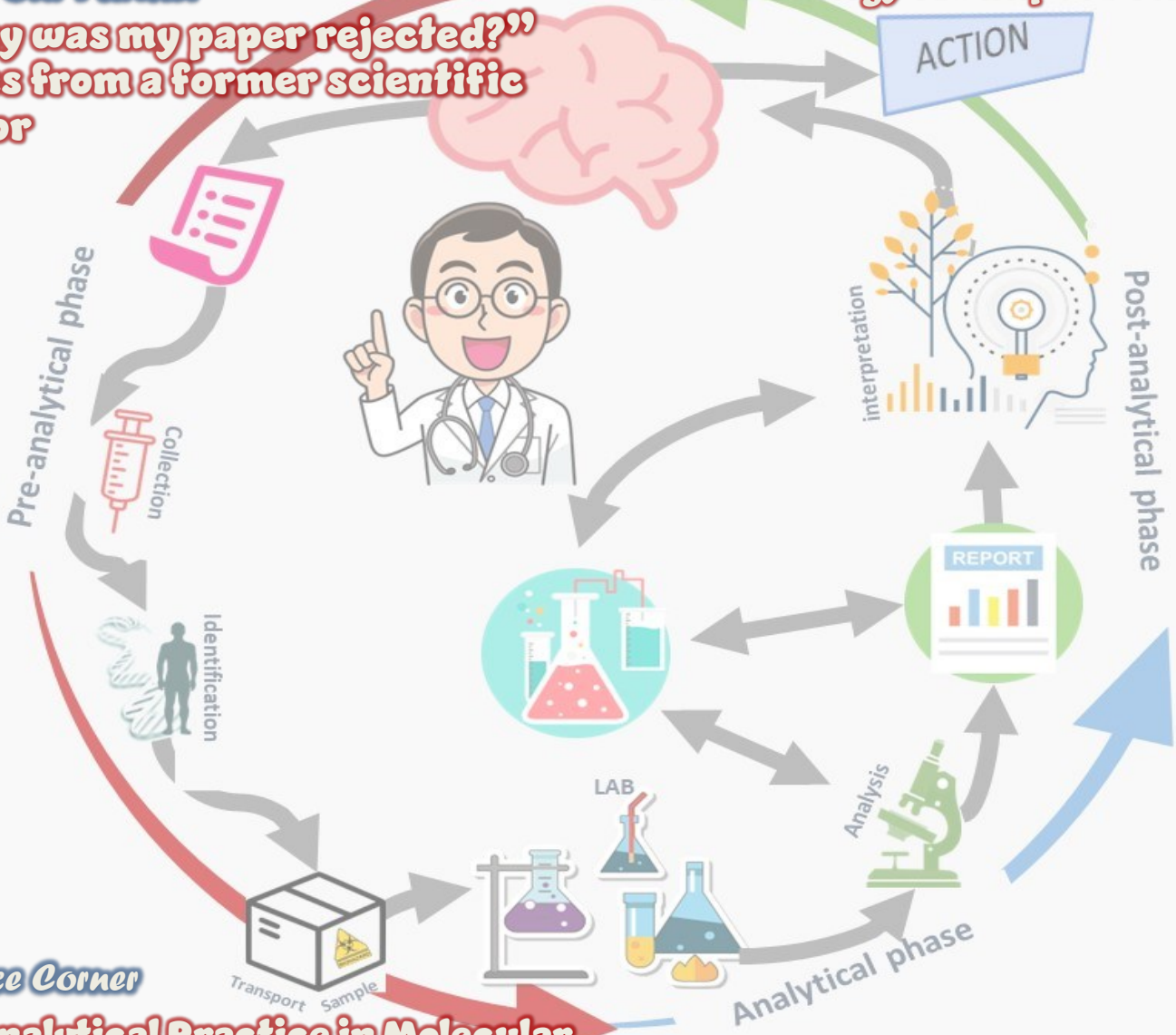

Science Corner

Preanalytical Practice in Molecular Assay in Clinical and Research Setting

HEALTH POLICY AGENCY
MINISTRY OF HEALTH REPUBLIC OF INDONESIA
2023

INA-RESPOND newsletter

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FEATURES

INA-RESPOND

Newsletter

PROACTIVE Study Updates

By: Eka Windari R., I Wayan Adi Pranata, Lois E. Bang, Melinda Setiyaningrum, Nur Latifa Hanum, Retna Mustika Indah, Riza Danu Dewantara

