JOURNAL OF BALTIC SCIENCE EDUCATION

ISSN 1648-3898 /Print/
ISSN 2538-7138 /Online/

This is an open access article under the Creative Commons Attribution 4.0 International License

DEVELOPMENT AND VALIDATION OF THE GENETICS LITERACY AND REASONING TEST: A TOOL FOR EXPLORING GLOBAL GENETICS ISSUES

Hidayati Maghfiroh, Siti Zubaidah, Susriyati Mahanal, Hendra Susanto, Chun-Yen Chang

Abstract. *So far, instruments to measure genetic literacy that encompass global genetic issues are limited. In addition, instruments that assess practical knowledge and comprehensively evaluate genetic literacy skills have yet to be developed. Therefore, this research aimed to develop, validate, and improve an instrument based on a new conceptual framework of genetic literacy across grades. Six stages were conducted based on construct modeling to establish the Genetics Literacy and Reasoning Test. In the development process, numerous sources of evidence were collected, including evaluation from an expert panel to examine face validity, a pilot study to ensure comprehension, and testing involving 250 pre-service biology teachers. The results showed that the Genetics Literacy and Reasoning Test generally has good quality regarding dimensionality, reliability and separation, item fit, person–item mapping, and other data collected from interviews. This study highlights the importance of developing reliable and valid instruments to evaluate students' genetic literacy and recommends it as a valuable tool for research and practice.*

Keywords: *genetics literacy, instrument validation, Rasch analysis, science education, scientific reasoning*

Hidayati Maghfiroh, Siti Zubaidah, Susriyati Mahanal, Hendra Susanto
State University of Malang, Indonesia
Chun-Yen Chang
State University of Malang, Indonesia
National Taiwan Normal University, Taiwan

Introduction

Advances in genetic technologies are transforming both environmental sustainability and human health. For example, breakthroughs in genomics and molecular genetics have been applied across agriculture, medicine, and conservation—driving improvements in crop resilience, personalized therapies, and ecosystem restoration (Boerwinkel et al., 2017; Little et al., 2022). With advances in molecular genetics, society and people from around the world should be kept informed of the latest genetic research (Middleton et al., 2023; Reydon et al., 2012). For example, broadening access to direct-to-consumer genetic tests indicates the importance of requiring social consciousness for global citizens to understand their advantages and implications (Ruhl et al., 2020; Stern & Kampourakis, 2017). In other words, the advancement of genetic technology is not solely a local concern. It requires global communities to take responsibility for making decisions on global genetic issues.

The tremendous growth in genetic technology has led to global genetic issues such as stem cell research, the COVID-19 pandemic, genetically modified organisms, and cancer (Angraini et al., 2022; Cebesoy & Oztekin, 2018; Fauzi et al., 2021; Han-Tosunoglu & Ozer, 2022). Genetic issues that are controversial in society are described as global genetic issues, which are commonly addressed in three major fields: agriculture, medicine, and the social implications of genetics (Snustad & Simmons, 2016; Wang et al., 2023). Global citizens should actively participate in debates on global genetics issues, make thoughtful decisions using reasoning based on the evidence from the core concepts of genetics knowledge, and enact socio-political actions to address issues about genetics in global society (Dawson & Venville, 2010; Han-Tosunoglu & Ozer, 2022). Therefore, the overarching goal of biology educators is to prepare students to pursue their lives responsibly as global citizens in a globalized society.

The impact of current advanced genetics and genomics technologies has been discussed in biology courses and encourages the aim of biology teaching

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

to reform educated genetically literate citizens (Aivelo & Uitto, 2021). Many education policies in several countries acknowledge science literacy as an inseparable part of genetic literacy, which is considered a primary educational goal (National Research Council, 2012; Zimani et al., 2021). Science education standards demonstrate that to promote students as future citizens in order to become genetically literate, they should have sufficient core concepts of genetics knowledge, as well as provoke their awareness to be proactive in resolving global genetics issues by arguing for and against positions using appropriate reasoning and argumentation (McKnight et al., 2021; Shea et al., 2015; Stern & Kampourakis, 2017). Thus, the understanding of genetics literacy for biology educators and teachers who take a role in cultivating students' genetics literacy is more in demand and crucial in this respect nowadays.

Given the importance of understanding genetic literacy, it is therefore necessary to revisit what genetic literacy means, which is relevant to the era of global change, by referring to what new conceptual framework for genetic literacy is needed in the post-genomic era (Boerwinkel et al., 2017; Maghfiroh et al., 2023). There have been many debates on the meaning of genetic literacy, particularly focusing on emphasising the core concept of genetics in the knowledge dimension. However, prominent theorists have recently agreed that genetic literacy comprises knowledge and skills dimensions. We agree with Shea et al. (2015), Stern and Kampourakis (2017), and Daly and Kaphingst (2023) that genetic literacy is related to the interconnection between genetic concepts and practice for making decisions using appropriate reasoning and argumentation to solve global genetic issues.

This research conceptualizes twenty-first-century genetics literacy as encompassing students' proficiency not only in fundamental genetics concepts but also in the critical decision-making abilities necessary to address global genetics challenges (Daly & Kaphingst, 2023; Maghfiroh et al., 2023; Shea et al., 2015). Biology teachers, as lifelong learners, play a significant role in supporting students' genetic literacy skills, enabling effective responses to genetic phenomena. It is essential to develop students' ability to provide sufficient justification for their claims regarding gene therapy (Högström et al., 2024; Sadler & Fowler, 2006). The focus is on provoking students' informal reasoning, enabling interdisciplinary thinking, and encouraging consideration of the risks and benefits when addressing global genetics issues (Boerwinkel et al., 2017). Emphasis is also placed on training students in decision-making, enabling them to determine solutions through logical considerations (Böttcher & Meisert, 2013; Högström et al., 2024). This new direction is expected to enable students to become global citizens equipped with the skills to tackle major challenges—particularly in the environmental, health, and sustainability domains (Boerwinkel et al., 2017).

Although calls to educate students with a genetics literacy vision have persisted throughout this century, implementation has remained limited. Since early 1994, concerns about courses designed to promote genetic literacy have significantly increased with some spillover to the assessment of genetics literacy (Andrews, 1994; Bowling et al., 2008; Daly & Kaphingst, 2023). Many useful instruments have been developed to measure students' genetic literacy concepts and attitudes, as documented by Bowling et al. (2008) and Chapman et al. (2017). Nonetheless, these instruments were developed over two decades ago and were not designed to measure the competencies that global society needs to reform. Coincident with this shift, this study focuses on developing the instrument of genetics literacy, called the Genetics Literacy and Reasoning Test (GLRT), corresponds to global demands and reflects the new conceptualization of twenty-first-century genetics literacy.

Literature Review

Conceptualization of Genetics Literacy for the Twenty-First Century

Early concepts of genetic literacy focused on genetics concepts, especially in the knowledge dimension (Bowling et al., 2008). Regarding the knowledge dimension, the core genetics concepts were agreed to consist of six main genetics concepts, including genetics material, genetics transmission, regulation of genes, expression of genes, evolution, and genetics and society (Bowling et al., 2008). Nevertheless, evolution and natural selection topics are excluded, as are many other genetic concepts linked to genetic literacy (Boerwinkel et al., 2017). In the post-genomic era, fostering an understanding of gene technology is crucial (Stern & Kampourakis, 2017). Due to recent advances in genetics and gene technology, it is also critical to understand genetics determinism and essentialism (Aivelo & Uitto, 2021). Therefore, the reconceptualization of core genetics concepts encompasses the nature of genetic material, transmission, gene regulation, gene expression, genetic technologies, genetic determinism, and essentialism.

Nowadays, the emphasis on genetic literacy in the twenty-first century has shifted to foster the student's development of skills and knowledge related to genetics literacy to solve global genetic issues in their everyday lives (Boerwinkel et al., 2017; Shea et al., 2015). Numerous studies have identified the main genetic literacy skills that students must master before completing their education. Dawson and Venville (2010) and Beatty et al. (2023)

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

argued that biology teachers have a significant role in helping students develop argumentation skills related to global genetic issues, such as the genetically altered tomato, as well as prenatal genetic testing on cystic fibrosis, through creating informed justifications and providing credible evidence in support of their claims. Han-Tosunoglu and Ozer (2022) revealed that pre-service biology teachers are crucial to developing students' informal reasoning and decision-making skills during the COVID-19 pandemic. Wood et al. (2003) and Yamada-Kurebayashi et al. (2023) showed the importance of teachers cultivating students' awareness and decision-making skills, specifically on cancer genetics services. However, these related skills to genetic literacy need further articulation into measurable constructs to evaluate students' mastery of these genetic literacy skills effectively.

Exploring from extensive literature review and investigating biology educators' views of genetics literacy have been conducted to get a more precise characterisation for global citizens. This research also synthesized a framework for the skills dimension of genetics literacy that consisted of informal reasoning, argumentation, and decision-making. *Informal reasoning* is how students make reasons, which has three elements: interdisciplinary thinking, criteria-setting priority, and decision-making mode (Han-Tosunoglu & Ozer, 2022; Sadler & Zeidler, 2005). *Argumentation* is how the student can create an argument involving two elements: justification quality and evidence credibility (Kulju et al., 2024; Zohar & Nemet, 2002). *Decision-making* is how the student can decide and reflect on choices on global issues, which has two elements, including social interaction and meta-decision (Becker et al., 2023; Böttcher & Meisert, 2013). The key genetics concepts were then articulated, including the nature of genetic material, transmission, gene regulation, gene expression, genetic technology, genetic determinism, and essentialism. Therefore, these two dimensions must be integrated to promote pre-service biology teachers' understanding and necessary skills to solve the complex global genetics issues they may face.

Efforts for Measuring Genetics Literacy

In the last few decades, scholars have designed and developed assessments for evaluating students' genetics concepts on the knowledge dimension, such as genetics information, genetics concept assessment, and genetics literacy assessment instruments. Chattopadhyay (2005) attempted to develop an assessment to evaluate the understanding of genetics information with the concepts focused on classical genetics, molecular genetics, and cell biology among students in class XII. Smith et al. (2008) designed and developed 25 multiple-choice items to measure genetics concept assessment, which concerns the congenital diseases, inheritance of various traits, and transmission to major and non-major undergraduate students. Bowling et al. (2008) developed 30 multiple-choice items GLAI to measure genetics concepts, which many educational researchers have widely used to date, that focused on the six main genetics concepts, including genetics material, genetics transmission, regulation of genes, expression of genes, evolution, and genetics and society for nonmajors in biology undergraduate students. Cebesoy and Oztekin (2018) revised some of the multiple-choice items developed by Bowling et al. (2008) to be suitable for Turkish culture based on Turkish human rights and biomedical legislation, assessing science teachers' genetics literacy.

Although the previously developed instruments are useful for assessing students' genetics conceptual knowledge, these instruments did little to evaluate students' skills related to genetic literacy, and they did not focus on applicable knowledge of genetics literacy needed in the current demands of society. Given the impact of science on global society, it is time to reconceptualize genetic literacy. In order to achieve the goal of being literate in genetics, students are not limited to understanding genetic concepts but also be skilled in making decisions that are now needed as global citizens by considering their social consciousness. This gap undermines students' ability to critically evaluate genetic applications—such as gene therapy, GM crops, and genomic data privacy—potentially leading to misinformed public debate and policy decisions. Therefore, including this critical knowledge and skills related to genetic literacy has become urgent.

