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The Effect of Using BLAST (Basic Local Alignment Search Tool) on the Conceptual Understanding of Students on Evolutionary Concepts

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Abstract

This study aimed to determine the effect of using the Basic Local Alignment Search Tool (BLAST) on students' learning independence and conceptual understanding of evolution at the senior high school level. The research uses a quantitative approach with a weak experimental, one-group pretest-posttest design. The study population consists of Grade XII Science students at a public senior high school in Tangerang, Indonesia. A random sample of 70 students formed the experimental group. Data collection used non-test methods, such as questionnaires for learning autonomy and essay tests for conceptual understanding. The average learning independence score was 79.1, indicating high independence. The average concept understanding score was 57.9, categorized as sufficient. Data analysis for learning independence used the Paired-Samples Test, while concept understanding was analyzed with the nonparametric Wilcoxon test. Results showed the use of BLAST had a significant effect on improving students' learning independence and conceptual understanding, with a p-value of $<0.001 < 0.05$.

Keywords: BLAST, Computational Inquiry-based Teaching, Evolution, Conceptual Understanding, Bioinformatics Learning.

INTRODUCTION

Biology education is a medium for scientific thinking, which students greatly need. It develops critical thinking skills that require self-motivation (Firmansah, 2021). Most students view biology as a complicated subject because it is abstract. Therefore, it requires learning supported by concrete evidence to validate the science, especially in the case of evolution. As science and technology rapidly advance, learning activities can adapt to maximize their impact through better facilities, infrastructure, and teaching and learning processes. Technology provides various learning media, including bioinformatics. Bioinformatics combines biology, computer science, information systems, mathematics, and statistics to support the analysis of large data sets (Mahrus et al., 2021).

Bioinformatics uses software and databases to study genes, proteins, and genomes in an organism (Ningrum et al.; Zulkifli et al., 2021). It can help organize large amounts of genetic data for analysis. This is useful for students studying evolutionary relationships among living organisms (Pratiwi et al., 2018). Many bioinformatics resources are available online for free. One relevant tool for learning evolutionary concepts is BLAST on the NCBI website. BLAST (Basic Local Alignment Search Tool) can be used to reconstruct species phylogeny. It provides reference data, including accurate sequence information for a species, quickly (Wangiyana, 2022). Another bioinformatics resource is e-BiMo. It covers bioinformatics and related tools for biology education. e-BiMo presents three themes: genetic disease, forensic science, and evolution. It uses the CIbT (Computational Inquiry-based Teaching) model, which includes Orientation, Conceptualization, Investigation, Conclusion, and Discussion for each theme (El Islami & Sari, 2023). These stages include pre-learning questions, relevant videos, and case examples that encourage student discussions. There are also self-guided practice exercises with guidelines for using BLAST and for building a phylogenetic tree. These activities are expected to enhance students' understanding of abstract biological material.

Conceptual understanding is a process where an individual understands and categorizes something (Hikmah et al., 2017). It is a cognitive process in which one can accurately and coherently explain a concept and flexibly apply this knowledge across different contexts. This view aligns with the idea that conceptual understanding is more than theory. It includes the ability to transfer and use knowledge in new situations (Mestre, 2002; Kulasegaram et al., 2017; Perkins & Salomon, 1992; Schönborn & Bögeholz, 2009). Teachers can use conceptual understanding as a benchmark for assessing their teaching. If students understand a concept, the models and methods used can be considered successful. A student is considered to understand a concept if they can grasp its meaning and explain it in their own words, thereby making learning meaningful (Nahdi et al., 2016).

The success of students' understanding of concepts is measured through tests based on indicators by Anderson and Krathwohl (2001): 1) Interpreting: the ability to translate or explain something verbally, in writing, or in images. Students not only remember information, but also process it for different situations. 2) Exemplifying: the ability to find illustrations and provide examples. Students give relevant examples from their own experience, connecting theory to concrete situations. 3) Classifying: the ability to group items into categories. Students identify features of a concept and sort items by shared traits or rules. 4) Summarizing: the ability to present the main ideas in a shorter, concise way without losing meaning. 5) Drawing inferences: the ability to make logical conclusions not directly stated, based on available evidence. 6) Comparing: the ability to connect or contrast two ideas, objects, or phenomena—to identify similarities and differences. 7) Explaining: the ability to clearly describe a concept, process, or phenomenon in a logical way that others understand.

