



**The Impact of Case Based Learning on Students' Understanding
of Real World Applications of Genetics for Better Academic
Performance**

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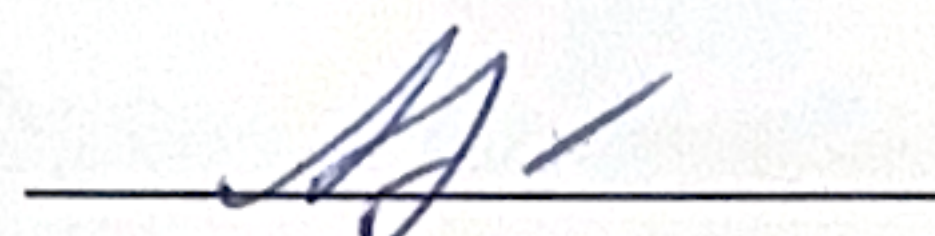
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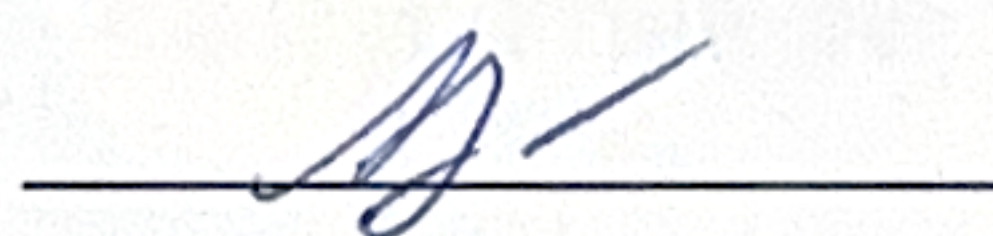
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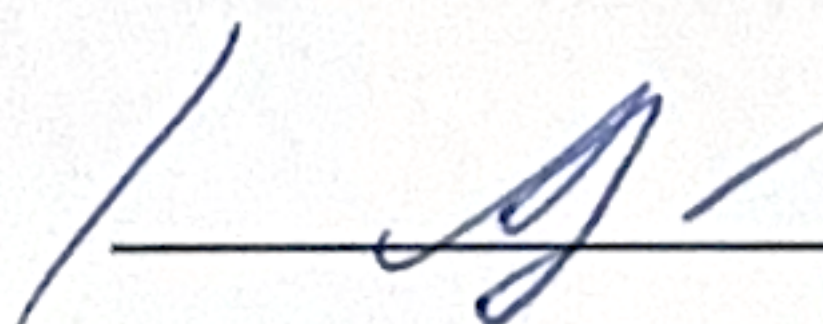


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LIST OF ABBREVIATIONS

ANCOVA - Analysis of Covariance

ARCS - Attention, Relevance, Confidence, and Satisfaction

CBL - Case-Based Learning

CLT - Cognitive Load Theory

COPUS - Classroom Observation Protocol for Undergraduate STEM

CVI - Content Validity Index

HOTS - Higher Order Thinking Skills

IMMS - Instructional Materials Motivation Survey

PBL - Problem-Based Learning

PLS - Partial Least Squares

PSI - Problem-Solving Inventory

RT-qPCR - Reverse Transcription Quantitative Polymerase Chain Reaction

SDT - Self-Determination Theory

SEM - Structural Equation Modelling

STEM - Science, Technology, Engineering, and Mathematics

ABSTRACT

This study examined the impact of case-based learning (CBL) on undergraduate students' academic performance in a genetics course and explored the role of motivation across different instructional contexts. Using a quasi-experimental design, 70 students at SDU University participated in four CBL case studies delivered in two formats: theory-based seminars and laboratory-based practical classes. Academic performance was assessed through pre-tests and case-specific post-tests, while motivation was measured using Keller's Instructional Materials Motivation Survey (IMMS) based on the ARCS model. ANCOVA results showed that CBL significantly improved performance in laboratory-based cases but not in theory-based cases, indicating that CBL effectiveness is context-dependent. Hierarchical regression analysis revealed that laboratory-based CBL produced substantially greater learning gains than theory-based instruction ($B = 18.517$, $p < 0.001$, $\Delta R^2 = 0.197$). Regarding motivation, Satisfaction was the only ARCS subscale significantly predicting learning gains in theory-based classes, while motivational variables did not predict outcomes in laboratory settings, where the instructional environment itself appeared sufficiently engaging. These findings suggest that CBL is most effective in contextually rich, hands-on environments and that intrinsic satisfaction plays a key motivational role in less stimulating instructional settings. The results offer practical guidance for designing active learning interventions in undergraduate genetics education.

Keywords: *case-based learning, genetics education, academic performance, ARCS model, IMMS, laboratory-based learning, quasi-experimental design, undergraduate biology, constructivist learning, motivation*

АНДАТПА

Бұл зерттеуде кейс-негізделген оқытудың (CBL) генетика курсындағы бакалавриат студенттерінің академиялық үлгіріміне әсері бағаланды және әртүрлі оқыту контексттеріндегі мотивацияның рөлі зерделенді. Квазиэксперименттік дизайнды қолдана отырып, СДУ Университетінің 70 студенті екі форматта: теориялық семинарлар мен зертханалық практикалық сабақтарда ұсынылған төрт CBL кейс-стадияне қатысты. Академиялық үлгірім алдын ала тестілеу (pre-test) және кейске тән кейінгі тестілеу (post-test) арқылы бағаланды, ал мотивация ARCS моделіне негізделген Келлердің оқу материалдарына мотивация сауалнамасы (IMMS) арқылы өлшенді. ANCOVA нәтижелері CBL зертханалық кейстерде үлгірімді айтарлықтай жақсартқанын, бірақ теориялық кейстерде нәтиже бермегенін көрсетті; бұл CBL тиімділігінің контекске тәуелді екенін білдіреді. Иерархиялық регрессиялық талдау зертханалық CBL теориялық оқытуға қарағанда әлдеқайда жоғары білім алу көрсеткіштерін көрсеткенін анықтады ($B=18.517$, $p<.001$, $\Delta R^2=.197$). Мотивацияға келетін болсақ, «Қанағаттану» (Satisfaction) теориялық сабақтардағы білім алу деңгейін айтарлықтай болжайтын жалғыз ARCS субшкаласы болды, ал мотивациялық айнымалылар зертханалық жағдайларда нәтижелерді болжай алмады, өйткені бұл жерде оқыту ортасының өзі жеткілікті деңгейде қызықты болды. Бұл тұжырымдар CBL мән-мәтінге бай, практикалық ортада барынша тиімді екенін және ішкі қанағаттану сезімі ынталандыру деңгейі төменірек оқыту жағдайларында негізгі мотивациялық рөл атқаратынын көрсетеді. Нәтижелер бакалавриаттағы генетикалық білім беруде белсенді оқыту интервенцияларын жобалау бойынша практикалық нұсқаулықтар ұсынады.

Түйін сөздер: кейс-негізделген оқыту, генетикалық білім беру, академиялық үлгірім, ARCS моделі, IMMS, зертханалық оқыту, квазиэксперименттік дизайн, бакалавриат биологиясы, конструктивистік оқыту, мотивация

АННОТАЦИЯ

В данном исследовании изучалось влияние кейс-метода (CBL) на академическую успеваемость студентов бакалавриата в рамках курса генетики, а также исследовалась роль мотивации в различных контекстах обучения. В рамках квазиэкспериментального дизайна 70 студентов Университета СДУ приняли участие в четырех кейс-стади CBL, реализованных в двух форматах: теоретических семинарах и лабораторно-практических занятиях; академическая успеваемость оценивалась с помощью пре- и пост-тестов, а мотивация - с использованием опросника IMMS (модель ARCS). Результаты ANCOVA показали, что CBL значительно повысил успеваемость в лабораторных кейсах, но не дал значимого эффекта в теоретических, что указывает на контекстную зависимость его эффективности; иерархический регрессионный анализ подтвердил существенно больший прирост знаний в лабораторном формате ($B=18.517$, $p<.001$, $\Delta R^2=.197$). Субшкала «Удовлетворение» оказалась единственным значимым мотивационным предиктором прироста знаний на теоретических занятиях, тогда как в лабораторных условиях мотивационные переменные не прогнозировали результаты, поскольку сама среда обеспечивала достаточную вовлечённость. Полученные результаты свидетельствуют о том, что кейс-метод наиболее эффективен в контекстно-насыщенной практической среде, и предлагают практические рекомендации для проектирования методов активного обучения в высшем биологическом образовании.

Ключевые слова: кейс-метод, генетическое образование, академическая успеваемость, модель ARCS, IMMS, лабораторное обучение, квазиэкспериментальный дизайн, бакалавриат биологии, конструктивистское обучение, мотивация

INTRODUCTION

Genetics is one of the key disciplines for biology education since it supplies means to explain inheritance and variation and provides information about molecular mechanisms; moreover, genetics is related to modern scientific and social concerns. Indeed, the instruction in genetics at universities has increased greatly over time and is frequently associated with reforms towards active learning to promote greater understanding and skills in science (Smith & Wood, 2016). Furthermore, knowledge in genetics became important from the standpoint of genetic testing, genomics, biotechnologies, and public debates regarding genetics and personal identity (Chattopadhyay, 2005; Smith & Wood, 2016). Thus, enhancing the way genetics is being taught can be considered an educational challenge, which should become an essential part of developing scientific literacy among future scientists.

Meanwhile, recently the interest in Case-Based Learning (CBL), a learner-centered method aimed at promoting deep reasoning, understanding, and application, has grown significantly. According to a recent meta-analysis summarizing research findings on effectiveness of problem-oriented teaching strategies, including CBL, such techniques demonstrate positive impacts on motivation of students in comparison with traditional teacher-centered instruction, which depend on the quality of implementation and educational domain (Wijnia et al., 2024). Indeed, because of its focus on real-life scenarios, which involve interpretation and making decisions by students, CBL may prove particularly useful for disciplines, where the application of theoretical knowledge to specific cases is necessary (Srinivasan et al., 2007; Wijnia et al., 2024). For these reasons, the examination of the effect of CBL in genetics education is relevant and educationally meaningful.

Even though it plays an essential role, genetics is known to be considered as one of the most difficult subjects among all students. Genetics study includes multi-level thinking from micro, macro and molecular levels. Transitioning between those is usually difficult for students (Murray-Nseula, 2011). In cases when the material is presented as a set of sequential units, the students fail to create an integrated

explanation but instead come up with fragmented knowledge structures (Murray-Nseula, 2011). The literature also shows that misconceptions about genetics mechanisms persist and that it relates both to the lack of understanding of central dogma and difficulties with interpretation of genetic information within the process of reproduction and transmission of genes (Briggs et al., 2016; Chattopadhyay, 2005). Literature reviews conducted in the field of secondary education point out that genetic information is difficult to understand, and common misconceptions persistently influence the learning processes (Machová & Ehler, 2023).

In this context, CBL has already been studied in several educational settings as a means of increasing applicability. According to Srinivasan et al. (2007), PBL and CBL were compared after the curricular change, and many students reported preferring CBL to PBL due to fewer tangents and decreased busywork. That means that CBL can be introduced in a dense curriculum and help students learn more efficiently. Moreover, there is evidence that CBL can be introduced in a manner that would increase motivation and promote the development of necessary learning skills. According to Alizadeh et al. (2024), participation in virtual CBL was associated with a significant increase in the motivation to learn basic science concepts among first- and second-year medical students. Those also reported high perceptions of relevancy ("applicability") and interest. Additional evidence from biochemistry education states that the use of CBL (and combined CBL-PBL approach) increases student interest, class participation, and grades compared with conventional methods (Dong & Zeng, 2017). As for biology education, Wikanta and Susilo (2022) show that case-based biochemistry learning allows achieving high-level cognitive goals among biology education students.

Furthermore, biology education literature also contains examples of case integration into the genetics field. Murray-Nseula (2011) implemented case studies in an undergraduate genetics course and achieved good results in terms of student perception; however, the impact on student performance was mixed, pointing to possible factors influencing the quality of CBL implementation and assessment

methods as well as learner preparedness. In line with the findings in STEM areas, this example reflects evidence from the research that the effectiveness of CBL can vary according to learner characteristics and cognitive readiness; Rhodes et al. (2020) used cognitive load theory to make a point that CBL approaches can create extra cognitive burden for novices in a certain subject matter.

Despite the wealth of research available for both fields, there is one significant gap in the connection between them. The literature on genetics education is extensive regarding common student misunderstandings about genetics, determinism, and difficulties with multiple levels of mechanistic explanation (Briggs et al., 2016; Jamieson & Radick, 2017; Machová & Ehler, 2023; Murray-Nseula, 2011). At the same time, CBL studies regularly report positive impacts on motivation, satisfaction, and practical skills development in health education and science-related programs (Alizadeh et al., 2024; Bi et al., 2019; Gholami et al., 2021; Wijnia et al., 2024). Nevertheless, very few studies directly examine whether CBL improves learners' ability to use genetic knowledge in the real world. Furthermore, even fewer explore whether this improved ability leads to academic achievement improvement in undergraduate genetics courses.

There are several reasons why additional research in the area of concern is necessary. First, despite strong support for CBL effects coming from health education (Alizadeh et al., 2024; Bi et al., 2019; Gholami et al., 2021), its applicability to genetics education can differ significantly. Second, case studies in genetics are known to have had varied success in improving academic achievement (Murray-Nseula, 2011), making it vital to determine the circumstances of their effective use. Finally, although motivational effects are often explored, their connection to transferable skills development and further academic achievement requires further analysis. Although meta-analysis proves that problem-solving approaches promote motivation (Wijnia et al., 2024), it does not guarantee increased skills related to genetics applications and improved performance.

Aim of the study

To examine the impact of case-based learning on students' academic performance in an undergraduate genetics course.

Objectives

- To develop and conduct a case-based learning (CBL) teaching approach for selected genetics topics for the experimental group and provide the same genetics lessons to the control group using the conventional lecture approach.
- To compare the effects of the CBL approach and conventional lecture on the academic achievement of the students.
- To assess the motivation of the students toward the genetics lessons using the Instructional Materials Motivation Survey (IMMS) by Keller.
- To compare the academic performance of both the groups based on their performance measures such as quizzes, test, case report score, etc.
- To find the correlation between motivation and academic performance.

Research Questions

RQ1. To what extent does case-based learning affect the academic performance of undergraduate genetics students in comparison to traditional instruction?

RQ2. Is there a significant difference in learning gains between theory-based and lab-based CBL instruction in genetics?

RQ3. What is the relationship between motivation and academic performance in genetics, and does this relationship differ between theory-based and lab-based instructional contexts?

Hypothesis

H1. Students who experience case-based learning will achieve significantly higher academic performance outcomes than students taught via traditional instruction.

H2. Students in lab-based CBL classes will demonstrate significantly greater learning gains than students in theory-based CBL classes.

H3. Motivation as measured by the IMMS ARCS subscales will significantly predict academic performance, and the strength of this relationship will differ between theory-based and lab-based instructional contexts.

There are many reasons why the present study will be important.

Firstly, difficulties with genetics are well known to educators in relation to learning molecular mechanisms (Briggs et al., 2016); persistent misunderstanding and abstractness (Machová & Ehler, 2023); and integration of multi-level concepts (Murray-Nseula, 2011). The purpose of this dissertation is to test the CBL approach to address the above-mentioned problem. That is, an attempt to develop the educational method to solve long-standing issues in genetics will be made.

Secondly, real-life genetic issues become increasingly important as far as their influence on individual and social decision-making is concerned. There is proof that genetics instruction may actually lead to a distorted interpretation of genetics from an overly deterministic/essentialist point of view (Aivelo & Uitto, 2021; Donovan, 2019; Jamieson & Radick, 2017). It is expected that using real-world cases will make it easier for the students to think in a more scientific way based on probabilities.

Thirdly, studies on CBL stress the importance of high-quality instruction (Rhodes et al., 2020). As a result, this work will add not only knowledge of the outcomes, but will also include an account of how genetics cases were implemented, measured, and evaluated in accordance with academic criteria. It will also rely on methodological practices in CBL used to assess motivation and learning processes, such as using the IMMS (Gholami et al., 2021; Keller, 2010).

Finally, in case of success, the present study would provide instructors with a practical strategy to implement genetics instruction in an active way in compliance with reforms in undergraduate biology education (Smith & Wood, 2016). In any case, if the results are mixed or depend on individual learners' preparedness, as was found in other works (Murray-Nseula, 2011; Rhodes et al., 2020), further improvements could be considered.

Theoretical framework

In summary, the current research project is largely underpinned by the Constructivist Learning Theory, while the ARCS Model of Motivational Design (Keller, 1987, 2010) and Cognitive Load Theory (Sweller, 1988) provide explanations for the motivational and cognitive mechanisms through which constructivist instruction impacts on learning outcomes in undergraduate genetics education.

First and foremost, the Constructivist Learning Theory represents the broad theoretical base underlying the current research. According to constructivism, individuals do not learn by receiving information passively from their environment but by interacting with their surroundings and constructing their knowledge actively (Bodner, 1986; Vygotsky, 1978). Within a constructivist approach, optimal learning occurs within the framework that provides contextual grounding, social mediation, and active construction of new knowledge as opposed to its rote memorization. In other words, CBL represents an implementation of the constructivist teaching paradigm in practice – by exposing students to realistic and complex case scenarios requiring the application of disciplinary knowledge to interpret the facts and justify their conclusions, CBL enables the creation of meaningfully transferable knowledge (Srinivasan et al., 2007; Kantar, 2013). As noted earlier, this process becomes especially important in genetics education, where students often end up creating fragmented and non-transferable knowledge structures and persisting misconceptions about the mechanisms of gene inheritance (Murray-Nseula, 2011; Briggs et al., 2016; Machová & Ehler, 2023).

According to constructivism, the richness of the instructional environment also impacts how students construct knowledge. In laboratory-based courses, the instructional environment is naturally constructivist: students observe natural phenomena, conduct and analyze experiments, and draw connections between their empirical observations and theoretical explanations, thereby building rich concrete referents needed for constructing multi-level knowledge about genetics (Smith & Wood, 2016; Wikanta & Susilo, 2022). Although theory-based seminar courses also involve constructivism via discussion and problem-solving approaches, there is less room for concrete referent

objects within the instructional environment of such classes. Therefore, this theoretical distinction directly informs the research question about CBL effectiveness in theory-based vs. laboratory-based courses (RQ2).

In line with the theoretical rationale, the constructivist process of active knowledge creation is complemented by motivational theories that explain why motivation plays an important role in CBL. According to Keller (1987, 2010), the ARCS Model of Motivational Design explains motivational factors that make active learning possible. From the constructivist perspective, it is essential to distinguish two different motivational functions of interest – a condition and an effect of active learning processes. The ARCS model identifies four motivational aspects – attention, relevance, confidence, and satisfaction. In terms of the ARCS model, the latter represents the ultimate phase at which motivation reinforces active constructivist learning efforts. If the environment of a learning course has rich sources that can support learner engagement, then intrinsic motivational factors related to satisfaction will activate automatically. However, if there are few external supportive elements of the learning environment, individual differences related to satisfaction will play a key role in motivating learners to actively engage with knowledge construction processes (Gholami et al., 2021; Wijnia et al., 2024).

Cognitive Load Theory (Sweller, 1988) offers a cognitive model that integrates well with the constructivist paradigm, specifying the boundary conditions necessary for effective knowledge acquisition through active processes. Active engagement of learners' cognition, as required by constructivism, becomes feasible only if their working memory is not overloaded by the dual demands of difficult material and novel learning approaches. Thus, given the necessarily high cognitive load associated with undergraduate genetics education, the initial combination of high-content learning and case-based reasoning will initially be too much for novice learners, making their knowledge construction process less effective (Rhodes et al., 2020). Over time, learners become increasingly familiar with CBL approach, alleviating extraneous load, and allowing them to engage in productive knowledge acquisition activities, such as

the constructive, active processes assumed by constructivism. This progression precisely explains the increased effectiveness of CBL found in this experiment in later cases.

Combining these theories into a coherent framework leads to an important theoretical hypothesis: constructivist CBL instruction will promote the greatest depth of learning if the learning occurs in a rich context conducive to active knowledge acquisition, provided that learners already know how to work within the constraints of the CBL format and motivated Satisfaction ensures continued engagement in learning processes.

LITERATURE REVIEW

2.1 Genetics as a Core Discipline in Biology Education

One of the foundational fields in biology is genetics. This field focuses on studying the storage, expression, and transmission of biological information between generations and how the differences in this biological information result in phenotypic diversity. Genetics, when included in school or college courses, typically ties in multiple "stories" - inheritance, molecular-level processes, and developmental pathways for phenotype formation. This combination of features makes genetics not only an important conceptually for teaching purposes but also socially relevant – genetic concepts are often used in public discourse and decision-making. According to Aivelo and Uitto (2021), knowledge of genetics has increasingly gained social relevance, with genetics-related issues like gene technology and genetic testing becoming prevalent among people. The social relevance of genetics is further demonstrated by the growing integration of disease-focused genetics research into undergraduate curricula. Forte et al. (2023) showed that engaging students with real human disease gene variants through a course-based research experience not only deepened their understanding of genetic mechanisms but also significantly increased their sense of scientific identity and relevance. This underscores that genetics education is most powerful when anchored in authentic biological problems students can connect to the real world.

Significantly, teaching genetics isn't just about conveying information; it's way more complex than that. Students bring their own ideas and beliefs to class, which really shapes how they understand new genetic stuff. So, each learning experience is super unique and dependent on the situation. According to Donovan (2022), genetic concepts are used a lot in discussions about social inequality and human differences both in public debates and academic circles. What ends up in the curriculum and how it's explained becomes super important. This matters a lot because it can either reinforce faulty views about essentialism or help tear them down, depending on how teachers choose to use the material and for what goal.

2.2 Student Difficulties in Genetics Education

One of the reasons why genetics is complicated is due to its abstraction and integration across different levels of biological organization-gene ↔ DNA ↔ chromosome ↔ cell ↔ organism ↔ population, in addition to process reasoning. In the literature on genetics education, genetics is continually cited as complex and intellectually challenging for students. For example, according to Smith and Wood (2016), genetics learning and teaching are challenging not just because genetics is probabilistic but also because learners have incorrect knowledge or beliefs about concepts in genetics.

Another area of research on secondary students is one that emphasizes the abstractness of genetics learning as one of the challenges. According to the literature review on misconceptions in secondary school genetics, learners find it tough to learn about genetics due to the complexity and abstraction of genetic content (Machová & Ehler, 2023). This is critical since it emphasizes the notion that genetics learning entails more than learning terms and definitions but also entails applying concepts – precisely the application of genetics.

Moreover, students are expected to combine "mechanistic" (how does it happen?) and "representational" (how do symbols/models represent a process?) forms of reasoning while learning genetics. In their studies on misconceptions about the central dogma, Briggs et al. (2016) argue that some concepts of molecular biology are conceptually and representationally challenging for learners, such that misconceptions about such concepts are tracked through instruction. This is important since central dogma reasoning is crucial for interpreting modern genetics information. The persistence of errors in genetics problem-solving has been further documented at the secondary level. Lee and Byun (2022) identified systematic error patterns in students' genetic reasoning, showing that most mistakes were not random but reflected deeply embedded faulty models - particularly around the relationship between genotype, phenotype, and probability. Their finding that students applied memorized procedural rules without genuine conceptual understanding directly supports the argument that

genetics instruction must move beyond declarative knowledge toward case-based reasoning and application.

It can be concluded from studies that an important feature of learners' genetics is its fragmentation. Students usually manage to learn definitions and terminology but do not manage to construct the model explaining these phenomena properly (Chattopadhyay, 2017). The study of the genetic information understanding among high school students also reports misunderstanding, confusion and poor grasp of essential genetic concepts showing that students might struggle building scientifically correct models in their mind.

It is especially relevant for genetics that simplified narratives used by teachers can reinforce misconceptions. Thus, in his discussion of 'myth-conceptions,' Allchin (2003) claims that there are cases when instructors tend to present science in terms of oversimplified and heroic linear narratives which mislead students and condition them to believe that the scientific discovery process follows certain rules. In relation to genetics instruction, this means that oversimplification encourages students to build incorrect ideas of heredity and genes' roles in the organism's development.