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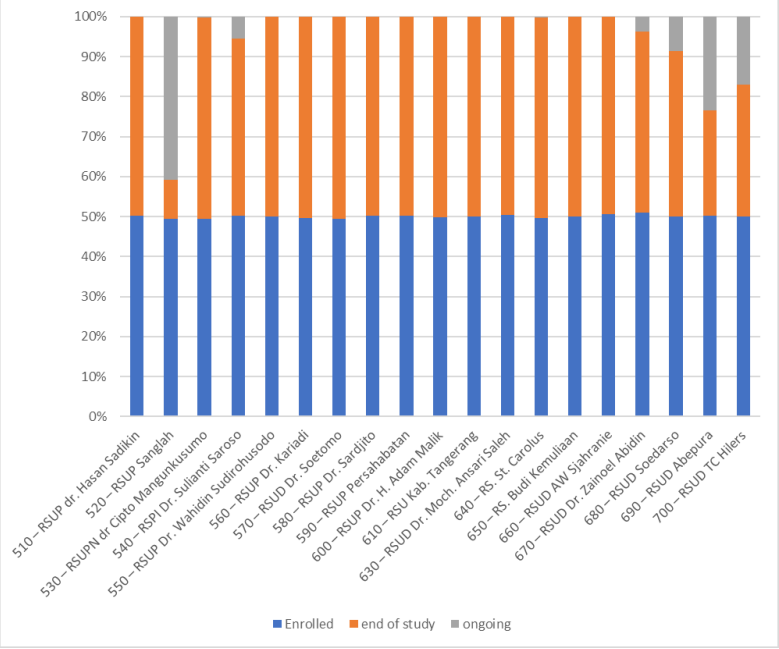
As of 3 January 2023, out of 4,336 subjects enrolled, 4,042 (93.22%) subjects have ended their study, and 294 (6.78%) are still ongoing. For the End-of-Study, 3,313 subjects had already completed the study until the Follow-up Visit Month 36, 405 subjects were lost to follow-up, 247 subjects died, 38 subjects moved to the city without a PROACTIVE Site, 32 subjects withdrew consent, five subjects were HIV negative, and two subjects were suspended (imprisoned). The study progress from each site is described in the Figure on the right, while detailed information on the End-of-Study participants is available in Table 1.



After the completion of the follow-up at site 610 - RSU Kabupaten Tangerang in September 2022, sites 510, 550, 560, 580, 590, 600, 630, 640, 650, and 660 also completed the follow-up for all their subjects. The previously mentioned sites will have a site monitoring visit by appointment and site close-out visits within six months from the last follow-up before archiving the documents the following month. For the monitoring activity, two on-site monitoring visits are scheduled for early 2023, namely site 600 – Adam Malik Hospital on 17-20 Jan 2023, site 510 – Hasan Sadikin Hospital on 28-20 Jan 2023, site 590 – Persahabatan Hospital in Feb 2023, Site 560 – Kariadi Hospital in Feb 2023, Site 670 – Zainoel Abidin Hospital in Feb 2023 and Site 540 in March 2023.

No.	Sites	Date
1.	550 – RSUP Dr. Wahidin Sudirohusodo	13 – 15 December 2022
2.	560 – RSUP Dr. Kariadi	22 – 24 November 2022
3.	570 – RSUD Dr. Soetomo	26 – 28 October 2022
4.	580 – RSUP Dr. Sardjito	22 – 24 November 2022
5.	610 – RSU Kabupaten Tangerang	20 – 22 September 2022
6.	630 – RSUD Dr. M. Ansari Saleh	11 – 13 October 2022
7.	640 – RS St. Carolus	26 – 28 December 2022
8.	650 – RSU Budi Kemuliaan Batam	1 – 3 November 2022
9.	660 – RSU A. Wahab Sjahranie	23 – 25 November 2022

The last monitoring visit dates that have been conducted for some sites

No	Site	End of Study Duration/ Complete	Withdrew Consent	Participants with HIV negative	Moved	Death	Investigator Discretion	Lost to Follow Up	Other	Total
1.	510 – RSUP Dr. Hasan Sadikin	189	1	0	5	5	0	6	0	206
2.	520 - RSUP Sanglah	24	0	0	1	3	0	0	0	28
3.	530 – RSUPN Dr. Cipto Mangunkusumo	283	0	0	0	17	0	15	0	315
4.	540 – RSPI Dr. Sulianti Saroso	133	0	0	3	8	0	16	0	160
5.	550 – RSUP Dr. Wahidin Sudirohusodo	240	0	0	5	25	0	67	0	337
6.	560 – RSUP Dr. Kariadi	199	1	3	0	15	0	16	0	234
7.	570 – RSUD Dr. Soetomo	261	13	0	4	21	0	21	0	320
8.	580 – RSUP Dr. Sardjito	168	1	0	5	6	0	38	0	218
9.	590 – RSUP Persahabatan	186	0	1	0	37	0	22	0	246
10.	600 – RSUP Dr. H. Adam Malik	253	3	0	2	21	0	61	0	340
11.	610 – RSU Kabupaten Tangerang	272	6	0	4	20	0	22	2	326
12.	630 – RSUD Dr. M. Ansari Saleh	215	1	0	1	7	0	17	0	241
13.	640 – RS St. Carolus	211	0	0	0	1	0	15	0	227
14.	650 – RSU Budi Kemuliaan Batam	179	3	0	5	9	0	33	0	229
15.	660 – RSU A. Wahab Sjahranie	183	0	0	2	6	0	26	0	217
16.	670 – RSUD Zainoel Abidin	89	0	0	0	11	0	12	0	112
17.	680 – RSUD Soedarso	74	0	0	0	11	0	10	0	95
18.	690 – RSUD Abepura	56	2	1	1	7	0	5	0	72
19.	700 – RSUD TC Hillers	98	1	0	0	17	0	3	0	119
	Total	3313	32	5	38	247	0	405	2	4042