Several factors influence students' conceptual understanding: 1) Teaching methods. How teachers interact with students strongly affects understanding. Direct, engaging methods help students understand better. 2) Learning interest. Students with low interest often struggle to understand and are less motivated to study. In contrast, students with high interest are more diligent and achieve higher understanding. 3) Individual cognitive ability. Each student has unique cognitive skills. Those with above-average ability learn concepts more easily, while those below average find it harder (Safitri et al., 2021).

Relevant research by Mahrawi et al. (2019) used Project-Based Learning (PJBL) to study outcomes in evolution courses. The study found that the PJBL model improves learning results in the evolution course. Other studies show web-based and blended learning environments help students' conceptual understanding and learning independence in mathematics (Mlotshwa et al., 2020; Tong et al., 2022). Therefore, this study uses the CIbT model and the NCBI website to measure students' conceptual understanding.

Based on the context above, the research needs to be modified to use the BLAST tool to analyze variable y: students' understanding of evolution. School needs analysis at School A and School B found that School B has better facilities and uses e-learning and various technologies. However, biology has not been taught using bioinformatics. The research aimed to determine whether BLAST influences students' understanding of biology concepts, particularly evolution.

METHOD

The research method used was a weak experimental design with a One-Group Pretest-Posttest design. In Arikunto's (2018) research design, the pretest was administered before learning with e-BiMo; then students received treatment with e-BiMo and were given the opportunity to create phylogenetic trees manually (unplug) and using the BLAST tool on e-BiMo (plug). Finally, the posttest was administered after the treatment to determine the extent of the treatment's effect. The research was conducted at a public senior high school in Tangerang, Indonesia. The research subject was determined using random sampling from 7 biology classes, with 70 Grade XII MIPA students selected as the experimental class. The research object was students' learning outcomes after using the new learning medium, the BLAST bioinformatics tool. Data collection techniques included a test consisting of 7 essay questions to measure students' conceptual understanding and an observation sheet to measure BLAST achievement.

The collected data were analyzed using inferential statistical techniques in SPSS version 29.0, namely the Shapiro-Wilk test for normality, the Levene's test for homogeneity, and the Paired Sample Test for hypothesis testing. If the data analysis revealed that the data were not normally distributed or homogeneous, the nonparametric Wilcoxon Signed-Rank test was used for hypothesis testing.

RESULTS AND DISCUSSION

Students' conceptual understanding was analyzed by comparing pretest and posttest scores in the experimental class. The data showed an increase in students' conceptual understanding of evolutionary material when using the bioinformatics tool Basic Local Alignment Search Tool (BLAST). In the experimental class, the average pretest score was in the very low category (27.3), while the average posttest score was in the moderate category (57.9). This data indicates a 30.6-point increase in the learning process after treatment using the Basic Local Alignment Search Tool (BLAST). The significant difference between the pretest and posttest scores was due to the fact that most students had never received similar material at school or in their daily lives, so many students answered the pretest questions with little knowledge or did not answer at all. Then, there was an improvement after the treatment, in the form of evolution learning, using the Computational Inquiry-based Teaching (CIbT) method with the bioinformatics tool Basic Local Alignment Search Tool (BLAST). The comparison of pretest and posttest scores for students' conceptual understanding is shown in Figure 1.