Previous studies showed that most instruments designed to measure genetic concepts were in a multiple-choice question. The format of multiple-choice items has a significant and valuable role in large-scale and small-scale assessments because the advantages of using multiple-choice questions are scoring accuracy, quick to score, and cost-effectiveness (Riggs et al., 2020; Roediger & Marsh, 2005). However, the previous instrument for assessing genetic literacy relied on the raw scores of standardised tests and did not consider the psychometric properties. This approach has limitations when it comes to generalising findings about students' genetic literacy, as the unknown psychometric properties can affect the accuracy of the results (Fauzi et al., 2021; Gormally et al., 2012).

To address these limitations, the GLRT was designed as a large-scale assessment comprising multiple-choice items that span comprehensive competencies within the genetics literacy construct, and Rasch measurement was employed to evaluate its psychometric properties. Previous education research also used Rasch measurement to

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

measure validity and showed a good index (Fauzi et al., 2021; Yang et al., 2018). Rasch measurement has a unique property in which item difficulty and ability are independent of one another because the ability scores are calibrated on an infinite scale that can avoid the effect of upper and lower bounds. Therefore, Rasch calibrated scores provide a more accurate estimate of student ability than raw scores (Bond & Fox, 2010; Tesio et al., 2024).

Research Aim

This research aimed to develop, validate, and refine an instrument for evaluating genetics literacy called the Genetics Literacy and Reasoning Test (GLRT). As a first step, a detailed description of the rigorous development process of the GLRT was provided. Next, evidence supporting the unidimensionality, validity, and reliability of the GLRT across different grade levels was presented. The development of the GLRT represents the initial phase of a research project integrating theoretical knowledge with advanced analytical and problem-solving abilities. The resulting instrument demonstrates reliability and validity for measuring twenty-first-century genetic literacy competencies. This study was conducted with second- and fourth-year biology teacher candidates.

Research Methodology

Developing Instruments

The Genetics Literacy and Reasoning Test (GLRT) was designed following Gormally et al. (2012) and its construct validity approach was adopted from Yang et al. (2018). Content validity was maximized through a robust theoretical framework that synthesized critical features of twenty-first-century genetic literacy aligned with documented global genetics applications. Key features of genetic literacy required by society were identified and synthesized from the literature. Table 1 presents the items constructed based on key characteristics of the Genetics Literacy and Reasoning Test.

Table 1
Items Constructed Based on Key Characteristics of the Genetics Literacy and Reasoning Test

Categories of genetics literacy skills	Elements	Global Genetics Issues		
		Pandemic Coronavirus Disease (p)	Genetically Modified Organisms (g)	Cancer (c)
Informal reasoning	Interdisciplinary thinking (I)	pNogI1	gNogI8	cNogI15
	Decision-making mode (D)	pTraD2	gTraD9	cTraD16
	Criteria setting and priority (C)	pExpC3	gExpC10	cExpC17
Argumentation	Justification quality (J)	pRegJ4	gRegJ11	cRegJ18
	Evidence credibility (E)	pTecE5	gTecE12	cTecE19
Decision-making	Social interactions (S)	pEssS6	gEssS13	cEssS20
	Meta-decision (M)	pDetM7	gDetM14	cDetM21

Note:
a. for the first letter: *p* pandemic coronavirus disease, *g* genetically modified organisms, *c* cancer;
b. for the second letter*: Nog* Nature of genetics material, *Tra* Transmission gene, *Exp* Expression of the gene, *Reg* Regulation of the gene, *Tec* Technology gene, *Ess* Essentialism gene, *Det* Determinism gene;
c. for the third letter*: I* interdisciplinary thinking, *D* decision-making mode, *C* criteria setting and priority, *J* justification quality, *E* evidence credibility, *S* social interactions, *M* Meta-decision
d. for the last letter*:* the number of the item

A new framework and constructs for genetics literacy assessment were synthesized by integrating essential skills and core concepts (see Appendix A). Prior research indicated that argumentation, informal reasoning, and decision-making are critical competencies for mastering genetic literacy in the context of global issues (Böttcher

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

& Meisert, 2013; Sadler & Zeidler, 2005; Shea et al., 2015). Informal reasoning was defined as students' ability to generate reasons about global genetics issues across three dimensions: interdisciplinary thinking, criteria prioritization, and decision-making mode (Sadler & Zeidler, 2005). Argumentation was operationalized as the capacity to construct arguments based on justification quality and evidence credibility (Zohar & Nemet, 2002). Decision-making was measured by students' selection of appropriate solutions to global issues, encompassing social interaction and meta-decision processes (Böttcher & Meisert, 2013). Core genetics concepts—namely, the nature of genetic material, transmission, gene regulation, gene expression, genetic technologies, genetic determinism, and essentialism—were then mapped to these skills to capture how content knowledge is applied to complex global problems (Aivelo & Uitto, 2021; Boerwinkel et al., 2017; Bowling et al., 2008; Stern & Kampourakis, 2017).

The second step involved selecting global genetics issues with relevant across diverse domains. Snustad and Simmons (2016) identified three major application areas of genetics: society, agriculture, and medicine. Issues for each domain were selected based on prior recommendations (Boerwinkel et al., 2017; Han-Tosunoglu & Ozer, 2022; Snustad & Simmons, 2016). The societal application of genetics was exemplified by the Coronavirus Disease (COVID-19) pandemic (Han-Tosunoglu & Ozer, 2022); the agricultural application was represented by the genetically modified organisms (GMO) issue (Boerwinkel et al., 2017); and the medical application was illustrated through the cancer issue (Snustad & Simmons, 2016). The third step involved constructing the item blueprint of the Genetics Literacy and Reasoning Test (GLRT), which was informed by the selected genetics issues and data from current and widely publicized sources. The GLRT was developed in the form of multiple-choice questions, following established practices in instrument design (Bowling et al., 2008; Gormally et al., 2012; Romine et al., 2017).

Fourth, the content validity of the GLRT was evaluated through face validity by a panel of experts, consisting of five professors with expertise in genetics education and five in assessment design. The genetics education experts evaluated each item for genetic accuracy, relevance, and clarity, while the assessment design experts assessed each item for comprehension, clarity, and relevance. The GLRT was subsequently revised to improve item quality based on the experts' comments and suggestions.

Fifth, Munby (1997) and Cabouat et al. (2025) suggested that instruments should be designed to be easily understandable by the target audience. Therefore, overreliance on experts as the sole determinant of face validity in the instrument validation process must be critically reconsidered. To enhance readability and understandability, informal interviews were conducted with three second-year and three fourth-year pre-service biology teachers. As the development of the GLRT followed an iterative process, the items were revised based on the feedback provided by the pre-service biology teachers to ensure item clarity and quality. Figure 1 presents examples of revised items. For further details, the item specification table and the complete instrument are included in Appendices B and C.

Sixth, a large-scale implementation was conducted involving a broader population of pre-service biology teachers. A two-stage stratified cluster sampling method was employed to obtain representative samples across different proficiency levels. As a result, the sample included both second-year and fourth-year pre-service biology teachers. Finally, Rasch analysis was performed to validate the assessment based on the results of the large-scale implementation.

Participants

Ethical approval was obtained from the university affiliated with the primary researcher, and Informed consent was obtained from all participants. This aligns with the ethical guidelines emphasizing the importance of informed consent and participant autonomy in studies involving genetic information and education. The study involved 250 pre-service biology teachers, divided equally between second-year (n = 125; 109 females, 17 males; aged 19–20) and fourth-year students (n = 125; 95 females, 31 males; aged 21–22). The second-year participants had not yet undertaken genetics courses, while the fourth-year participants had completed such coursework. This stratification was intentional to assess the instrument's sensitivity in distinguishing between varying levels of genetics knowledge, a practice supported by the expert–novice paradigm in educational research.

The instrument validation involved 250 pre-service biology teachers responding to the 21-item Genetics Literacy and Reasoning Test (GLRT). This sample size met established guidelines for Rasch analysis, which typically recommend a minimum of 10 participants per item (Boone et al., 2014; Linacre, 2019). With a ratio of nearly 12 participants per item, the sample provided adequate power to detect misfitting items, estimate person and item parameters reliably, and evaluate the functioning of the scale. In the context of test development, DeVellis (2016) suggested participant-to-item ratios of 5:1 to 10:1 for psychometric analyses such as item calibration and construct validation. The Genetics Literacy and Reasoning Test (GLRT) was administered to both cohorts to evaluate its ef-

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

fectiveness in measuring genetic literacy across different knowledge levels. The use of equivalent sample sizes enhances the validity of comparative analyses, ensuring that observed differences are attributable to the variable of interest—in this case, genetics knowledge. Rasch analysis was employed to validate the instrument, providing a robust statistical framework for assessing item difficulty and participant ability.

Figure 1

Figure 1 illustrates examples of revised GLRT items (pTraD2, gExpC10, cEssS20), reflecting modifications made based on expert feedback and pilot testing to enhance clarity and relevance

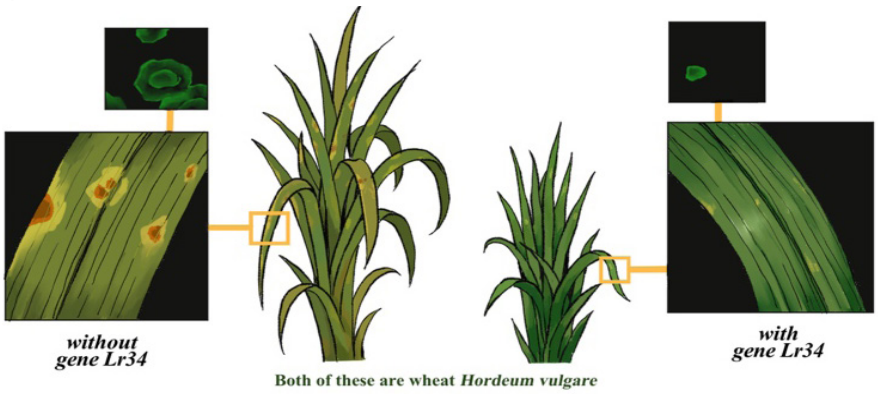
1. Look at the table below!

No	Exposure	Average viral genome copy reduction (log)
1	Dry control	0,20
2	Hand sanitiser	0,14
3	Hand soap	0,94
4	Water rinse	0,75

Disinfection is the critical step in interrupting the transmission of the SARS-CoV-2 genome, but there is debate about the effectiveness of some disinfection practices. The table above shows the average difference in viral genome copy reduction. The data was obtained from the results of virus inoculation on the fingertips of 20 volunteers, who were then given different disinfection exposures. A healthcare professional wants to suggest the best disinfection practice to prevent replication of the SARS-CoV-2 genome. Based on the table above, determine **the most effective** practice to avoid the replication of the SARS-CoV-2 genome!

A. Hand soap, as it damages capsid proteins and RNA.
B. Hand soap, as it damages lipid membranes and DNA.
C. Water rinse, as it damages spike proteins and mRNA.
D. Hand sanitiser, as it damages capsid proteins and RNA.
E. Hand sanitiser, as it damages lipid membranes and DNA.

2. Look at the picture below!



A scientist conducted genetic engineering by inserting the *Lr34* gene from wheat (*Triticum aestivum*) into the wheat gene (*Hordeum vulgare*). Based on the picture above and the expression of the *Lr34* gene, evaluate the **role** and **consequence** of the insertion of the *Lr34* gene in *H. vulgare*!

A. *Lr34* gene encodes resistance gene but decreases growth rate.
B. *Lr34* gene encodes resistance tRNA and increases growth rate.
C. *Lr34* gene encodes resistance protein and increases growth rate.
D. *Lr34* gene encodes resistance cDNA but decreases growth rate.
E. *Lr34* gene encodes resistance protein but decreases growth rate.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

3. Based on data from Global Cancer Statistics 2022, breast cancer has a high incidence rate globally. Coinciding with World Cancer Day, the government has initiated an early detection programme using functional DNA biomarkers to identify breast cancer. However, this detection method raises concerns about the potential access to patients' private genetic information. From a **scientific ethics** perspective, do you agree with the practice of early breast cancer detection?