However, apart from wrong facts themselves, misconception problem is characterized by wrong causality explanation of various genetic phenomena. Thus, molecular genetic misconceptions were found to change during instruction which showed that the issue persisted despite the lessons' presence. Another important aspect discussed in the secondary misconceptions review is that due to high level of abstraction of genetics, learners may memorize certain facts and be unable to apply them (Briggs et al. 2016).

2.3 Genetic determinism and essentialist reasoning

One more problem associated with genetics learning involves students' interpretative rather than cognitive misunderstanding. In genetics, genetic determinism, which is essentially an essentialist view on genes, represents one such challenge. Genetic determinism refers to the idea that genes have a significant influence on individuals, resulting in their traits developing regardless of any other

circumstances. As a consequence, genetic determinism can make students believe in the absolute role of genes, ignore the importance of environment and gene-environment interplay, and reduce complex phenomena to simple concepts of a gene for. This topic is discussed in several articles. For instance, in the paper by Jamieson & Radick (2017), the authors demonstrate that curriculum emphasis plays an important role in developing students' deterministic interpretation of genetics. In turn, Bapty (2022) also emphasizes that genetic determinism can influence students' self-limitations if they think that they do not have a particular gene for a skill. Finally, Aivelo & Uitto (2021) find that hereditary emphasis in the work of teachers or in textbooks contributes to negative attitudes and belief in genetic determinism. The importance of avoiding genetic determinism is further explained in the paper by Thomas et al. (2015). According to these researchers, people frequently talk about a "gene for" some behaviors or skills. At the same time, the data indicate that genetic predispositions for skills are extremely low. Thus, educators need to understand how this finding impacts educational approaches because proper interpretation of genetics is important for maximizing educational achievements.

In summary, genetics learning problems involve significant cognitive and interpretative issues that are related to multi-level reasoning, inability to grasp abstraction, persisting misunderstandings, and deterministic beliefs about genetics. Consequently, students may not develop the necessary skills to analyze genetics because they do not know how to reason between different genetic levels, fail to understand mechanisms, and accept the "gene for" paradigm. According to Donovan (2022), the connection between genetic learning difficulties and their effects is confirmed. She discusses how essentialist views misinterpret genetic processes, and stresses the importance of teaching to help students spot the flaws in this type of reasoning. This shows that genetics education is about more than just delivering facts. Additionally, Aivelo and Uitto (2021) point out that how teachers present genetics material really affects student attitudes. So, the way genetics is taught matters a lot, shaping how engaged students are and how well they understand the topic.

2.4 Case Based Learning

Case-based learning (CBL) is a learner-centered educational approach, which involves using cases that describe authentic situations to solve problems by applying disciplinary concepts and interpreting information in order to make justified conclusions and decisions. An important element of the definition is the fact that the "case" forms the framework for the lesson – in small-group formats, students explore concepts as tools for problem-solving and learning rather than as isolated pieces of knowledge. The guided inquiry CBL is among the most popular formats because it allows the teacher to facilitate students' reasoning without sacrificing structure (Srinivasan et al., 2007).

In general, CBL is regarded as one of the best methods for achieving higher levels of learning (e.g., analysis, application, synthesis, problem solving), as argued by Rhodes, Wilson, and Rozell (2020). Case-based learning typically consists of a description of an actual situation that learners need to solve through information processing; importantly, the format and length of the case varies widely depending on the content, meaning that "CBL" should be considered a family of different strategies (Rhodes et al., 2020). Most effective CBL strategies include individual preparatory work, small group discussions, and guided reasoning facilitated by a teacher, thus making it particularly useful for addressing complex topics prone to misconceptions and rote memorization.

In the CBL literature, an important development is the concept of multi-episode or unfolding CBL, when learners need to repeatedly update their understanding and reasoning based on information presented at each step. According to Gholami et al. (2021), single episode CBL in the field of health often focuses exclusively on the disease and omits psychosocial aspects of an illness journey, which reduces learners' reasoning abilities; however, multi-episode CBL allows updating decisions in each step and, therefore, helps develop core competencies. For example, a quasi-experimental within-subject design employed by Gholami et al. (2021) involved implementation of multi-episode CBL in five steps and revealed significant differences in learners'

problem-solving skills and motivational beliefs assessed using the Problem-Solving Inventory and IMMS (Gholami et al., 2021). It is important to note that these authors also encourage researchers to investigate potential generalizability of these gains to a wide range of real situations – an issue directly relevant to your dissertation topic (Gholami et al., 2021). The superiority of CBL over traditional lectures in science-adjacent disciplines is further evidenced by recent experimental work. Raghuwanshi et al. (2025) conducted a crossover quasi-experimental study with 100 undergraduate medical students in clinical biochemistry, finding that CBL significantly outperformed traditional lectures in both test sessions (CBL mean: 37.9 vs. lecture mean: 31.2, $p < 0.001$), with 88% of students reporting improved ability to apply biochemistry concepts to clinical practice. Crucially, the benefit was consistent across two separate topic modules - suggesting that CBL gains are not topic-specific but reflect a durable instructional advantage, which is directly relevant to assessing CBL's potential in multi-topic genetics courses.

For this reason, an iterative cycle between evidence and explanation will be highly relevant when applying CBL to genetics education since new evidence (pedigree analysis, genotype or molecular testing, variable penetrance, phenotype analysis) often alters interpretations, which require probabilistic reasoning. CBL can facilitate modeling of genetics reasoning in practice because it allows designing such a process. Your genetics education literature supports such an idea by stating that genetics reasoning involves multiple levels of analysis (micro, macro, molecular), while a lack of understanding may result from compartmentalized education preventing learners from combining knowledge on meiosis, inheritance, and molecular level phenomena (Murray-Nseula, 2011). The need for increased case-based relevance and integration in genetics education at the university level explains why case-based learning in genetics is often promoted (Murray-Nseula, 2011).

A connection between case analysis and active cognitive engagement needed to facilitate meaningful learning also justifies CBL in education. Evidence from virtual CBL can be used to support this pathway via the motivational role of perceived

relevance of cases for learning. In their quasi-experimental study involving peer instruction and the flipped classroom, Alizadeh et al. (2024) show that participation in CBL facilitated by structured virtual discussions was associated with higher students' motivation to learn basic sciences. It appears that group discussions and getting the correct answer were particularly motivating experiences for students, which allowed them to perceive that the knowledge gained was applicable to the practice of basic sciences in their profession (Alizadeh et al., 2024). For genetics, relevance to the "real world" seems to be a major mediating factor between case-based learning and the intended outcomes of your research.

2.5 Implementing CBL in education: core design features

The quality of implementation is another recurring topic in CBL-related research articles. Commonly, authors mention multiple practical features that affect the results of the activity:

Case reality and relevancy

Often, cases are created to reflect reality and local specifics while evoking emotions. Gholami et al. describe the development of cases based on real-life scenarios, locally-relevant situations, and realistic details to maximize the interactivity of the cases. Authentic cases can be created in genetics by exploring family inheritance, ethics, genetics testing, and population genetics for specific problems.

Facilitated collaboration and discussion

In many cases, CBL practice includes peer interaction, group discussion, and the role of the instructor. According to Alizadeh et al., items included in questionnaires in virtual CBL are specifically aimed at reflecting peer interaction and group discussion as motivators of the learning process. The importance of collaborative discussion within CBL is supported by Scholten and Timmermans (2022), who compared a tutor-driven CBL format with a more collaborative version featuring small breakout group discussions. The collaborative format significantly improved exam scores and student engagement, with 90% of students and 92% of tutors endorsing the more interactive design. For genetics instruction, this evidence reinforces that shifting discussion

control from the instructor to students - while maintaining structured guiding questions - is a key design feature for maximizing CBL's cognitive and motivational benefits.

Facilitation, scaffolding, and prompting

Since complex cases require higher-level thinking, instructors must guide the process to avoid surface-level discussion. The necessity to provide facilitation arises from the fact that cases can be too challenging for the learners' existing knowledge base. Consequently, students can fall back on their common-sense reasoning or determinism. At the same time, the literature that criticizes one-dimensional case studies also argues that cases need to encourage multidimensional reasoning (Emblen-Perry, 2022).

Multi-facet assessment

As an outcome of CBL, students' conceptual understanding, reasoning, and decision-making skills are assessed through multi-component tests. Specifically, Zhang (2025) stresses the importance of multi-level evaluation techniques for enhanced CBL. Thus, it appears that evaluating CBL-based learning cannot be done by one measure only (for instance, performance, engagement, and conceptual understanding).

2.6 Distinctions Between PBL and CBL

One common differentiation that can be found in literature is that while PBL usually starts from the presentation of an ill-structured problem with an expectation for students to find and define their own issues, CBL normally involves a structured case story where issues and goals for learning are defined by an instructor. The latter point was highlighted in the article by Srinivasan et al., who compare PBL and CBL frameworks and mention differences in terms of structure, facilitation, and the use of learning sources (Srinivasan et al., 2007). While PBL can be considered relatively unstructured, CBL tends to be highly structured and oriented toward predetermined educational goals, which makes it easier to incorporate into a curriculum with set standards of coverage and evaluation (Wikanta et al., 2022).

This difference is relevant for genetics lessons since the subject entails high cognitive load and numerous misconceptions, making guided approaches such as CBL especially efficient for explaining concepts through real-life situations.

Moreover, when comparing CBL and PBL, one can notice that CBL features an advantage in relation to problems connected with numerous misconceptions since there is always an opportunity for the facilitator to guide the discussion and address incorrect assumptions made by learners. This is mentioned by Srinivasan et al. (2007), who state that CBL proponents claim facilitators' capability to correct incorrect assumptions as well as to reduce the impact of opinion leaders in groups. On the other hand, there are some concerns associated with facilitators acting as lecturers, providing ready answers without stimulating curiosity (Srinivasan et al., 2007). In terms of genetics education, CBL can benefit from prompts aimed at justifying the position of learners, providing answers only after reasoning by students, and addressing misconceptions specifically during the process of debriefing (Guo et al., 2020). A qualitative comparison of the cognitive processes activated by PBL and CBL further clarifies this distinction. Khoiriyah and Wijaya (2022) analyzed video-recorded discussion sessions of medical students and found that while both methods activated cumulative reasoning and exploratory questioning, CBL students engaged more frequently in procedural interaction - the structured step-by-step application of knowledge to case data. PBL students, meanwhile, asked more open-ended exploratory questions. For genetics education, where procedural reasoning (e.g., tracing inheritance patterns, interpreting molecular assay data) is essential, CBL's structured scaffolding of this process appears particularly well-suited.

2.7 Effectiveness of CBL

Case-based learning is considered effective in terms of learning across all disciplines, although the magnitude and generalizability of CBL effects highly depend on the quality of the instructional design, chosen outcome measures, and participants' characteristics. According to the evidence collected in syntheses of the literature, CBL tends to increase the academic achievement of learners and their case analysis skills;

however, research outcomes tend to differ substantially, showing some cases of very high effects alongside others with low effects (Tsekhmister, 2023). Beyond domain-specific studies, meta-analytic synthesis across disciplines provides stronger evidence for CBL's general effectiveness. Wu et al. (2023) conducted a meta-analysis specifically examining CBL in psychology teaching and found a statistically significant positive effect of CBL on academic performance compared to traditional instruction. Importantly, subgroup analyses revealed that CBL was most effective when cases were closely aligned with course objectives, when group discussions were facilitated rather than lecture-driven, and when sample sizes were moderate - conditions directly comparable to the genetics course context in the present study. Similar variability of results can be observed in relation to the wider evidence base for active-learning strategies in STEM courses, where moving learners from passive listeners to active sense-makers tends to enhance learning but can vary depending on the implementation, structure of course activities, and assessments (Freeman et al., 2014). As such, one can expect CBL to yield measurable results if (a) cases align well with the course content and desired learning outcomes and are assessed against clearly specified criteria, (b) scaffolded approach is applied, and (c) cognitive load in relation to case content is well managed by the instructor.

Studies based on comparative and quasi-experimental designs suggest that CBL can yield better or comparable outcomes to conventional lectures, especially in terms of problem-solving skills, reasoning, and learners' motivation. One such example is provided by the results of the study conducted by Gholami et al. (2021): in a course in emergency nursing, the authors employed a within-subjects pretest–posttest design. Participants were involved in two phases (lecture-based learning vs. CBL) in multi-episode cases. Results of the study showed positive changes in the perception of their problem-solving skills at different stages of the course and demonstrated an especially high effect in increased motivation during CBL as opposed to lecture phase of learning (Gholami et al., 2021). Specifically, this design illustrates one of the main strengths of

CBL – creating opportunities for repeated application of knowledge under real-life conditions, including decision-making and other cognitive activities.

More generally in higher education contexts, researchers posit that CBL facilitates development of multi-faceted thinking and transferable skills like critical thinking, collaboration, and problem solving-in cases where there is no oversimplification of situations. For example, Emblen-Perry (2022) highlights how text-only case study exercises tend to foster “backward reasoning” and insufficient student engagement, and offers an improved strategy based on use of mixed-media cases combined with a structured “audit” process. The audit encourages students to collect, analyze, and present multidimensional data and arguments, leading to greater depth of reasoning. Though Emblen-Perry's case study framework is intended for sustainability education, the underlying principle applies widely: reasoning skills improve when students have to consider multi-factor interactions, make informed decisions about compromises between conflicting goals, and formulate defensible conclusions. It is immediately clear how CBL fits within genetics education: real-world problems in genetics involve multilevel reasoning (such as genotype-phenotype mapping, penetrance/expressivity, gene-environment interaction, sampling issues), and usually have some moral dilemmas involved. With appropriate case studies, learning genetics could be transformed from “finding the correct answer” into evidence-supported argumentation. Nonetheless, it is crucial not to adopt an overly simplistic view that suggests that CBL works in all situations.

As an opposing example, Rhodes, Wilson, and Rozell (2020) offer an intermediate physiology case study with intriguing findings in terms of learning outcomes when compared to lectures: they found that case-based teaching did not consistently lead to better learning than lecture teaching, depending on individual characteristics of the students enrolled. Applying cognitive load theory, they explain how extraneous load caused by more complex processes involved in case instruction would disproportionately affect less-prepared or less-experienced students-unless proper scaffolding was available (Rhodes et al., 2020). This is important to keep in

mind both from a pedagogical and a dissertation-writing point of view: even if the outcome does not prove superiority of CBL, that does not mean it is ineffective overall. Rather, the effectiveness may depend on whether students' cognitive and metacognitive capabilities match with case complexity and the amount of scaffolding.

Collectively, the research literature supports a valid synthesis – CBL will work best when approached as a designed learning system, not just “add cases.” For the highest impact, the recommendation includes alignment of cases to learning objectives and assessment formats, sequenced difficulty of cases (particularly for novices), prompts and feedback in learning experiences, and assessments measuring higher-order learning such as application, quality of reasoning, and transfer (not just recall). Meta-analytic studies of the effectiveness of CBL within professional education reveal that CBL has potential to help improve academic achievement and analysis skills generally, while exhibiting wide variance depending upon implementation strategies (Tsekhmister, 2023). Further, cross-disciplinary evidence from STEM fields reveals that active learning environments correlate with lower failure rates and better test scores, supporting the general idea that active engagement is essential to learning (Freeman et al., 2014; Hake, 1998). While there is evidence that CBL can be highly impactful, it will depend upon good learning designs, aligned assessment approaches, and the demographics of the learner groups. Such an understanding provides a framework in which to understand variable findings and offers theoretical rationales and explanations for mixed results, such as cognitive load (Rhodes et al., 2020; Emblen-Perry, 2022).

2.8 CBL in biology education and undergraduate genetics

One such example in relation to biology education is the study conducted by Murray-Nseula, demonstrating the effectiveness of the case-based strategy in teaching genetics at the undergraduate level through an introductory genetics course, proving the feasibility of cases in genetics concepts education, fostering reasoning skills among students over simple memorization. Regarding biochemistry and molecular biology topics directly relevant to genetics lessons, Dong and Zeng (2017) state their successful

use of CBL together with PBL approaches in biochemistry education, implying that there may exist hybrid models of cases that could be adopted when both guiding (CBL) and encouraging self-inquiry (PBL) are needed for complex topics. This may come handy if, according to your curriculum, both content understanding and investigative projects have to be completed. The evidence regarding the feasibility of CBL in biochemistry and molecular biology comes from Wikanta and Susilo (2022) in relation to cultivating higher-level critical skills among biochemistry learners using cases in science education. Moreover, Zhang (2025) shows the ongoing development of CBL models, along with a multi-layered assessment framework for biochemistry/molecular biology cases. More recent evidence reinforces the case for real-world case integration in genetics and molecular biology education. Shahoy et al. (2024) examined whether undergraduate biology students could apply central dogma knowledge to explain how COVID-19 mRNA vaccines work - a precisely the kind of authentic genetics application your Case 2 addresses. Their findings showed that while students possessed some foundational molecular biology knowledge, they struggled to connect it coherently to real-world mechanisms without guided instructional support. This confirms that real-world case scenarios in genetics do not spontaneously activate application skills - they require structured CBL-type facilitation to bridge declarative knowledge and functional understanding.

Concurrently, the literature on misconceptions in genetics provides additional explanations for the necessity of adopting CBL when teaching genetic topics. Namely, if learners possess established genetic misconceptions associated with the molecular level (Briggs et al., 2016) or understand genetic information in a fragmented way (Chattopadhyay, 2017), one needs to develop activities that will prompt their application of concepts for justification or explanation purposes.

2.9 CBL, Motivation, and Academic Engagement

Moreover, motivation is one of the key mechanisms through which CBL impacts academic performance, particularly in more complex disciplines like genetics. Some of your references link motivation directly to CBL and include specific measures that

could be used as part of your dissertation methodology. For instance, Gholami et al. measured motivation using the Instructional Materials Motivation Survey (IMMS) and found motivation was significantly higher after CBL compared to lecture-based learning.

Alizadeh et al. take the motivational argument one step further and consider how it works in an online/virtual context, using a Self-Determination Theory approach. Their motivational items are quite specific about how CBL allows for appreciation of practical application and encourages peer interactions, thus fostering motivation-both points very pertinent to the way you design the case if it involves discussing the application of genetics knowledge.

The higher-level perspective of educational psychology synthesis is reinforced by a meta-analysis included in Educational Psychology Review (Wijnia et al., 2024). It deals with motivational effects from a wide variety of student-centered pedagogical techniques, including CBL. Although, meta-analyses usually serve as a good empirical basis for predicting increased motivation if instruction is meaningful, interactive, and relevant-which is precisely what CBL is. The relationship between instructional practice and motivation quality has been examined specifically in undergraduate biology contexts. Stieha et al. (2024) used the Classroom Observation Protocol for Undergraduate STEM (COPUS) alongside a self-determination theory-based motivation survey to analyze active learning and motivation simultaneously in biology courses. Their mixed-methods findings revealed that not all active learning practices equally support motivation - the alignment of instructional activities with students' needs for autonomy, competence, and relatedness was the key differentiating factor. For genetics education using CBL, this suggests that case design should intentionally address all three need dimensions: student choice within cases (autonomy), appropriately challenging content (competence), and peer collaboration (relatedness).

Furthermore, motivation matters to the study of genetics in particular because attitudes can play a role. In the case of studying attitudes toward learning genetics and

belief in genetic determinism, it is clear that both motivation and attitudes could be measured in your study.

2.10 Challenges, limitations, and risks of CBL

Labor-intensive development and preparation.

A successful use of CBL requires resources, effort, and iterations. Challenges listed by Emblen-Perry explicitly include labor intensity of the case development itself and lack of preparation of the learners. As such, for the implementation in genetics class, you may need to develop, test and iterate through your cases and also make sure that they align with learning outcomes of your course.

Potential of fostering superficial reasoning when cases are single-dimensional or poor at facilitating critical thinking.

In case only shallow features of the story are provided or there is only one answer, then, according to Emblen-Perry, the student will not develop his/her reasoning skills because the traditional approach based on single-dimensional cases can be problematic. For genetics, this means that your case should not be too simplistic and foster deterministic view ("gene X causes trait Y").

High reliance on the facilitation quality and classroom environment.

CBL often involves discussions. When facilitation is not appropriate, learners might not correct their misconceptions, but, rather, reinforce them. The concern here is aligned with genetic misconception research where authors point out that these misconceptions are usually coherent (Briggs et al., 2016). As such, CBL in genetics should involve instructor prompts that would force students to support their claims with genetic evidence.

Diversity of students and uneven participation.

According to Rhodes et al. (2020), individual characteristics of the learners can influence the benefits gained by them during the case study sessions. In small groups, better-prepared students are likely to dominate in reasoning while less-able ones may stay passive if there are no mechanisms in place to ensure involvement. Therefore, effective CBL implementation requires deliberate facilitation strategies, such as

structured role assignment, rotating discussion leadership, and targeted questioning, to ensure equitable participation and prevent knowledge asymmetry from undermining the learning experience for less-prepared students.

Self-reporting bias in evaluations.

Many CBL evaluations depend on students' reflections. These methods can be helpful, but suffer from the inherent bias that makes self-reporting a rather unreliable measurement. As such, Emblen-Perry describes discussions about this issue and mentions that sometimes even improved performance does not imply increased learning.

2.11 CBL as an Evidence-Based Approach to Real-World Genetics Application and Academic Performance

Genetics education studies unambiguously demonstrate that many learners face difficulties with abstract and multi-level reasoning and keep many misconceptions in this discipline (Allchin, 2003; Briggs et al., 2016; Chattopadhyay, 2017).

Additionally, their attitudes and deterministic views influence how they perceive genetic rationales and interact with complex ideas (Jamieson & Radick).

On the other hand, the CBL research highlights that appropriately designed cases enhance motivation, problem-solving, and application skills (Gholami et al., 2021; Alizadeh et al., 2024), while biology-related studies have shown viability in genetics/biochemistry (Murray-Nseula, 2011; Wikanta & Susilo, 2022; Zhang, 2025; Dong & Zeng). Nevertheless, there is an apparent doctoral-level deficiency, as most studies measure the effectiveness of CBL by general academic achievement or satisfaction, whereas few examine its impact on linking genetics knowledge to practical uses as a strategy for improving grades.

METHODOLOGY

3.1 Research Design and Approach

The present study used a quasi-experimental design combined with quantitative methodology to investigate the impact of CBL on academic performance in the undergraduate genetics course, and to explore the association between motivational factors and academic success under various teaching approaches. In educational settings, quasi-experiments are frequently used in cases when randomization is impracticable due to class integrity, but causal inference can still be drawn when proper controls are applied (Shadish, Cook, & Campbell, 2002). This study considered the following three research questions: Does CBL affect academic performance relative to conventional instruction (RQ1)? Is there a difference in learning gains between theory-based and lab-based CBL implementation (RQ2)? Is student motivation (using the ARCS model) associated with academic success in different instructional contexts (RQ3)?

Instructional intervention included four CBL case studies conducted within two distinct instructional formats: theory-based classes (Cases 1 and 2) and lab-based classes (Cases 3 and 4). Theory-based classes referred to seminar-style lectures focusing on the conceptual framework, mechanisms, and discussions of genetic principles. Lab-based classes were laboratory experimental sessions in which students participated in genetics exercises and case analysis. CBL refers to a learner-centered instructional strategy where students analyze authentic scenarios and use discipline-specific knowledge to analyze data and suggest solutions (Srinivasan et al., 2007). The method has been extensively utilized in scientific and health education for promoting critical thinking, problem-solving skills, and involvement (Gholami et al., 2021; Rhodes et al., 2020; Wikanta & Susilo, 2022). CBL has also been applied in undergraduate genetics instruction to promote hierarchical reasoning and prevent fragmented learning (Murray-Nseula, 2011).

The present study employed a design in which different groups of students were exposed to experimental and control conditions depending on the case under

examination. Specifically, all students received CBL instruction during the semester, though not simultaneously across groups. Groups A and B were assigned to the CBL condition for Cases 1 and 3 respectively, while Groups C and D participated in CBL for Cases 2 and 4, as presented in Table 3.1.