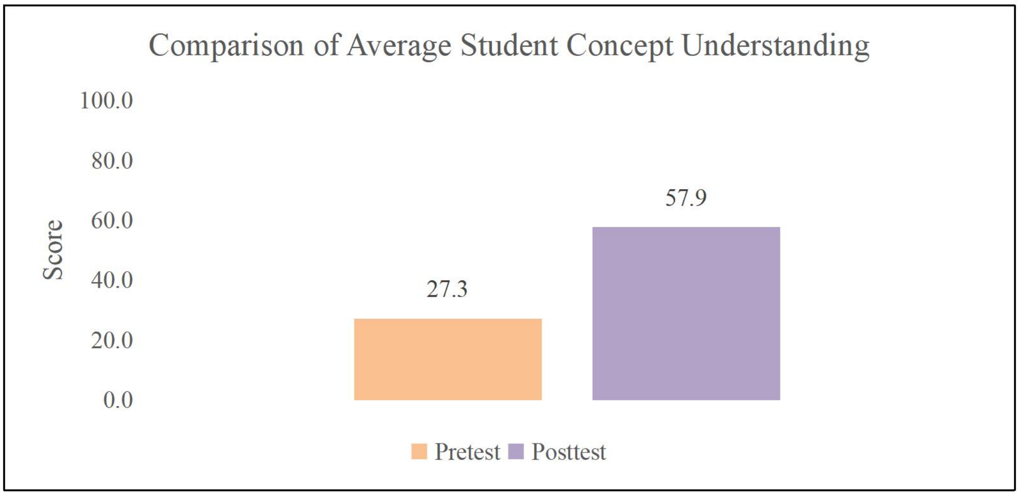

Figure 1. Average Student Conceptual Understanding

The average results were then tested for normality and homogeneity before hypothesis testing in SPSS version 29.0. In the normality test, the pretest results for the experimental class showed a p-value < 0.001, and the posttest results showed a p-value of 0.003. Based on the normality test results of the pretest and posttest, the p-value was <0.05, indicating that the data were not normally distributed. In the homogeneity test, the p-value was 0.109 (p-value > 0.05), indicating that the data were homogeneous. The hypothesis test used was the non-parametric Wilcoxon Ranked-Sign test because the data did not meet the prerequisites (the data was not normally distributed). In the non-parametric Wilcoxon Ranked-Sign test, the Asymp.sig value was <0.001 (Asymp.sig < 0.05), indicating a significant difference between the pretest and posttest scores in both experimental classes, consistent with the rejection of the null hypothesis (H0) and acceptance of the alternative hypothesis (Ha) (The use of the BLAST tool influences high school students' understanding of evolutionary concepts at SMA Negeri 2 Kota Tangerang). This aligns with the average concept understanding scores (Figure 1), which show a positive effect of the BLAST tool on students' concept understanding. The results of the SPSS test on the effect of the BLAST tool on students' conceptual understanding are shown in Table 1.

Table 1. Results of Concept Understanding Data Analysis

Normality Test	*p-value* = <0,001	*p-value* = 0,003	·The pretest yielded a p-value < 0.05, which means that the data is not normally distributed.
Normality Test	*p-value* = <0,001	*p-value* = 0,003	·The posttest yielded a p-value < 0.05, which means that the data is not normally distributed.
Homogenity Test	*p-value* = 0,109	*p-value* = 0,109	A p-value > 0.05 means that the data variation within the group is homogeneous.
Non-Parametric Test (Wilcoxon)	<0,001	<0,001	The Wilcoxon test yielded a value of Asymp.sig < 0.005, meaning that H0 is rejected and Ha is accepted.

The influence of the BLAST bioinformatics tool on students' understanding of concepts is further reinforced by data on the percentage of students who understand each concept (Figure 2). The pretest percentage scores showed an average of 0% in the very high category, 1% in the high category, 3% in the sufficient category, 13% in the low category, and 83% in the very low category. Then, the post-test percentage results for the very high category were 4%, the high category 26%, the sufficient category 39%, the low category 31%, and the very low category 0%. There was an increase in students' conceptual understanding: pretest scores were predominantly in the very low category, but after treatment with the BLAST bioinformatics learning tool, scores were predominantly in the moderate category. This indicates that using the BLAST tool in learning can improve students' conceptual understanding in science, including the concept of evolution. There was an increase in students' conceptual understanding: pretest scores were predominantly in the very low category, but after treatment with the BLAST bioinformatics learning tool, scores were predominantly in the moderate category. This indicates that using the BLAST tool in learning can improve students' conceptual understanding in science, particularly of the concept of evolution. This finding is consistent with previous studies showing that bioinformatics tools such as BLAST facilitate students' understanding of complex biological concepts by enabling exploration of sequence similarity and evolutionary relationships (Kerfeld & Scott, 2011;

Kovarik et al., 2013; Martins et al., 2020; Sari et al., 2022). Furthermore, integrating bioinformatics-based learning has been shown to promote deeper conceptual engagement and improve students' ability to interpret abstract concepts in genetics and evolution through data-driven inquiry. The percentages of students' conceptual understanding scores in each category are shown in Figure 2.