A. Disagree, as it may lead to public concern.
B. Agree unconditionally, as it may hinder tumor cell division.
C. Neutral, as early detection must be balanced with genetic data protection.
D. Disagree, as it may violate the privacy of an individual's genetic information.
E. Agree, with patient consent, as early detection can help prevent cancer cell metastasis.

Data Analysis

Rasch measurement. The Rasch measurement model was developed by the Danish mathematician George Rasch (Rasch, 1993) was used to analyse the Genetics Literacy and Reasoning Test (GLRT). This model tested the construct validity and reliability of the GLRT as applied to second-year, fourth-year, and pooled data. Rasch (1993) stated that the probability of a person answering an item correctly can be represented through a mathematical equation under the item response theory (IRT). The model assumes that a person with higher ability is more likely to answer difficult items correctly, while easier items are more likely to be answered correctly by individuals with varying abilities. Probability is modeled as the difference between a person's ability and the item's difficulty.

Assessment of unidimensionality. The unidimensionality of the GLRT was examined using the principal component analysis (PCA) method. PCA identified response patterns that deviated from the Rasch model (Bond & Fox, 2007). In this context, PCA aimed to detect clusters of items displaying unexpected variance patterns. The Rasch dichotomous model was applied to the multiple-choice format of the GLRT (scored as 0 = incorrect; 1 = correct). PCA was deemed suitable for assessing the dimensionality of dichotomous responses. According to Raiche (2005) and Linacre and Tennant (2009), residuals showing randomness with a first eigenvalue around two suggest adequate unidimensionality. However, Galli et al. (2008) proposed a stricter threshold of three for practical utility.

Reliability and separation. In addition to unidimensionality, the structure and reliability of the GLRT were analysed across contexts. Rasch person separation and reliability indices were calculated to determine the precision of the instrument. Reliability was computed as the ratio of true variance to observed variance, while separation reflected the ratio between true variance and error variance. Item reliability and separation indices were also reviewed to confirm the hierarchy of item difficulty. Item reliability indicates the precision of measuring latent traits (such as abilities or dispositions), and item separation refers to the scale's ability to differentiate between individuals with varying levels of the trait. Reliability values ranged from 0 to 1, with higher values indicating greater measurement precision (Wright & Masters, 1982).

Item–level construct validity. Item-level construct validity was examined using infit and outfit mean square (MNSQ) statistics calculated with WINSTEPS software. These statistics compared observed and expected responses. The optimal MNSQ value is 1.0, with values between 0.5 and 1.5 considered productive for measurement (Wright & Linacre, 1994). For low-stakes assessments, a stricter range of 0.7–1.3 is often applied (Bond & Fox, 2007). An MNSQ value exceeding 1.0 suggests more error than expected, while values above 1.5 typically reflect misfit responses—such as when high-ability participants miss easy items or low-ability participants guess correctly (Linacre & Tennant, 2009).

Person–item mapping. Person–item mapping was used to evaluate how well the GLRT items were targeted to the participants. This visual analysis facilitated the interpretation of whether the test items were too easy or too difficult for the sample. Item and participant locations on the Rasch continuum were plotted to evaluate the functioning of the test for second-year, fourth-year, and pooled data. Person–item mapping also added qualitative meaning to the logit measures. Participants located above an item on the scale were more likely to answer it correctly, whereas those below an item were less likely to do so (Wright & Linacre, 1994).

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Research Results

Unidimensionality

The Genetics Literacy and Reasoning Test (GLRT) unidimensionality was determined using principal component analysis (PCA) on the residuals associated with the Rasch method. The study results showed that the GLRT fulfilled the criteria of unidimensionality, which represented a single dimension (Table 2). The total variance explained by the measures exceeded 20%, while the percentage of unexplained variance in the first contrast was below 10% for the second year, fourth year, and pooled data. The values for the PCA for the first eigenvalue of the residuals were 2.64, 2.32, and 2.09 for the second year, fourth year, and pooled data (the metrics when both cohorts' data are analysed together), respectively. Most items were within the factor loading range of -.4 to +.4, except for items gNogI8 and gExpC10, which require further analysis.

Table 2
The PCA Report for Two Grades and Pooled Data

Component Assessed	Second-year	Fourth-year	Pooled
Raw variance explained by measures (%)	23.1	20.1	20.8
Raw unexplained variance (%)	76.9	80.2	79.2
Unexplained variance in 1st contrast (%)	9.7 (2.64)	8.9 (2.32)	7.9 (2.09)
Items out of range	gExpC10, gTecE12	cExpC17, gNogI8	gNogI8, gExpC10

Reliability and Separation

The GLRT was determined to meet the reliability criteria, indicating its utility in a particular context. Nevertheless, its utility did vary significantly depending on the application (Table 3). When it was used with second-year pre-service biology teachers, the person reliability value was .63 (separation = 1.30). Hence, when used with fourth-year pre-service biology teachers, the person reliability value increased to .70 (separation = 1.51). The person reliability further increased to .71 (separation = 1.57) when applied to the pooled data. These results indicated that the person reliability and separation values were acceptable for the second-year data but more robust for the fourth and polled data.

Additionally, the reliability and item separation depend on item difficulty variance and respondent sample size. Item reliabilities for second-year, fourth-year, and pooled data were measured at .95, .91, and .96. Moreover, item separation for the second-year, fourth-year, and pooled data were estimated at 4.39, 3.26, and 5.06. This high item reliability and separation showed that this sample size provided adequate precision for establishing the construct validity of the test.

Item–Level Validity

The fit statistics of all GLRT items are calculated in the mean square of fit (MNSQ) in Table 3. Most items fit the Rasch Model, demonstrating the usefulness of items for differentiating pre-service biology teachers along the Genetics Literacy and Reasoning Test. All items in the GLRT had values of infit and outfit MNSQ ranging between .7 and 1.3, indicating the items had a generally good model fit. The lowest infit values for second-year, fourth-year, and pooled data were measured at .84 (item gRegJ11), .85 (item cExpC17), and .87 (item cExpC17), and the highest values were calculated at 1.17 (item gTraD9), 1.20 (item pNogI1), and 1.21 (item pNogI1). When the GLRT was used for second-year pre-service biology teachers, the outfit values for Item cEssS20 were outside the range at 1.51. However, item cEssS20 fits well when used for fourth-year and pooled data, with outfit values of .90 and 1.16, suggesting this item's predictions were less accurate.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Table 3
The Results of Evaluating Item-Level Validity for GLRT

Component Assessed		Second-year			Fourth-year			Pooled	
Reliability of person		.63			.70			.71	
Separation of person		1.30			1.51			1.57	
Reliability of item		.95			.91			.96	
Separation of item		4.39			3.26			5.06	
MNSQ	**Measure**	**Infit**	**Outfit**	**Measure**	**Infit**	**Outfit**	**Measure**	**Infit**	**Outfit**
pNogI1	-.09	1.12	1.09	.81	1.20	1.21	.34	1.21	1.24
pTraD2	1.10	.96	.92	.97	1.01	1.05	1.03	.98	.98
pExpC3	-.31	.96	.93	-1.00	.94	.98	-.60	.92	.90
pRegJ4	-.73	1.12	1.07	.22	1.10	1.09	-.28	1.15	1.17
pTecE5	.77	1.02	1.05	.38	.92	.89	.57	.95	.94
pEssS6	-.93	1.07	1.03	.10	.97	1.01	-.45	1.07	1.12
pDetM7	-.69	.88	0.86	-.77	.98	.92	-.73	.92	.88
gNogI8	1.44	1.16	1.19	.89	.98	.98	1.13	1.03	1.03
gTraD9	1.02	1.17	1.28	.78	.99	.97	.88	1.06	1.10
gExpC10	.06	.94	.98	.26	1.08	1.04	.15	1.01	1.01
gRegJ11	.24	.84	.79	.30	1.01	.97	.26	.92	.88
gTecE12	1.24	.95	.92	.54	1.08	1.07	.86	.98	.97
gEssS13	.42	.89	.89	-.72	.95	.92	-.08	.88	.86
gDetM14	-.27	.87	.82	-1.34	.94	.77	-.68	.87	.76
cNogI15	.53	1.15	1.17	-.29	.92	.81	.15	.99	.98
cTraD16	.53	1.00	1.08	.30	1.11	1.16	.41	1.04	1.10
cExpC17	.50	.91	.90	.38	.85	.78	.43	.87	.83
cRegJ18	-2.40	.96	.76	-1.49	1.01	1.01	-1.97	1.00	1.03
cTecE19	.06	.93	.89	.81	1.00	1.04	.41	1.01	1.03
cEssS20	-1.63	1.05	1.51	-.42	1.00	.90	-1.04	1.08	1.16
cDetM21	-.85	1.06	1.07	-.72	.95	.87	-.80	1.01	.97

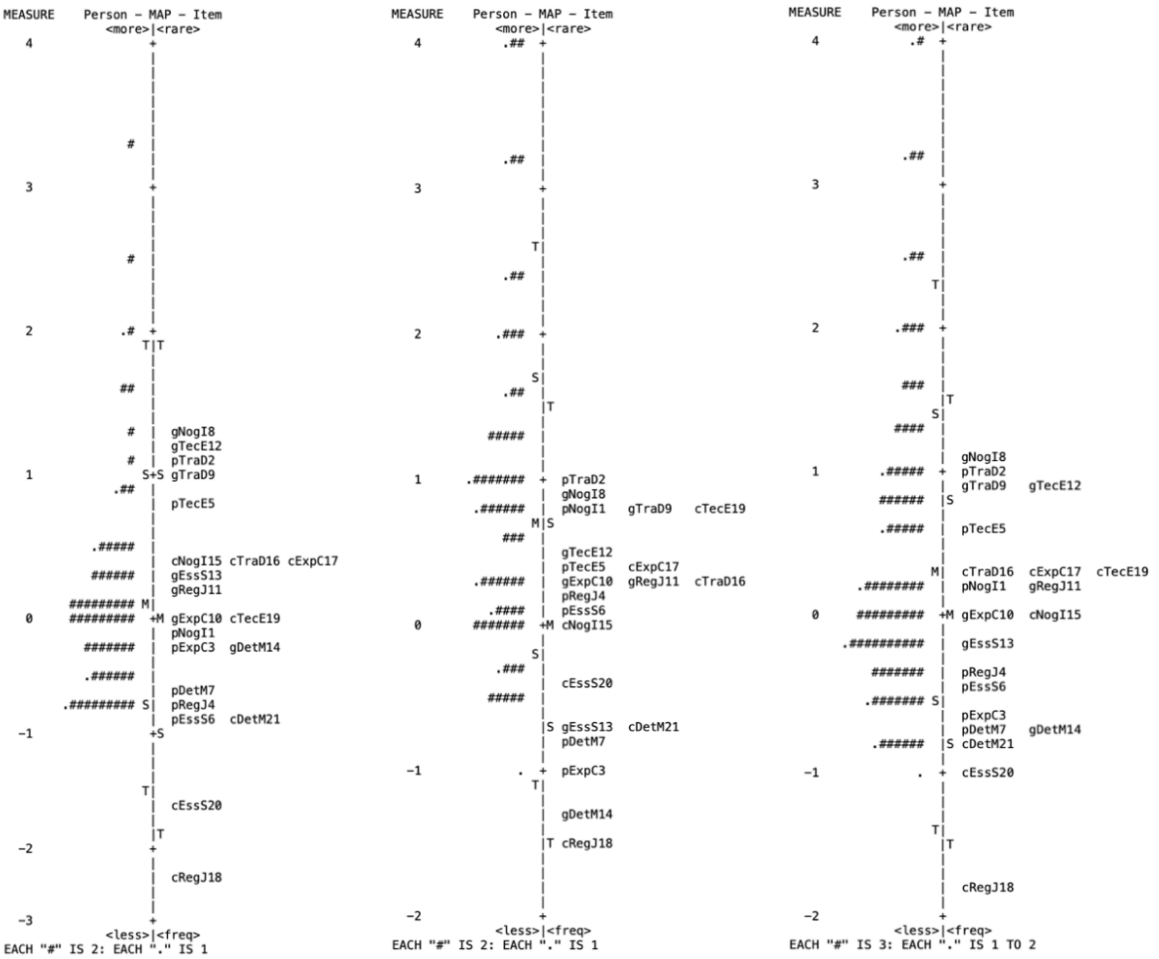
Person–Item Mapping

Person–item maps were generated to assess targeting and construct validity for second-year, fourth-year, and pooled data (Figure 2). The maps showed a good spread of item difficulties and student abilities. Items located below a respondent's ability level were generally answered correctly, whereas those above their ability level were more often missed. For example, a second-year participant with an ability estimate of –1 logits correctly answered items gNogI8 and cEssS20 but failed the more difficult items. The most difficult items were gNogI8 for second-year and pooled data, and pTraD2 for fourth-year data; the easiest item across all groups was cRegJ18. The dashed line at zero logits indicates average difficulty and ability. Finally, items gExpC10, cTecE19, and cNogI15 each showed approximately a 50% probability of correct response in their respective cohorts, suggesting borderline targeting efficiency.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Figure 2
The Result of the Wright Map