Table 3.1 Experimental and Control groups

	Case 1	Case 2	Case 3	Case 4
Experimental (CBL)	Groups A, B	Groups C, D	Groups A, B	Groups C, D
Control (Traditional)	Groups C, D	Groups A, B	Groups C, D	Groups A, B

The present study examined two dependent variables: student academic performance and learning motivation. Motivation was assessed using Keller's Instructional Materials Motivation Survey (IMMS), an instrument grounded in the ARCS model of motivational design, which conceptualises motivation along four dimensions - Attention, Relevance, Confidence, and Satisfaction (Keller, 2010). The IMMS was selected on the basis of its established use in CBL research, where it has demonstrated sufficient sensitivity to detect meaningful differences in instructional quality and format (Alizadeh et al., 2024; Gholami et al., 2021).

3.2 Participants and Setting

This research took place in an upper-level university class called Genetics which was offered in one semester of the academic year. This course involved both theoretical seminars and practical laboratory sessions as is common for undergraduate life science education courses (Smith & Wood, 2016). CBL cases were used in both instructional environments to test if CBL effectiveness would differ between different types of instructions.

3.2.1 Participant recruitment and exclusion

A total of 70 students were enrolled in the genetics course at the beginning of the semester. Students self-selected into one of four lab and practice groups at the start of the semester following standard course enrolment procedures, resulting in four intact groups:

- Group A: 25 students
- Group B: 12 students
- Group C: 24 students
- Group D: 9 students

As the students have formed their own groups as opposed to being allocated randomly, this experimental setup can be referred to as quasi-experimental. To minimize any possible impact of selection biases on the results obtained, baseline equivalence among the groups has been investigated using pre-test scores as a covariate in all ANCOVA tests.

Before analyzing the data, some students were eliminated from the sample on the basis that: 3 students who performed poorly enough in the course to fail it were dropped from the sample since their performance could not properly reflect the learning process; 7 students were excluded from particular case analyses because of their failure to participate in the pre-test or post-test administrations. In total, 64-65 students were analyzed in class theory analyses (Case 1 & Case 2), while 65 students were analyzed in class laboratory analyses (Case 3 & Case 4). All remaining students in the sample were exposed to the CBL approach in at least two cases out of four, and took part in the IMMS motivation questionnaire at the end of the semester.

3.3 Data Collection Instruments

All the tests administered in this study, including the pre-test test and the post-tests related to each CBL case, were developed by the researcher to align with the course objectives and content of each CBL lesson. Before the data gathering process was done, all the instruments underwent content validity and reliability checks to

confirm that they are suitable and consistent. This is discussed in further detail in the sub-sections below, while the results of which are presented in the Results chapter (Section 4.1).

3.3.1 Validity

The content validity of the three assessments was determined based on expert ratings using the Content Validity Index (CVI), according to the procedure suggested by Lynn (1986) and Polit & Beck (2006). For that purpose, a panel of three experts in the matter, namely three teachers of biology or biological sciences at SDU University, was recruited to assess each item of the tests separately.

An individual test item was assessed based on four aspects: (C1) its suitability for assessing a specified concept in genetics, (C2) clarity and absence of ambiguity of this item, (C3) adequacy and plausibility of the possible answers to the question, and (C4) adequate difficulty level for a third-year undergraduate student.

The Item Content Validity Index (I-CVI) for each test item was calculated as the percentage of experts who gave a rating of at least Good (4) or Excellent (5) to it, with the acceptable minimum value being $I-CVI \geq 0.78$ when there were three experts (Lynn, 1986). The Scale Content Validity Index (S-CVI) was then calculated as the average I-CVI for all items in the test instrument, with the acceptable minimum being $S-CVI \geq 0.80$ (Polit & Beck, 2006). The CVI calculation was performed using R Studio (R Core Team, 2023).

3.3.2 Reliability

The internal consistency reliability of all three measurement tools was established through the computation of Cronbach's Alpha (α) from student responses to individual items using R Studio (R Core Team, 2023). Cronbach's Alpha represents the extent to which all the test items consistently measure the same construct. The minimal requirement for internal consistency was set at $\alpha \geq 0.70$ because this value represents the commonly accepted standard in the educational literature (Nunnally, 1978). The range of 0.70-0.79 indicates satisfactory internal consistency, while values in the range

of 0.80-0.89 are considered good, and those above 0.90 are considered excellent. Reliability findings are reported in the Results section along with validity results.

3.3.3 Pre-test

A pre-test comprising 25 questions was given to all students at the start of the intervention phase before exposing them to any of the four CBL cases. The pre-test served two main purposes: first, as a means of achieving baseline equivalence among the different groups of participants prior to the instruction phase; second, as a covariate in ANCOVA when evaluating differences between groups based on post-test scores. During the hierarchical regression analysis of research questions 2 and 3, pre-test scores were also included as control variables during Block 1, which allows for an evaluation of the independent contributions of instructional context and motivation, assuming that pre-test scores account for prior knowledge. The inclusion of pre-test scores as covariates in the analyses is in line with the methodological guidelines in conducting quasi-experimental research in education (*Appendix 3*).

3.3.4 Post-tests and Gain Scores

After exposure to each of the four CBL cases, a case-specific post-test was conducted among students. Each post-test evaluated the achievement of learning objectives related to the specific topic addressed by the case study. Post-test scores served as the dependent variables for each intervention. Gain scores, calculated as the difference between post-test and pre-test scores, expressed in percentage points, were the primary dependent variables in research questions 2 and 3 (*Appendix 4&5*).

3.3.5 Motivation Survey – Keller’s IMMS

The motivation level of students was measured by means of Keller’s Instructional Materials Motivation Survey (IMMS) (*Appendix 2*), grounded on the ARCS model that includes the following components: Attention, Relevance, Confidence, and Satisfaction (Keller, 2010). It is a reliable survey containing 36 questions which can be answered using a five-point Likert scale. This test measures the effect of instructional materials and learning activities on motivation levels of students.

It was conducted only once during the last week of the semester for all students who experienced CBL in at least two out of four situations because of the counterbalancing procedure.

3.4 Research Procedures

These were conducted in the following manner:

Step 1. Group formation: At the start of the semester, students self-allocated themselves to one of four lab and practice groups (A-D) through standard course enrolment practices.

Step 2. Pre-test: All students completed the 25-question pre-test prior to the introduction of any of the case studies, providing baseline knowledge of all students across all groups at the outset of any instructional intervention.

Step 3. Introduction of the four case studies: The four case studies were delivered in the respective courses units throughout the semester where Case 1 & 2 (*Appendix 6*) were delivered in theory-based seminars while Case 3 & 4 (*Appendix 7*) were delivered in laboratory based practical classes.

The following cases were employed as experimental interventions throughout the study:

- Case 1: RT-qPCR Case Study - Detection of SARS-CoV-2
- Case 2: Cystic Fibrosis and the Central Dogma
- Case 3: From the Wild to the Mutant - *Drosophila Melanogaster*
- Case 4: The Genetic Code Unfolds - From F₂ to Discovery

For experimental conditions, instructions were structured around the CBL case study whereby the students engaged in the analysis of an authentic situation, applying genetic knowledge in order to interpret evidence and make well-supported conclusions. In line with research on the potential impacts of student characteristics on the effectiveness of CBL, structured facilitation and scaffolding of students' reasoning processes were provided to minimize unproductive cognitive load (Rhodes et al., 2020). Conceptual integration and discussion were encouraged in the case-based

learning in theory-based seminar settings while the case-based learning in the practical settings took place within the context of a laboratory experiment. Control conditions comprised of a traditional approach whereby instructors explained the topics and students practiced related skills, but without the use of the case-based scenario.

Step 4. Post-test: A case-specific post-test was delivered to all students immediately after each case.

Step 5. IMMS motivation survey: At the end of the semester following completion of all case studies, all students completed the Keller IMMS instrument (Keller, 2010).

Step 6. Exclusion of incomplete records: If students did not complete the pre-test or post-test for a particular case, then they were not included in the specific case analyses. Those students who had failed the course were also excluded from all analyses.

3.5 Characteristics of the Implementation of CBL

For the experimental condition, the CBL process was centered on realistic cases, based on current genetics and molecular biology topics. The selection of such cases aimed at promoting the connection between real-life applications, such as clinical diagnosis, molecular procedures, genetics of model organisms, and inheritance processes, and genetics content, according to recommendations for an application-oriented teaching of genetics in order to promote the use of genetics knowledge and avoid fragmentation of such knowledge (Murray-Nseula, 2011; Machová & Ehler, 2023).

In CBL, students engaged in discussions about case contents following guiding questions, which were designed to promote mechanistic reasoning and to use knowledge about genetics in problem-solving. The use of such questions follows recommendations for CBL implementation, which allow for a balance between providing some structure to the lesson while still requiring the learner to engage in mechanistic reasoning, with instructors being able to focus the discussion on certain goals, with justifications required and peer discussion (Srinivasan et al., 2007). Additionally, facilitation was oriented to provide explanations only after reasoning by

students, address specific misconceptions related to genetics knowledge, and ask students to explain their answers by relating them to genetic mechanisms - as recommended for CBL of genetics (Murray-Nseula, 2011; Briggs et al., 2016).

CBL was delivered either as theory-based (in seminars) or as lab-based (in laboratories), reflecting the instructional organisation of the course. In the former case, the delivery of CBL included case discussion and applying theoretical knowledge from genetics. Lab-based CBL entailed discussing cases and carrying out experiments, with case discussion embedded in laboratory activities – as shown to be feasible in case-based approaches to biochemistry and biology (Wikanta & Susilo, 2022; Zhang et al., 2025).

Control conditions entailed instruction based on the standard approach of the course, which included instructor presentations and examples, practice tasks, and explanations – but without CBL case structure.

3.6 Data Analysis

Preparation and screening

All data were analyzed in R Studio (R Core Team, 2023). Missing data, outliers, and normality of distributions were checked before analysis; students who did not have complete pre-test and post-test data for a given case were not considered in the corresponding analysis.

Pre-test equivalence

To investigate whether there were differences between intact groups at the beginning of the experiment, pre-test scores were compared between experimental and control groups in each case. It was done to provide a justification for using ANCOVA.

ANCOVA of post-tests (RQ1)

To evaluate the impact of CBL on academic performance in each case, one-way ANCOVA with post-test score as a dependent variable, instructional approach as a factor (CBL vs traditional), and pre-test score as a covariate was used. ANCOVA is the best option because this design compares outcomes of interest after controlling for the effects of the covariate, which is typical for quasi-experiments and non-randomized

designs where pre-test score is used to account for differences in prior knowledge. Such assumptions as normality (Shapiro-Wilk tests, Q-Q plots), linearity (scatterplots), homogeneity of regression slopes (scatterplots), and homogeneity of variances (Levene's test) should be checked in advance. Pairwise comparisons of adjusted estimated marginal means and effect sizes (partial η^2 , small = 0.01, medium = 0.06, large = 0.14, according to Cohen, 1988) were used.

Learning gains by instructional context (RQ2)

In order to compare the influence of theory- and laboratory-based instructional contexts on learning gains, a hierarchical regression model was used. As a covariate, pre-test score was put in Block 1; in Block 2, instructional context (theory-based vs. lab-based) was entered. The R^2 change (ΔR^2) associated with the introduction of the second block was obtained.

Motivation and academic performance (RQ3)

In order to investigate the relationship between ARCS motivational dimensions and academic performance and if this relationship varies based on instructional setting, hierarchical regression analyses were performed separately for theory and laboratory-based courses. In both analyses, the pre-test score was introduced in Block 1, whereas the four subscales of IMMS (Attention, Relevance, Confidence, Satisfaction) were introduced in Block 2 simultaneously. R^2 change between Blocks 1 and 2 represented the motivational contribution to learning outcomes, which was additional to the learners' previous knowledge base. Such an analysis is in line with the hierarchical regression procedures applied in studies exploring CBL motivation and the suggestions for investigating predictors of achievement outcomes while accounting for previous knowledge. Assumptions of regression were checked, including normality of the residuals, homoscedasticity (Residuals vs Fitted Plot and Scale-Location Plot), lack of outliers (Cook's distance) and multicollinearity (Variance Inflation Factor, $VIF < 10$).

RESULTS

4.1 Validity and Reliability of Assessment Instruments

4.1.1 Validity testing outcomes

The findings of expert evaluation are provided in Table 4.1. Three assessments exhibited a good content validity. The pre-test obtained the maximum possible S-CVI score of 1.000, because all 14 items were assessed by two raters as Good and Excellent across all four criteria (mean ratings per criterion = 4.86/5.00, SD = 0.36). Theory-based post-test (18 items) scored S-CVI = 0.972, with 16 of 18 items having I-CVI = 1.00 and two items – I-CVI = 0.88, exceeding the minimum threshold of 0.78. The only issue noted by raters regarding these two items concerned criterion C4 (Difficulty Level). Both items were kept unchanged due to an acceptable I-CVI. Lab-based post-test (12 items) got the S-CVI = 0.990, with 11 of 12 items having I-CVI = 1.00 and one item having I-CVI = 0.88. None of the items was deleted in all three assessment tools, ensuring their high content validity prior to distribution to students.

Table 4.1 Expert Content Validity Index Results - All Assessment Instruments

Instrument	N Items	Items Passed (I-CVI $\geq$.78)	Items Flagged	S-CVI	Result
Pre-test	14	14	0	1.000	Acceptable
Post-test Theory	18	16	2	0.972	Acceptable
Post-test Lab	12	12	0	0.990	Acceptable

4.1.2 Reliability

Internal consistency reliability of the three tests was determined using Cronbach's Alpha, where item-level responses provided by students on all three tests were analyzed using R Studio software. See Table 4.2 for results. The pre-test revealed

satisfactory internal consistency ($\alpha = 0.78$; 14 items), suggesting that the 14 items measured a common construct of genetics knowledge before any lessons on the subject were undertaken. The theory-based post-test also revealed satisfactory internal consistency ($\alpha = 0.84$; 18 items), while the lab-based post-test also showed good internal consistency ($\alpha = 0.82$; 12 items). All three tests had internal consistency that was equal to or exceeded the accepted standard of $\alpha = 0.70$ in educational research studies, ensuring the reliability of the tests used in this study. When considered alongside the expert content validity results described above, these results prove that all three tests were valid and reliable measures of student knowledge of genetics.

Table 4.2 Reliability Analysis of Knowledge Assessments

Assessment	Number of Items	Cronbach's Alpha (α)	Interpretation
Pre-test	14	0.78	Acceptable
Post-test Theory	18	0.84	Good
Post-test Lab	12	0.82	Good

4.2 Impact of Case-Based Learning on Academic Performance in Genetics

The first step in exploring if there was a significant effect of CBL on performance was to run one-way ANCOVA tests for each of the four post-test measures that corresponded to each particular case. In every test, post-test measure was used as a dependent variable, instructional method as a fixed variable, while each respective pre-test was used as a covariate.

4.2.1 Assumption checks

Before conducting any analysis of covariance, the assumptions were checked. The normality of residuals in each condition was tested using the Shapiro-Wilk test and QQ

plots. Homogeneity of variances was tested using the Levene's test. The assumption of homogeneity of regression slopes, where the association between the covariate and the dependent variable is the same across all groups, was tested using the interaction term between condition and the pretest.

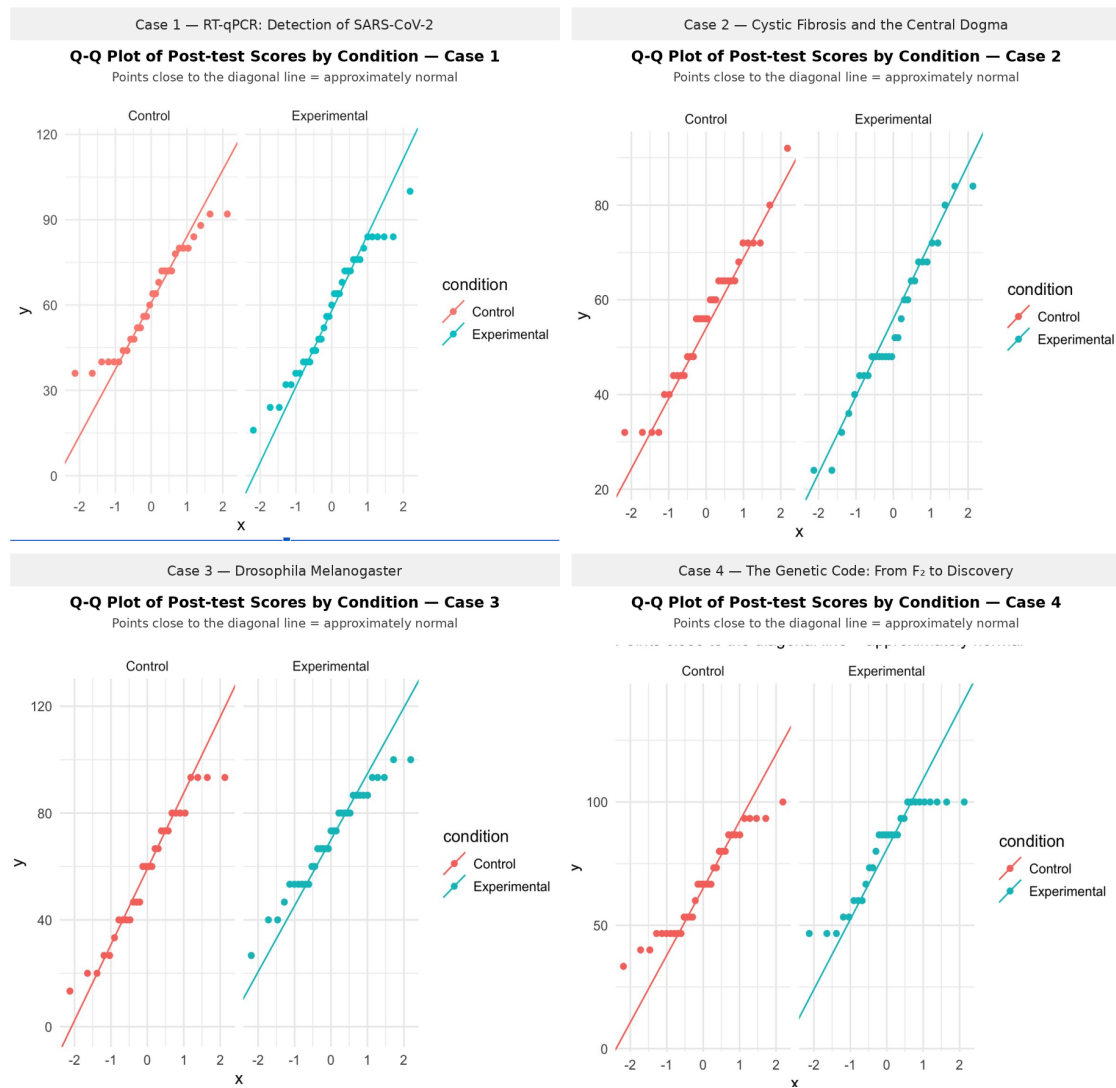
Table 4.3 Normality test: Shapiro- wilk

Cases	Method	W statistics	P value
Case 1	Control	0.935	0.0664
	Experimental	0.964	0.303
Case 2	Control	0.962	0.281
	Experimental	0.964	0.397
Case 3	Control	0.947	0.142
	Experimental	0.963	0.283
Case 4	Control	0.935	0.0398
	Experimental	0.856	0.000814

Post-test scores' normality for each condition was tested using Shapiro-Wilk normality test and visual inspection through Q-Q plots, shown in Figure 4.1. In Case 1, there was no significant deviation from normality found in the Control group ($W=0.935$, $p=0.066$) and the Experimental group ($W=0.964$, $p=0.303$). Likewise, in Case 2, there was evidence of normality of distribution in both Control ($W=0.962$, $p=0.281$) and Experimental ($W=0.964$, $p=0.397$) groups. The same applies to Case 3 where there was also support for the normality assumption in the Control group ($W=0.947$, $p=0.142$) and the Experimental group ($W=0.963$, $p=0.283$). In Case 4, on the other hand, the Control group displayed borderline results ($W=0.935$, $p=0.040$), while in the Experimental group there was an apparent significant deviation from normality ($W=0.856$, $p<0.001$). From the visual inspection using Q-Q plots, it could

be observed that points were almost aligned along the diagonal line in Cases 1-3 for both Control and Experimental groups, but for the Experimental group in Case 4, deviation was observed, which could be partially explained by ceiling effect occurring in the Experimental group at 100%. Therefore, the results of the ANCOVA analysis should be cautiously interpreted for Case 4.

Figure 4.1 Q-Q Plots of Post test Scores by Condition



The assumption of homogeneity of variance was tested using Levene's Test for Equality of Variances (refer to Table 4.4). The findings revealed that the assumption held true for all the four cases: Case 1, $F(1, 63) = 1.185$, $p = 0.281$; Case 2, $F(1, 62) =$

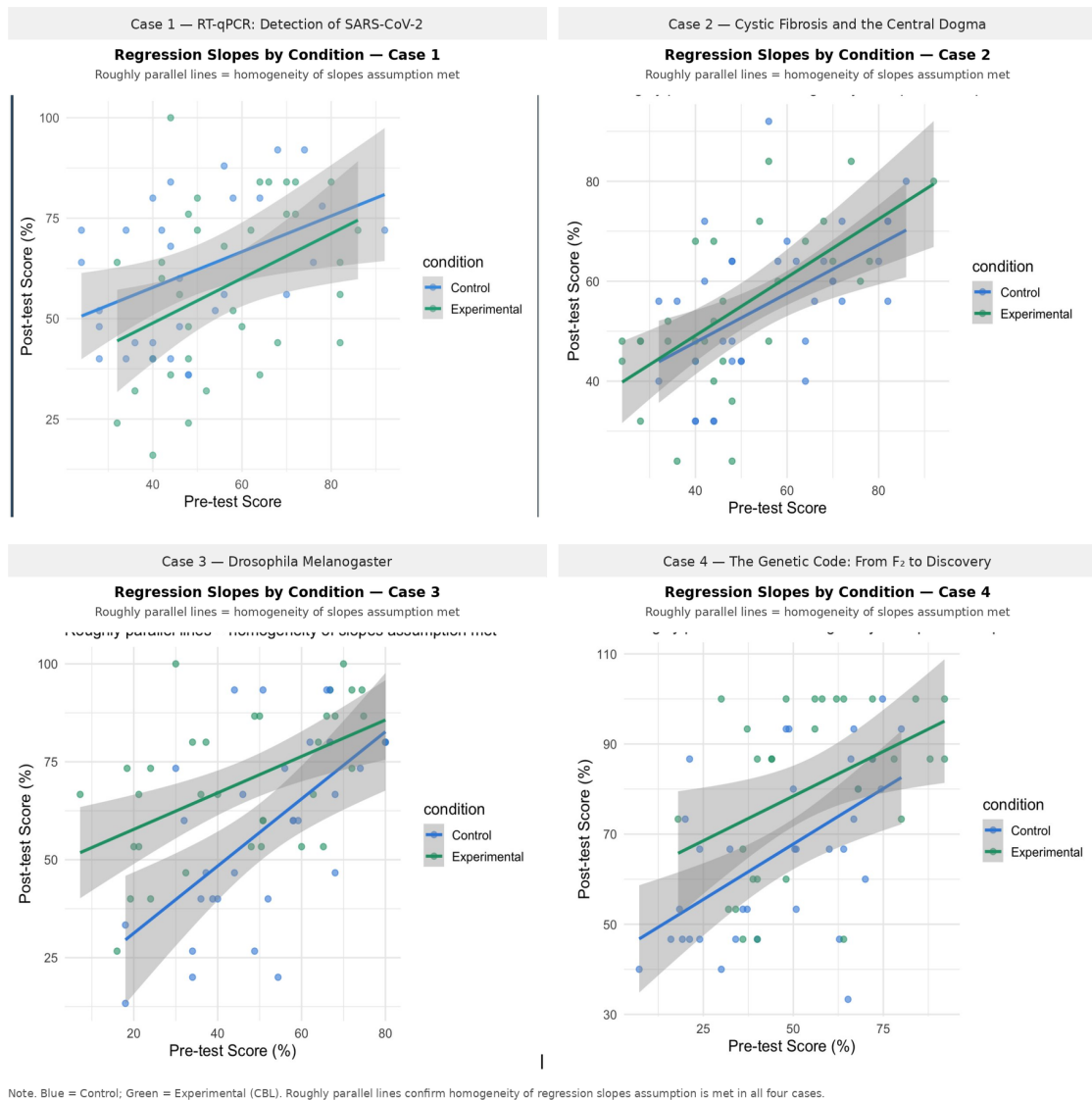
0.186, $p = 0.668$; Case 3, $F(1, 63) = 2.961$, $p = 0.090$; Case 4, $F(1, 63) = 0.099$, $p = 0.754$. Despite Case 3 obtaining a borderline significance level ($p = 0.090$), it remained above the conventional threshold of $\alpha = 0.05$, indicating that the variances between the CBL and control groups were not statistically significantly different.