Table 1. Subjects' end of study reasons

INA-RESPOND Newsletter

PREANALYTICAL PRACTICE IN MOLECULAR ASSAY IN CLINICAL AND RESEARCH SETTINGS

By: Yan Mardian

Pre-analysis refers to all the complex steps that must take place before a sample can be analyzed. Over the years, a series of studies identified that 32% to 75% of all testing errors occur in the preanalytical phase, and technological advances and quality assurance procedures have significantly reduced the number of analytic-based errors. This has exposed the pre-analysis stage as a major source of residual "error" and/or variables that can affect test results. Preanalytic factors include patient-related variables (diet, age, sex, etc.), specimen collection and labeling techniques, specimen preservatives and anticoagulants, specimen transport, and processing and storage. Potential sources of error or failure in this process include improperly ordered tests, sample misidentification, improper timing, improper fasting, improper anticoagulant/blood ratio, improper mixing, incorrect order of draw, and hemolyzed or lipemic specimens.

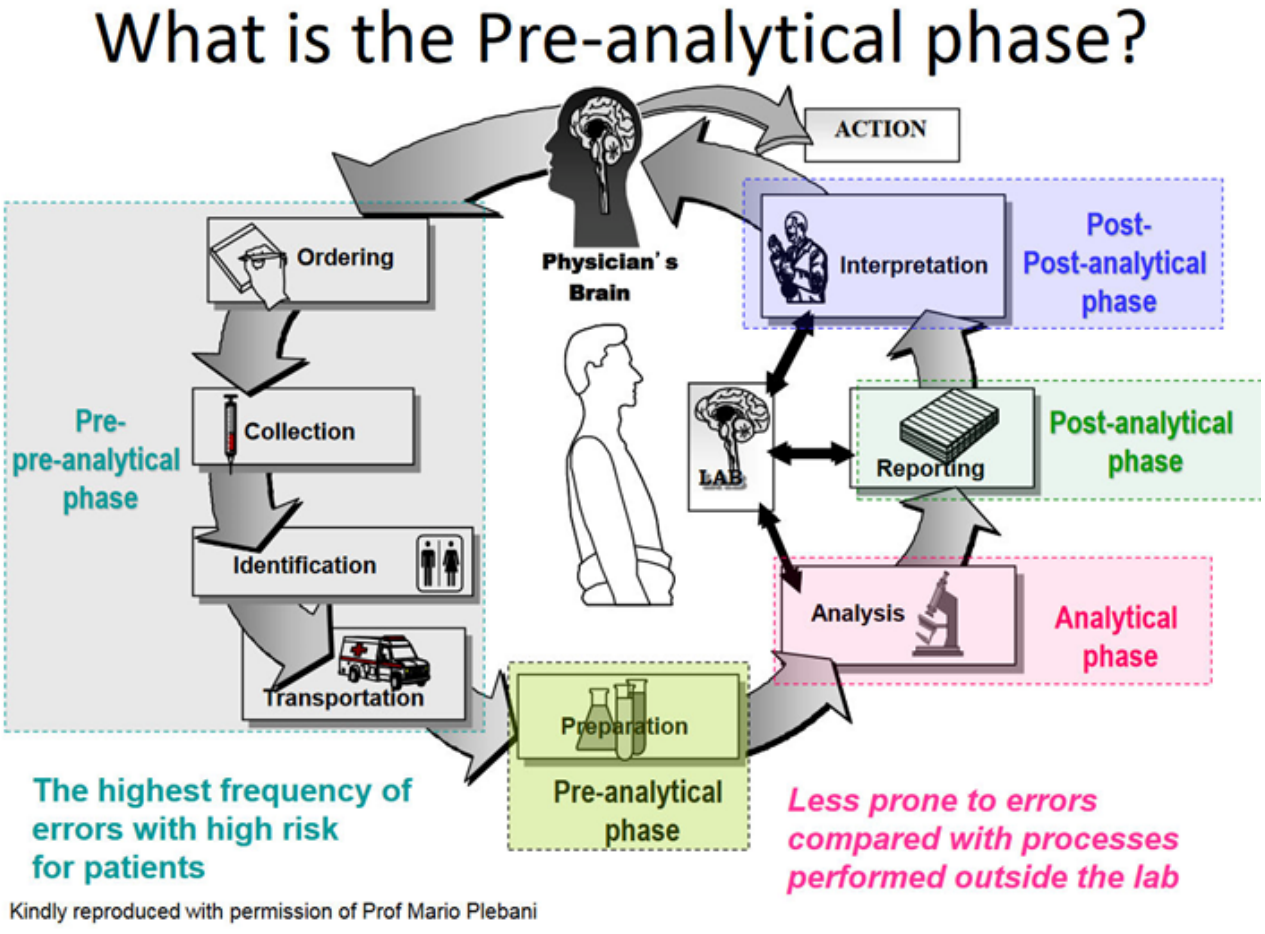


Figure 1. Preanalytical phase components.

The most frequent preanalytic errors include improperly filling the sample tube, placing specimens in the wrong containers or preservatives, and selecting the incorrect test.