Discussion

The present study aimed to develop and validate a Genetics Literacy and Reasoning Test (GLRT) encompassing overarching constructs that integrate key concepts and essential skills of genetic literacy and target pre-service biology teachers in different grades. Specifically, six design steps were used to guide the assessment design process, and Rasch measurement was applied to evaluate the GLRT. Specifically, six design steps were used to guide the assessment design process, and Rasch measurement was applied to assess the GLRT. The following section presents empirical evidence for the GLRT and highlights design issues related to providing continuous, comprehensive information. In addition, GLRT limitations and implications for future research are addressed.

The global understanding of genetic literacy requires a multifaceted background in genetics issues across different domains such as society, agriculture, and healthcare. Consequently, collecting reliable, valid, and unidimensional measures presents a significant challenge. Incorporating global issues into the GLRT enabled an accurate and unidimensional assessment of multiple constructs. Regarding the study's aim, the Rasch measurement demonstrated that the GLRT, as a multiple-choice test, reliably assessed continuous latent traits within a new global genetics literacy framework for pre-service biology teachers. Rasch measurement was the best model to analyse the dichotomous responses, not only for the sample (pooled data) but also for each group (second and fourth year) (Avinç & Doğan, 2024; Bond & Fox, 2007).

A thorough analysis of the residuals using principal component analysis (PCA) demonstrated that the GLRT was unidimensional. These findings indicated that the GLRT is a single-dimension instrument according to the Rasch

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

model, with acceptable interference from some items (Bond et al., 2020; Linacre & Tennant, 2009). Thus, the design of GLRT, which involved multiple genetic issues, was not a problem to remain unidimensional. Although these values are slightly over the strict criteria for unidimensionality based on simulation studies (Linacre & Tennant, 2009; Raiche, 2005; Wind & Schumacker, 2021), these values remained well below three and indicated low inter-item interdependence, so that the GLRT can be regarded as a unidimensional construct (Ha et al., 2025; Linacre & Tennant, 2009). Items gNogI8 and gExpC10 were slightly out of range in PCA, which indicates that these items might not fit into the construct. Factor loadings in these ranges indicated that most items measured the same dimension (Liu, 2010).

Secondly, the reliability values for the second-year cohort were deemed acceptable at .63, while those for the fourth-year cohort were deemed sufficient at .70. The adequate and sufficient levels of person reliability and separation highlighted the strong ability of the GLRT to distinguish between high-performing and low-performing participants. Previous studies showed that these values of person reliability proved the GLRT could distinguish between high- and low-ability students to compare within groups (Dabaghi et al., 2020; Tennant & Conaghan, 2007). The reliability of the items is between .91 and .96, and the separation of items is between 3.26 and 5.06, indicating measurements with high precision. The high reliability and item separation precision indicated a sufficient sample size and item variability for appropriately comparing items (Boone, 2016). Furthermore, the high reliability and separation values confirmed that the GLRT covers a wide range of item difficulty levels that can be effectively differentiated.

Thirdly, the infit and outfit item mean squares values are around .7 and 1.3, showing that these items provide a good model fit (Wright & Linacre, 1994). However, item cEssS20 displayed extreme outfit values of 1.51 when GLRT was used for second-year pre-service biology teachers. This indicates that students with an extremely low ability to guess item cEssS20 correctly and students with an extremely high ability missed item cEssS20 (Bond & Fox, 2007). Fourth, person-item mapping showed evidence for an accepted GLRT needing easier items. The average item difficulty for second-year and fourth-year items was items gExpC10 about gene expression, item cTecE19 about genetics technology, and item cNogI15b about the nature of genetic material. According to Wright and Masters (1982), efficiency is maximized when every item has a distinct location along the latent continuum.

Overall, the GLRT has acceptable construct validity based on the criteria of unidimensionality, reliability, and separation, item-level validity, and then person-item mapping. Hence, the designed GLRT provided satisfactory quality for the early phase of such iterative development. Nevertheless, the development of the instrument is an iterative process. Thus, there is a need for further improvements to make the GLRT widely applicable.

Although this study extends the empirical evidence of the validity and reliability revealed by Rasch's measurement, there are some limitations. The two grades had different values of person reliability, indicating that the GLRT could distinguish between second-year and fourth-year pre-service biology teachers. Future research could further explore the strengths of the GLRT by involving pre-service biology teachers from various universities, employing diverse sampling methods, and conducting scale analyses that account for clustering effects such as ethnicity, gender, and urban or rural backgrounds, factors beyond the scope of this study. Additionally, Rasch measurement can provide validity and reliability values, particularly for each item. Future studies may also investigate differential item functioning and factor analysis to enhance the robustness of the instrument.

Moreover, it could be noted that the development of GLRT could potentially provide a psychometrically sound instrument for assessing genetics literacy and reasoning. A major advantage is that this study builds foundations by designing tests involving essential skills and core genetics concepts representing global genetics issues. Empirical evidence was also provided to demonstrate the GLRT's validity and reliability across different educational levels. Therefore, this study represents strong empirical evidence of the global genetics literacy test. In addition, researchers and educators may use GLRT to assess the students' global genetic literacy across different countries, thus enabling international comparisons. The GLRT can also be a tool to evaluate or compare effective teaching practices to promote global genetic literacy for life in the present century.

These findings suggest that this research can prompt the global scientific community to reconsider the notion of genetic literacy and redefine the meaning of "knowing" genetics well in the twenty-first century context. While the findings of research using the GLRT have the potential to contribute to the development of novel standards in genetics education, teaching practices, institutional development, and the synchronization between these various elements, the GLRT is accessible to educators and scholars across the globe. Overall, the GLRT is readily accessible to many teachers and researchers worldwide as the instrument has good psychometric characteristics. The GLRT has already proved its significant value for the science education literature. Finally, these findings encourage scholars and educators to utilise the GLRT in order to measure and evaluate students' global genetic literacy, both in the context of academic research and practice in the field of science education.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Conclusions and Implications

Although genetic literacy has become an essential and widely discussed topic in recent years, studies related to assessment involving global genetics issues are still in the beginning stages. The development of the GLRT has the potential to provide academics with an instrument of good psychometric quality to assess genetic literacy in the twenty-first century. The peculiarity of the GLRT enables a higher level of accuracy for analysing how students master competencies in this era. Even though other instruments can also be used to measure genetic literacy, the GLRT is specifically designed to measure genetics literacy and reasoning with an approach that differs from past views. Taking into account that the GLRT integrates essential genetic literacy skills such as argumentation, informal reasoning, and decision-making, it also integrates core concepts of genetics, such as the nature of genetic material, transmission, expression of genes, regulation of genes, technology of genetics, determinism, and essentialism of genetics. All of these aspects represent current definitions and measurements of genetic literacy. Overall, as the GLRT is readily accessible to scientists worldwide and its psychometric characteristics are sound, this instrument contributes significantly to the literature of educational science. Furthermore, it offers valuable insights for reforming genetics curricula, redesigning learning approaches, and being useful for educators and researchers in measuring genetics literacy competencies towards the twenty-first century.

Funding

This research was supported by the Master's Education towards Doctorate for Excellent Graduates (Pendidikan Magister menuju Doktor untuk Sarjana Unggul/PMDSU) program and the Enhancing International Publication Program (Peningkatan Kualitas Publikasi Internasional/PKPI), funded by the Ministry of Education, Culture, Research, and Technology of the Republic of Indonesia through a research grant with project number 3.5.22/UN32.14.1/LT/2024.

Acknowledgements

The authors would like to express their sincere gratitude to all individuals and institutions who contributed to and supported the completion of this research.

Declaration of Interest

The authors declare no competing interest.

References

Aivelo, T., & Uitto, A. (2021). Factors explaining students' attitudes towards learning genetics and belief in genetic determinism. *International Journal of Science Education*, *43*(9), 1408–1425. https://doi.org/10.1080/09500693.2021.1917789

Andrews, L. B. (1994). *Assessing genetic risks: Implications for health and social policy*. National Academy Press.

Angraini, E., Zubaidah, S., Susanto, H., & Omar, N. (2022). Enhancing creativity in genetics using three teaching strategies-based TPACK model. *Eurasia Journal of Mathematics, Science and Technology Education*, *18*(12), Article em2196. https://doi.org/10.29333/ejmste/12697

Avinç, E., & Doğan, F. (2024). Digital literacy scale: Validity and reliability study with the Rasch model. *Education and Information Technologies*, *29*(17), 22895–22941. https://doi.org/10.1007/s10639-024-12662-7

Beatty, A. E., Driessen, E. P., Clark, A. D., Costello, R. A., Ewell, S., Fagbodun, S., Klabacka, R. L., Lamb, T., Mulligan, K., Henning, J. A., & Ballen, C. J. (2023). Biology instructors see value in discussing controversial topics but fear personal and professional consequences. *CBE Life Sciences Education*, *22*(3), ar28. https://doi.org/10.1187/cbe.22-06-0108

Becker, F., Wirzberger, M., Pammer-Schindler, V., Srinivas, S., & Lieder, F. (2023). Systematic metacognitive reflection helps people discover far-sighted decision strategies: A process-tracing experiment. *Judgment and Decision Making*, *18*, Article e15. https://doi.org/10.1017/jdm.2023.16

Boerwinkel, D. J., Yarden, A., & Waarlo, A. J. (2017). Reaching a consensus on the definition of genetic literacy that is required from a twenty-first-century citizen. *Science & Education*, *26*(10), 1087–1114. https://doi.org/10.1007/s11191-017-9934-y

Bond, T. G., & Fox, C. M. (2007). *Fundamental measurement in the human sciences* (2nd ed.). Mahwah.

Bond, T. G., & Fox, C. M. (2010). *Applying the Rasch model: Fundamental measurement in the human sciences ; [free Rasch software CD enclosed]* (2. ed., reprinted). Routledge.