Table 4.4 Homogeneity of Variance: Levene's Test Results Across All Four Cases

Case	df1	df2	F value	p value
Case 1	1	63	1.185	0.281
Case 2	1	62	0.186	0.668
Case 3	1	63	2.961	0.090
Case 4	1	63	0.099	0.754

The second assumption tested, the homogeneity of regression slopes, is based on the assumption that there is a consistent pattern of association between the covariate and post-test score in each instructional condition. Homogeneity of regression slopes is tested in each case using an interaction term between the condition and pre-test covariate variable, as well as a visual test via a plot of regression slopes (see Figure 4.2). It is important to ensure homogeneity of regression slopes as a basis for making sure that the covariate adjustment made by ANCOVA is done equally on all participants so as to ensure that the differences observed between groups are purely due to instructional conditions. The interaction between condition and covariate was not statistically significant in any of the four cases. In addition, as seen from Figure 4.2, the regression lines in the Control and Experimental conditions were parallel in all four cases, with Cases 1 and 2 showing almost identical regression lines between the two groups. Based on these results, homogeneity of regression slopes can be seen to have been satisfied in all cases, making ANCOVA valid as the analysis tool in these cases.

Figure 4.2 Regression Slopes by Condition



4.2.2 Case 1 Results: RT-qPCR - Detection of SARS-CoV-2

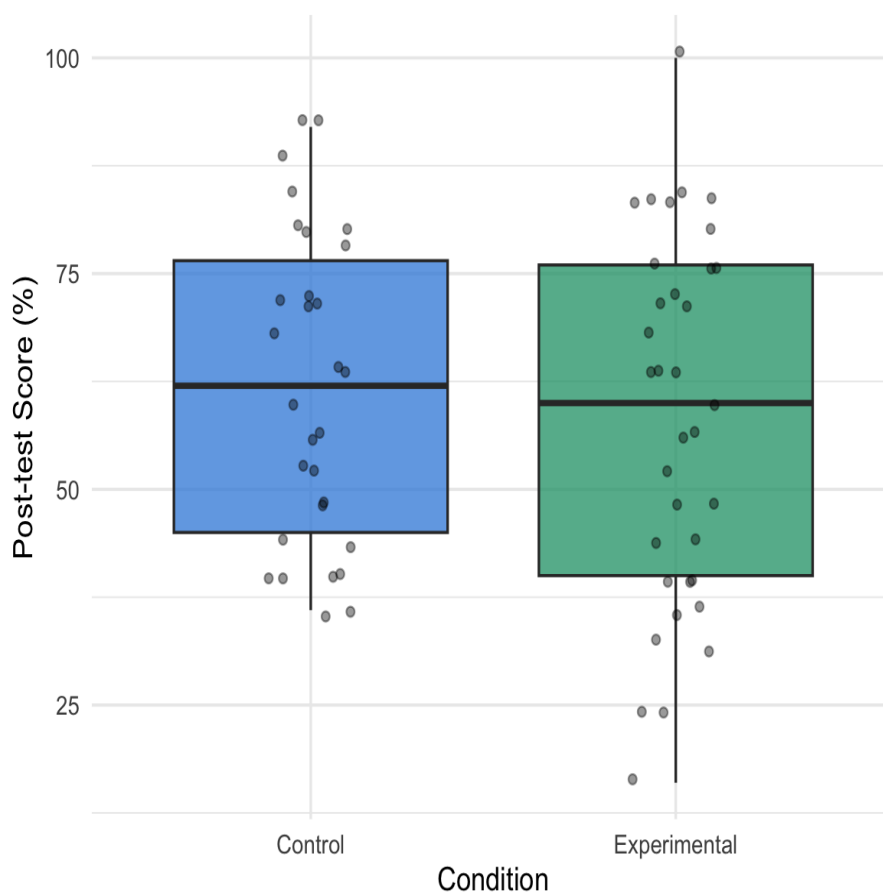
The descriptive statistics related to Case 1 are outlined in Table 4.3. In the control group 30 participants, whereas in the experimental group 35 participants. In relation to the pretest results, there was found to be a significant difference between the control and the experimental group, as the latter performed better ($M = 56.5\%$, $SD = 15.6$) compared to the former ($M = 48.8\%$, $SD = 17.5$). In the case of the post-test, the results were found to be as follows: $M = 61.7\%$ ($SD = 17.8$, min-max: 36–92%) for the control group and $M = 58.1\%$ ($SD = 21.3$, min-max: 16–100%) for the experimental group. The distribution of post test results is demonstrated in Figure 4.5 below.

Table 4.5 Descriptive Statistics - Case 1: RT-qPCR: Detection of SARS-CoV-2

Condition	n	Pre-test Mean	Pre-test SD	Post-test Mean	Post-test SD	Post-test Min	Post-test Max
Control (Traditional)	30	48.8	17.5	61.7	17.8	36	92
Experimental (CBL)	35	56.5	15.6	58.1	21.3	16	100

Note. Pre-test and post-test scores are expressed as percentages. SD = standard deviation.

Figure 4.3 Distribution of Post-test Scores by Condition - Case 1: RT-qPCR: Detection of SARS-CoV-2



A one-way ANCOVA was carried out to test for any effect of instruction on post-test achievement, with the pre-test score used as the covariate. Full ANCOVA findings are displayed in Table 4.6. Pre-test covariates were found to be statistically significant predictors of post-test achievement, $F(1, 62) = 12.983$, $p < 0.001$, partial $\eta^2 = 0.15$, which demonstrated that the pre-test score played a significant role in predicting the post-test scores, thereby supporting the inclusion of pre-test score as a covariate. However, after accounting for any variations due to pre-test score, the impact of instruction was not statistically significant, $F(1, 62) = 2.573$, $p = 0.114$.

Table 4.6 ANCOVA Results for Case 1: RT-qPCR: Detection of SARS-CoV-2

Source	Sum of Squares	df	F value	p value
(Intercept)	8075.40	1	24.578	< 0.001***
Pre-test (covariate)	4265.73	1	12.983	< 0.001***
Condition (CBL vs. Traditional)	845.29	1	2.573	0.114
Residuals	20370.82	62	—	—

Note. Significance codes: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

According to Table 4.7 η^2 of the condition factor was 0.04 (95% confidence interval [0.00, 1.00]), which is regarded as a small effect size based on Cohen's (1988) standards. This implies that instructional conditions accounted for about 4% of the total variation in test scores after considering prior knowledge. Although this finding is not statistically significant, the positive value of the effect size provides evidence of a meaningful practical effect that cannot be detected by the current sample size. The pre-test covariate had a large effect size ($\eta^2 = 0.15$, 95% confidence interval [0.05, 1.00]) compared to the condition factor, indicating the strong influence of prior knowledge

on test scores. Taken together, these effect size estimates confirm that prior knowledge was the dominant predictor of post-test performance in Case 1.

Table 4.7 Partial Effect Sizes (η^2) - Case 1: RT-qPCR: Detection of SARS-CoV-2

Source	Partial η^2	95% CI	Interpretation
Pre-test (covariate)	0.15	[0.05, 1.00]	Large
Condition (CBL vs. Traditional)	0.04	[0.00, 1.00]	Small

Note. Effect size benchmarks follow Cohen (1988): small = 0.01, medium = 0.06, large = 0.14.

The estimated marginal means, having accounted for pre-test scores presented in Table 4.8. After statistically controlling for prior knowledge, the Control group obtained an adjusted post-test mean score of 63.7% (SE = 3.36, 95% CI = [57.0, 70.4]), while the Experimental CBL group achieved a mean of 56.3% (SE = 3.10, 95% CI = [50.1, 62.5]). Despite the apparent numerical advantage of the Control group, this difference did not reach statistical significance ($t(62) = 1.604$, $p = 0.114$), as evidenced by the overlapping confidence intervals between the two conditions. It is important to note that the non-significant result does not necessarily indicate that CBL was ineffective in Case 1; rather, the small effect size ($\eta^2 = 0.04$) suggests that the current sample size may have been insufficient to detect a meaningful difference. Furthermore, the Experimental group entered Case 1 with a higher pre-test mean (56.5%) compared to the Control group (48.8%), meaning that ceiling effects may have partially limited the relative gains achievable by CBL students after statistical adjustment. These results should therefore be interpreted cautiously, as the absence of statistical significance in Case 1 may reflect contextual and methodological constraints rather than a true absence of CBL effect. Taken together, the adjusted means and overlapping confidence intervals indicate that CBL and traditional instruction produced comparable post-test outcomes in Case 1 once prior knowledge differences were accounted for.

Table 4.8 Adjusted Means and Pairwise Comparison - Case 1: RT-qPCR: Detection of SARS-CoV-2

Condition	Adjusted Mean	SE	df	95% CI	Mean Difference	t ratio	p value
Control (Traditional)	63.7%	3.36	62	[57.0, 70.4]	+7.43	1.604	0.114
Experimental (CBL)	56.3%	3.10	62	[50.1, 62.5]	—	—	—

Note. Adjusted means control for pre-test scores. Mean difference reflects Control minus Experimental. The non-significant result ($p = 0.114$) indicates the 7.43-point advantage of the Control group did not reach statistical significance after controlling for prior knowledge.

Figure 4.4 Individual Student Score Trajectories from Pre-test to Post-test by Condition - Case 1: RT-qPCR: Detection of SARS-CoV-2

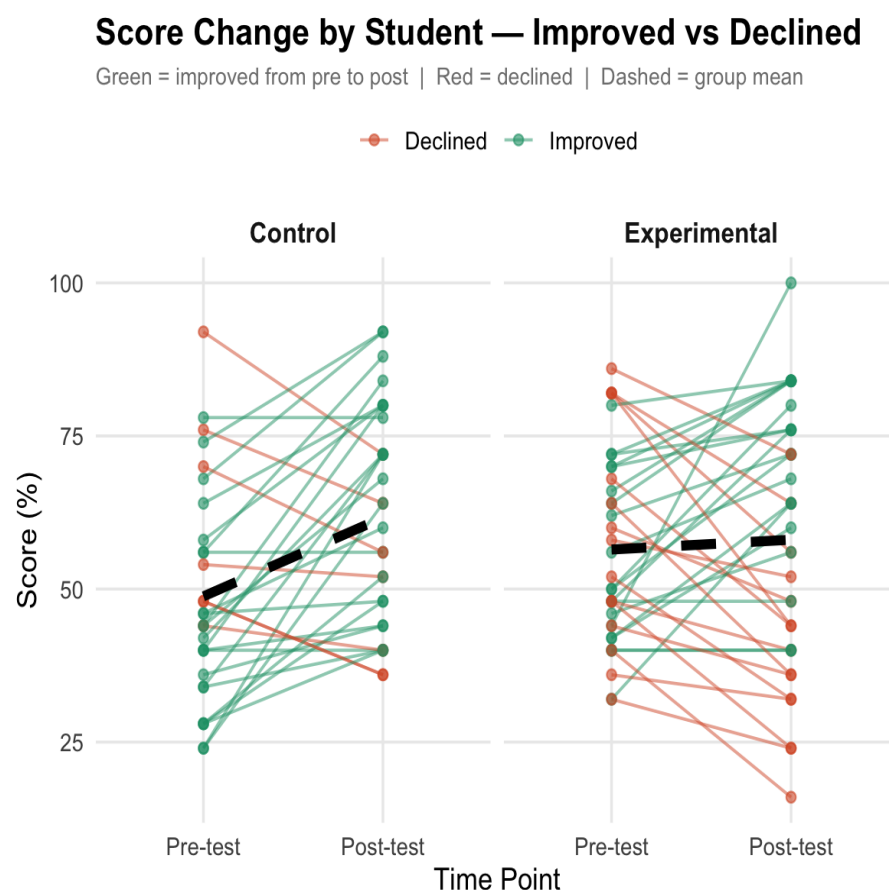


Figure 4.4 presents the results of each student's score progression from pre-test to post-test for each instructional method. For the Control group, most students made gains between their pre- and post-test scores, and overall the group average score increased from about 48.8% to 61.7%. For the Experimental group, however, there was more heterogeneity, including a proportion of students that decreased in their post-test scores compared to their pre-test scores, accounting for the greater variability seen in the post-test results. This variation among participants within the CBL group indicates that some were able to gain more out of the experience than others, perhaps due to their level of preparation, engagement with the information, or understanding of the case-based learning experience.

Overall, Case 1 had no statistically significant impact on the two instructional methods under analysis. While after controlling for the pre-test effect, the Control group scored an additional 7.43 percentage points higher than the CBL group on the post-test, this finding was not significant at all ($p = 0.114$) and the effect size was small, with partial η^2 of only 0.04. Prior knowledge was found to be the main predictor of post-test performance and individual trajectory plots indicated that CBL conditions featured much higher variability. Overall, it seems that in the first case of the semester, students were still learning the case-based format, a trend that will be analyzed in subsequent cases.

4.2.3 Case 2 Results: Cystic Fibrosis - The Central Dogma

Statistical description of case study number two can be seen in Table 4.9. There were 34 respondents in the Control group and 30 in the Experimental group. In the pre-test, the Control group had a higher pre-test average mark ($M=56.6\%$, $SD=15.8$) than the Experimental group ($M=48.8\%$, $SD=17.5$), meaning there was an existing difference in their prior knowledge in favor of the Control group. For the post-test, the Control group scored an average of 55.9% ($SD=14.6$; Range: 32-92%), while the Experimental group got a mark average of 54.3% ($SD=15.9$; Range: 24-84%). Their distribution of scores for the post-test is shown in Figure 4.5. Both groups had an

almost similar interquartile range, although the Experimental group's distribution is slightly wider compared to the Control group.

Table 4.9 Descriptive Statistics -Case 2: Cystic Fibrosis and the Central Dogma

Condition	n	Pre-test Mean	Pre-test SD	Post-test Mean	Post-test SD	Post-test Min	Post-test Max
Control (Traditional)	34	56.6	15.8	55.9	14.6	32	92
Experimental (CBL)	30	48.8	17.5	54.3	15.9	24	84

Note. Pre-test and post-test scores are expressed as percentages. SD = standard deviation.

Figure 4.5 Distribution of Post-test Scores by Condition - Case 2: Cystic Fibrosis and the Central Dogma

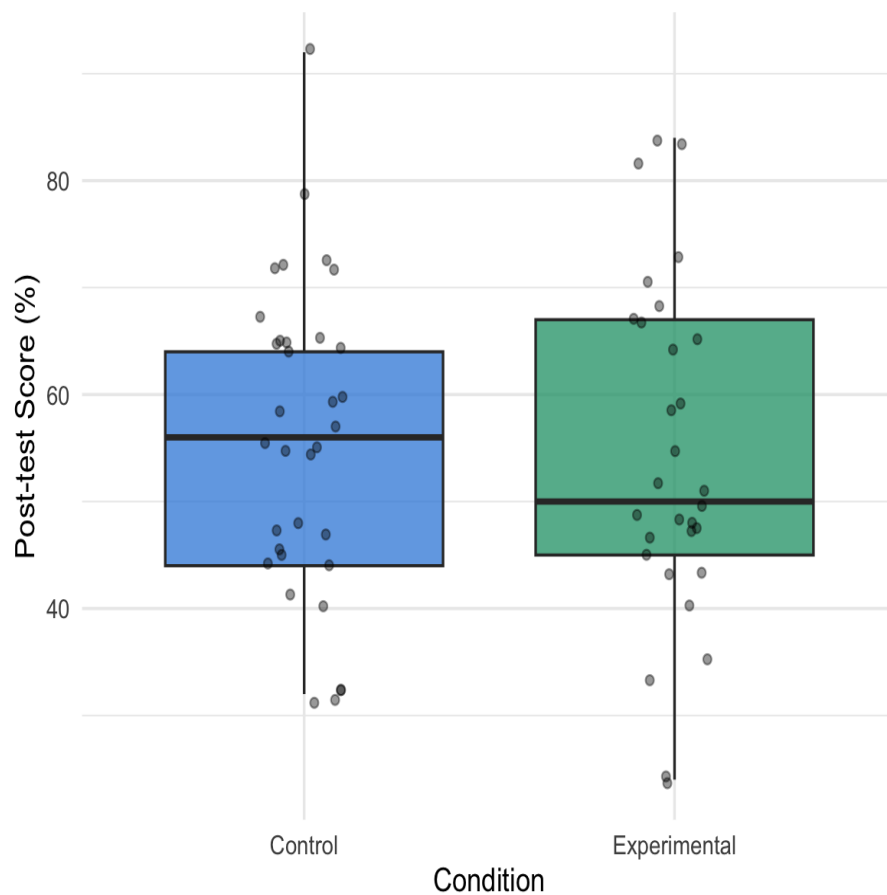


Table 4.10 ANCOVA Results - Case 2: Cystic Fibrosis and the Central Dogma

Source	Sum of Squares	df	F value	p value
(Intercept)	2998.49	1	19.314	< 0.001***
Pre-test (covariate)	4935.30	1	31.790	< 0.001***
Condition (CBL vs. Traditional)	99.46	1	0.641	0.427
Residuals	9470.10	61	—	—

Note. Significance codes: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

One way ANCOVA test was done using post test score as the outcome, instructional condition as the fixed factor, and pre test score as the covariate. The results are shown in Table 4.10. Pre-test was a highly significant predictor of post test scores, $F(1,61) = 31.790$, $p < 0.001$, partial $\eta^2 = 0.34$, where pre test accounted for 34% of the variation in the post test – an increase from the percentage obtained in Case 1. Instructional condition did not predict post test performance, $F(1,61) = 0.641$, $p = 0.427$.

Table 4.11 Partial Effect Sizes (η^2) - Case 2: Cystic Fibrosis and the Central Dogma

Source	Partial η^2	95% CI	Interpretation
Pre-test (covariate)	0.34	[0.19, 1.00]	Large
Condition (CBL vs. Traditional)	0.01	[0.00, 1.00]	Negligible

Note. Effect size benchmarks follow Cohen (1988): small = 0.01, medium = 0.06, large = 0.14.

According to Table 4.11, partial η^2 for the condition factor was 0.01 (95% CI [0.00, 1.00]), which is equivalent to a negligible effect size. This means that the instructional condition accounted for merely 1% of the variation in the post-test score

after controlling for prior knowledge, suggesting that the choice between CBL and traditional instruction had virtually no practical impact on student performance in Case 2. Pre-test was found to be a significant contributor to the post-test score, showing a large effect size of 0.34 (95% CI [0.19, 1.00]), which indicates that students' prior knowledge was by far the strongest predictor of their post-test achievement in this case.

Table 4.12 Adjusted Means and Pairwise Comparison - Case 2: Cystic Fibrosis and the Central Dogma

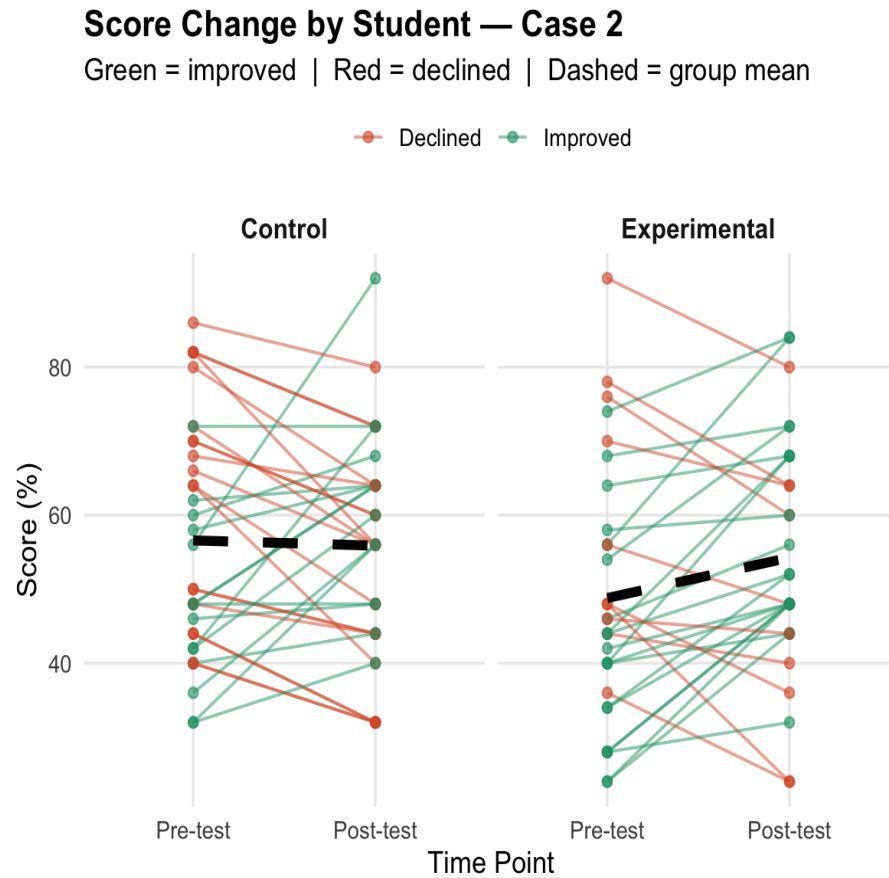
Condition	Adjusted Mean	SE	df	95% CI	Mean Difference	t ratio	p value
Control (Traditional)	53.9%	2.16	61	[49.6, 58.3]	-2.57	-0.800	0.427
Experimental (CBL)	56.5%	2.31	61	[51.9, 61.1]	—	—	—

Note. Adjusted means control for pre-test scores. Mean difference reflects Control minus Experimental. Negative value indicates CBL group scored marginally higher.

Adjusted means, taking into account pre-test scores, can be seen in Table 4.12 above. Once the covariates were controlled for, the Experimental CBL group showed a slightly higher adjusted mean score ($M = 56.5\%$, $SE = 2.31$, 95% CI [51.9, 61.1]) compared to the Control group ($M = 53.9\%$, $SE = 2.16$, 95% CI [49.6, 58.3]). This is in contrast to Case 1 in which the Control group had performed better. The difference in mean scores between the groups was 2.57, which was not statistically significant, $t(61) = -0.800$, $p = 0.427$.

Figure 4.6 depicts individual student scores' trajectory changes from pre- to post-test in both conditions. In the Control condition, the mean for the group remained almost stable across the two measurement occasions, with an almost equal number of students having either increased or decreased. In the Experimental condition, there was a slight increase in the group mean; however, this is not devoid of individual variability, since many students declined from pre- to post-test while others improved. Both groups exhibited a high level of heterogeneity among individual changes in their scores.

Figure 4.6 Individual Student Score Trajectories from Pre-test to Post-test by Condition - Case 2: Cystic Fibrosis and the Central Dogma



Overall, it can be concluded that Case 2 showed no statistical difference between the two groups based on prior knowledge ($p = 0.427$; partial $\eta^2 = 0.01$). The adjusted mean difference was relatively small, at 2.57 points, and contrary to Case 1, favored the experimental group somewhat. The main contributor to post-test score differences was students' prior knowledge, which accounted for 34% of variability. A very low effect size ($\eta^2 = 0.01$) suggests that the instructional condition had no meaningful effect on the post-test performance in Case 2, making it the least effective example of CBL out of all four cases. Finally, overlap of confidence intervals for both conditions (Control Group – 57.8%, 95% CI; Experimental Group – 60.4%, 95% CI) once again confirms that after taking into account prior knowledge, the groups were performing equally. In this regard, findings in Case 2 correspond with those in Case 1, confirming no academic advantage of theory-based CBL used at an early stage of a semester.