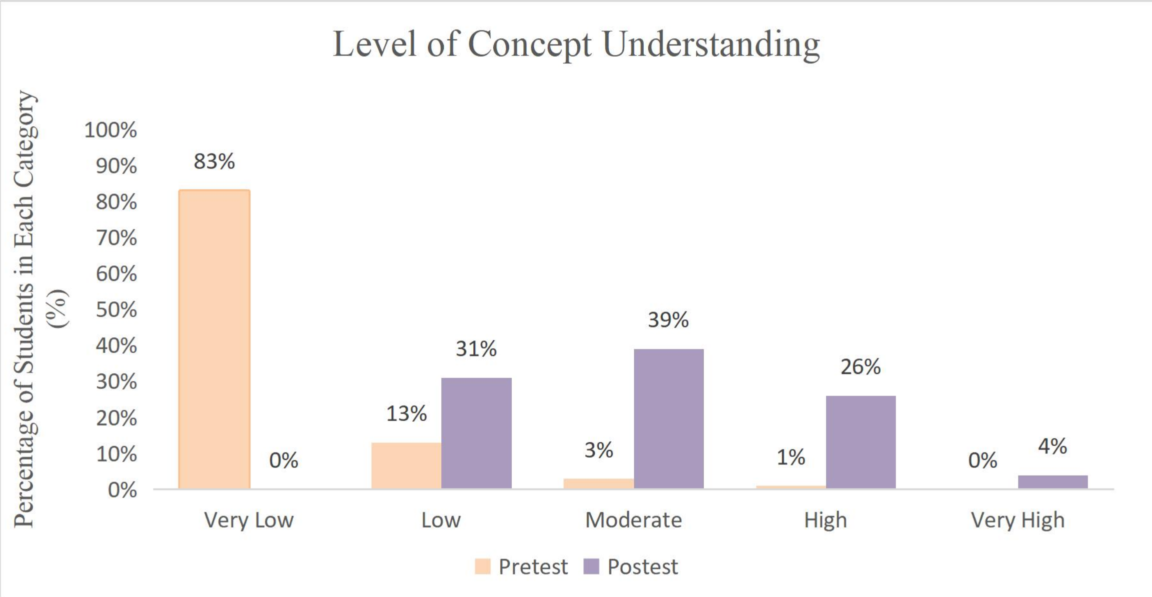

Figure 2. Percentage of Students' Conceptual Understanding Levels in Each Category

This learning activity uses e-BiMo as an application of the BLAST bioinformatics tool through the Computational Inquiry-based Teaching (CIbT) method with the syntax orientation, conceptualization, investigation, conclusion, and discussion developed by Sari et al. (2022). The CIbT syntax, consisting of orientation, conceptualization, investigation, conclusion, and discussion, provides space for students to actively engage in the learning process in line with the concept understanding indicators according to Anderson and Krathwohl (2001) in Susanti et al. (2021), namely interpreting, classifying, summarizing, drawing inferences, comparing, and explaining.