Bond, T., Yan, Z., & Heene, M. (2020). *Applying the Rasch model: Fundamental measurement in the human sciences* (4th ed.). Routledge. https://doi.org/10.4324/9780429030499

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Boone, W. J. (2016). Rasch Analysis for instrument development: Why, when, and how? *CBE—Life Sciences Education*, *15*(4), Article rm4. https://doi.org/10.1187/cbe.16-04-0148

Boone, W. J., Staver, J. R., & Yale, M. S. (2014). *Rasch analysis in the human sciences* (1st ed. 2014). Springer: Imprint: Springer. https://doi.org/10.1007/978-94-007-6857-4

Böttcher, F., & Meisert, A. (2013). Effects of direct and indirect instruction on fostering decision-making competence in socioscientific issues. *Research in Science Education*, *43*(2), 479–506. https://doi.org/10.1007/s11165-011-9271-0

Bowling, B. V., Acra, E. E., Wang, L., Myers, M. F., Dean, G. E., Markle, G. C., Moskalik, C. L., & Huether, C. A. (2008). Development and evaluation of a genetics literacy assessment instrument for undergraduates. *Genetics*, *178*(1), 15–22. https://doi.org/10.1534/genetics.107.079533

Cabouat, A.-F., He, T., Isenberg, P., & Isenberg, T. (2025). PREVis: Perceived readability evaluation for visualizations. *IEEE Transactions on Visualization and Computer Graphics*, *31*(1), 1083–1093. https://doi.org/10.1109/TVCG.2024.3456318

Cebesoy, U. B., & Oztekin, C. (2018). Genetics literacy: Insights from science teachers' knowledge, attitude, and teaching perceptions. *International Journal of Science and Mathematics Education*, *16*(7), 1247–1268. https://doi.org/10.1007/s10763-017-9840-4

Chapman*, R., Likhanov, M., Selita, F., Zakharov, I., Smith-Woolley, E., & Kovas, Y. (2017). *Genetic literacy and attitudes survey (lglas): International population-wide assessment instrument*. 45–66. https://doi.org/10.15405/epsbs.2017.12.6

Chattopadhyay, A. (2005). Understanding of genetic information in higher secondary students in Northeast India and the implications for genetics education. *Cell Biology Education*, *4*(1), 97–104. https://doi.org/10.1187/cbe.04-06-0042

Dabaghi, S., Esmaielzadeh, F., & Rohani, C. (2020). Application of Rasch analysis for development and psychometric properties of adolescents' quality of life instruments: A systematic review. *Adolescent Health, Medicine and Therapeutics*, *11*, 173–197. https://doi.org/10.2147/AHMT.S265413

Daly, B. M., & Kaphingst, K. A. (2023). Variability in conceptualizations and measurement of genetic literacy. *PEC Innovation*, *2*, Article 100147. https://doi.org/10.1016/j.pecinn.2023.100147

Dawson, V. M., & Venville, G. (2010). Teaching strategies for developing students' argumentation skills about socioscientific issues in high school genetics. *Research in Science Education*, *40*(2), 133–148. https://doi.org/10.1007/s11165-008-9104-y

DeVellis, R. F. (2016). *Scale development: Theory and applications* (Fourth edition). SAGE Publications.

Fauzi, A., Saefi, M., Kristiana, E., Adi, W. C., & Lestariani, N. (2021). Factor and Rasch analysis on COVID-19 genetics literacy assessment instrument. *Eurasia Journal of Mathematics, Science and Technology Education*, *17*(11), Article em2032. https://doi.org/10.29333/ejmste/11264

Galli, S., Chiesi, F., & Primi, C. (2008). The construction of a scale to measure mathematical ability in psychology students: An application of the Rasch model. *TPM-Testing, Psychometrics, Methodology in Applied Psychology*, *15*(1), 3–18.

Gormally, C., Brickman, P., & Lutz, M. (2012). Developing a test of scientific literacy skills (TOSLS): Measuring undergraduates' evaluation of scientific information and arguments. *CBE—Life Sciences Education*, *11*(4), 364–377. https://doi.org/10.1187/cbe.12-03-0026

Ha, H. T., Nguyen ,Duyen Thi Bich, & and Stoeckel, T. (2025). A comparison of Yen's Q3 coefficient and Rasch testlet modeling for identifying local item dependence: Evidence from two vocabulary matching tests. *Language Assessment Quarterly*, *22*(1), 56–76. https://doi.org/10.1080/15434303.2025.2456953

Han-Tosunoglu, C., & Ozer, F. (2022). Exploring pre-service biology teachers' informal reasoning and decision-making about COVID-19. *Science & Education*, *31*(2), 325–355. https://doi.org/10.1007/s11191-021-00272-5

Högström, P., Gericke, N., Wallin, J., & Bergman, E. (2024). Teaching socioscientific issues: A systematic review. *Science & Education*. https://doi.org/10.1007/s11191-024-00542-y

Kulju, P., Hämäläinen, E. K., Mäkinen, M., Räikkönen, E., & Kiili, C. (2024). Pre-service teachers evaluating online texts about learning styles: There is room for improvement in justifying the credibility. *Frontiers in Education*, *9*. https://doi.org/10.3389/feduc.2024.1451002

Linacre, J. M. (2019). *Winsteps® Rasch measurement computer program user's guide*. Winsteps.com.

Linacre, J., M., & Tennant, A. (2009). *More about critical eigenvalue sizes (variances) in standardised-residual principal components analysis (PCA)*. *23*(3).

Little, I. D., Koehly, L. M., & Gunter, C. (2022). Understanding changes in genetic literacy over time and in genetic research participants. *The American Journal of Human Genetics*, *109*(12), 2141–2151. https://doi.org/10.1016/j.ajhg.2022.11.005

Liu, X. (2010). *Using and developing measurement instruments in science education: A Rasch modeling approach*. Information Age Publishing.

Maghfiroh, H., Zubaidah, S., Mahanal, S., & Susanto, H. (2023). Definition and conceptual model of genetics literacy: A systematic literature review. *International Journal of Public Health Science (IJPHS)*, *12*(2), Article 554. https://doi.org/10.11591/ijphs.v12i2.22679

Maghfiroh, H., Zubaidah, S., Mahanal, S., & Susanto, H. (2024). Biology lecturers' perceptions of genetics literacy in Indonesia: An explanatory sequential mixed methods. *Journal of Biological Education, 59*(1), 139-161. https://doi.org/10.1080/00219266.2024.2308302

McKnight, L., Pearce, A., Willis, A., Young, M.-A., & Terrill, B. (2021). Supporting teachers to use genomics as a context in the classroom: An evaluation of learning resources for high school biology. *Journal of Community Genetics*, *12*(4), 653–662. https://doi.org/10.1007/s12687-021-00550-3

Middleton, A., Adams, A., Aidid, H., Atutornu, J., Boraschi, D., Borra, J., Bircan, T., Burch, C., Costa, A., Dickinson, A., Enticknap, A., Galloway, C., Gale, F., Garlick, E., Haydon, E., Henriques, S., Mitchell, M., Milne, R., Monaghan, J., … Parkinson, S. (2023). Public engagement with genomics. *Wellcome Open Research*, *8*, Article 310. https://doi.org/10.12688/wellcomeopenres.19473.2

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Munby, H. (1997). Issues of validity in science attitude measurement. *Journal of Research in Science Teaching*, *34*(4), 337–341. https://doi.org/10.1002/(SICI)1098-2736(199704)34:4<337::AID-TEA4>3.0.CO;2-S

Murni, D., Lestari, S. R., Indriwati, S. E., Zubaidah, S., Susanto, H., & Paidi, P. (2024). Students' ICT literacy and conceptual knowledge correlation: From a genetic course and a gender perspective. *International Journal of Evaluation and Research in Education (IJERE)*, *13*(1), Article 580. https://doi.org/10.11591/ijere.v13i1.25237

National Research Council. (2012). *A framework for K-12 science education: Practices, crosscutting concepts, and core ideas* (p. 13165). National Academies Press. https://doi.org/10.17226/13165

Raiche, G. (2005). Critical eigenvalue sizes in standardised residual principal components analysis. *Rasch Measurement Transactions, 19*(1), 1010–1013.

Rasch. (1993). *Probabilistic models for some intelligence and attainment tests*. Retrieved from ERIC database (ED419814)

Reydon, T. A., Kampourakis, K., & Patrinos, G. P. (2012). Genetics, genomics and society: The responsibilities of scientists for science communication and education. *Personalized Medicine*, *9*(6), 633–643. https://doi.org/10.2217/pme.12.69

Riggs, C. D., Kang, S., & Rennie, O. (2020). Positive impact of multiple-choice question authoring and regular quiz participation on student learning. *CBE—Life Sciences Education*, *19*(2), Article ar16. https://doi.org/10.1187/cbe.19-09-0189

Roediger, H. L., & Marsh, E. J. (2005). The positive and negative consequences of multiple-choice testing. *Journal of Experimental Psychology: Learning, Memory, and Cognition*, *31*(5), 1155–1159. https://doi.org/10.1037/0278-7393.31.5.1155

Romine, W. L., Sadler, T. D., & Kinslow, A. T. (2017). Assessment of scientific literacy: Development and validation of the Quantitative Assessment of Socio-Scientific Reasoning (QuASSR): Development and validation of QuASSR. *Journal of Research in Science Teaching*, *54*(2), 274–295. https://doi.org/10.1002/tea.21368

Ruhl, G. L., Hazel, J. W., Clayton, E. W., & Malin, B. A. (2020). Public attitudes toward direct to consumer genetic testing. *AMIA Annual Symposium Proceedings*, *2019*, 774–783.

Sadler, T. D., & Fowler, S. R. (2006). A threshold model of content knowledge transfer for socioscientific argumentation. *Science Education*, *90*(6), 986–1004. https://doi.org/10.1002/sce.20165

Sadler, T. D., & Zeidler, D. L. (2005). The significance of content knowledge for informal reasoning regarding socioscientific issues: Applying genetics knowledge to genetic engineering issues. *Science Education*, *89*(1), 71–93. https://doi.org/10.1002/sce.20023

Shea, N. A., Duncan, R. G., & Stephenson, C. (2015). A tri-part model for genetics literacy: Exploring undergraduate student reasoning about authentic genetics dilemmas. *Research in Science Education*, *45*(4), 485–507. https://doi.org/10.1007/s11165-014-9433-y

Smith, M. K., Wood, W. B., & Knight, J. K. (2008). The genetics concept assessment: A new concept inventory for gauging student understanding of genetics. *CBE—Life Sciences Education*, *7*(4), 422–430. https://doi.org/10.1187/cbe.08-08-0045

Snustad, D. P., & Simmons, M. J. (2016). *Principles of genetics* (Seventh edition). John Wiley & Sons.

Stern, F., & Kampourakis, K. (2017). Teaching for genetics literacy in the post-genomic era. *Studies in Science Education*, *53*(2), 193–225. https://doi.org/10.1080/03057267.2017.1392731

Tennant, A., & Conaghan, P. G. (2007). The Rasch measurement model in rheumatology: What is it and why use it? When should it be applied, and what should one look for in a Rasch paper? *Arthritis Care & Research*, *57*(8), 1358–1362. https://doi.org/10.1002/art.23108

Tesio, L., Caronni ,Antonio, Simone ,Anna, Kumbhare ,Dinesh, & and Scarano, S. (2024). Interpreting results from Rasch analysis 2. Advanced model applications and the data-model fit assessment. *Disability and Rehabilitation*, *46*(3), 604–617. https://doi.org/10.1080/09638288.2023.2169772

Wang, G., Kong, Q., Wang, D., & Asmi, F. (2023). Ethical and social insights into synthetic biology: Predicting research fronts in the post-COVID-19 era. *Frontiers in Bioengineering and Biotechnology*, *11*, Article 1085797. https://doi.org/10.3389/fbioe.2023.1085797

Wind, S. A., & Schumacker, R. E. (2021). Exploring the impact of missing data on residual-based dimensionality analysis for measurement models. *Educational and Psychological Measurement*, *81*(2), 290–318. https://doi.org/10.1177/0013164420939634

Wood, F., Prior, L., & Gray, J. (2003). Translations of risk: Decision making in a cancer genetics service. *Health, Risk & Society*, *5*(2), 185–198. https://doi.org/10.1080/1369857031000123957

Wright, B., D., & Linacre, J., M. (1994). *Reasonable mean-square fit values*. *8*(3).