4.2.4 Case 3 Results: From the Wild to the Mutant - *Drosophila Melanogaster*

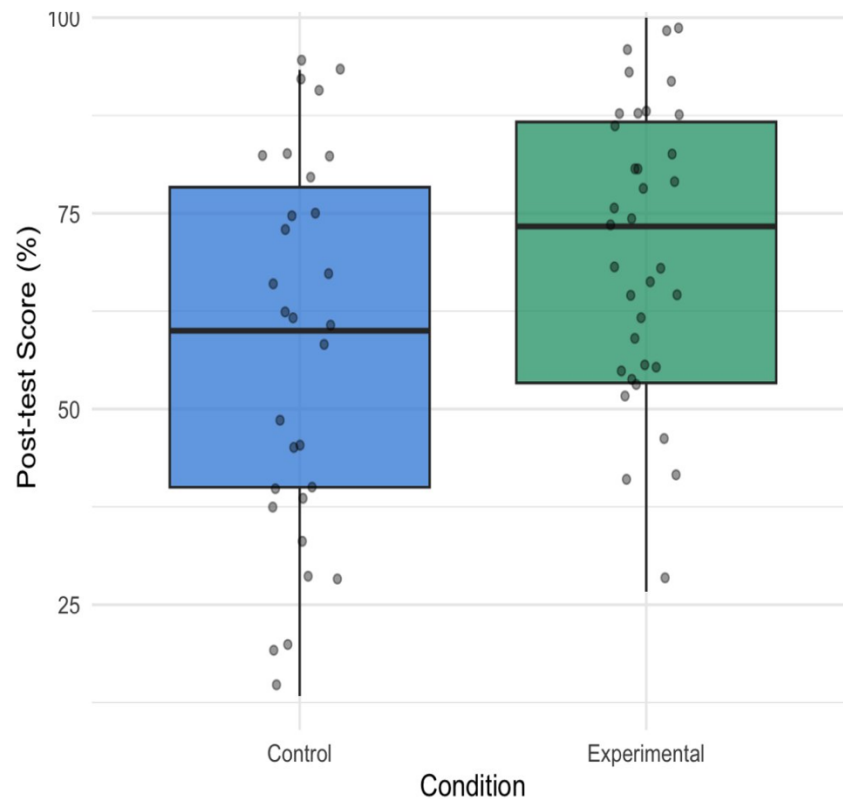
The descriptive statistics of Case 3 are provided in Table 4.13. The Control group contained 30 participants, whereas the Experimental group consisted of 35 participants. As seen from Table 4.13, at the pre-test stage of the experiment, the participants' means were almost equal for both groups, with the Control group having a slightly higher pre-test mean value ($M = 50.69\%$, $SD = 16.82$) compared to the Experimental group ($M = 46.93\%$, $SD = 21.19$), reflecting a relatively small gap in prior knowledge between the two conditions at baseline. On the post-test, however, there was a noticeable distinction in the groups' post-test results, with the Experimental CBL group obtaining a much higher mean score ($M = 70.29\%$, $SD = 18.39$) than the Control group ($M = 57.56\%$, $SD = 24.16$). The mean difference between the groups amounted to 12.73 percentage points and was the largest among all four cases. It is also notable that the Experimental group entered Case 3 with a lower pre-test mean than the Control group, yet achieved a considerably higher post-test mean. Furthermore, the wider standard deviation in the Control group ($SD = 24.16$) relative to the Experimental group ($SD = 18.39$) points to greater heterogeneity in learning outcomes under traditional instruction compared to the more consistent performance observed in the CBL condition. The distribution of post-test scores is visualized in Figure 4.7 below.

*Table 4.13 Descriptive Statistics - Case 3: From the Wild to the Mutant: *Drosophila Melanogaster**

Condition	n	Pre-test Mean	Pre-test SD	Post-test Mean	Post-test SD	Post-test Min	Post-test Max
Control (Traditional)	30	50.69	16.82	57.56	24.16	13.33	93.33
Experimental (CBL)	35	46.93	21.19	70.29	18.39	26.67	100.00

Note. Pre-test and post-test scores are expressed as percentages. SD = standard deviation.

Figure 4.7 Distribution of Post-test Scores by Condition - Case 3: From the Wild to the Mutant: Drosophila Melanogaster



A one-way ANCOVA was performed with the post-test score as the dependent variable, instructional condition as the fixed factor, and pre-test score as the covariate. The covariate pre-test significantly predicted the post-test scores, $F(1, 62) = 26.499$, $p < 0.001$, partial $\eta^2 = 0.27$, showing that prior knowledge made a substantial contribution to the variation in outcomes. Significantly, after controlling for differences at pre-test levels, the instructional condition significantly affected the outcome, $F(1, 62) = 11.204$, $p = .001$, representing the first statistically significant influence of CBL on post-test scores among the four cases. The medium-to-large effect size associated with the condition factor ($\eta^2 = 0.15$) indicates that instructional condition accounted for approximately 15% of the variance in post-test scores after controlling for prior knowledge. This result marks a notable and statistically reliable difference between the CBL and traditional instruction groups in the laboratory-based Case 3, confirming that the two instructional approaches produced meaningfully different academic outcomes in this context. See Table 4.14 below for complete findings

Table 4.14 ANCOVA Results - Case 3: From the Wild to the Mutant: Drosophila Melanogaster

Source	Sum of Squares	df	F value	p value
(Intercept)	5112.60	1	15.915	< 0.001***
Pre-test (covariate)	8512.38	1	26.499	< 0.001***
Condition (CBL vs. Traditional)	3599.12	1	11.204	0.001**
Residuals	19916.61	62	—	—

Note. Significance codes: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

Table 4.15 Partial Effect Sizes (η^2) - Case 3: From the Wild to the Mutant: Drosophila Melanogaster

Source	Partial η^2	95% CI	Interpretation
Pre-test (covariate)	0.27	[0.13, 1.00]	Large
Condition (CBL vs. Traditional)	0.15	[0.04, 1.00]	Large

Note. Effect size benchmarks follow Cohen (1988): small = 0.01, medium = 0.06, large = 0.14.

According to Table 4.15 the partial η^2 for the condition factor was 0.15 (95% confidence interval [CI] [0.04, 1.00]), which is considered a large effect size based on Cohen's (1988) criteria. This suggests that instructional condition explained about 15% of the variability in post-test performance scores after accounting for prior knowledge

- which is equivalent to the pre-test effect size from Case 1 and larger than those found in Cases 1 and 2. The pre-test factor showed a large effect size (partial $\eta^2 = 0.27$, 95% CI [0.13, 1.00]) as well.

Table 4.16 Adjusted Means and Pairwise Comparison - Case 3: From the Wild to the Mutant: Drosophila Melanogaster

Condition	Adjusted Mean	SE	df	95% CI	Mean Difference	t ratio	p value
Control (Traditional)	56.3%	3.28	62	[49.8, 62.9]	-15.00	-3.347	0.001
Experimental (CBL)	71.3%	3.04	62	[65.3, 77.4]	—	—	—

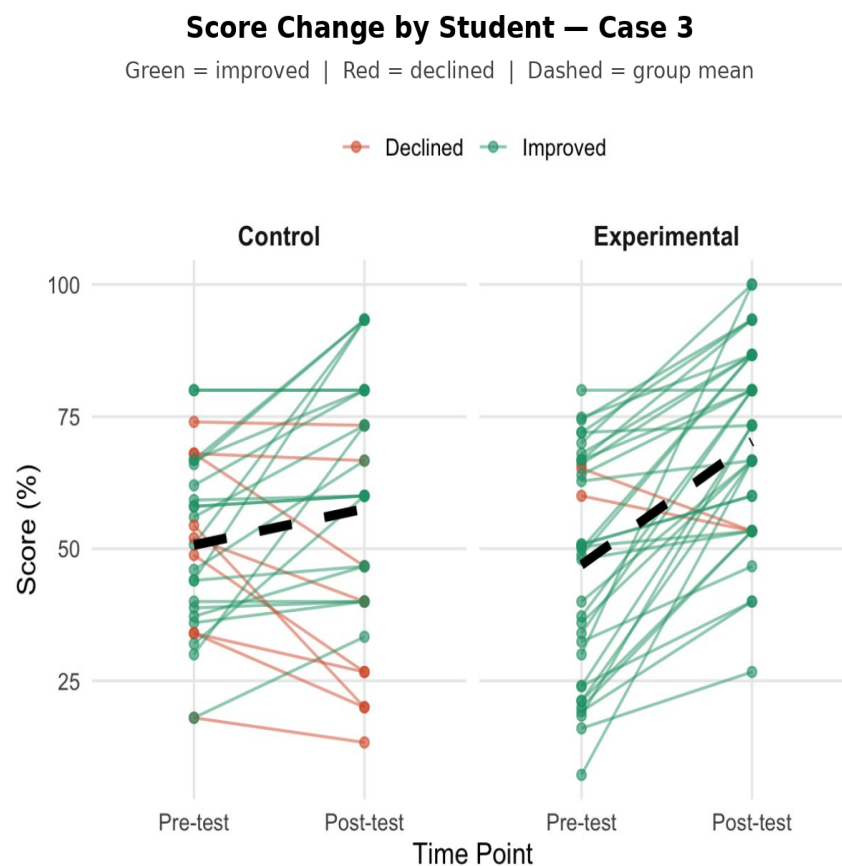
Note. Adjusted means control for pre-test scores. Mean difference reflects Control minus Experimental. Negative value indicates CBL group scored significantly higher.

The adjusted means, taking into account the effects of pre-test scores as covariates, can be seen in Table 4.16 above. Post-test results, after adjusting for the initial levels of knowledge of the subjects, showed that the Experimental CBL group outperformed the Control group significantly ($M = 71.3\%$, $SE = 3.04$, 95% CI [65.3, 77.4] compared to $M = 56.3\%$, $SE = 3.28$, 95% CI [49.8, 62.9]), with overlapping confidence intervals further confirming the differences between the groups' post-test scores. Indeed, a gap of 15 percentage points in favor of the CBL group emerged, which was found to be statistically significant, $t(62) = -3.347$, $p = 0.001$. This indicates that the CBL group scored better than the Control group, meaning that the CBL instruction yielded significant benefits as compared to the traditional teaching method in this context.

The score trajectories for individual students before and after the test from Figure 4.8 show how individual performance changed in both groups over time. In the Control condition, the trajectory trend was mixed – even though there was an observable upward trend in the mean score, many students scored lower after than

before the test, and the post-test distribution was relatively wide. By contrast, the Experimental CBL condition had a more consistent trend – most trajectories were green (showing improvement), the mean improved noticeably between tests, and fewer students showed declining scores than in the control condition. The consistent trend observed among individuals in this case is consistent with the ANCOVA finding and the effect size observed in this case.

Figure 4.8 Individual Student Score Trajectories from Pre-test to Post-test by Condition - Case 3: From the Wild to the Mutant: Drosophila Melanogaster



In conclusion, Case 3 yielded a statistically significant improvement due to CBL over traditional instruction, adjusted for prior knowledge, $F(1, 62) = 11.204$, $p = 0.001$, partial $\eta^2 = 0.15$. While the mean post-test score for the CBL group after adjustment was significantly higher, at 71.3%, by 15.0% compared to the mean adjusted post-test score for the control group of 56.3% ($p = 0.001$).

4.2.5 Case 4 Results: The Genetic Code Unfolds - From F₂ to Discovery

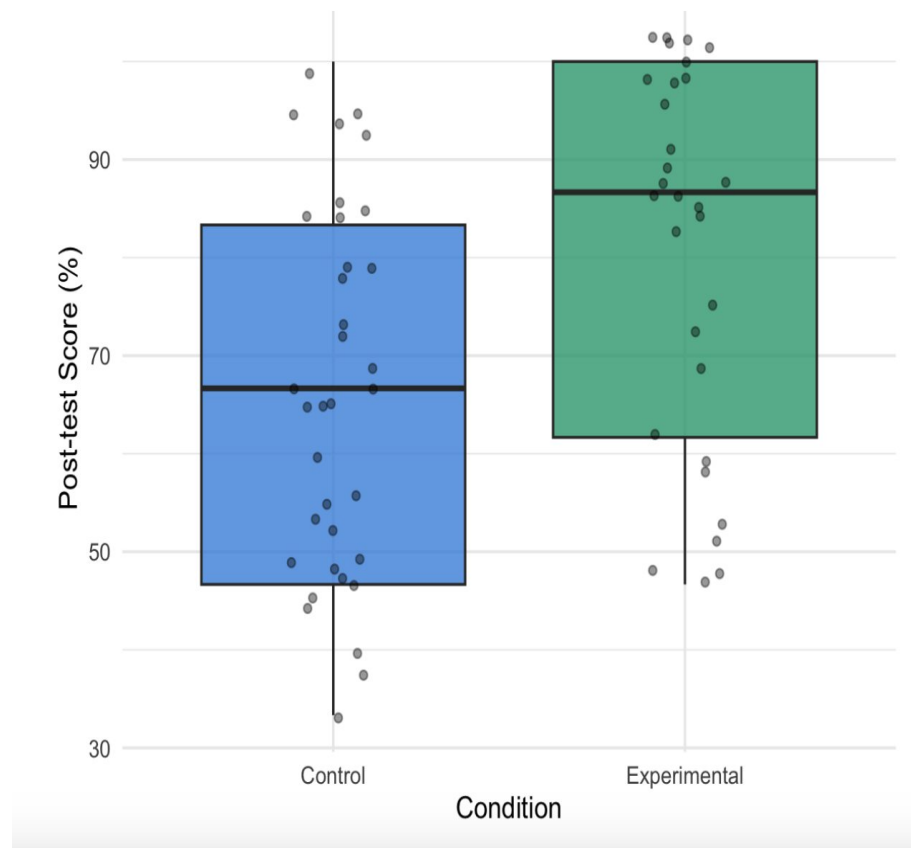
Table 4.17 provides the descriptive statistics for Case 4. The Control group had 35 participants while the Experimental group had 30 participants. The Experimental group exhibited a significantly higher pre-test mean ($M = 55.07\%$, $SD = 20.40$) relative to the Control group ($M = 46.93\%$, $SD = 21.19$). In other words, at the outset of the experiment, there was already an existing gap between the two groups with respect to their levels of prior knowledge where the CBL group had a higher score. On the post-test, the Experimental CBL group attained a significantly higher mean score ($M = 80.44\%$, $SD = 19.01$, range: 46.67–100%) relative to the Control group ($M = 66.29\%$, $SD = 18.99$, range: 33.33–100%). In other words, the mean difference between the scores of the two groups was 14.15 percentage points. Additionally, there was a slight difference between the standard deviations of both groups in the post-test scores where the standard deviation was 19.01 in the experimental group while the other one had a standard deviation of 18.99. Figure 4.9 demonstrates the post-test scores of the two groups wherein it can be observed that the experimental group's interquartile range was noticeably above the Control group

Table 4.17 Descriptive Statistics - Case 4: The Genetic Code Unfolds: From F₂ to Discovery

Condition	n	Pre-test Mean	Pre-test SD	Post-test Mean	Post-test SD	Post-test Min	Post-test Max
Control (Traditional)	35	46.93	21.19	66.29	18.99	33.33	100
Experimental (CBL)	30	55.07	20.40	80.44	19.01	46.67	100

Note. Pre-test and post-test scores are expressed as percentages. SD = standard deviation.

Figure 4.9. Distribution of Post-test Scores by Condition - Case 4: The Genetic Code Unfolds: From F₂ to Discovery



A one-way ANCOVA was conducted with the post-test score as the dependent variable, instructional condition as the fixed factor, and pre-test score as the covariate. Prior to examining the main results, it should be mentioned that the assumption of normal distribution was violated for the Experimental group (Shapiro-Wilk Test for Normality; $W = 0.856$, $p < 0.001$). Nevertheless, it was assumed that a violation of the assumption of normality would not be a major concern in the present case study because the procedure of ANCOVA tends to be robust regarding such an assumption, especially when sample sizes are relatively equal (Field, 2018). The results of ANCOVA are presented in Table 4.18. The pre-test score was found to be a statistically significant covariate, $F(1, 62) = 19.916$, $p < 0.001$, partial $\eta^2 = 0.29$. This means that the effect of prior knowledge accounted for a considerable portion of the variability in post-test scores which is consistent with the results of Cases 1 and 2. Importantly, after

taking into consideration the effect of the covariate, the difference between instructional conditions was found to be statistically significant, $F(1, 62) = 6.169$, $p = 0.016$.

Table 4.18 ANCOVA Results - Case 4: The Genetic Code Unfolds: From F_2 to Discovery

Source	Sum of Squares	df	F value	p value
(Intercept)	18702.47	1	67.358	< 0.001***
Pre-test (covariate)	5529.88	1	19.916	< 0.001***
Condition (CBL vs. Traditional)	1712.83	1	6.169	0.016*
Residuals	17214.68	62	—	—

Note. Significance codes: *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$.

Table 4.19 Partial Effect Sizes (η^2) - Case 4: The Genetic Code Unfolds: From F_2 to Discovery

Source	Partial η^2	95% CI	Interpretation
Pre-test (covariate)	0.29	[0.14, 1.00]	Large
Condition (CBL vs. Traditional)	0.09	[0.01, 1.00]	Medium

Note. Effect size benchmarks follow Cohen (1988): small = 0.01, medium = 0.06, large = 0.14.

Partial η^2 for the condition factor was found to be 0.09 (95% CI [0.01, 1.00]), which corresponds to a medium effect based on Cohen's (1988) criteria. This shows that instructional condition was responsible for 9% of variance in post-test scores after adjusting for prior knowledge. Though less powerful compared to the large effect in case three ($\eta^2 = 0.15$), this medium effect size in case four implies that there is a practically significant superiority of CBL over other conditions. The pre-test factor showed a large effect (partial $\eta^2 = 0.29$, 95% CI [0.14, 1.00]).

Table 4.20 Adjusted Means and Pairwise Comparison - Case 4: The Genetic Code Unfolds: From F₂ to Discovery

Condition	Adjusted Mean	SE	df	95% CI	Mean Difference	t ratio	p value
Control (Traditional)	67.5%*	4.23	62	—	-10.50	-2.484	0.016
Experimental (CBL)	78.0%*	4.23	62	—	—	—	—

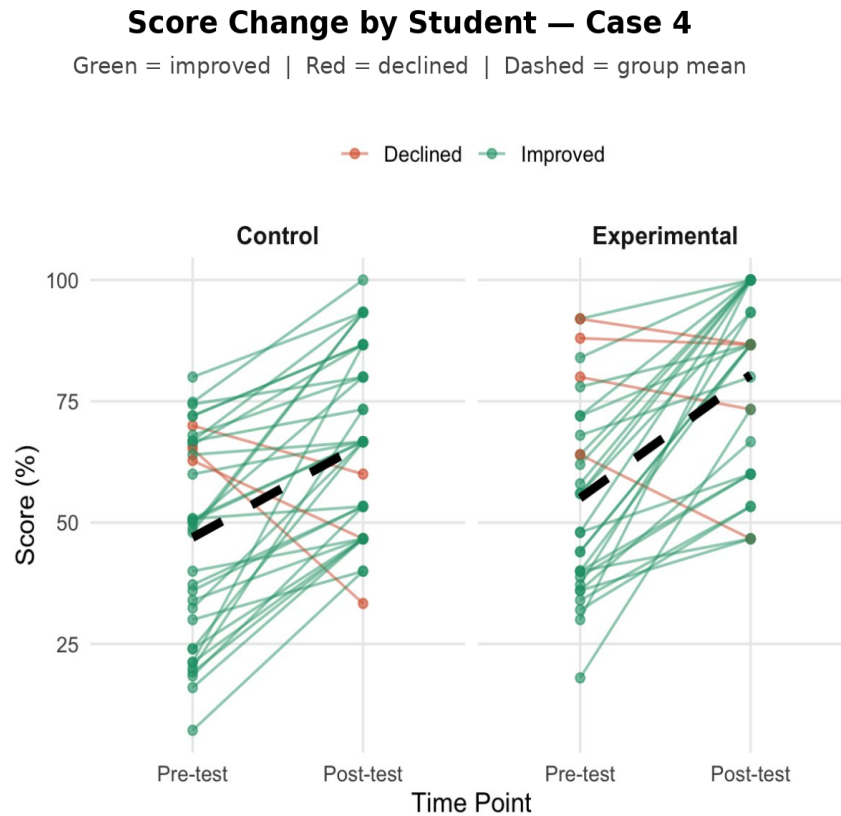
Note. Adjusted means control for pre-test scores. Mean difference reflects Control minus Experimental. Negative value indicates CBL group scored significantly higher.

The adjusted means, taking into account the pre-test scores, are displayed in Table 4.20. As indicated in the table below, the Experimental CBL group had a higher mean score of 78.0% on the post-test than the Control group, which had a mean score of 67.5%. The mean difference between the two groups was 10.5%, and this difference was statistically significant, $t(62) = -2.484$, $p = 0.016$.

Figure 4.10 illustrates individual students' scores' trajectories from pre- to post-test for both groups. In the Control condition, while most students improved their scores from pre- to post-test, some deteriorated, and the average score trajectory in the group revealed a noticeable but not too dramatic upward trend. However, in the Experimental CBL condition, the majority of individual trajectories demonstrated a

very strong tendency toward growth; the group mean grows dramatically from pre- to post-test, and there are few deteriorating trajectories among all participants.

Figure 4.10. Individual Student Score Trajectories from Pre-test to Post-test by Condition - Case 4: The Genetic Code Unfolds: From F₂ to Discovery



To summarize, the current case demonstrated a statistically significant superiority of CBL over traditional teaching techniques when adjusting for prior knowledge, $F(1, 62) = 6.169$, $p = 0.016$, partial $\eta^2 = 0.09$. The post-test mean score adjusted by previous knowledge of students in the experimental CBL group exceeded that of the control group by about 10.5 percent and was statistically significantly different ($p = 0.016$). Thus, the results confirm the significance of the CBL advantage established in Case 3. It may be concluded that, indeed, CBL demonstrates better effects in the later, more complicated cases of the intervention series. The violation of normality in the experimental group is considered the limitation of the present analysis.

4.3 Motivation and Academic Performance Across Instructional Contexts

To examine the relationship between motivation and academic performance across instructional contexts, hierarchical multiple regression analyses were conducted separately for theory-based (Practice Classes: Cases 1 and 2) and lab-based (Lab Classes: Cases 3 and 4) instructional settings. In each analysis, the gain score (post-test minus pre-test) served as the dependent variable, with the pre-test score entered in Block 1 as a covariate to control for prior knowledge, and the four ARCS motivational subscales (Attention, Relevance, Confidence, and Satisfaction) entered in Block 2 as predictors.

4.3.1 Assumptions checks

Before conducting the hierarchical regression analyses, the key statistical assumptions of both models were systematically examined to ensure the validity of the results. Multicollinearity was assessed through the Variance Inflation Factors (VIF) for all predictors, as presented in Table 4.21.