There is now incontrovertible evidence that the preanalytical phase is the major source of errors in laboratory testing when used for either diagnostic or research purposes. The molecular assay is not an exception, whereby many potential preanalytical errors are similar to those occurring in other different diagnostic areas, whilst others can be classified as specific. Molecular assays for the detection of nucleic acids in biologic specimens are valuable diagnostic tools supporting clinical diagnoses and therapeutic decisions. Pre-analytical errors, contribute a significant role in common errors that take place in molecular laboratories. Certain practices in specimen collection, transportation, and storage can affect the integrity of nucleic acids before analysis. Although diagnostic errors can occur almost always and everywhere in healthcare, the vulnerability of error in molecular assays pre-analytic phase is enormously magnified when the staff is forced to work in high-throughput settings, as seen in the COVID-19 pandemic. In the case of infectious outbreaks, the generation of false-positive or false-negative test results not only jeopardizes the health of the individual patient but may also derange and disrupt the efficacy of public health policies, emergency plans, and restrictive measures established by national and international authorities for containing the outbreak.

This article addressed correct practices in specimen collection, transportation, preservation, and storage in most biological samples which are routinely received and processed in translational research laboratories. Laboratory manipulations of nucleic acids are susceptible to interferences at various stages, including specimen collection and processing. Blood and its components are among the most common samples received in molecular laboratories. Most of the received samples contain anticoagulants, therefore awareness about the possible confounding effects of each anticoagulant and selection of the proper one has paramount importance in ensuring the accuracy of reports. The introduction of inhibitory substances and contamination with false-positive signals are among the significant interferences. Currently, K2/K3 -EDTA and acid citrate dextrose (ACD) are the recommended anticoagulants for molecular assays. Blood specimens for nucleic acid testing are generally collected into EDTA anticoagulant to inhibit enzymes that might break them down. Heparin is a poor choice for anticoagulant in this application because it can be coextracted with DNA and inhibits DNA polymerase in polymerase chain reactions (PCRs). There are some reports implying that heparin, even at low concentrations, may suppress DNA amplification. Overall, it is recommended to avoid the usage of a heparinized sample as much as possible in molecular assays, but in certain situations such as only one sample or emergency states, a heparinized sample should not be rejected.

Hemin from hemolysis in plasma or serum can also inhibit DNA polymerase. RNA is labile in blood or tissues; thus, these specimens must be stored appropriately by rapid freezing in liquid nitrogen if the extraction will be delayed. Extraction of nucleic acids from clinical specimens such as plasma (e.g., for viral load measurement), blood cells (e.g., for genetic testing), or tissues (e.g., for analyzing mutations in tumors) entails lysing cells and separating nucleic acids from proteins and lipids. Reagents for extraction include salts, proteases, and phenol-chloroform to denature the substances complexed with nucleic acids. This process must be optimized for specimen type to recover high-quality nucleic acids with good quantitative yield. Care must be taken to avoid contamination of specimens with target nucleic acids

from other specimens or with amplified targets from specimens that have been analyzed previously in that vicinity. Accordingly, laboratories practicing nucleic acid amplification, especially PCR, should have separate preamplification, amplification, and post-amplification

The effect of freeze–thaw cycles on nucleic acid quantity and quality is under debate. As a general rule, freezing and thawing have detrimental effects on the concentration of all analytes. Ross et al. observed more than 25% decrease in blood DNA concentration after a single freeze–thaw cycle but the quality of DNA did not change even after multiple freeze–thaw cycles. According to Chan et al., a single freeze-thaw cycle of plasma has no significant effect on DNA integrity but repeated (3 times) freezing and thawing of plasma (but not extracted DNA) leads to fragmentation of DNA. Kopreski et al. reported that a single freeze–thaw cycle results in a marked decrease of c-abl and tyrosinase mRNAs in serum (87), however a similar study by Tsui et al. showed no significant difference for RNA concentrations between untreated serum/plasma and frozen/thawed samples. Detection of nucleic acids of infectious agents by molecular methods may be individually considered. According to CLSI, for RNA viruses like human immunodeficiency virus (HIV) (and hepatitis C virus (HCV)), the plasma should be separated from whole blood into a second tube within four hours of specimen collection and WHO/UNAIDS guidelines recommend storing serum and plasma at 4°C –8°C for up to a maximum of one week. For longer storage, the specimens should be frozen at –20°C or lower. HIV is a biologically stable virus. It has been stated that HIV-1 RNA is stable in EDTA-whole blood for up to 72 hours and if the plasma is separated by centrifugation within 12 hours the genomic content of the virus can be evaluated for up to 7 days at RT.