Wright, B. D., & Linacre, J. M. (1994). Reasonable mean-square fit values. *Rasch Measurement Transactions, 8*(3). https://www.rasch.org/rmt/rmt83b.htm

Wright, B., D., & Masters, G. (1982). *Rating scale analysis: Rasch measurement*. MESA Press.

Yamada-Kurebayashi, F., Sasaki, M., Kuga, A., Kojima, R., & Miyake, H. (2023). Human genetics education as part of the Japanese Cancer Education Comprehensive Support Project. *Journal of Community Genetics*, *14*(2), 163–174. https://doi.org/10.1007/s12687-022-00623-x

Yang, Y., He, P., & Liu, X. (2018). Validation of an instrument for measuring students' understanding of interdisciplinary science in grades 4-8 over multiple semesters: A Rasch measurement study. *International Journal of Science and Mathematics Education*, *16*(4), 639–654. https://doi.org/10.1007/s10763-017-9805-7

Zimani, A. N., Peterlin, B., & Kovanda, A. (2021). Increasing genomic literacy through national genomic projects. *Frontiers in Genetics*, *12*, Article 693253. https://doi.org/10.3389/fgene.2021.693253

Zohar, A., & Nemet, F. (2002). Fostering students' knowledge and argumentation skills through dilemmas in human genetics. *Journal of Research in Science Teaching*, *39*(1), 35–62. https://doi.org/10.1002/tea.10008

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Appendix A: Development Framework and Constructs of the Genetics Literacy and Reasoning Test

The Genetics Literacy and Reasoning Test (GLRT) was designed by integrating core genetics concepts with genetic reasoning skills. The core genetics concepts include: (1) the nature of genetic material, (2) transmission gene, (3) expression of the gene, (4) regulation of the gene, (5) genetic technology, (6) essentialism gene, and (7) determinism gene. Meanwhile, the genetic reasoning skills indicators consist of: (1) interdisciplinary thinking, (2) decision-making mode, (3) criteria setting and priority, (4) justification quality, (5) Evidence credibility, (6) social interactions, and (7) meta-decision.

The GLRT was developed using three case studies, each representing one of the major domains of global genetic applications. This framework is informed by Snustad and Simmons (2016), who identified society, agriculture, and medicine as key fields in which genetics is applied. The specific case studies were selected based on recommendations from Snustad and Simmons (2016), Boerwinkel et al. (2017), and Archila et al. (2021). These include the coronavirus disease pandemic to represent societal applications, genetically modified organisms for agricultural applications, and cancer for medical applications.

References:

Snustad, D. P., & Simmons, M. J. (2016). *Principles of genetics* (7th ed.). Wiley.
Boerwinkel, D. J., Yarden, A., & Waarlo, A. J. (2017). Reaching a consensus on the definition of genetic literacy that is required from a twenty-first-century citizen. *Science & Education*, *26*(10), 1087–1114. https://doi.org/10.1007/s11191-017-9934-y
Archila, P. A., Danies, G., Molina, J., Truscott de Mejía, A.-M., & Restrepo, S. (2021). Towards COVID-19 literacy. *Science & Education*. https://doi.org/10.1007/s11191-021-00222-1

Appendix B: Genetics Literacy and Reasoning Test Item Specification Table

No (Code)	Context Domain	Core Genetics Concepts	Genetics Reasoning Skills	Description	Cognitive Level	Correct Answer
1 (pNogI1)	Coronavirus disease pandemic	Nature of the genetic material	Interdisciplinary thinking	Analyse the relationship between the issue of diagnostic method selection for SARS-CoV-2 and the concept of genetic material structure from both chemical and biological perspectives.	Analyse (C4)	A
2 (pTraD2)	Coronavirus disease pandemic	Transmission gene	Decision-making mode	Evaluate preventative solutions for inhibiting the replication of SARS-CoV-2 genetic material based on data regarding the mean reduction in viral genome copies.	Evaluate (C5)	A
3 (pExpC3)	Coronavirus disease pandemic	Expression of the gene	Criteria setting and priority	Evaluate the role and impact of vaccine development in both stable and unstable environmental conditions, with reference to the expression of the SARS-CoV-2 spike (S) gene.	Evaluate (C5)	B
4 (pRegJ4)	Coronavirus disease pandemic	Regulation of the gene	Justification quality	Analyse the issue of SARS-CoV-2 infection across various tissues and organs by incorporating findings from recent studies on ACE2 gene expression regulation.	Analyse (C4)	D
5 (pTecE5)	Coronavirus disease pandemic	Technology gene	Evidence credibility	Demonstrate the credibility of genetic information by integrating concepts of enzymes utilised in genetic engineering.	Evaluate (C5)	B
6 (pEssS6)	Coronavirus disease pandemic	Essentialism gene	Social interactions	Evaluate the administration of vaccines to individuals previously infected with SARS-CoV-2, taking into account scientific ethics and genetic information.	Evaluate (C5)	D
7 (pDetM7)	Coronavirus disease pandemic	Determinism gene	Meta-decision	Determine the optimal vaccination strategy through logical consideration of each vaccine's composition, type, and replication mechanism.	Evaluate (C5)	C

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

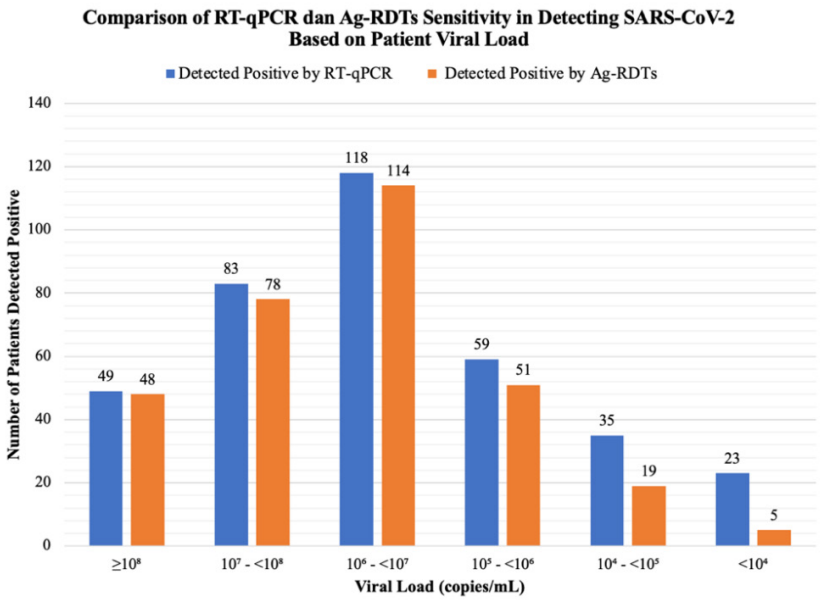
No (Code)	Context Domain	Core Genetics Concepts	Genetics Reasoning Skills	Description	Cognitive Level	Correct Answer
8 (gNogI8)	Genetically Modified Organisms	Nature of the genetic material	Interdisciplinary thinking	Analyse the issue of genetic engineering based on the concept of genetic material structure from both biological and chemical perspectives.	Analyse (C4)	D
9 (gTraD9)	Genetically Modified Organisms	Transmission gene	Decision-making mode	Evaluate decisions concerning the utilisation of transgenic crops in light of the increased cultivation area of Bacillus thuringiensis maize and the corresponding decrease in insecticide usage.	Evaluate (C5)	E
10 (gExpC10)	Genetically Modified Organisms	Expression of the gene	Criteria setting and priority	Evaluate the role and consequences of inserting the Lr34 gene across different wheat species.	Evaluate (C5)	E
11 (gRegJ11)	Genetically Modified Organisms	Regulation of the gene	Justification quality	Analyse the social issues related to genetically modified food (GMF), incorporating recent research findings on gene regulation.	Analyse (C4)	C
12 (gTecE12)	Genetically Modified Organisms	Technology gene	Evidence credibility	Evaluate the credibility of genetic engineering techniques by considering the most effective research findings to date.	Evaluate (C5)	B
13 (gEssS13)	Genetically Modified Organisms	Essentialism gene	Social interactions	Assess genetic information based on scientific ethics and gene expression principles.	Evaluate (C5)	C
14 (gDetM14)	Genetically Modified Organisms	Determinism gene	Meta-decision	Determine a rational solution regarding the use of transgenic rice, taking into account ethical, social, and scientific considerations.	Evaluate (C5)	E
15 (cNogI15)	Cancer	Nature of the genetic material	Interdisciplinary thinking	Analyse the relationship between carcinogenic substances and alterations in the structure of genetic material.	Analyse (C4)	D
16 (cTraD16)	Cancer	Transmission gene	Decision-making mode	Determine the most effective preventative practice to inhibit the transmission of breast cancer based on relevant genetic information.	Evaluate (C5)	E
17 (cExpC17)	Cancer	Expression of the gene	Criteria setting and priority	Evaluate the role and impact of tumor suppressor gene expression under both normal and mutated conditions.	Evaluate (C5)	D
18 (cRegJ18)	Cancer	Regulation of the gene	Justification quality	Analyse methods for the early detection of breast cancer by incorporating the most recent scientific research.	Analyse (C4)	B
19 (cTecE19)	Cancer	Technology gene	Evidence credibility	Evaluate the credibility of oncolytic virotherapy mechanisms with reference to viral vectors and replication methods.	Evaluate (C5)	A
20 (cEssS20)	Cancer	Essentialism gene	Social interactions	Assess early breast cancer detection strategies from the perspective of scientific ethics.	Evaluate (C5)	E
21 (cDetM21)	Cancer	Determinism gene	Meta-decision	Evaluate experimental data on gene expression to determine the most scientifically and ethically appropriate next steps in cancer research.	Evaluate (C5)	E

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

Appendix C: Genetics Literacy and Reasoning Test

No (Code)	Questions
1 (pNogI1)	Examine the graph below!



Coronavirus Disease-2019 (COVID-19) is caused by Severe Acute Respiratory Syndrome-Coronavirus-2 (SARS-CoV-2). The selection of SARS-CoV-2 diagnostic methods has been a topic of debate, particularly between Antigen-Rapid Diagnostic Tests (Ag-RDTs) and Real Time-quantitative Polymerase Chain Reaction (RT-qPCR). Based on a comparative graph of sensitivity and the characteristics of detected genetic materials, which SARS-CoV-2 diagnostic method is **the most accurate**?

A. RT-qPCR detects cDNA polymers with higher sensitivity than Ag-RDTs.
B. Ag-RDTs detect RNA monomers with lower sensitivity than RT-qPCR.
C. RT-qPCR detects mRNA polymers with higher sensitivity than Ag-RDTs.
D. Ag-RDTs detect DNA monomers with lower sensitivity than RT-qPCR.
E. RT-qPCR detects rRNA polymers with higher sensitivity than Ag-RDTs.

2 (pTraD2) Look at the table below!