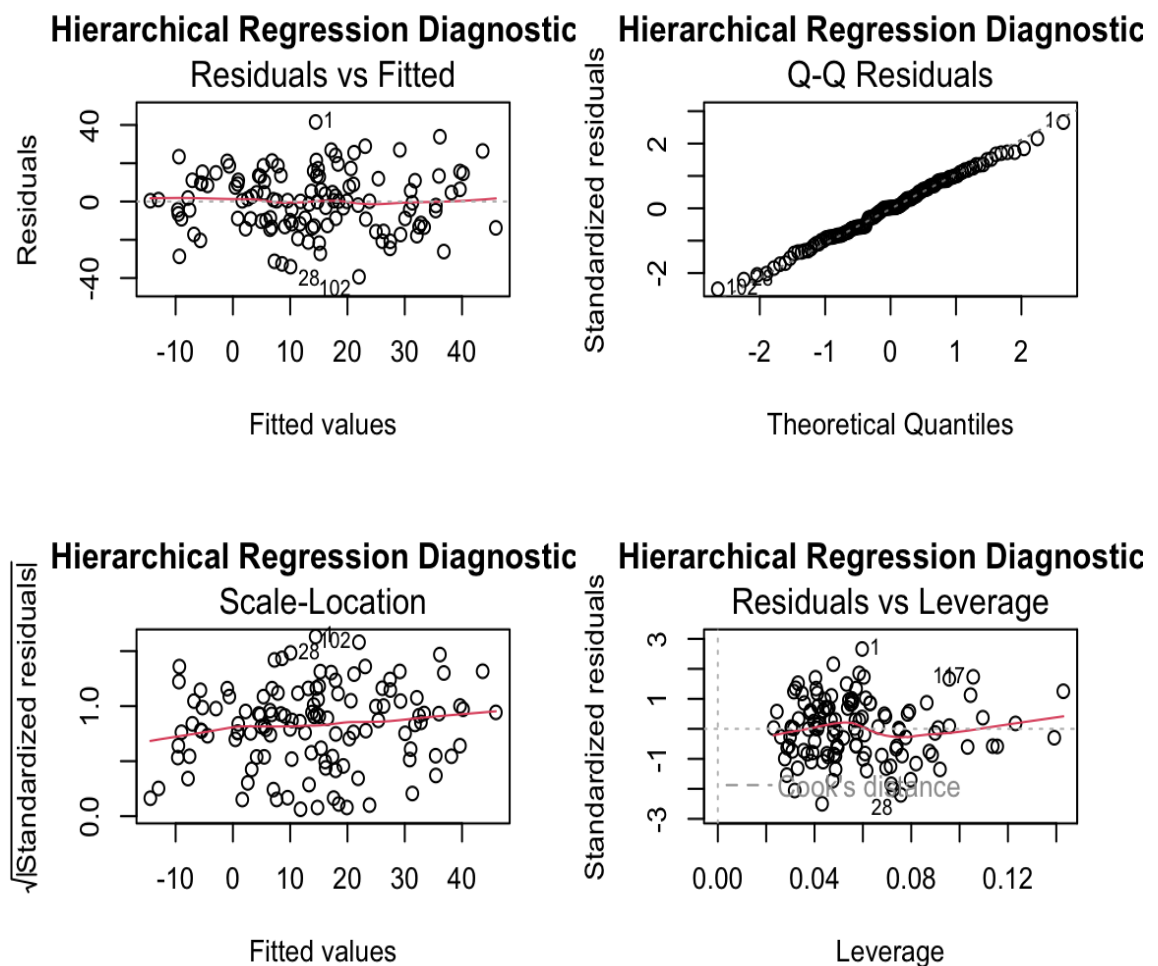
Table 4.21 Multicollinearity Diagnostics - Variance Inflation Factors (VIF)

Predictor	Practice Model VIF	Lab Model VIF
Pre-test	1.13	1.07
Attention	4.60	4.51
Relevance	6.61	6.59
Confidence	3.11	2.88
Satisfaction	4.23	4.32

Note. VIF values below 10 are generally considered acceptable. The elevated VIF for Relevance indicates moderate multicollinearity with other ARCS subscales, which should be considered when interpreting individual subscale coefficients

All VIF values fell below the commonly accepted threshold of 10 (Hair et al., 2019). The pre-test covariate demonstrated minimal multicollinearity in both the Practice model ($VIF = 1.13$) and the Lab model ($VIF = 1.07$), confirming its independence from the motivational predictors. Among the ARCS subscales, Attention ($VIF = 4.60; 4.51$), Confidence ($VIF = 3.11; 2.88$), and Satisfaction ($VIF = 4.23; 4.32$) all returned acceptable values, while Relevance recorded the highest VIF values across both models ($VIF = 6.61; 6.59$), reflecting moderate multicollinearity with the other ARCS subscales.

Figure 4.11 *Hierarchical Regression Diagnostic Plots - Combined Model*



Note. Top left: Residuals vs Fitted - points scattered randomly around zero indicating linearity and homoscedasticity. Top right: Q-Q plot of standardized residuals - points track closely along the diagonal confirming approximate normality of residuals. Bottom left: Scale-Location plot - relatively horizontal trend line indicates homoscedasticity. Bottom right: Residuals vs Leverage - no points exceed Cook's distance threshold, indicating no highly influential outliers.

Regression diagnostic plots for the combined model are presented in Figure 4.11 and provide visual confirmation that the core assumptions of linear regression were adequately met. The Residuals vs. Fitted plot displayed a random scatter of residuals around zero with no discernible pattern. The normal Q-Q plot of standardized residuals revealed that the points tracked closely along the diagonal reference line, confirming approximate normality of residuals. The Scale-Location plot showed a relatively horizontal trend line across the range of fitted values. Finally, the Residuals vs. Leverage plot indicated that no data points exceeded Cook's distance threshold.

4.3.2 Hierarchical Regression Results Across Instructional Contexts

Table 4.22 presents descriptive statistics based on case types. There were almost equal pre-test means for both groups (Practice group (Cases 1 and 2): $M = 13.30$; Lab group (Cases 3 and 4): $M = 13.20$). Furthermore, the four sub-scales of ARCS motivation had almost equivalent mean values in both groups, i.e., Attention ~ 3.77 - 3.78 , Relevance ~ 3.90 - 3.91 , Confidence ~ 3.62 - 3.63 , and Satisfaction ~ 4.04 . However, the gain in mean values was significantly different in both groups; the substantially higher mean gain observed in the Lab group ($M = 23.20$, $SD = 19.90$) relative to the Practice group ($M = 4.59$, $SD = 17.70$) represents an 18.61 percentage point difference.

Table 4.22 Descriptive Statistics by Case Type

Case Type	n	Pre-test		Gain		ARCS Subscale Means			
		<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	A	R	C	S
Practice (Cases 1 & 2)	61	13.30	4.27	4.59	17.70	3.77	3.90	3.62	4.04
Lab (Cases 3 & 4)	60	13.20	5.00	23.20	19.90	3.78	3.91	3.63	4.04

Note. A = Attention; R = Relevance; C = Confidence; S = Satisfaction. Gain score = post-test minus pre-test. ARCS subscale scores are reported on a 5-point scale.

Table 4.23 Hierarchical Regression Results - Practice Classes (Cases 1&2)

	Block 1: Prior Knowledge	Block 2: + IMMS
(Intercept)	28.449*** (6.782)	34.762** (11.135)
pre_test	-1.792*** (0.486)	-1.506** (0.499)
attention		-2.222 (5.390)
relevance		-3.078 (5.809)
confidence		-7.232 (4.346)
satisfaction		9.021* (4.259)
Num.Obs.	61	61
R ²	0.188	0.293
R ² Adj.	0.174	0.229

Note. + $p < 0.1$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

The results for the Practice Classes model are summarized in Table 4.23. In Block 1, pre-test score served as the predictor. The model was significant and had a variance explained value of 18.8% ($R^2 = 0.188$, adjusted $R^2 = 0.174$). The pre-test coefficient was negative and significant ($B = -1.792$, $p < 0.001$). In Block 2, all four motivation subscales were included in one block. As a result, the model variance explained value was raised to 0.293 (adjusted $R^2 = 0.229$), meaning an increment of R^2 value by 0.106. Thus, the motivation subscales together contributed an additional 10.6% of variance in gain scores after controlling for pre-test scores. Of the motivation subscales, Satisfaction was found to be significantly predictive ($B = 9.021$, $p < 0.05$),

which shows that high levels of satisfaction led to greater gain in the practice condition. Attention ($B = -2.222$, $p > 0.05$), Relevance ($B = -3.078$, $p > 0.05$), and Confidence ($B = -7.232$, $p > 0.05$) did not have significant coefficients, however, the Confidence subscale showed a notable trend in the same direction.

Table 4.24 Hierarchical Regression Results - Lab Classes (Cases 3 & 4)

	Block 1: Prior Knowledge	Block 2: + IMMS
(Intercept)	52.654***	52.339***
	(6.150)	(11.833)
pre_test	-2.221***	-2.128***
	(0.435)	(0.459)
attention		1.192
		(5.915)
relevance		1.362
		(6.398)
confidence		-5.313
		(4.596)
satisfaction		2.110
		(4.734)
Num.Obs.	60	60
R ²	0.310	0.330
R ² Adj.	0.298	0.268

Note. + $p < 0.1$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

Table 4.24 presents the results of analysis using the Lab Classes model. Block 1 yielded a significant effect of pre-test score on gain scores, where the predictor variable acted as a negative correlate ($B = -2.221$, $p < 0.001$). In this model, 31.0% of variance was explained by the predictors ($R^2 = 0.310$, adjusted $R^2 = 0.298$). The four ARCS subscales were added in Block 2. The result was a marginal increase in model R^2 to

0.330 (adjusted $R^2 = 0.268$), a difference in R^2 of 0.020. The small improvement shows that IMMS subscales collectively explained an additional 2.0% of variance in gain scores beyond pre-test score in the lab setting – a smaller effect size compared to practice classes. None of the ARCS subscales were found to be a significant predictor in the current context (Attention: $B = 1.192$, $p > 0.05$; Relevance: $B = 1.362$, $p > 0.05$; Confidence: $B = -5.313$, $p > 0.05$; Satisfaction: $B = 2.110$, $p > 0.05$). The adjusted R^2 dropped from Block 1 (0.298) to Block 2 (0.268). The hierarchical combined model (Table 4.25) validated the findings from the separate models.

Table 4.25 R^2 Change Summary

Model	R^2	ΔR^2	Interpretation
Combined Block 1 (Prior knowledge)	0.205	0.205	Prior knowledge baseline
Combined Block 2 (+ Case type)	0.402	0.197	Case type adds 19.7%
Combined Block 3 (+ IMMS)	0.439	0.037	IMMS adds 3.7%
Practice Block 1 (Prior knowledge)	0.188	0.188	Prior knowledge baseline
Practice Block 2 (+ IMMS)	0.293	0.106	IMMS adds 10.6%
Lab Block 1 (Prior knowledge)	0.310	0.310	Prior knowledge baseline
Lab Block 2 (+ IMMS)	0.330	0.020	IMMS adds 2.0%

Overall, the IMMS motivation scale contributed additional variance in gain scores beyond that of prior knowledge; however, the level and nature of contribution varied depending on the instructional setting. In the practice settings, the IMMS subscales increased explained variance significantly, explaining an additional 10.6% of variance, with Satisfaction being the only significant predictor of gain scores. In the lab conditions, the incremental increase in R^2 due to IMMS was negligible (0.020) and none of the IMMS subscales approached statistical significance.

DISCUSSION

4.4 Overview of Findings

The present research investigated the effect of CBL on academic achievement in an undergraduate genetics course, the differential effects of theory-based and lab-based CBL instruction on learning gains, and the role of motivation in academic performance depending on the type of instruction. The results yielded three major observations. First, CBL yielded significant improvements in academic achievement compared to conventional teaching in lab-based cases (Cases 3 and 4), whereas in theory-based cases (Cases 1 and 2) no differences were found, thus suggesting that the effects of CBL vary depending on its context of application and are not generalized. Second, CBL instruction in laboratory settings significantly improved learning gains compared to theory-based instruction with the former yielding learning gains of about 18.5 percentage points more than the latter after adjusting for initial knowledge level. Third, satisfaction was the only significant predictor of learning gains in theory-based CBL instruction, whereas motivation did not account for much variance in gains obtained from lab-based CBL instruction. These findings are discussed below.

4.5 CBL Influence on Academic Performance Compared to Traditional Instruction

The ANCOVA test showed an uneven performance of the CBL method in the four cases. There was no significant difference in the post-test performance between CBL and traditional instruction cases after controlling for pre-test score among the theory-based cases (case 1: $F(1,62)=2.573$, $p=0.114$, $\eta^2=0.04$; case 2: $F(1,61)=0.641$, $p=0.427$, $\eta^2=0.01$). In contrast, the lab-based cases demonstrated statistically significant advantage of the CBL over the traditional teaching cases (case 3: $F(1,62)=11.204$, $p=0.001$, $\eta^2=0.15$; case 4: $F(1,62)=6.169$, $p=0.016$, $\eta^2=0.09$). Students in CBL group performed better than control group students by 15.0% and 10.5% in cases 3 and 4 respectively after adjusting the covariance effect.

The absence of significant performance difference in Cases 1 and 2 is supported by the evidence that suggests that active learning does not always perform better compared to traditional teaching – its effectiveness highly depends on its proper implementation (Andrews et al., 2011). The large-scale observational study conducted by Andrews et al. (2011) did not find any positive correlation between the use of active learning methods and the gains of the students' academic performance. Andrews et al. (2011) argue that active learning can be effective if and only if it is properly implemented. In the current research, cases 1 and 2 were presented during theoretical seminars which took place at the beginning of the semester when CBL was a completely new format for students. The absence of significant performance difference in Cases 1 and 2 may also be related to unmet psychological needs in the early instructional phase. González-Arias et al. (2025) demonstrated that basic psychological need satisfaction - specifically autonomy, competence, and relatedness - significantly mediates the relationship between motivation and academic performance in higher education. When students encounter a new instructional format like CBL without sufficient scaffolding, their sense of competence may be undermined, limiting motivation's capacity to translate into achievement gains.

Cognitive load theory also contributes to the null results obtained in the first two cases. Rhodes et al. (2020) showed that case-based learning may increase extraneous cognitive load among novices unless the learning experience is well scaffolded. Simultaneous exposure to new content and to the new learning method could mean that students are divided in terms of cognitive resources allocation. It was similarly pointing out that the lack of familiarity of both CBL and case materials among students is known to lead to lower learning outcomes when the method is improperly implemented (Mostert, 2007; Abercrombie, 2011). In seminar sessions focused on theory, where the core learning process happens through discussion and concept-based learning, adding CBL requirements might have put too much pressure on students' cognitive resources.

A number of recent findings provide support for the significant and substantial CBL effects found in the two other cases included in the current paper. As shown by

Gholami et al. (2021), CBL is a more effective method than traditional lecturing for improving problem solving skills and motivation in the context of an emergency nursing course – if used consistently. Multi-episode use of this technique led to substantial improvements in students' performance. Similarly, Bi et al. (2019) discovered that multi-session use of CBL is better than lectures for increasing students' exam results, improving overall satisfaction with the course and boosting their problem-solving skills. In Case 3 and 4 involving genetics of *Drosophila* and the structure of the genetic code, CBL techniques were used in laboratory sessions later during the semester. By that time, students already had some experience in using CBL cases.

The finding of the growing effectiveness of CBL throughout the semester aligns with the results presented by Zhang et al. (2025), according to which enhanced CBL resulted in gradual progress in knowledge acquisition and increased learning satisfaction among the students progressing through the intervention. Felemban et al. (2025) found that although there were no significant differences in performance between CBL and lecture-based instruction, the former provided better learning outcomes in terms of long-term retention. It can be hypothesized that despite no significant differences after the post-test stage, CBL could provide some grounds for further success in Case 1, as well as establish a foundation for subsequent improvements in Cases 2, 3, and 4.

Mixed achievements obtained in the four cases align with the mixed results of achievement attained in the study conducted by Murray-Nseula (2011) when integrating cases into the curriculum of an undergraduate genetics course; although positive perceptions had been observed, improved results were not noted. The reasons provided by the author can be regarded as relevant to the present study: poor integration of CBL, lack of alignment in assessments, and low learner preparedness have been recognized as reasons for failure (Murray-Nseula, 2011). These factors can explain why CBL was more effective in the laboratory setting than in other contexts. In other words, it is possible to conclude that Hypothesis 1 holds conditionally: CBL yielded

significantly higher academic achievement than the traditional instruction format, although its impact was gradual.

4.6 Differences in Learning Between Theory-Based and Lab-Based CBL Instruction

As indicated by hierarchical regression analysis, instructional context was identified as the predictor with the largest impact on learning gains in the current research. Even after accounting for differences in pretest scores, laboratory-based CBL classes demonstrated higher learning gains in comparison with theory-based CBL ($B = 18.517$, $p < 0.001$, $\Delta R^2 = 0.197$). On average, students from lab-based CBL gained about 18.5 percentage points more in comparison with their peers in theory-based CBL. Thus, the results clearly support Hypothesis 2 and may be considered one of the most important findings of the study.

There are several potential explanations of why lab-based CBL proved more successful than theory-based CBL in this study. First, laboratory-based teaching per se creates a context-rich environment which enhances case-based reasoning processes. Students in laboratories get to interact with physical material and observe biological phenomena which creates tangible references for theoretical genetic knowledge. According to Tegginamani and Vanishree (2024), CBL should focus on integration of theory and practice. Lab-based cases in the present study focused precisely on integration of practical observation and case-based genetic reasoning, thus facilitating learning.

The second explanation for the results of Case 3 and Case 4 concerns the inherent nature of the lab-based cases. Wikanta and Susilo (2022) found that CBL instruction of biochemistry resulted in the development of high-level HOTS, specifically analysis and evaluation abilities. These skills are naturally promoted by laboratory activities, where students have to analyse and interpret real or virtual data, which naturally facilitates the development of such skills. Both cases require the use of multi-level reasoning. In Case 3, students are required to infer genotypic characteristics from phenotypic variations in wild type and mutant *Drosophila*. Case 4 also requires multi-

level reasoning, because students are asked to analyse the genetic code based on inheritance patterns in F₂ generations. Such reasoning naturally aligns with multi-level laboratory-based learning (Smith & Wood, 2016). This advantage of lab-based contexts for developing higher-order thinking is consistent with systematic review evidence. Vansteenacker et al. (2023) found that student-centered learning environments grounded in constructivist theory - such as problem-based and project-based learning - demonstrate stronger higher-order thinking outcomes when they involve concrete, real-world problem engagement rather than purely abstract discussion. Laboratory settings, with their inherent emphasis on data collection and inference, provide precisely this kind of concrete grounding.

Thirdly, the fact that Cases 3 and 4 were presented at the end of the course means that students gained experience using the CBL format earlier during the course. Knight et al. (2022) demonstrated that the improvement in metacognitive accuracy throughout the course resulted in higher academic achievements, which means that learning how to learn in a certain format promotes better outcomes independently of the topic's difficulty. Having completed two other CBL cases before starting with Cases 3 and 4, students learned how to interact effectively with case materials, discuss evidence with peers, and build genetic explanations. The growing effectiveness of CBL from Cases 1–2 to Cases 3–4 aligns with metacognitive development theory. Stanton et al. (2021) demonstrated that metacognitive regulation skills - students' ability to monitor and adjust their own learning - have a more dramatic impact on academic outcomes than metacognitive awareness alone, and that these skills improve with structured, repeated practice. By the time students reached lab-based Cases 3 and 4, their familiarity with CBL reasoning had strengthened their metacognitive regulation, enabling them to engage more productively with case materials.

Fourthly, Allchin (2013) noted that there are certain characteristics of CBL that promote its effectiveness, such as contextualisation, complexity, and application/generation of knowledge. Lab-based cases are high on contextualisation, as students can easily observe the organisms, inheritance patterns, and link case

materials to their observations. In theory-based cases, students have to visualise unseen phenomena. That is why contextualisation can account for significant differences in student achievement in lab-based and theory-based CBL activities.

The fact that context is more significant than instructional approach by itself presents a number of implications for the way CBL should be approached in genetic teaching. Incorporation of case-based approaches into a theory seminar without modification of the learning situation in any significant way might be insufficient to enhance the learners' performance. As it was discussed by Emblen-Perry (2022), case work in its traditional one-dimensional form is limited in its scope, and for the purpose of encouraging in-depth thinking on the matter, multi-faceted case work should be encouraged – which is more likely in laboratory CBL.

4.7 Motivation, Academic Performance, and the Role of Instructional Context

Hierarchical regressions showed different contributions of ARCS subscales to learning gains in theory-based versus lab-based courses. Specifically, inclusion of the ARCS subscales in Block 2 of the theory-based regression accounted for an important incremental 10.6% ($\Delta R^2 = 0.106$) variance in gain scores beyond prior knowledge, with Satisfaction being the only significant independent ARCS contributor ($B = 9.021$, $p < 0.05$). By contrast, in lab-based classes, motivation played a very minor role in explaining the variances in gain scores ($\Delta R^2 = 0.020$) and none of the ARCS subscales were statistically significant. Therefore, Hypothesis 3 received partial support, namely, motivation predicted learning gains in theory-based classes, but not lab-based classes. It is of theoretical significance that Satisfaction was the only significant ARCS subscale predictor of learning gains. According to Keller (1987, 2010) in her ARCS framework, Satisfaction is the highest motivational level attained – how rewarding students find their learning process. It follows from Keller (1987) that Satisfaction motivates students to persist in their efforts, as it is the most crucial motivational factor that influences students' academic performance. As there were no environmental supports for learning in the theory-based class format, students' feeling satisfied with

the course experience can be seen as a motivating element compensating for the lack of extrinsic support. That is, the sense of satisfaction students had due to the CBL approach used encouraged them to put in efforts necessary to analyse cases and achieve higher gain scores.

Support for this interpretation can be found in the literature: Hartfield (2010) found that CBL increased both student satisfaction and academic achievements, with student satisfaction and alignment of their learning increasing each other. Similarly, Yang and Junsuwan (2025) confirmed that motivational strategies based on ARCS positively influence learning achievement through enhancing learning value and satisfaction. The finding that Satisfaction uniquely predicted learning gains in theory-based CBL - while the lab context made motivational predictors largely redundant — is consistent with self-determination theory. Wang et al. (2024), in a meta-analytic review, found that autonomous forms of motivation, including intrinsic satisfaction, positively predict academic achievement specifically when external instructional supports are weak or absent. In theory-based seminars, where the learning environment provides fewer concrete props and feedback loops, intrinsic satisfaction functions as the primary driver of sustained effort - consistent with Keller's (2010) account of Satisfaction as the highest-level ARCS motivator

Moreover, the absence of motivational predictors in the lab-based context seems to be just as informative and logically justified. Specifically, when the instruction is carried out within the framework of a laboratory class, which can be seen in Case 3 and 4, the learning process becomes highly motivating per se since it allows for actively engaging in experimenting with real-life genetics-related phenomena, receiving timely feedback, and working on interesting content. Thus, in the lab environment, it might be irrelevant whether individual differences in motivational orientations affect the performance of students as the actual instructional process is engaging enough regardless of personal motivation to learn the material presented.

Finally, the similarity in ARCS subscale scores across theory-based and lab-based groups with no more than 0.02-point differences between them is yet another

supporting factor for the above-mentioned interpretation. Indeed, although the level of motivation was almost equal in both cases (ARCS scores of all subscales were high: from 3.62 to 4.04 points on a five-point scale), students demonstrated markedly different learning results. That is, one can interpret the results as the proof of the fact that motivational variables were a necessary but not sufficient component in learning outcomes in theory-based lessons, whereas in lab-based settings, motivational factors did not matter at all.

It can be inferred from the high levels of Satisfaction recorded (4.04 on average in both scenarios) that CBL had positive motivational results for the participants, consistent with CBL literature. In particular, Alizadeh et al. (2024) showed that virtual CBL increased learners' motivation specifically regarding relevance and applicability, whereas Gholami et al. (2021) found significant improvements in all IMMS dimensions in the context of multi-episode CBL versus lectures. It may thus be concluded that CBL was satisfying enough for participants, even though there was no increase in their performance levels in theory-based CBL situations. The current results corroborate Murray-Nseula's (2011) finding about CBL increasing student perceptions even without improvement in performance outcomes.

However, it is necessary to consider the potential threat to statistical inferences caused by the high level of multicollinearity among ARCS subscales (Relevance VIF = 6.61). Specifically, because ARCS subscales are interrelated (students who perceive the material as relevant also pay more attention to it, are more self-confident, and are more satisfied), the multiple regression analysis used in this research experienced difficulties isolating independent factors. This could be the reason for only Satisfaction being significant in the theory-based CBL regression model, whereas all subscales were high on the average. Further research in this direction should be conducted using more complex analytical techniques such as SEM or PLS. The high multicollinearity observed among ARCS subscales (Relevance VIF = 6.61) reflects a structural issue documented in the broader ARCS literature. Lo and Hew (2023), in a systematic review of 55 empirical studies using the ARCS/IMMS framework, noted that the four

subscales are theoretically and empirically interrelated, as students who perceive material as relevant tend to also report higher attention, confidence, and satisfaction. The authors recommend that future researchers address this collinearity either by using composite ARCS scores or by applying more robust multivariate techniques such as SEM - a recommendation directly aligned with the present study's limitations.