Nasopharyngeal specimens for Respiratory viruses diagnosis (Influenza, Respiratory Syncytial Virus, Parainfluenza virus, Human Metapneumovirus, Rhinovirus, Enterovirus, Adenovirus, Coronavirus) are collected by sterile dacron/nylon swab. Nylon flocked swabs are more efficient in comparison with other synthetic ones like rayon swabs. The most common acceptable specimen for detecting Influenza Viruses is nasopharyngeal swabs along with washes or aspirates. Throat swabs and/or nasal swabs (two sterile dry polyester swabs with aluminum or plastic shafts) are also acceptable. However, more viral loads can be obtained by nasopharyngeal swabs in comparison with oropharyngeal swabs. The swab should be transported into sterile VTM at 4°C. If the shipment is delayed by 3 to 4 days, the samples should be kept at -70°C. Sputum specimens should be obtained in a sterile container and then transported at RT for DNA analysis. If transportation time is anticipated to be longer than 30 minutes, samples should be transported to the laboratory at 4 to 8°C. The transport media that have been developed for culture may not be suitable for molecular tests and the media developed for molecular tests are not suitable for culture. The sputum specimens which are not going to be tested immediately should be refrigerated for up to 7 days. If longer storage time is needed, the specimen can be stored for a few years at -70°C. For M. tuberculosis, it is recommended to first apply N-acetyl-L-cysteine-NaOH for decontamination, then directly put thick particles of sputum on FTA cards with a foam-tipped applicator and spread over an area of 2.5 cm. Subsequently, the samples should be air-dried for 1 hour and finally put in a storage packet and stored at RT. Ethanol fixation of sputum samples does not affect the rate of M. tuberculosis detection, so the cytology slides of sputum sediments can be used for PCR detection. Stomach acidic fluid should be neutralized with phosphate buffer before DNA isolation. After the final centrifugation, the pellet can

also be used for DNA isolation. . After final centrifugation, the pellet can also be used for DNA isolation.

Dried blood spots (DBSs) can be used to detect viral genomes and can be prepared on filter paper with optimal blood volumes as low as 50 µL. Even six hours lag time between blood collection and its application on DBS can lead to reliable results. The drying procedure takes 3 hours at RT in a safety cabinet (even longer in high humidity) or 1 hour at 37°C in an oven. One of the great advantages of DBS is easy handling and shipping even in rural areas with unavailable cold chain. RNA in DBS samples is stable for at least 3 months at RT. However, some studies show that RNAs are usable for as long as 1 year at RT. High

Specimen type	Target	Temperature	Duration
Whole blood	DNA	RT	up to 24h
		2-8°C	up to 72h optimal, but possible up to 6 days
Whole blood	DNA (HBV)	RT	4-6h
	RNA (HIV, HCV)	4°C	72h
Serum	DNA	RT	24h
	DNA (CMV)	RT	less than one day
	DNA (CMV)	4°C	2 days
	DNA (HBV)	RT	24h
	DNA (HBV)	4°C	7 days
Plasma	DNA	RT	24h
		2-8°C	5 days
		-20 °C	longer than 5 days
		-80°C	9 to 41 months
Plasma	RNA	4°C	up to 24h
Plasma	DNA (HBV)	RT	24 h,28 days
		4°C	7 days, 28 days
Plasma	RNA (HIV, HCV)	4–8°C	1 week
	HIV	RT	30h
	HIV	RT	7 days
	HIV	5°C	14 days
	HCV	RT	72h
	HCV	25°C	14 days
	HCV	RT	3 months
Dried blood spot	RNA	RT	up to 3 months
		4°C	up to 1 year
		-20°C	up to 4 years
Stool	DNA	RT	4h
		4°C	24-48h
		-20°C	few weeks
		-80°C	2 years
Nasopharyngeal swabs (in VTM)	Respiratory viruses	4°C	3-4 days
		-70°C	more than 3-4 days

The table above summarizes pre-analytical recommendation for molecular analysis using various biological specimens.

temperature (37°C) results in progressive degradation of RNA but has less effect on DNA. RNA progressive loss at 37°C is remarkable after two months. Refrigerated (in a zip bag with a desiccant pack) and frozen DBS samples can be stored for 1 year and a period of 4 years, respectively, with reliable recovery of HIV1 RNA.

Stool sample preservation in cold conditions (4°C) is recommended during transportation. Allowable transportation time at 4°C is 24-48 hours. This time is 4 hours at RT without preservation. Fixatives/ preservatives such as TotalFix, Unifix, Zinc- or copper -based polyvinyl alcohol (PVA), and Ecofix can preserve specimens for storing and transporting at RT. DNA stabilizer can be utilized for sample preservation to protect DNA and/o RNA and prevent degradation after collection. One of the most famous stabilizers is RNAlater, which prevents RNA as well as DNA degradation at ambient temperature for one week. Another common and economic stabilizer for fecal DNA is 95% Ethanol. The procedure contains mixing 2.5 mL of 95% ethanol with approximately 1–2 g of stool. For microbiome studies, it is ideal to transport fecal specimens immediately at -20°C or -80°C. These specimens can be stored at -80°C for up to 2 years with unremarkable alteration in stool microbial composition. The storage time is reduced to a few weeks at -20°C. Viral infections can be detected in urine using PCR, using sterile containers for urine sample collection and transport at 4°C. Urine can be stored at 4°C for Epstein–Barr virus (EBV) and CMV until processing is done in one week. The specimen should be shipped on wet ice within one week for CMV evaluation. Collection of the first 10-20 mL of voided urine for HSV (first catch) and transportation within 3 hours has been recommended. The specimens can be kept at -70°C for up to 3 months, but individual manufacturer's instructions should also be considered for storage conditions.