No	Exposure	Average viral genome copy reduction (log)
1	Dry control	0,20
2	Hand sanitiser	0,14
3	Hand soap	0,94
4	Water rinse	0,75

Disinfection is the critical step in interrupting the transmission of the SARS-CoV-2 genome, but there is debate about the effectiveness of some disinfection practices. The table above shows the average difference in viral genome copy reduction. The data was obtained from the results of virus inoculation on the fingertips of 20 volunteers, who were then given different disinfection exposures. A healthcare professional wants to suggest the best disinfection practice to prevent replication of the SARS-CoV-2 genome. Based on the table above, determine **the most effective** practice to avoid the replication of the SARS-CoV-2 genome!

A. Hand soap, as it damages capsid proteins and RNA.
B. Hand soap, as it damages lipid membranes and DNA.
C. Water rinse, as it damages spike proteins and mRNA.
D. Hand sanitiser, as it damages capsid proteins and RNA.
E. Hand sanitiser, as it damages lipid membranes and DNA.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

No (Code)	Questions
3 (pExpC3)	Scientists have been working to control the COVID-19 pandemic by developing a vaccine based on the SARS-CoV-2 spike protein. The spike protein encoded by the *S* gene binds to the ACE2 receptor on host cells, making it the primary target of the vaccine to prevent infection. In a stable environment (low transmission), the structure of the spike protein remains relatively unchanged, allowing the vaccine to effectively trigger immunity. However, in an unstable environment (high transmission), intense viral replication leads to the accumulation of spontaneous mutations in the *S* gene. These mutations can change the structure of the spike protein, thereby reducing the ability of antibodies to recognise the virus. Based on this, which is the correct statement about **the role** of the *S* gene and **the impact** of its mutation? A. The *S* gene encodes the spike protein as an antigen, but mutation of the *S* gene increases vaccine immugenity. B. The *S* gene encodes the spike protein as an antigen, but mutation of the *S* gene decreases vaccine effectiveness. C. The *S* gene encodes the membrane protein as an antigen, but mutation of the *S* gene reduces vaccine stability. D. The *S* gene encodes the envelope protein as an antigen, but mutation of the *S* gene increases vaccine reactivity. E. The *S* gene encodes the nucleocapsid protein as an antigen, but mutation of the *S* gene decreases vaccine sensitivity.
4 (pRegJ4)	A report from December 2019 indicated that SARS-CoV-2 can cause COVID-19 by infecting epithelial cells of the respiratory organs. The mechanism involves the spike protein on the virus surface, which functions as a ligand binding to the ACE2 receptor on host cells. Subsequently, a March 2020 report confirmed that the ACE2 receptor is also expressed in epithelial cells of the digestive tract. Further, data from the Genotype-Tissue Expression (GTEx) Project in April 2020 expanded these findings by demonstrating that the ACE2 receptor is expressed in 31 human tissues. Based on these three reports regarding the regulation of *ACE2* gene expression, it can be concluded that SARS-CoV-2 is capable of infecting .... A. All tissues or organs B. Only digestive organs C. Only respiratory organs D. Multiple tissues or organs E. Both respiratory and digestive organs
5 (pTecE5)	Currently, vaccination is an effective method for preventing COVID-19. Researchers have developed the Zydus Cadila vaccine through genetic engineering, by cutting plasmids using specific enzymes and inserting a fragment of the *S* gene from SARS-CoV-2 into the plasmid. To verify claims regarding the enzymatic processes involved, one must evaluate the functional compatibility of these enzymes with established genetic engineering protocols. Which of the following statements about enzymes is **the most scientifically credible** in supporting this process? A. The protease enzyme cuts the plasmid and the lipase enzyme inserts the *S* gene. B. The restriction enzyme cuts the plasmid and the ligase enzyme inserts the *S* gene. C. The sucrase enzyme cuts eight base pairs of DNA and the ligase enzyme inserts the *S* gene. D. The ligase enzyme cuts the S gene and the restriction enzyme inserts twelve base pairs of DNA. E. The restriction enzyme cuts 21 base pairs of the plasmid and the lipase enzyme inserts the *S* gene.
6 (pEssS6)	Consider the following data, which provide information on several respondents. **Respondent ID** / **Previous Infection Status** / **Vaccination Stage** / **Log Value of IgG (S-RBD)** / **Age** / **Cormorbidity** 001 / Infected / Before vaccination / 5.6 / 45 / Hypertension 002 / Not infected / Before vaccination / 0.2 / 30 / - 003 / Infected / After dose 1 / 8.7 / 50 / Diabetes 004 / Not infected / After dose 1 / 7.9 / 29 / - 005 / Infected / After dose 2 / 11.5 / 48 / Hypertension 006 / Not infected / After dose 2 / 9.3 / 31 / Individual X is a 45-year-old male who was infected with SARS-CoV-2 four months ago and has a medical history of hypertension as a comorbidity. He is currently considering whether to receive a COVID-19 vaccination. Based on the data and the principles of scientific ethics, what would be **the most appropriate** vaccination decision for Individual X? A. Vaccination should be decided with family consent, given the broader social implications of the decision. B. Vaccination is not required if the individual feels healthy, as antibody levels are already sufficiently high. C. Vaccination is not necessary, as antibodies have already been developed from the previous infection. D. Vaccination is recommended with a doctor's approval, as age and comorbidity require further medical evaluation. E. Vaccination should proceed based on the individual's own decision, as evidence shows antibody levels increase post-vaccination.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

No (Code) | **Questions**

7 (pDetM7)

Look at the table below!

No	Vaccine Name	Composition	Vaccine Type	Genetic Material Replication Mechanism
1	Pfizer Comirnaty	SARS-CoV-2 Spike mRNA	mRNA	mRNA does not replicate; it is only translated into the Spike protein
2	Moderna Spikevax	SARS-CoV-2 Spike mRNA	mRNA	mRNA does not replicate; it is only translated into the Spike protein
3	Sinovac CoronaVac	Inactivated whole virus	Inactivated	No replication occurs (virus is non-viable)
4	BBV152 (Bharat Biotech)	Inactivated whole virus	Inactivated	No replication occurs (virus is non-viable)
5	AstraZeneca Vaxzevria	Non-replicating viral vector + Spike DNA	Viral vector	Spike DNA does not replicate; it is only transcribed
6	Janssen (Johnson & Johnson)	Non-replicating viral vector + Spike DNA	Viral vector	Spike DNA does not replicate; it is only transcribed

Since the onset of the COVID-19 pandemic, various types of vaccines have been developed using different mechanisms to trigger an immune response. A female patient with immunodeficiency is currently considering the safest type of COVID-19 vaccine. Based on the composition, type, and replication mechanism of the genetic material, evaluate which vaccine type would be safer for individuals with immunodeficiency!

A. Vaccines 1 and 2, as the Spike mRNA is translated into amino acids.
B. Vaccines 1 and 2, as the Spike mRNA is a product of DNA transcription.
C. Vaccines 3 and 4, as the virus has been inactivated and cannot replicate.
D. Vaccines 3 and 4, as the inactivated whole virus is capable of self-replication.
E. Vaccines 5 and 6, as the viral vector Spike DNA can trigger an immune response.

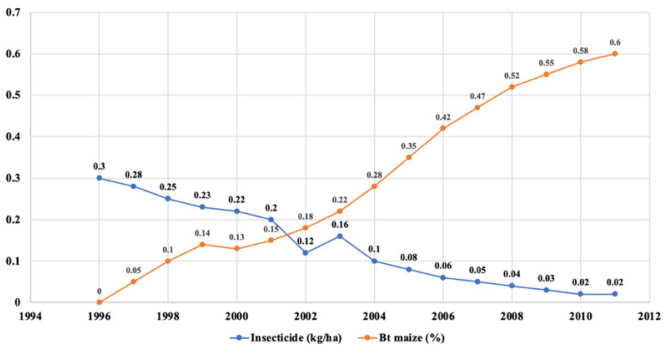
8 (gNogI8)

The high demand for maize consumption has prompted researchers to perform genetic engineering on the maize genome. Researchers inserted a variant of the *Cry9c* gene from *Bacillus thuringiensis* into the maize genome, resulting in insect-resistant maize. Gene integration occurs through chemical bonds formed between the hydroxyl group (OH) on the C3 nucleotide and the phosphate group on another C5 nucleotide. Analyse the mechanism of *Cry9c* gene integration into the maize genome!

A. Integration of the *Cry9c* gene and maize alleles occurs via hydrogen bonds between nucleotides.
B. Integration of the *Cry9c* gene and maize proteins occurs via hydrogen bonds between nitrogenous bases.
C. Integration of the *Cry9c* gene and maize chromatids occurs via hydrophobic interactions between nucleotides.
D. Integration of the *Cry9c* gene and maize DNA occurs via covalent phosphodiester bonds between nucleotides.
E. Integration of the *Cry9c* gene and maize cells occurs via covalent phosphodiester bonds between nitrogenous bases.

9 (gTraD9)

Observe the graph below!



Transgenic crops are a revolutionary outcome of genetic engineering, now being cultivated on a commercial scale in many countries, such as *Bacillus thuringiensis* (Bt) maize. Bt maize is a genetically modified variety in which the genetic material has been integrated with the *Cry9c* gene from Bt, making it resistant to insect pests. The graph above presents a comparison between the percentage of land cultivated with Bt maize and the level of insecticide usage. Based on the graph and the genetic information provided, do you agree with the increasing adoption of Bt maize?

A. No, because the increase in Bt maize cultivation has led to a reduction in insecticide use.
B. Yes, because the percentage of land planted with Bt maize continues to increase.
C. No, because the increase in Bt maize cultivation leads to a decline in the overall insect population.
D. Yes, because the expression of the *Cry9c* gene encodes resistance to insects, thereby reducing the use of insecticides.
E. Yes, because the expression of the *Cry9c* gene encodes a protein that is resistant to insect pests, thereby reducing insecticide usage.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

No (Code)	Questions
10 (gExpC10)	Look at the picture below!  Both of these are wheat *Hordeum vulgare* A scientist conducted genetic engineering by inserting the *Lr34* gene from wheat (*Triticum aestivum*) into the wheat gene (*Hordeum vulgare*). Based on the picture above and the expression of the *Lr34* gene, evaluate the **role** and **consequence** of the insertion of the *Lr34* gene in *H. vulgare*! A. *Lr34* gene encodes resistance gene but decreases growth rate. B. *Lr34* gene encodes resistance tRNA and increases growth rate. C. *Lr34* gene encodes resistance protein and increases growth rate. D. *Lr34* gene encodes resistance cDNA but decreases growth rate. E. *Lr34* gene encodes resistance protein but decreases growth rate.
11 (gRegJ11)	One approach to improving the quality of tomatoes involves the use of genetically modified food (GMF) technology, such as the insertion of genes regulating the production of flavonols and anthocyanins from maize (*Zea mays*) into the genome of the tomato (*Lycopersicon esculentum*). A study conducted in 1995 demonstrated that these genes could regulate flavonol and anthocyanin production in maize. However, a 2002 study showed that the insertion of these genes into tomatoes resulted in increased flavonol production, but no corresponding increase in anthocyanin production. This was attributed to the low expression of other genes required in the anthocyanin biosynthesis pathway within the tomato. Based on this information and the differential regulation of gene expression among plant species, which of the following statements is **the most accurate**? A. Insufficient flavonol gene expression in tomatoes leads to reduced anthocyanin production. B. Limited anthocyanin gene expression in tomatoes causes an increase in flavonol production. C. A lack of supporting gene expression for anthocyanin biosynthesis in tomatoes results in anthocyanin levels remaining low. D. Flavonol gene expression is higher than anthocyanin gene expression, resulting in increased flavonol levels in tomatoes. E. Anthocyanin gene expression is lower than flavonol gene expression, leading to increased flavonol levels in tomatoes.
12 (gTecE12)	Global data indicate that nearly 250 million people suffer from vitamin A deficiency. In response to this issue, a team of researchers attempted to introduce the β-carotene gene into rice plant cells. In the first experiment, the gene was delivered using a high-velocity gene gun. This method did not result in any change in seed colour. In the second experiment, the β-carotene gene was inserted into a plasmid vector of Agrobacterium tumefaciens, which was then used to transform rice cells. In this case, the seeds turned orange, indicating successful gene expression. Based on the outcomes of these two experiments, which of the following genetic engineering techniques is **the most effective**? A. Plasmid vector transfer, as it can prevent DNA damage. B. Plasmid vector transfer, as it enables stable gene integration into the plant genome. C. Microinjection via gene gun, as it delivers genes directly into the plant cell nucleus. D. Microinjection via gene gun, as it can deliver a large quantity of genes into plant cells. E. Plasmid vector transfer, as it allows for precise control over the gene's base pair length.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

No (Code)	Questions

13 (gEssS13) Observe the table below!