CONCLUSION

The current study explored the impact of case-based learning (CBL) on the academic achievement of undergraduate biology students enrolled in a genetics class in SDU University, specifically focusing on the differential effectiveness of CBL based on its delivery in a theory and laboratory environment and the role of motivation – defined by the ARCS model by Keller – in predicting the academic outcomes of CBL. In this regard, the current study included 70 undergraduate biology students in their third year of studies taking part in four CBL cases during one academic semester.

With regard to Research Question 1, the ANCOVA findings reveal a context-specific trend in the efficacy of CBL. There were no statistically significant positive differences between CBL and traditional instruction in theory-based scenarios (Cases 1 and 2): $F(1, 62) = 2.573$, $p = 0.114$, $\eta^2 = 0.04$ for Case 1 and $F(1, 61) = 0.641$, $p = 0.427$, $\eta^2 = 0.01$ for Case 2. In laboratory-based scenarios (Cases 3 and 4), in turn, significant differences in favor of CBL learning were revealed: $F(1, 62) = 11.204$, $p = 0.001$, $\eta^2 = 0.15$ for Case 3 and $F(1, 62) = 6.169$, $p = 0.016$, $\eta^2 = 0.09$ for Case 4. After controlling for prior knowledge, CBL learners were shown to perform better than traditional instruction learners by about 15.0 percentage points in Case 3 and about 10.5 percentage points in Case 4. Therefore, Conditional Hypothesis 1 is partially confirmed by the findings as CBL positively impacts academic outcomes only within laboratory-based instructional contexts. The non-significant findings regarding CBL learners in theory-based classes are explained by Cognitive Load Theory that assumes that simultaneous exposure to new material and a new instructional technique at the beginning of the semester may have depleted students' cognitive capacities.

Concerning the second research question, the results of the hierarchical regression analysis confirmed Hypothesis 2. Having controlled the effect of prior knowledge, CBL implemented in the laboratory setting led to significantly higher (18.5 percentage points) gains in learning in comparison with CBL relying on theoretical materials ($B = 18.517$, $p < 0.001$, $\Delta R^2 = 0.197$). Thus, instructional context, rather than prior knowledge or motivational orientation, was identified as the most influential

factor affecting learning gains in the current sample. This evidence suggests that it is not the method of CBL, per se, which explains the success of learning. On the contrary, the effectiveness of the method depends on contextual factors related to the learning environment's authenticity.

Addressing the third research question, the results of the regression analysis provided partial confirmation for Hypothesis 3. Within the framework of the theory-based instructional context, the incorporation of motivational subscales of the ARCS model into Block 2 accounted for 10.6% more variability in students' learning gains over their prior knowledge ($\Delta R^2 = 0.106$). In particular, Satisfaction turned out to be the only statistically significant ARCS subscale predicting students' learning ($B = 9.021$, $p < 0.05$). As can be observed from the results of regression analysis, in the absence of an interesting learning environment, intrinsic students' satisfaction with the achieved results becomes the only motivational force behind sustained efforts and higher learning gains. Conversely, within the framework of laboratory-based CBL, motivational variables had virtually no effect on explaining students' learning gains ($\Delta R^2 = 0.020$).

Overall, the results obtained during the study suggest that CBL can be maximally effective only when used in practice-oriented educational setting involving authentic biological processes and application of various levels of reasoning in the process, as well as building on CBL competencies developed over the whole period of one semester. For the purposes of practice, the mentioned conclusions mean that it would not be effective to use CBL in theoretical seminars without any additional changes in the educational environment. Moreover, taking into account that in theory-based settings only Satisfaction is a reliable motivational variable, it is critical to design intrinsically motivating experiences in cases in such types of instructional setting. The present study adds to the overall body of literature related to active learning strategies in higher education. It can serve as a basis for further development of CBL strategies in the field of genetics teaching in Kazakhstan.

LIMITATIONS

Several limitations of the present study need mentioning. Firstly, the use of a quasi-experimental design with intact groups poses restrictions on causal inferences. Although covariates were taken into account in the analysis of pre-test results, the potential role of confounding factors – student ability, pre-intervention motivation, and unequal participation in CBL sessions – remains unconsidered (Andrews et al., 2011). Secondly, although the sample sizes (about 60–65 students in each case) were sufficiently large to find medium-sized effects, smaller effects could not be detected – as evidenced by the non-significance of small effects in Case 1 and Case 2. Thirdly, the measurement of IMMS motivation could be conducted only in those students who had participated in CBL and only once after the completion of the course, preventing comparison of motivations between the CBL and control groups and insight into the dynamics of the former. Fourthly, the current study was carried out in a single course of genetics offered at one university, restricting its generalisability.

Recommendations for Future Research

Based on the findings and limitations of the present study, several recommendations for future research can be formulated. Firstly, future research should be designed to explore the effectiveness of CBL in genetics education using either randomised or quasi-randomised designs with multiple samples of students and several cohorts. Secondly, future longitudinal studies should assess how CBL contributes to long-term retention of material taught in genetics by measuring students' knowledge weeks or even months after the course – similarly to what Felemban et al. (2025) did in their study and found more prolonged benefits of the CBL approach in terms of increased retention. Thirdly, assessing the level of motivation at several points of the course – instead of only one at the end – will help in studying the dynamics of motivation development when exposed to CBL format and will allow researchers to see whether it predicts performance improvement. Fourthly, conducting focus group interviews with participants and analysing class observations will facilitate understanding of the mechanisms of lab-based CBL's effectiveness and allow

researchers to see what precisely in case design, facilitation, and lab sessions is beneficial for students. Fifthly, future research is needed to test whether CBL is more effective in practice labs than in lecture halls when teaching not only genetics but other disciplines of the life sciences domain.

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APPENDICES

Appendix 1. Approval from Ethics Committee

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Зерттеу этикасы комитеті

Research Ethics Committee

Dear Shynar Dumanbek,

The Research Ethics Committee has reviewed "*The impact of case based learning on students' understanding of real world applications of genetics for better academic performance*" and has granted ethical approval based on the information provided in the application, and on the condition that the study is conducted in accordance with ethical standards and institutional guidelines.

Approval No.	11-12-06
Project title	The impact of case based learning on students' understanding of real world applications of genetics for better academic performance
Approval date	07 April 2026
Expiry date	06 April 2028
Decision	Approved

Please ensure that you contact the Research Ethics Committee at rethics@sdu.edu.kz if there are any changes to the study, so that any implications for ethics approval can be considered. Please quote the application number in all correspondence.

Chairwoman of the Research Ethics Committee

Secretary

K. Smakova

A. Kaukenova

Appendix 2. IMMS Survey questions

Instructions: Please answer each item based on your experience with the genetics case-based learning activities in this course. There are no right or wrong answers. Circle or tick one response for each item.

Нұсқаулық: Осы курс бойынша генетикадағы кейс-тапсырмаларға сүйеніп, әр сұраққа жауап беріңіз. Дұрыс немесе бұрыс жауап жоқ. Әр сұрақ үшін бір жауапты белгілеңіз.

Rating Scale / Бағалау шкаласы:

1 = Not true / Мүлде дұрыс емес 2 = Slightly true / Аздап дұрыс 3 = Moderately true / Орташа дұрыс 4 = Mostly true / Көбіне дұрыс 5 = Very true / Толық дұрыс

*Note. Items marked with * are reverse-scored. / Ескерту. * белгісімен белгіленген сұрақтар кері бағаланады.*

Item / Сұрақ	Not true Мүлде дұрыс емес	Slightly true Аздап дұрыс	Moderately true Орташа дұрыс	Mostly true Көбіне дұрыс	Very true Толық дұрыс
Section A: Attention (A) / А бөлімі: Назар аудару					
1. The beginning of the genetics case activity included something that captured my attention. <i>Генетика кейсінің басында назарымды аудартқан нәрсе болды.</i>	☐	☐	☐	☐	☐
2. The case materials (slides/handouts/visuals) were visually engaging. <i>Кейс материалдары (слайдтар/таратпалар/көрнекіліктер) көз тартарлық болды.</i>	☐	☐	☐	☐	☐
3. The clarity and quality of the text/explanations helped me stay attentive. <i>Мәтін/түсіндірмелердің анықтығы мен сапасы назарымды сақтауға көмектесті.</i>	☐	☐	☐	☐	☐
4. The genetics case activity felt so abstract that it was hard to maintain my attention.* <i>Генетика кейсі тым абстрактілі болып көрінді, сондықтан назарымды ұстап тұру қиын болды. *</i>	☐	☐	☐	☐	☐
5. The case materials looked dull or unappealing.* <i>Кейс материалдары қызықсыз немесе тартымсыз көрінді. *</i>	☐	☐	☐	☐	☐
6. The way information was arranged in the case helped me keep my attention. <i>Кейс ішіндегі ақпараттың берілу тәртібі назарымды сақтауға көмектесті.</i>	☐	☐	☐	☐	☐
7. The genetics cases included elements that stimulated my curiosity. <i>Генетика кейстерінде қызығушылығымды оятатын элементтер болды.</i>	☐	☐	☐	☐	☐
8. Too much repetition in the case activities made me bored at times.* <i>Кейс тапсырмаларында қайталау тым көп болып, кейде жалығып кеттім. *</i>	☐	☐	☐	☐	☐
9. I learned some genetics ideas that were surprising or unexpected.	☐	☐	☐	☐	☐

Item / Сұрақ	Not true Мүлде дұрыс емес	Slightly true Аздап дұрыс	Moderately true Орташа дұрыс	Mostly true Көбіне дұрыс	Very true Толық дұрыс
<i>Мен күтпеген немесе таңқаларлық генетикалық идеяларды үйрендім.</i>					
10. Variety (questions, tasks, visuals, discussion) helped keep my attention during the case. <i>Түрлілік (сұрақтар, тапсырмалар, көрнекілік, талқылау) кейс кезінде назарымды сақтауға көмектесті.</i>	☐	☐	☐	☐	☐
11. The writing/wording style in the case materials was boring.* <i>Кейс материалдарындағы жазу/сөйлеу стилі қызықсыз болды.*</i>	☐	☐	☐	☐	☐
12. There was so much text in the case materials that it felt irritating or overwhelming.* <i>Кейс материалдарында мәтін тым көп болды, сондықтан ол мазамды алып/қызықсыздандырды.*</i>	☐	☐	☐	☐	☐
Section B: Relevance (R) / B бөлімі: Өзектілік					
13. It was clear how the genetics case content connected to what I already knew. <i>Генетика кейс мазмұнының бұрыннан білетініммен қалай байланысты екенін түсіну оңай болды.</i>	☐	☐	☐	☐	☐
14. The cases included examples that showed why genetics knowledge matters in real life. <i>Кейстерде генетикалық білімнің өмірде не үшін маңызды екенін көрсететін мысалдар болды.</i>	☐	☐	☐	☐	☐
15. Successfully completing the case activities was important to me. <i>Кейс тапсырмаларын сәтті орындау мен үшін маңызды болды.</i>	☐	☐	☐	☐	☐
16. The genetics case content was relevant to my interests. <i>Генетика кейс мазмұны менің қызығушылықтарыма сәйкес болды.</i>	☐	☐	☐	☐	☐
17. The cases showed how genetics is used in real situations (health, testing, inheritance, biotech). <i>Кейстер генетиканың нақты жағдайларда (денсаулық, тестілеу, тұқымқуалау, биотехнология) қалай қолданылатынын көрсетті.</i>	☐	☐	☐	☐	☐
18. The content and style of the cases made the genetics topic feel worth learning. <i>Кейстердің мазмұны мен стилі генетиканы оқуға тұрарлық екенін көрсетті.</i>	☐	☐	☐	☐	☐
19. The cases were not relevant to my needs because I already knew most of the content.* <i>Кейстер менің қажеттіліктеріме сәйкес болмады, себебі мен мазмұнның көбін бұрыннан білетінмін.*</i>	☐	☐	☐	☐	☐

Item / Сұрақ	Not true Мүлде дұрыс емес	Slightly true Аздап дұрыс	Moderately true Орташа дұрыс	Mostly true Көбіне дұрыс	Very true Толық дұрыс
20. I could relate the genetics case content to things I have seen, done, or thought about in my own life. <i>Генетика кейс мазмұнын өз өмірімде көрген/жасаған/ойлаған нәрселермен байланыстыра алдым.</i>	☐	☐	☐	☐	☐
21. I believe the genetics knowledge from these cases will be useful to me. <i>Осы кейстерден алған генетикалық білім маған пайдалы болады деп ойлаймын.</i>	☐	☐	☐	☐	☐
Section C: Confidence (C) / C бөлімі: Сенімділік					
22. At first glance, I felt the genetics case activities would be manageable for me. <i>Бір қарағанда, генетика бойынша кейс-тапсырмалар мен үшін орындауға болатын сияқты көрінді.</i>	☐	☐	☐	☐	☐
23. The genetics case materials were harder to understand than I would have liked.* <i>Генетика кейс материалдарын түсіну мен қалағаннан да қиын болды.*</i>	☐	☐	☐	☐	☐
24. After reading the case introduction, I felt clear about what I was expected to learn. <i>Кейс кіріспесін оқығаннан кейін, менен не үйрену күтілетінін анық түсіндім.</i>	☐	☐	☐	☐	☐
25. There was so much information in the case materials that it was difficult to identify and remember the key points.* <i>Кейс материалдарында ақпарат тым көп болды, сондықтан негізгі ойларды ажыратып, есте сақтау қиын болды.*</i>	☐	☐	☐	☐	☐
26. While working on the cases, I felt confident that I could learn the genetics content. <i>Кейстермен жұмыс істеген кезде, генетика мазмұнын меңгере алатыныма сенімді болдым.</i>	☐	☐	☐	☐	☐
27. The tasks/exercises in the case activities were too difficult for me.* <i>Кейс-тапсырмалардағы жаттығулар мен үшін тым қиын болды.*</i>	☐	☐	☐	☐	☐
28. After working on the cases for a while, I felt confident I could pass a test on this genetics topic. <i>Кейстермен біраз жұмыс істегеннен кейін, осы генетика тақырыбынан тестті тапсыра алатыныма сенімді болдым.</i>	☐	☐	☐	☐	☐
29. I could not understand a significant part of the genetics material in the case activities.* <i>Кейс-тапсырмалардағы генетика материалының едәуір бөлігін түсіне алмадым.*</i>	☐	☐	☐	☐	☐
30. The way the genetics case content was organized increased my confidence that I could learn it.	☐	☐	☐	☐	☐

Item / Сұрақ	Not true Мүлде дұрыс емес	Slightly true Аздап дұрыс	Moderately true Орташа дұрыс	Mostly true Көбіне дұрыс	Very true Толық дұрыс
<i>Генетика кейс мазмұнының ұйымдастырылуы оны меңгере алатыныма сенімді арттырды.</i>					
Section D: Satisfaction (S) / D бөлімі: Қанағаттану					
31. Completing the case tasks gave me a satisfying sense of achievement. <i>Кейс тапсырмаларын аяқтау маған жетістік сезімін берді.</i>	☐	☐	☐	☐	☐
32. I enjoyed the genetics cases enough that I would like to learn more about these topics. <i>Генетика кейстері маған ұнады, сондықтан осы тақырыптарды көбірек оқығым келеді.</i>	☐	☐	☐	☐	☐
33. I genuinely enjoyed learning genetics through these case activities. <i>Мен генетиканы осы кейс-тапсырмалар арқылы оқуды шын мәнінде ұнаттым.</i>	☐	☐	☐	☐	☐
34. It felt good to successfully complete the genetics case activities. <i>Генетика кейс тапсырмаларын сәтті аяқтау жағымды болды.</i>	☐	☐	☐	☐	☐
35. Overall, it was pleasant to work with these well-designed genetics case materials. <i>Жалпы алғанда, жақсы құрастырылған генетика кейс материалдарымен жұмыс істеу жағымды болды.</i>	☐	☐	☐	☐	☐

Total items: 35 | Subscales: A (12 items), R (9 items), C (9 items), S (5 items)

Source: Adapted from Keller, J. M. (2010). *Motivational design for learning and performance: The ARCS model approach*. Springer.

Appendix 3. Pre test questions

Name surname _____

1. What was a key feature of the traits Mendel studied in peas?
 - A) They showed many intermediate forms between two extremes
 - B) They were clear-cut, either-or traits without intermediates
 - C) They blended together in offspring
 - D) They only appeared in female plants
2. In people with cystic fibrosis, what is the result of having two recessive alleles for the CFTR gene?
 - A. Excess water enters the cells, causing them to swell
 - B. A functional CFTR protein is produced, leading to dehydration.
 - C. The cells retain water, leading to thick, dehydrated mucus building up outside the cells.
 - D. The CFTR protein functions normally, but chloride ions are not absorbed.
3. Have a "spike" on their dorsal surface at the rare
 - A. Male drosophila
 - B. Female drosophila
 - C. both of them
 - D. none of them
4. What is the purpose of a testcross?
 - A. To determine if an individual has a homozygous or heterozygous genotype.
 - B. To predict the phenotype of future offspring.
 - C. To test the strength of dominant alleles.
 - D. To find out whether two traits are linked on the same chromosome.
5. In a testcross, if a yellow pea plant of unknown genotype (Y-) is crossed with a green pea plant (yy) and half of the offspring are yellow and half are green, what is the genotype of the yellow parent?
 - A. Yy
 - B. YY
 - C. yy
 - D. Y-
6. Which of the following statements about Mendel's law of segregation is false?
 - A. Gametes carry only one allele for each trait.
 - B. The two alleles for each gene segregate during gamete formation.
 - C. Each parent contributes two alleles to their offspring.
 - D. The random fusion of gametes at fertilization restores two copies of each gene
7. In a dihybrid cross (Yy Rr x Yy Rr), what proportion of the offspring will have the genotype Yy rr?
 - A. 1/16
 - B. 2/16
 - C. 3/16
 - D. 4/16
8. In eukaryotic cells, DNA is organized into chromatin. What is the key difference between euchromatin and heterochromatin?
 - A. Euchromatin is tightly packed, while heterochromatin is loosely packed
 - B. Euchromatin is transcriptionally active, while heterochromatin is transcriptionally inactive.
 - C. Heterochromatin is found only in the nucleus, while euchromatin is found in the cytoplasm.
 - D. Heterochromatin contains more genes than euchromatin.
9. How did Mendel explain the reappearance of green peas in the F2 generation?
 - A. The green trait was lost in the F1 generation but reappeared due to mutation in F2
 - B. The green trait was recessive and remained hidden in the F1 hybrids, reappearing in F2.
 - C. The yellow trait dominated in the F1 generation, and blending occurred in F2.
 - D. The green trait became dominant in the F2 generation.
10. In animal cells, how is the process of cytokinesis accomplished?
 - A) By the formation of a contractile ring that pinches the cell into two.
 - B) By the formation of the spindle fibers that help divide the cytoplasm.
 - C) By the creation of a cell plate that separates the two daughter cells.
 - D) By the elongation of the microtubules, which pull the cytoplasm apart.
11. What structure forms during the zygotene stage of prophase I to align homologous chromosomes?
 - A) Chiasmata
 - B) Centromere
 - C) Recombination nodules
 - D) Synaptonemal complex
12. According to Bridges, what happens to zygotes with the abnormal XXX and OY karyotypes?
 - A) They develop into viable adults with abnormal traits.
 - B) They die during embryonic development and do not produce progeny.
 - C) They result in sterile offspring that cannot reproduce.
 - D) They develop into individuals with ambiguous sex phenotypes.
13. Why is a sperm much smaller than an ovum?
 - A) Sperm cells contain more genetic material than the ovum, making them more efficient.
 - B) Sperm are designed to be motile, concentrating all their energy and chromosomal material in the head and tail.
 - C) Sperm only contain half the chromosomes needed for fertilization, while the ovum contains a full set.
 - D) Sperm cells mature faster and do not have time to grow as large as ova.
14. What happens to alleles after crossing-over during meiosis, according to Mendel's first law?
 - A) Crossing-over combines maternal and paternal alleles into one chromatid, violating Mendel's first law.
 - B) Crossing-over causes alleles to segregate randomly into different gametes, maintaining Mendel's first law.
 - C) Crossing-over exchanges alleles between chromatids, but they still segregate into different gametes as per Mendel's law of segregation.
 - D) Crossing-over eliminates the possibility of segregation by mixing up all the alleles.

Appendix 4. Post test questions for Seminar classes

Variant A

Name _____ Surname _____ group _____

1. Which observation from the Luria–Delbrück fluctuation test provided the strongest evidence for spontaneous mutation?
A) Identical resistant colonies on all plates
B) Rapid adaptation after phage addition
C) Wide variation in resistant colony numbers among plates
D) Complete absence of resistant colonies
2. A thymine-thymine dimer escaped photorepair but was bypassed by an error-prone polymerase. Which post-replicative outcome is most likely?
A) Transition at the 5' T of the dimer
B) Small deletion opposite the lesion
C) Replication fork reverts
D) Double-strand break during the next cell cycle
3. When proofreading and mismatch repair are both disabled, the overall base-substitution spectrum skews toward transitions rather than transversions because ...
A) tautomeric shifts favor purine↔purine mispairing
B) polymerase inserts random bases with equal probability
C) depurination dominates over oxidative damage
D) transversions are selectively repaired by AP endonuclease
4. What is the most direct molecular result of depurination?
A) Frameshift insertion
B) Apurinic site formation
C) Thymine-thymine dimerization
D) Chromosomal inversion
5. Suppose a 5-bromouracil-induced mutation reverts after replication in the *absence* of further mutagen. Which mechanistic explanation fits best?
A) Spontaneous tautomer re-shift restores correct pairing
B) Base-excision glycosylase replaced the analog
C) Direct photolyase cleavage
D) Unequal crossing-over removed the analog base
6. The proofreading function of DNA polymerase depends on which enzymatic activity?
A) 5'→3' exonuclease
B) 3'→5' exonuclease
C) Endonuclease cleavage
D) Helicase unwinding
7. Predict the mutation type if replication occurs across an apurinic site followed by mismatch repair guided to the *wrong* strand.
A) True reversion
B) Transition
C) Transversion
D) Small deletion
8. Which process explains the origin of red–green color blindness?
A) Transition mutation in opsin gene
B) Unequal crossing-over between homologous genes
C) Chromosomal translocation
D) Transversion in photoreceptor RNA
9. Why are spontaneous mutation rates lower in bacteria than in humans?
A) Shorter genomes
B) Fewer cell divisions before gamete formation in bacteria
C) Absence of recombination
D) Less exposure to mutagens
10. Which type of mutagenic agent most likely induces double-strand breaks leading to deletions?
A) Base analogs
B) Hydroxylamine
C) Intercalators
D) X-rays
11. The purpose of the extension step at 72 °C is to
A) denature secondary structures in the template.
B) allow Taq polymerase to synthesize new DNA strands from the annealed primers.
C) favor re-annealing of short fragments.
D) stabilize primers without synthesis.
12. In an RT-PCR detecting *CFTR* gene expression, only the negative control well shows amplification (Ct = 28). Interpretation?
A) Contamination of reagents—experiment invalid.
B) Negative control expected to amplify.
C) Target gene overexpressed.
D) Fluorescent threshold too low.
13. Which factor most directly determines primer specificity during PCR?
A) Mg²⁺ concentration
B) Annealing temperature
C) dNTP ratio
D) Extension time
14. The correct order of thermal steps in standard PCR is
A) Denaturation → Annealing → Extension
B) Extension → Annealing → Denaturation
C) Annealing → Denaturation → Extension
D) Denaturation → Extension → Annealing
15. The role of reverse transcriptase is to
A) Convert RNA → cDNA
B) Convert DNA → RNA
C) Join primers
D) Synthesize proteins

Appendix 5. Post test for Lab classes

Id _____

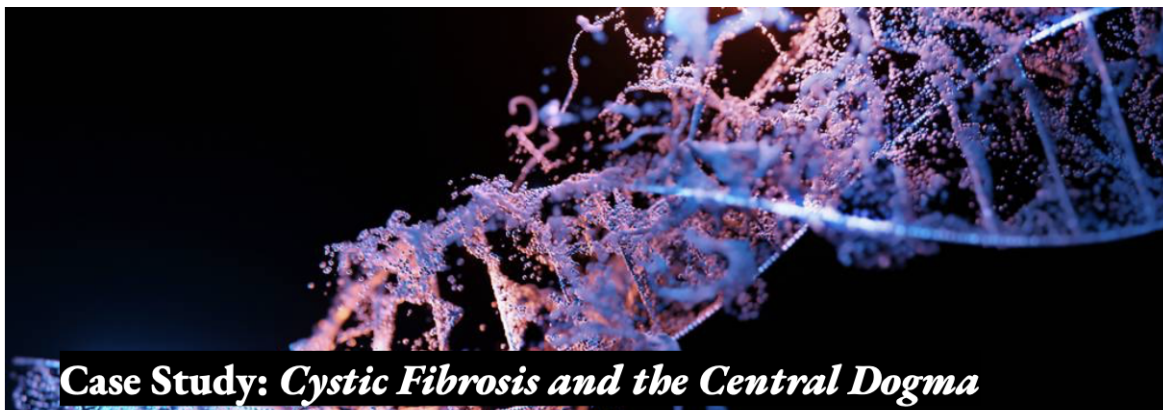
1. A student collected flies from a trap placed in a very humid area. After transfer to the vial, most larvae drown in the medium. What is the MOST scientifically valid explanation?
 - A. Medium lacked yeast
 - B. Medium absorbed environmental moisture and became too wet
 - C. Wild flies carry moisture-sensitive mutations
 - D. Low humidity is required for larval feeding
2. While preparing *Drosophila* medium, one student added propionic acid before cooling the mixture. The next day, mold appeared. What is the BEST explanation?
 - A. Acid evaporated at high temperature and lost antifungal function
 - B. Sugar neutralized the acid
 - C. Yeast activity blocked acidity
 - D. Agar prevented proper mixing
3. A student misidentified a female mutant as a male because the abdomen tip appeared dark. Which trait should have been evaluated FIRST to avoid misidentification?
 - A. Body size
 - B. Wing length
 - C. Sex comb presence
 - D. Bristle number
4. Virgin females were collected 14 hours after emergence. What is the MOST likely resulting issue?
 - A. Females will not lay eggs
 - B. Cross results will mix paternal genotypes
 - C. F₁ will be sterile
 - D. Sex ratio will become imbalanced
5. Which stage of *Drosophila* is immobile and undergoes metamorphosis?
 - A. Egg
 - B. Larva
 - C. Pupa
 - D. Adult

Question(5 points)

During your *Drosophila* cross, the F₁ generation showed phenotypes that did not match your predicted ratios. Using evidence from your procedures (virgin collection, sex identification, medium preparation, and environmental conditions), analyze the possible sources of error and evaluate which factor most likely influenced the unexpected results. Justify your reasoning with specific observations from your experiment.