In the orientation stage, students are directed toward a contextual problem that stimulates their curiosity, prompting them to interpret initial information and connect it to their prior knowledge. The conceptualization stage encourages students to summarize information and compare relevant concepts to build a theoretical foundation. The investigation stage represents the core of the CIbT learning process, in which students explore data through both unplugged activities (e.g., manually sorting and comparing DNA sequences) and plugged activities (e.g., using BLAST bioinformatics software). During this stage, students classify data, identify patterns, and compare similarities and differences, which supports analytical and higher-order thinking skills. In the conclusion stage, students are encouraged to draw evidence-based inferences and determine the phylogenetic relationships of *Homo sapiens* based on the constructed phylogenetic tree. Finally, during the discussion stage, students present their findings to the class, thereby enhancing their communication skills and reinforcing their conceptual understanding. These findings are consistent with previous studies indicating that inquiry-based and bioinformatics-supported learning environments improve students' conceptual understanding, data interpretation skills, and engagement in learning complex biological concepts such as evolution and genetics (Kerfeld & Scott, 2011; Kovarik et al., 2013; Magana et al., 2014; Goller et al., 2021; Martins et al., 2020; Jungck & Weisstein, 2013). Furthermore, active learning strategies involving data analysis and collaborative discussion have been shown to promote deeper learning and meaningful knowledge construction, particularly in science education contexts (Freeman et al., 2014; Prince, 2004; Michael, 2006). Therefore, the CIbT approach not only facilitates cognitive understanding but also fosters an active, meaningful, and data-driven learning experience. Thus, the use of the CIbT method aligns with the concept understanding indicators proposed by Anderson and Krathwohl (2001) in Susanti et al. (2021), which serve as a reference for tests to measure students' concept understanding.

The conceptual understanding data results, per indicator, show an increase from the pretest to the posttest (Figure 3). The indicator with the highest percentage is the classification indicator, and the lowest is the comparison indicator. The conceptual understanding component data, per indicator, are shown in Figure 3.