Plant	Event	Trait	Gene	Description
Cotton	MON1445	Herbicide tolerance	CP4 EPSPS	△
Soybean	MON87701	Insect resistance	cry1Ac	◯
Maize	NK603	Herbicide tolerance	CP4 EPSPS	☐
Sugarcane	NXI-1T	Drought tolerance	BetA	◯

Noted:
△ = Public field trials have been completed for 60 days.
☐ = Results of public field trials have been submitted to the Secretariat of the Biosafety Commission.
◯ = Food safety recommendation has been issued by the Biosafety Commission to the Food and Drug Supervisory Agency.

The Ministry of Agriculture (MoA) has established the types of genetically modified crops that have been granted environmental safety certification. Based on the data presented in the table and gene expression characteristics, which of the following genetically modified crops is considered the **safest to cultivate**?

A. Soybean MON87701 contains the *cry1Ac* gene, which encodes an insect resistance gene.
B. Sugarcane NXI-1T contains the *BetA* gene, which encodes DNA responsible for drought tolerance.
C. Soybean MON87701 contains the c*ry1Ac* gene, which encodes a protein responsible for insect resistance.
D. Maize NK603 contains the *CP4 EPSPS* gene, which encodes DNA responsible for herbicide tolerance.
E. Cotton MON1445 contains the *CP4 EPSPS* gene, which encodes DNA responsible for herbicide tolerance.

14 (gDetM14) Observe the table below!

Rice Type	Micronutrient content in rice samples (mg/100 g ± SEM)		
	Thiamine	Vitamin B6	Riboflavin
Control	0,18+ 0,01	0,40 + 0,02	1,20 + 0,05
Transgenic	0,31+ 0,02	0,56 + 0,03	1,25 + 0,04

In an effort to enhance nutritional quality, a scientist performed genetic modification by incorporating a soybean gene into rice plant cells. Subsequently, the nutrient composition of rice derived from both control and transgenic plants was analysed. Based on the data presented in table, and considering current government regulations, do you agree with the cultivation of transgenic rice?

A. Disagree, because the riboflavin content in transgenic rice is nearly equivalent to that of the control.
B. Agree, because the thiamine content in transgenic rice is higher, with authorisation from the landowner.
C. Disagree, because the thiamine content in transgenic rice is not significantly different from that of the control.
D. Agree, because the vitamin B6 content in transgenic rice is higher, with the consent of the local community.
E. Agree, because the vitamin B6 content in transgenic rice is higher, subject to approval from the Food and Drug Authority.

15 (cNogI15) According to data from the Global Cancer Observatory (GCO) in 2022, it is estimated that there were more than 20 million new cancer cases worldwide, with lung, breast, and colorectal cancers being the three most common types. One of the primary causes is exposure to harmful chemical substances in the environment, such as cigarette smoke, pollutants, or compounds in processed foods that may contribute to genetic material damage. Exposure to these hazardous chemicals can induce mutations in genes that regulate the cell division cycle. Based on the case study above, analyse the fundamental molecular processes involved in cancer development!

A. Neurotoxic substances inhibit neurotransmitters, leading to impaired neural communication.
B. Mutagenic substances trigger random mutations in DNA, gradually increasing cell proliferation.
C. Free radicals damage cell membranes and proteins through oxidative stress, disrupting normal cellular function.
D. Carcinogenic substances activate oncogenes and deactivate tumor suppressor genes, leading to uncontrolled cell division.
E. Teratogenic substances induce chromosomal abnormalities during embryonic development, resulting in congenital defects.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

No (Code)	Questions
16 (cTraD16)	A patient has been diagnosed with advanced breast cancer. Medical examination shows that the cancer cells have been dividing uncontrollably, forming a tumor and metastasising to distant organs such as the lungs and liver. Based on this information, determine the most effective medical intervention to inhibit the spread of cancer cells in a patient with advanced breast cancer! A. Modified stem cell therapy to target malignant cancer cells. B. Surgery to remove the primary tumor to prevent local spread. C. Adjuvant radiation therapy to reduce symptoms in metastatic areas. D. Immunotherapy to stimulate the immune system in inhibiting cancer progression. E. Systemic chemotherapy to target cancer cells that have spread throughout the body.
17 (cExpC17)	Cancer researchers have identified two major gene groups that contribute to cancer development when mutated: proto-oncogenes and tumor suppressor genes. Under normal conditions, tumor suppressor genes function to inhibit excessive cell division and maintain cellular growth stability. However, mutations in these genes lead to a loss of inhibitory function, resulting in uncontrolled cell proliferation. Evaluate the **role** of tumor suppressor genes under normal physiological conditions and the **consequences** of their mutation! A. Tumor suppressor genes encode growth hormones; mutations inhibit cell differentiation. B. Tumor suppressor genes encode signal receptors; mutations impair intercellular communication. C. Tumor suppressor genes encode metabolic enzymes; mutations disrupt cellular energy production. D. Tumor suppressor genes encode cell cycle inhibitory proteins; mutations result in dysregulated cell division. E. Tumor suppressor genes encode DNA repair proteins; mutations lead to the accumulation of genetic damage.
18 (cRegJ18)	Early detection of breast cancer is a crucial step in reducing mortality rates associated with the disease. In the 1960s, mammography (low-dose X-ray imaging) was first proposed as a method for identifying changes in breast tissue. However, its effectiveness is limited in individuals with dense breast tissue. In contrast, a 1997 study demonstrated that blood sample analysis can detect mutations in the *BRCA1* gene, which is involved in DNA repair and cell cycle regulation. Mutations in this gene are known to significantly increase the risk of breast cancer. Based on the findings from both studies, which method is **more effective** for the early detection of breast cancer, and why? A. Mammography and blood testing are equally effective because both can detect *BRCA1* mutations. B. Blood testing is more effective than mammography because *BRCA1* mutations are present in all body cells. C. Mammography is more effective than blood testing because *BRCA1* mutations are only detectable in breast tissue. D. Blood testing is more effective than mammography because *BRCA1* mutations are present in some body cells. E. Mammography is more effective than blood testing because *BRCA1* mutations are only present in tumor tissue.
19 (cTecE19)	Gene therapy is a therapeutic approach that involves the transfer of genetic material to treat or manage diseases, one example being oncolytic virotherapy for breast cancer. In oncolytic virotherapy, viruses are genetically modified to selectively target and destroy rapidly dividing cancer cells. Based on their replication mechanisms, viruses that follow the lytic cycle replicate directly within the host cell and ultimately destroy it through cell lysis, whereas those following the lysogenic cycle integrate their genetic material into the host DNA and replicate passively with the host cell without immediate destruction. Considering the type of viral vector and its replication mechanism, which oncolytic virotherapy strategy is **the most effective**? A. A DNA virus that replicates through the lytic cycle. B. An RNA virus that replicates via the lytic cycle but has limited cytotoxicity. C. A DNA virus capable of alternating between the lytic and lysogenic cycles. D. An RNA virus that integrates its genome into the host DNA via the lysogenic cycle. E. A DNA virus that replicates through the lysogenic cycle and evades immune detection.
20 (cEssS20)	Based on data from Global Cancer Statistics 2022, breast cancer has a high incidence rate globally. Coinciding with World Cancer Day, the government has initiated an early detection programme using functional DNA biomarkers to identify breast cancer. However, this detection method raises concerns about the potential access to patients' private genetic information. From a **scientific ethics** perspective, do you agree with the practice of early breast cancer detection? A. Disagree, as it may lead to public concern. B. Agree unconditionally, as it may hinder tumor cell division. C. Neutral, as early detection must be balanced with genetic data protection. D. Disagree, as it may violate the privacy of an individual's genetic information. E. Agree, with patient consent, as early detection can help prevent cancer cell metastasis.

https://doi.org/10.33225/jbse/25.24.465

ISSN 1648–3898 /Print/
ISSN 2538–7138 /Online/

No (Code)	Questions
21 (cDetM21)	A researcher investigated the effect of soursop leaf extract (*Annona muricata* Linn) on the expression of the *Ki-67* gene, which is known to be active during cancer cell proliferation. The results are presented in the following table:

Rat Group	Percentage of Ki-67 Gene Expression
No extract (control)	100%
Dose of 200 mg/kg	78%
Dose of 400 mg/kg	52%
Dose of 600 mg/kg	47%

If the aim of the study is to determine a dose that effectively suppresses cancer gene expression without introducing excessive risk, **the most logical** next step in the research would be to...

A. Determine that the 400 mg/kg dose is the lowest, and therefore should proceed directly to human trials.
B. Conclude that the 200 mg/kg dose has begun to reduce gene expression, although it may not be optimal as the primary choice.
C. Consider that the control group is no longer necessary in future experiments, as all treatment groups showed reduced gene expression.
D. Assume that, since all doses reduced gene expression, the experiment can be concluded as successful and no further trials are needed.
E. Recognise that the 600 mg/kg dose is the most effective in lowering gene expression, but further testing is required to ensure it is not harmful to the rats.

Received: *December 18, 2024* Revised: *March 06, 2025* Accepted: *May 22, 2025*

Cite as: Maghfiroh, H., Zubaidah, S., Mahanal, S., Susanto, H., & Chang, C. Y. (2025). Development and validation of the genetics literacy and reasoning test: A tool for exploring global genetics issues. *Journal of Baltic Science Education*, *24*(3), 465–487. https://doi.org/10.33225/jbse/25.24.465

Hidayati Maghfiroh
Dr, Department of Biology, State University of Malang (Universitas Negeri Malang), Malang, 65145, Indonesia.
E-mail: hidayati.maghfiroh.2203419@students.um.ac.id
ORCID: https://orcid.org/0000-0003-4702-6120

Siti Zubaidah
(Corresponding author)
Dr, Professor, Department of Biology, State University of Malang (Universitas Negeri Malang), Malang, 65145, Indonesia.
E-mail: siti.zubaidah.fmipa@um.ac.id
ORCID: https://orcid.org/0000-0002-0718-6392

Susriyati Mahanal
Dr, Professor Department of Biology, State University of Malang (Universitas Negeri Malang), Malang, 65145, Indonesia.
E-mail: susriyati.mahanal.fmipa@um.ac.id
ORCID: https://orcid.org/0000-0001-5764-2184

Hendra Susanto
PhD, Professor, Department of Biology, State University of Malang (Universitas Negeri Malang), Malang, 65145, Indonesia.
E-mail: hendrabio@um.ac.id
ORCID: https://orcid.org/0000-0002-3935-4848

Chun-Yen Chang
PhD, Professor, Graduate Institute of Science Education, Department of Earth Sciences, and Science Education Center of National Taiwan Normal University, 162, Section 1, Heping E. Rd., Taipei City 106, Taiwan.
E-mail: changcy@ntnu.edu.tw
ORCID: https://orcid.org/0000-0003-2373-2004