6. What is the purpose of adding agar in the fly medium?
 - A. Nutrient source
 - B. Solidification
 - C. Acid buffering
 - D. Enhancing color
7. Which visible structure identifies a male *Drosophila*?
 - A. Larger body
 - B. Extra bristles on the abdomen
 - C. Sex combs on forelegs
 - D. Lighter abdomen color
8. How long is the complete *Drosophila* life cycle at 25 °C?
 - A. 3 days
 - B. 10 days
 - C. 20 days
 - D. 40 days
9. Which ingredient prevents mold in the medium?
 - A. Corn flour
 - B. Sugar
 - C. Propionic acid
 - D. Yeast
10. A student misidentified older females as virgins because their color seemed light. What should have been evaluated more carefully?
 - A. Presence of meconium indicating recent emergence
 - B. Length of the female abdomen indicates recent emergence only
 - C. Eye spacing in the female adult and meconium indicates virgins
 - D. Position of the female wings

Appendix 6. Case Example Seminar Class



Part I – Amina’s Illness: Clinical Features and Diagnosis

Amina, a 14-year-old girl from Almaty, has been suffering from frequent chest infections, wheezing, and digestive problems since childhood. Her parents noticed her skin tasted unusually salty when they kissed her. After repeated hospitalizations for pneumonia, her doctors performed a **sweat chloride test**, which confirmed elevated chloride levels. Genetic testing revealed that Amina carries the **$\Delta F508$ mutation** in the CFTR gene. Her care team now wants to help her understand *how a single gene mutation can cause such widespread health problems*.

Cystic fibrosis (CF) is an **autosomal recessive genetic disease** caused by mutations in the **CFTR gene**. The CFTR protein normally regulates chloride and sodium ion transport in epithelial cells.

Symptoms include:

- Persistent coughing and lung infections (due to thick, sticky mucus in airways).
- Salty-tasting skin (caused by abnormal salt regulation in sweat glands).
- Poor weight gain and digestive problems (due to blocked pancreatic ducts).
- Male infertility (caused by congenital absence of vas deferens).

Diagnosis

Doctors diagnose CF through a combination of:

- **Clinical symptoms** (chronic cough, malnutrition, salty sweat).
- **Sweat chloride test** (high salt levels in sweat are a hallmark).
- **Genetic testing** (to confirm CFTR mutations like $\Delta F508$ or G542X).

Part II – From Gene to Disorder: Mutations and Molecular Mechanisms

Students are asked to read the following article fully (for Part I of the case):

Gene therapy for Cystic Fibrosis: current status and future directions. [Journal/Source: ScienceDirect] (link:

<https://www.sciencedirect.com/science/article/pii/S0929693X20300439>)

[Link](#)

Questions for Understanding & Analysis

1. What does the CFTR gene normally do in human cells?
2. Why do people with cystic fibrosis often have salty-tasting skin?
3. According to the article, describe how mutations in the CFTR gene alter the normal flow from DNA → RNA → protein → cell function in CF. Provide specific examples from the article.
4. Based on the patient case (Amina) and the article's explanations, identify two clinical symptoms of CF and explain how each one is linked to molecular dysfunction described in the article.

Part III – Modeling Transcription and Translation in the CFTR Gene

Tools Needed

1. **ExPASy Translate Tool** – <https://web.expasy.org/translate/>
→ Converts DNA sequences into amino-acid chains.
2. **LabXchange: DNA to Protein Simulation** –
https://www.labxchange.org/library/pathway/lx-pathway:1d8c2b7c-2bcc-4b1c-a995-655c3107771d/items/lb:LabXchange:fb468b9e:lx_simulation:1/51903
https://www.labxchange.org/library/items/lb:LabXchange:fb468b9e:lx_simulation:1
→ Visualizes how transcription and translation occur step by step.

Given Sequences

1 Normal CFTR DNA (coding strand):

CTTCAGAGGGTAAAAATTAAGCACAGTGGGAAGAATTCATTCTGTTCTCAGT

Carefully read the article and **write down the exact mutation name/description** the authors state as causing cystic fibrosis

Record **both** levels:

- Protein-level
- DNA-level

Using the normal sequence above construct **mutated DNA cystic fibrosis** segment

Instructions

A. Transcription (DNA → mRNA)

1. Go to **LabXchange** simulation and complete the interactive module “*From DNA to mRNA*.”
 - Observe how RNA polymerase binds to the promoter, unwinds DNA, and synthesizes mRNA.
 - Note the rules of base pairing (A–U, T–A, G–C, C–G).
2. Manually transcribe both DNA sequences into mRNA in your notebook (replace every T with U).
3. Compare: does the mutation affect transcription itself?

B. Translation (mRNA → Protein)

1. Copy your **normal DNA sequence** and paste it into **ExPASy Translate**.
 - Choose **Frame 1**.
 - Record the amino-acid sequence.
2. Now, paste your **mutated DNA sequence** and translate it again.
3. Compare both amino-acid chains.

Questions

1. Which codon was deleted in the mutation and what is the name of the mutation?
2. Did the reading frame change?
3. Which amino acid is missing in the mutated sequence?
4. Explain how this mutation affects the CFTR protein structure and its function in the cell.
5. Did transcription or translation change more directly as a result of this mutation? Explain why.
6. Summarize the key steps of transcription and translation in your own words.

You've already modeled transcription and translation of normal and mutated *CFTR* DNA sequences. Now, you will analyze *how each molecular step contributes* to the creation of the CFTR protein and identify *where the mutation has its greatest impact*.

Mapping the Flow of Information

1. Draw a flowchart labeled **DNA → mRNA → Protein → Cellular Function**.
2. Under each stage, briefly write:
 - Location** (nucleus or cytoplasm)
 - Main enzyme(s)/molecules involved**
 - Key process happening**
 - Potential effect of mutation**
3. Highlight in red where the $\Delta F508$ or splicing mutation disrupts this flow.

Part IV – RNA Splicing and the CFTR Gene: When Cutting Goes Wrong

You previously learned that **Amina**, a 14-year-old from Almaty, was diagnosed with cystic fibrosis after recurrent chest infections and a positive sweat-chloride test.

Her doctors initially found the well-known **ΔF508 mutation**, but a deeper genetic analysis revealed that one of her CFTR alleles shows **abnormal splicing** in *intron 8*.

Instead of including **exon 9**, her cells sometimes skip it, creating a shorter mRNA.

Even though transcription and translation still occur, the missing exon means the resulting CFTR protein lacks an important part of its chloride-channel domain—so it folds incorrectly and is rapidly degraded.

After transcription, the newly formed **pre-mRNA** contains **exons** and **introns**.

The **spliceosome**—a complex of snRNPs—recognizes conserved **GU/AG** intron boundaries and removes introns, joining exons into a continuous mRNA.

Splicing often occurs **while RNA polymerase II is still elongating the transcript** (co-transcriptional splicing).

The *CFTR* gene's 27 exons must all be joined correctly to form a functional message.

A weak 3' splice-site sequence in intron 8 (containing a variable **UG-repeat**) can cause **exon 9 skipping**, producing a truncated CFTR protein that never reaches the cell surface.

Molecular Mechanism

- RNA polymerase II transcribes *CFTR* pre-mRNA; splicing factors (U1, U2, U4/U6, U5 snRNPs) assemble on splice sites.
- If the UG-repeat is too short, the 3' splice site is weak and the spliceosome **fails to recognize exon 9**. The mature mRNA therefore joins exon 8 directly to exon 10.
- Translation of this mRNA produces a CFTR protein missing ~25 amino acids in its first nucleotide-binding domain.
- The misfolded protein is degraded by quality-control pathways → **no functional chloride channel** → **thick mucus** and **recurrent infection**, just like Amina experiences.

Read this article for detailed information [LINK](#)

Student Tasks

1. Identify and Explain the Mutation

Read the case background and the supporting article summary.

Write, in your own words, what type of **splicing-related mutation** can cause CF.

Specify whether it affects the **5'-splice site**, **3'-splice site**, or **branch point**.

Connect to Transcription and Translation

Answer briefly:

1. At which step (transcription, splicing, translation) does this error arise?
2. How can RNA polymerase II speed influence exon inclusion (Kornblihtt et al., 2013)?
3. How would exon 9 skipping change the final mRNA and protein?
4. Compare this mechanism with the $\Delta F508$ mutation — which step of the central dogma does each affect?

3. Clinical Analysis

Explain how a splicing mutation could produce the same CF symptoms (thick mucus, infections) even without a coding-region deletion.

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Case Study — *From the Wild to the Mutant: Drosophila Melongaster*



Introduction — “The Fly Room Reimagined”

The sun was already high over the SDU campus when the research teams gathered in the biology lab, their tables lined with empty vials, bits of ripe banana, and the soft buzz of tiny wings. Today, each student had a mission: to follow in the footsteps of the scientists who first uncovered the laws of heredity — using one of the smallest, most powerful creatures in science — the **fruit fly, *Drosophila melanogaster***.

More than a century ago, *Drosophila* changed biology forever. In a small, crowded laboratory at Columbia University, Thomas Hunt Morgan and his students bred these flies to answer one great question: *Where are genes located?* When one of Morgan’s flies unexpectedly showed **white eyes** instead of red, he traced the trait to the **X chromosome**, proving that genes are carried on chromosomes — a discovery that won him the **Nobel Prize in 1933** (Morgan, 1910; Giansanti, 2025).

Since then, *Drosophila* has remained a favorite of scientists worldwide. The reasons are simple yet powerful: it grows fast, lives only ten days from egg to adult, and shows easily visible traits like eye color, wing shape, and body color (Moraes et al., 2021). Each fly carries just four pairs of chromosomes — yet more than half of its genes have human counterparts (Lürsen et al., 2019). In its tiny body, generations of researchers have found answers about **genetics, development, evolution, and disease**.

Part I – Catching the Wild Ones

You are now officially part of the SDU Genetics Research Team.

Your first challenge: to find and capture *Drosophila melanogaster* — the same wild flies that once flew into Thomas Hunt Morgan’s laboratory more than a century ago.

Just like those early geneticists, your mission begins not in a sterile lab, but in the open air — where the story of every fly starts.

The common fruit fly, *Drosophila melanogaster*, is naturally drawn to fermenting fruits and sweet, yeasty smells. These flies live in kitchens, gardens, orchards, and anywhere fruit sugars begin to break down. They play an important ecological role by decomposing organic material and spreading yeast spores. Because they reproduce quickly, they are also ideal for studying inheritance and development.

Task 1 — Build a Fruit Fly Trap and Collect Wild Flies

To collect wild *Drosophila* and observe their behavior and characteristics.

Materials Needed:

- 1 empty **plastic bottle or jar**
- **Ripe fruit** (banana, apple, or peach)
- A **paper funnel** or plastic wrap with holes
- Labels and permanent marker
- Gloves and small brush

Procedure:



1. Cut the top of the bottle to form a funnel shape or insert a paper funnel.
2. Place pieces of fruit and sprinkle yeast inside — the yeast will ferment and attract flies.
3. Label your trap with your **group name, location, and date**.
4. Leave the trap for **24–48 hours** in a warm, shaded place (e.g., near fruit trees or garbage bins).
5. When flies enter, gently cover the opening and bring the trap to the lab.
6. Use a **brush or aspirator** to transfer flies into a small vial with prepared medium.

Write down your observation

Parameter	Your Observation
Date and location of trap	
Type of fruit used	
Approximate number of flies collected	
Behavior (active, sluggish, attracted to light, etc.)	
Visible differences (eye color, wing shape, body size, etc.)	

Questions

1. Why do fruit flies prefer fermented or overripe fruit instead of fresh fruit?
2. What challenges did you face during trapping or transferring flies? How did you solve them?
3. Why are *Drosophila* ideal for genetics studies?
4. What ecological niche do they occupy?

Task 2 — Crossing the Wild Flies

Once your group has caught wild flies, you will cross them to establish your **wild-type line** in the lab.

Steps:

1. Select **3–4 females** and **2–3 males** from your trapped flies.
2. Transfer them to a clean vial with a fly medium.
3. Label it as **P generation (Wild × Wild)**.
4. Observe for **3–4 days** until eggs appear on the surface of the medium.
5. Keep the vial at **25 °C** and observe daily changes.

Your fly vials are now alive with activity — tiny white dots on the surface of the medium, small larvae twisting through the food, and brown capsules clinging to the walls.

You are witnessing what generations of scientists have marveled at: the **complete metamorphosis** of *Drosophila melanogaster*.

Just as Morgan's students once did, your task is to carefully observe, describe, and draw every stage of this transformation — from the tiny egg to the winged adult.

Drosophila melanogaster undergoes **holometabolous development**, which means it passes through four distinct life stages:

1. **Egg** → 2. **Larva** → 3. **Pupa** → 4. **Adult**

Each stage represents a major change in structure and function — and each can be clearly observed in your own culture vials if you look closely.

Task 3

1. Observe your vial daily and identify which stages are visible.
2. Use a **hand lens or stereomicroscope** to examine details of shape, movement, and color.
3. In your notebook, **draw or photograph** each stage.
4. Write a **brief description (2–3 sentences)** for every stage — focusing on morphology, color, size, and behavior.

Questions

1. How can you recognize the egg stage in your vial?
2. What differences can you see between early and late larvae?
3. Why do pupae attach to the walls of the vial instead of staying in the food?
4. How can you distinguish newly emerged adults from older ones?

Part II – “The Secret Recipe of Life”

The wild flies you caught have arrived safely in the lab. They hover restlessly in their vials, waiting for the food that will sustain their next generations.

But this time, there’s no ready-made medium on the shelf — *you* must create it.

Just as early geneticists did, your team will experiment with proportions, texture, and timing to prepare the perfect environment for *Drosophila melanogaster*.

The future of your colony depends on how carefully you mix science with precision.

Drosophila feed on simple carbohydrates and yeast that ferment to produce energy and vitamins. The medium also requires agar to solidify and an acid (like propionic acid or vinegar) to prevent mold. A well-prepared medium supports the full fly life cycle — egg, larva, pupa, and adult — in a small glass vial.

Flies cannot survive if the medium is too watery, too dry, or contaminated with fungi. Every step of preparation reflects the balance between chemistry and biology — turning ingredients into a living ecosystem.

To prepare and describe, in your own words, the procedure for making the standard *Drosophila* medium used in genetics laboratories.

Given Ingredients (per 1 liter of medium):

Ingredient	Amount
Corn flour	80 g
Sugar	40 g
Glucose/ Fructose	20
Agar	8 g
Dry yeast	15 g
Propionic acid or vinegar	2 mL
Distilled water	1 L

Task 4

1. You are provided with all ingredients and basic lab equipment and preparing medium for 200ml.
2. Using your understanding of cooking, chemistry, and logic, **write your own complete step-by-step procedure** for preparing the medium.

Questions

1. Why should yeast and acid be added only after the mixture has cooled?
2. How might incorrect measurements affect the life cycle or health of your flies?
3. What happens if the medium becomes too wet or too dry?

Part III – Discovering Mutations

Your wild-type flies are thriving in the medium you prepared — healthy, active, and red-eyed.

But on the next bench, the “Mutant Gallery” awaits: tiny flies with curled wings, strange body colors, or snow-white eyes. Each one tells a story written not in words, but in DNA.

As a research team in the SDU Genetics Lab, your new assignment is to become a *fly detective* — to observe, photograph, and describe how single genetic changes can reshape an organism’s entire appearance.

Mutations in *Drosophila melanogaster* often produce visible differences, called **phenotypes**, that can be easily observed under a stereomicroscope.

Although these differences are caused by changes in genes, at this stage your goal is **phenotypic observation** — training your eye to recognize and describe traits accurately and scientifically.

Each mutant line is a window into genetic variation. Careful observation builds the foundation for later experiments on inheritance and analysis

Task 5 — Identify and Classify

1. From the available laboratory mutants, choose any five lines
2. Observe each mutant and the wild-type fly under a stereomicroscope.
3. Take clear photos of each fly using a smartphone or digital camera (side and top view).
4. For each mutation, describe its key visible features (eye color, body color, wing shape, bristles, size, and general behavior).
5. Insert your photos and notes below.
6. Label all images with mutation name, date, and group number.

Questions

- How can you distinguish male mutants from female mutants?
- What does studying visible mutations in *Drosophila* teach you about how small DNA changes can lead to major physical effects?
- How might mutations that change color, wing shape, or bristles relate to underlying protein functions in the fly?

Part IV – “The First Cross: From Observation to Hypothesis”

Weeks of work have brought you here.

You have learned to catch wild flies, prepare their food, and recognize the mutations that make them unique.

Now, you step into the role of a true geneticist.

Your mission: to select two mutant lines, identify males and virgin females, perform your first controlled cross, and record the offspring of the next generation.

Every fly you count will bring you closer to answering a question that shaped modern biology — *how are traits inherited?*

Background Information

1. Sex Differences in *Drosophila melanogaster*

Male and female *Drosophila* are easily distinguished under a stereomicroscope:

Feature	Male	Female
Body size	Smaller and more compact	Larger and elongated
Abdomen tip	Dark, rounded tip	Light, pointed tip
Sex combs	Present – small black bristles on forelegs	Absent
Genital plate	Visible dark patch on ventral abdomen	Absent
Behavior	Often more active, courtship behavior	Usually calmer

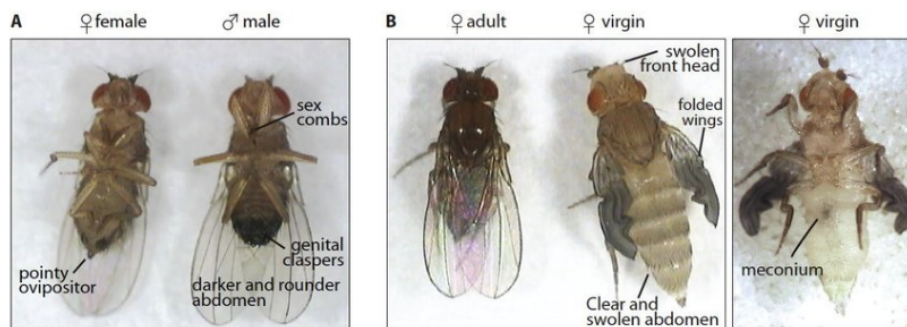
Virgin females are females that have not mated yet.

They must be collected within 8–10 hours after emergence from the pupa, before mating occurs.

Virgins are important because they guarantee that you know the exact parents in your cross.

Key visual cues:

- Lighter body color (not yet fully pigmented).
- Meconium (a small dark spot) visible inside the abdomen.
- Wings are still soft and held closed.
- They are often resting near empty pupal cases.



You have successfully performed your first *Drosophila* cross — selecting two mutant lines, identifying males and virgin females, setting up the cross, and observing the F₁ generation.

Now it's time to **document what you did**, step by step, as a scientist would in a real genetics report.

Remember, this section should not simply repeat instructions — it should show that you understand **how** and **why** each step was performed.

Task 6

Write a detailed description of how you performed your cross experiment.

Your description should include the following **stages**:

1.a. Identifying Parents

- a. How did you distinguish between **males and females**?
- b. How did you find or collect **virgin females**?
- c. What mutants did you choose for your cross?

2. b. Setting Up the Cross

- a. How many flies did you use?
- b. How did you transfer them to the vial?
- c. How did you label and store your vial?
- d. What were the environmental conditions (temperature, light, etc.)?

3. c. Observation and Documentation

- a. How did you document your setup? (e.g., taking photos, labeling, uploading to drive)
- b. How did you recognize when F₁ flies appeared?
- c. What phenotypes did you observe in F₁?
- d. How did you count and record your results?

4. Include Photos

- a. Attach or insert **your own photos** from the experiment:
 - i. Parental flies (male and female)
 - ii. Cross vial (with label visible)
 - iii. F₁ generation flies

5. Summarize your Observations

- a. How many F₁ flies did you count?
- b. What were their main visible traits?
- c. Were they similar to or different from the parental flies?

Questions

1. Which part of the procedure was the most challenging? Why?
2. How did you ensure that your cross involved only the chosen parent flies?
3. Why is labeling vials accurately important in *Drosophila* genetics?
4. What was the most noticeable difference between parent and F₁ flies?
5. What did this experiment teach you about precision and observation in genetics research?

Data Table – F₁ Generation

Phenotype (Describe in Words)	Photo / Sketch	Number of Flies Observed
Total Count:		

Task 7. Formulating Your Hypotheses

Before you perform the Chi-square test in the next section, you must create your hypotheses clearly and in testable form.

Type	Statement
Null Hypothesis (H ₀)	
Alternative Hypothesis (H ₁)	

only state the hypotheses

Questions

A. Identification and Technique

1. What were the most reliable features for distinguishing males from females?
2. How did you identify virgin females — what color or texture cues did you notice?
3. Why is using virgins essential for controlled crosses?

B. Observation and Data

4. How did the F_1 generation differ from the parental mutants?
5. Were all F_1 flies identical, or did you notice variation?
6. How might environmental factors (temperature, humidity) influence development or phenotype visibility?

C. Scientific Reasoning

7. What is the purpose of formulating a null and alternative hypothesis before analyzing data?
8. How does systematic counting improve the reliability of your results?
9. What problems might arise if male and female flies were misidentified?
10. What did this experiment teach you about the precision required in genetics research?

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