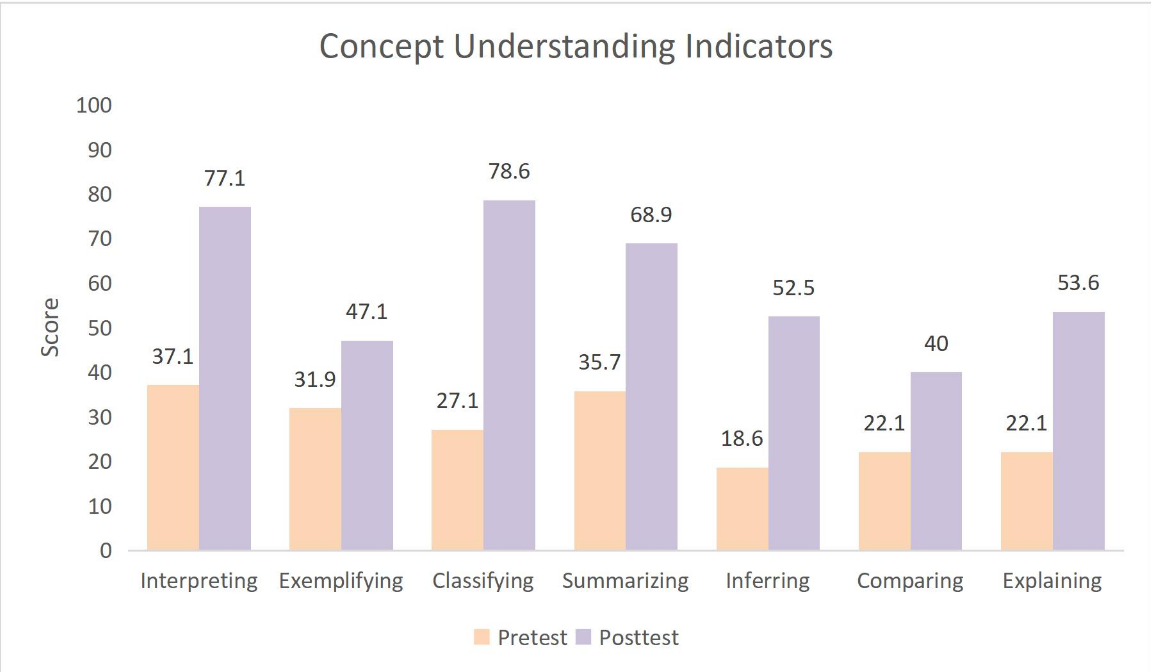

Figure 3. Score of Concept Understanding Indicators

The indicator was classified as high, with a pretest average of 27.1 and a posttest average of 78.6. The indicator showed a significant increase from the very low to the high category. Questions about the random extinction of species due to forest fires require students to analyze and classify the evolutionary mechanisms at work. Based on the test results for question 9, the majority of students correctly answered that genetic drift through the bottleneck effect causes changes in allele frequency. This shows that students can analyze evolutionary mechanisms and classify them according to the narrative questions provided. In learning activities using the CIbT method with the BLAST bioinformatics tool, students can classify closely related species based on their nucleotide base similarities. Learning using the CIbT method with the BLAST bioinformatics tool is an inquiry- and data-based approach that can help students practice classificatory reasoning. This aligns with the opinion of Prasetiyo & Rosy (2021) that students who are taught and learn through inquiry-based methods tend to be more motivated to develop critical thinking skills, one aspect of which is classifying ideas about objects. Based on the available percentage data, the highest percentage indicates that context-based questions presented in narratives or images are easier for students to understand, suggesting that students find it easier to understand concepts when presented in real-life cases or stories.

The indicator comparing fell into the low category, with an average pretest score of 22.1, and increased in the posttest, with an average of 40.0. Based on the difference between the pretest and posttest scores, the indicator increased from the very low to the low category, indicating an improvement in understanding, but it is still limited. The questions tested students' ability to distinguish between natural selection and adaptation, two evolutionary mechanisms that are often misunderstood because of their interconnection in the evolutionary process. According to the questionnaire results, most students mentioned only the definitions of natural selection and adaptation, but did not understand the key differences and characteristics of the two (Appendix 18). In the observation results, learning activities using the CIbT method with the BLAST bioinformatics tool allowed students to compare DNA sequences both manually (unplugged) and using the BLAST tool (plugged). These results demonstrate that although the use of the BLAST tool improved performance, some students still struggled to identify the conceptual differences between natural selection and adaptation. The comparison indicator had the lowest percentage among the indicators due to a lack of literacy skills and practice in comparing similar concepts, leading students to understand the concepts separately but struggle to explain their differences systematically. For example, in question 10, students mentioned the definitions of natural selection and adaptation separately, without explaining the fundamental differences between the two. In the question comparing natural selection and adaptation, students should not only know the definitions separately but also be able to relate and explain the differences between the two concepts in a structured manner, including their definitions, individual focus, and mechanisms. Sitanggang et al. (2024) state that students with high levels of science literacy will easily understand biological concepts, identify and analyze data, and draw appropriate conclusions.

The interpreting indicator is in the high category, with an average pretest score of 37.1 and a posttest score of 77.1. Interpreting is the process of understanding, organizing, and explaining the meaning of information, whether written, visual, or symbolic, into other forms of information that are easier to understand (Al Haq & Raicudu, 2023). The description questions that raise the phenomenon of natural selection in giraffes facilitate students' understanding and interpretation of concepts in context. Students are not asked to memorize; rather, they are directed to understand the biological context of the given situation, relate real phenomena to theoretical concepts, and explain scientific mechanisms based on the given narrative. Visual and narrative context-based questions will help students visualize abstract concepts, as seen in students' answers, which tend to interpret the mechanism of natural selection using the giraffe example. Then the ability to interpret students can be seen through learning activities using the CIbT method with the help of the BLAST tool, teaching media in the process of analyzing data based on case examples using BLAST, and then interpreting the phylogenetic tree visualization that has been made, so that simultaneously students' critical and conceptual thinking skills develop. This aligns with the research of Sari et al. (2022), which found that learning activities using the CIbT method with bioinformatics media support.

The exemplifying indicator is in the low category, with an average pretest score of 31.9, and has increased in the posttest, with an average of 47.1. Based on the difference in pretest and posttest scores, there is an increase in the exemplification indicator from the very low category to the low category, which means that some students have begun to understand the concept that two different species can be closely related by looking at existing evidence of evolution, but there are some students who are still lacking in exploring examples outside the material taught and lack of practice in generalizing the concept of evolutionary evidence so that there are still limitations in finding other examples. Learning with the CIbT method with BLAST media helps students create phylogenetic trees through DNA sequence analysis activities. In this process, students present examples of species with close kinship based on genetic sequence matches. For example, in the investigation activity, students can exemplify that humans are closely related to chimpanzees based on the level of genetic sequence similarity. In addition, in the conclusion activity, students discuss other species that are closely related. Based on the results of questionnaires and student observations, there is an increase in the indicator of exemplification, but further reinforcement is still needed for other examples to build students' ability to generalize a concept to examples they encounter around them. Al Haq & Raicudu (2023) stated that some students have not been able to provide examples or apply concepts to several other problems, so it is necessary to provide reinforcement in analyzing objects based on concepts, restating concepts with other representations, and linking concepts with examples that students can describe.