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INA-RESPOND Newsletter

"WHY WAS MY PAPER REJECTED?" NOTES FROM A FORMER SCIENTIFIC EDITOR

By: Caeul Lim

FROM OUR PARTNER

Introduction to the NIAID/DCR/CCRB laboratory team

The Collaborative Clinical Research Branch (CCRB) laboratory team within the Division of Clinical Research (DCR) at the National Institutes of Allergy and Infection Diseases (NIAID) is led by Dr. Katy Shaw-Saliba (Laboratory Research Scientist). The team includes Bonnie Dighero-Kemp (Scientific Program Manager), Mike Belson (Microbiologist), Dr. Aaron Neal (International Health Scientist, Indonesia Country Lead) and Dr. Caeul Lim (Research Scientist). All of the members have expansive expertise in laboratory operations, science, and clinical research.

The mission of the CCRB lab team is to provide laboratory expertise and support for science and operations associated with clinical trials and studies.

The team helps build laboratory and scientific capacity to accomplish high level clinical research across various international sites and within the US, in collaboration with other laboratory groups at and outside of NIAID. This includes every aspect of the laboratory related to clinical research including laboratory set up, day-to-day operations, monitoring, protocol development and implementation, data interpretation and publication/dissemination of results. Day-to-day operations include excellence in good laboratory practices and excellence in all aspects necessary for cutting edge clinical research including laboratory maintenance, assays, and biorepositories. The laboratory team is committed to development of areas of strategic interest in the government-to-government partnership. The team is also passionate about providing strong mentorship and support for scientists across all sites, including career development, scientific study design, and manuscript planning and writing.

The lab team is available to discuss and provide any guidance to promote rigorous clinical and basic studies, and we look forward to collaborating on developing sustainable and impactful clinical research capacity.

Understanding editorial rejections

Getting a rejection letter from a scientific journal after months if not years of hard work is probably one of the most frustrating yet common experience as a scientist. How could an editor evaluate the quality of my work in just a few days?

For over four years, I was a scientific editor at Cell Host & Microbe, a Cell Press journal that focuses on the interface of host and microbial interactions. In most papers I handled, I was the deliverer of bad news, rejecting the paper after editorial discussion - what we refer to as "desk rejection". However, except for the handful of studies that are easily recognizable as lacking scientific rigor, editors are in fact not evaluating the "quality" of the study, per se. Rather, the job of the scientific editor is to identify studies that best fit their journal's audience and scope. Many journals that are more selective and targeting a broader audience, including Cell Host & Microbe, also decide on how "impactful" a study is for a given field. (Figure 1)

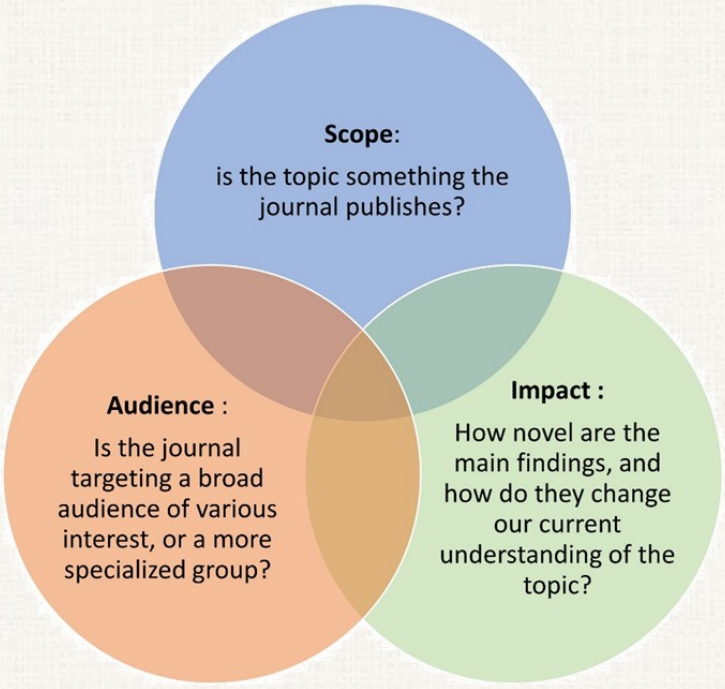

Figure 1 : The "trifecta" behind an editor's decision.

In this post I'm hoping to share some insights from an editorial point of view on why papers are rejected. I should note that these insights would be most relevant when submitting to a broad scope journal.

In my experience rejected papers usually do not fully meet the standards the journal editors have set in one or more of the factors described in Figure 1. Rejections often fall within specific patterns that are so common across journals and disciplines that my colleagues on another Cell Press journal, Matter, published an editorial outlining the four common types of rejections (Figure 2) [1] , which I'm briefly summarizing here.

The substitution

A paper is often rejected when the editors find that it effectively replicates and confirms a past finding, but with one component or parameter exchanged for another (for example, done in a different cell type, or a common immune function elicited by a different pathogen). Editors often ask, "how does this change the way we understand this phenomenon?". If the substitution provides similar conclusions to prior work, this may be grounds for a desk rejection.