The summarizing indicator is in the moderate category, with an average pretest score of 35.7 and an average posttest score of 68.9. In learning activities using the CIbT method with BLAST media, students can summarize the kinship of chimpanzees with Homo sapiens through the phylogenetic tree they create. Then, from the results of observations in the conclusion activity, students can draw conclusions at the conceptualization and investigation stages. The questionnaire results show that students understand the concept of biological kinship between Homo sapiens and chimpanzees, with 95% of students answering that humans and chimpanzees are closely related or share a common ancestor because they have genetic kinship, as evidenced by 95% DNA similarity. This shows that students understand the concept of kinship among living things by being able to extract core information from a phylogenetic tree based on BLAST analysis results and write it concisely. In line with the opinion of Susanti et al. (2021), that students who understand a concept have a basis for understanding complex concepts effectively organized.

The indicator of drawing inferences is in the low category, with an average pretest score of 18.6 and an increase in the posttest score to 52.4. The questions given require students to watch the video “Seven Million Years of Human Evolution” and then draw inferences about the evolutionary process, which will later be associated with students' initial understanding of evolution. The increase in the indicator of drawing inferences from the very low to the low category shows that students can connect visual information to concepts of evolutionary mechanisms such as natural selection, adaptation, and mutation. The use of the BLAST tool in DNA sequence analysis activities requires students to analyze genetic differences between humans and other organisms, then relate them to evolutionary theories such as natural selection mechanisms and genetic mutations. This process trains students to draw logical, scientific conclusions from sequence-matching results, thereby directly developing their inferential skills. In line with the opinion of Sari et al. (2022), learning bioinformatics by comparing and interpreting DNA sequences requires pattern recognition, which involves recognizing recurring patterns and generalizing them into conceptual understanding.

The explanation indicator was categorized as sufficient, with an average pretest score of 22.1 and an average posttest score of 53.6. This improvement indicates that students began to develop conceptual understanding and were able to reconstruct and communicate concepts using their own sentence structures. The assessment items required students to explain the concept of phylogenetic trees and their relationship to evolution. This is reflected in students' responses, which demonstrate their ability to describe phylogenetic trees as representations of relationships among species based on similarities in genetic and morphological characteristics, and to relate tree structures to evolutionary processes such as gradual change and common ancestry. These findings are consistent with previous studies indicating that students' conceptual understanding of evolution improves when they engage with visual representations and data-driven analysis, particularly through phylogenetic trees (Novick & Catley, 2013; Meir et al., 2007; Halverson et al., 2011). Furthermore, the use of bioinformatics tools such as BLAST supports students in interpreting molecular data and understanding evolutionary relationships, thereby facilitating the construction of scientific explanations (Kerfeld & Scott, 2011; Kovarik et al., 2013; Martins et al., 2020). Visualization of phylogenetic trees, combined with authentic data analysis, has also been shown to enhance students' ability to integrate abstract concepts into coherent scientific reasoning (Gregory, 2008; Baum et al., 2005). In line with the research of Sari et al. (2022), who found that BLAST is the most frequently used bioinformatics tool in high schools and tends to improve students' cognitive skills in Biology.

CONCLUSION

Based on the results of the study, it can be concluded that the use of the Basic Local Alignment Search Tool (BLAST) can significantly improve students' understanding of evolution material at the senior high school level, with a Wilcoxon nonparametric test p-value of <0.001 (<0.05). Concept understanding increased from the very low category to the moderate category with an average score of 57.9. The highest indicator of concept understanding is classifying, and the lowest is comparing. Based on these results, the use of the Basic Local Alignment Search Tool (BLAST) affects high school students' understanding of evolution.

SUGGESTIONS

The research was conducted with limited time and respondents, so it is suggested that future researchers conduct testing with more time and meetings to explore the BLAST feature more deeply. Future researchers are expected to expand the study by examining the influence of bioinformatics on other aspects, using a larger sample.

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