The incremental

Incremental advance is somewhat a subjective measure, and it is not necessarily bad. After all, science progresses thanks to incremental steps. However, it is often the cause for rejection if the size of the incremental step is considered too small or narrow. For example, you have identified a specific phosphorylation site on protein X. But we already knew that phosphorylation of Protein X is essential for its function. Although it is important to know the exact residue, if this finding does not change what we already know about Protein X and its function, this finding may be seen as incremental, and not enough to elicit broad interest.

A+B

Editors often refer to this archetype as the "connecting the dots" paper. This paper may do an excellent job combining two already known findings, but the conclusions are, in a way, expected. For example, let's say there is a therapeutic known to target a salmonella protein X. This protein is related to Protein Y found in E.coli. A study showing that this therapeutic is also efficient against E.coli by targeting protein Y may seem a bit obvious to the reader. (A+B = A+B)

Now, what would be interesting is if this therapeutic was not efficient against E.coli because of Protein Z that evolved to counteract it in e.coli (A+B = brand new C) !

Super niche

Finally, this archetype goes back to "scope" and "audience". Many journals of broad impact are looking for something that a lot of different researchers will find interesting. A study can be well done, novel and very interesting to the field, but still be rejected because editors just don't think a lot of people will read it.

As you can see, a rejection is rarely a reflection of the quality of your work. It is often a matter of whether the journal you submitted to, was the right fit for your study. Other journals also publish editorials explaining their decision making process (e.g., [2]).

As researchers, we can't avoid all rejections. But we can avoid some unnecessary ones by 1) choosing the right fit and 2) highlighting the significance of our work through clearly written cover letters and abstracts - topics that I would love to cover in future newsletters!

Reference:

1. Chin, S.M. and S.W. Cranford, 4 Archetype Reasons for Editorial Rejection. Matter, 2020. 2(1): p. 4-6.
2. Overcoming the Myths of the Review Process and Getting Your Paper Ready for Publication. The Journal of Physical Chemistry Letters, 2014. 5(5): p. 896-899.

Additional reading:

https://crosstalk.cell.com/blog/how-to-choose-the-right-journal-for-your-manuscript

https://crosstalk.cell.com/blog/what-should-i-do-if-my-paper-is-rejected-video

https://crosstalk.cell.com/blog/what-should-i-do-if-i-disagree-with-an-editors-decision-video

https://crosstalk.cell.com/blog/how-when-and-why-you-should-appeal-an-editors-decision

INA-RESPOND Newsletter

NEW YEAR, NEW YOU: HOW BEHAVIOUR CHANGING TECHNIQUES AND TECHNOLOGY CAN HELP YOU GET ACTIVE

By: Marco Ariono

As the new year comes, many of us make resolutions to improve our health and wellness. One way to do this is by increasing our physical activity levels, and several behavior-changing techniques and technologies can help us reach our fitness goals. Changing health-related behaviors can significantly impact people's risk of developing diseases linked to their lifestyles. This happens because lifestyle dramatically affects people's health and well-being (e.g., smoking, poor diet, lack of physical activity). According to research, social and cultural environments play a significant role in determining people's behavior patterns. 1–3

How to change a habit

It's hard to change behavior. Changing your own behavior is difficult, and convincing others to change their behavior is even more difficult. The good news is that it is achievable. One method of encouraging healthy behavior is through the use of technology, such as electronic or mobile health treatments. According to its definition, e- and m-health refer to "the use of information and communications technology, notably the internet, to improve or enable health and health care." These treatments have much potential because they can effectively reach many people at a relatively cheap cost while using a personalized and interactive approach.3,4

Many people struggle to live healthily despite knowing what a balanced diet looks like and how beneficial exercise is for them. Education may be crucial (for some, it may be sufficient to trigger a behavior change), but for many people, it won't be enough to change behavior. Therefore, using behavior change techniques (BCT) to support people in changing their physical activity and diet will increase the likelihood that they will make a change instead of simply providing information. At least five of the behavior change strategies (BCTs) included in successful dietary and physical activity treatments are shared by various health behavior theories (i.e., self-monitoring, intention formation, specific goal setting, review of behavioral goals, and feedback on performance).3,5

The term BCTs refers to elements of an intervention that are irreducible, observable, and replicable. BCTs are referred to as a part of an intervention that aims to change or redirect the causal mechanisms that control behavior in this way. In 2013, Michie et al. created the BCT Taxonomy (v1), a classification system for 93 hierarchically clustered approaches. The BCT Taxonomy aids in determining the efficacy of BCTs, especially those created by fitness app developers. Digital behavior change interventions (DBCIs) use digital technologies to support behavior change and can be applied to improve health.5–9 Goal setting, action planning, and self-monitoring are three of the most effective methods for improving physical activity.3

Goal Setting

Goal-setting is a widely used and accepted strategy for promoting physical activity. A goal is defined as "what an individual is trying to accomplish; it is the object or aim of an action." Examples of prominent PA promotion initiatives that involve the achievement of specific outcomes include the 10,000 steps challenge (based on either 10,000 steps per day or incremental increases such as 1500 more steps than last week). 3,10

The SMART criteria are a relatively well-known set of rules for goal specification. This acronym stands for Specific, Measurable, Achievable, Realistic, and Timed. Following these criteria, patients create specific goals with well-defined criteria for success. An example of a SMART goal is, "I will engage in 30 minutes of aerobic physical activity five days a week for the next four weeks." Well-defined goals are necessary for goal attainment because they help individuals focus their desires and intentions and create a standard by which success can be measured.3,10

A limitation of SMART goals, however, is that they do not specify how the goal will be implemented. In the example mentioned above, physical activity can be achieved in various ways: running on a track, going to the gym, one 30-minute bout of physical activity, or three 10-minute bouts of physical activity. To facilitate the implementation of SMART goals, clinicians can help patients develop action plans.3,10

Action Planning

Action plans help people organize the precise steps they will take to accomplish their specific goals by defining where, when, and how a goal will be implemented. Action plans must be created by the individual, shared with others, and have a short duration, among other important characteristics (i.e., one-week duration and reevaluated weekly). If a SMART goal is considered a long-term objective, then an action plan, which outlines the steps to accomplish the goal, is a short-term objective.10

Self Monitoring

It has been determined that self-monitoring, defined as keeping a record of a specific behavior as a method for changing behavior, is a promising behavior change technique to reduce sedentary behavior in adults. Self-monitoring procedures are no longer restricted to just pen and paper recordings, thanks to technological advancements over the past 20 years. In just one session, clinicians and other professionals can help clients set goals and identify target behaviors. Later that day, clients can log onto a website or receive an email with the data on the target behavior. The recording process is frequently more straightforward for the client and the clinician or other professional who needs to access the data. For instance, pedometers were frequently inaccurate and only tracked the number of steps taken, but modern technology like Fitbits provides a more precise way to track movement. Self-monitoring and technology cater to the specific requirements of people who regularly exercise.11,12

Conclusion

As we look towards the new year and the opportunity for fresh beginnings, we must consider how behavior-changing techniques and technologies can play in achieving our resolutions related to physical activity. By utilizing the strategies outlined in this article, we can effectively set ourselves up for success and make meaningful progress toward improving our health and well-being in the year ahead.

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INA-RESPOND Newsletter

OPENAI: GRAMMAR CORRECTION AND PARAPHRASING MONSTER

By: Aly Diana

COMIC CORNER

Some of us may or may not have heard about OpenAI, a "thing" that was quite shocking in my opinion. As a disclaimer, I am not tech-savvy, and conversations about machine learning, artificial intelligence (AI), or hardcore coding/modeling hurt my head. The first time I heard about OpenAI, it was introduced as a program to correct my grammar while writing a draft. I was interested, thinking that it might make my life easier. And yes, it's working (to some extent). In brief, I will give background information on OpenAI, its focus on natural language processing (NLP), and an explanation of GPT-3 and its potential use for grammar corrections and paraphrasing.

OpenAI is a private artificial intelligence research laboratory consisting of the for-profit OpenAI LP and its parent company, the non-profit OpenAI Inc. The company aims to promote and develop friendly AI in a responsible way and has released several widely used AI models, including Generative Pre-trained Transformer 3 (GPT-3), DALL-E and others. OpenAI has a strong focus on NLP, and the company's research in this area will likely lead to improvements in machine understanding of human language.

NLP involves the use of algorithms, statistical models, and machine learning techniques to process and analyze large amounts of natural lan-

guage data, such as text and speech. The goal of NLP is to enable computers to understand, interpret, and generate human language in a way that is both useful and effective. Some examples of NLP tasks include but are not limited to: a) Sentiment analysis: determining the emotional tone of a piece of text; b) Machine translation: translating text from one language to another; c) Text summarization: automatically generating a summary of a longer piece of text; d) Speech recognition: converting spoken language into a written text; and e) Dialogue systems: building computer systems that can hold a conversation with a human. Overall, NLP plays a crucial role in enabling computers to understand and process the vast amount of unstructured data that is generated by humans, such as social media posts, customer reviews, and customer support interactions.

OpenAI has developed several models capable of making grammar corrections in English, including GPT-3. GPT-3 is a state-of-the-art language model trained on a massive amount of text data, allowing it to generate high-quality text that is often indistinguishable from the human-written text. GPT-3 can also understand the context and perform a wide range of natural language processing tasks, such as grammar correction. However, it's important to note that GPT-3 and other models can make mistakes and may only catch some errors. The model's performance will depend on the quality of the training data and the specific task at hand.

Additionally, while GPT-3 can perform grammar correction well, it's not always perfect. OpenAI models show promising results in grammar correction and other natural language processing tasks, but they are not perfect and may not replace human editors in all cases. It's essential to use them as a tool to assist rather than to rely on them fully.

I believe that we may have many questions. It's probably also a good way to test the OpenAI by asking our burning questions and then evaluating the responses. OpenAI has some sub-specializations which can be seen on its website: https://openai.com/. The one that I have used is ChatGPT: https://chat.openai.com/chat. Happy exploring! FYI, sometimes the site was overloaded and showed error messages. Another thing, we need to log in to use the service.

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