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Original Article

A Comparative Review of Liquid Biopsy and AI-Powered Precision Medicine in Medulloblastoma: A Paradigm Shift in Diagnosis and Treatment

Sewanu Stephen Godonu, Aafrin Steffi Vijaya Kumar Glory

All American Institute of Medical Sciences

ABSTRACT

This study investigates revolutionary advancements in medulloblastoma treatment by combining liquid biopsy with AI-powered precision medicine. Early identification and individualized treatment plans are made possible by these technologies' non-invasive, real-time insights into tumor processes. The objectives of this strategy are to optimize patient-specific therapy, increase diagnostic accuracy, and eventually improve outcomes in pediatric neuro-oncology by examining biomarkers, such as circulating tumor DNA, and using sophisticated AI algorithms to understand complicated multi-omics data. One of the most difficult children brain tumors to diagnose and treat is medulloblastoma. This paper describes a revolutionary integrated strategy that combines liquid biopsy with AI-powered precision medicine to non-invasively monitor tumor dynamics and tailor treatment. In pediatric neuro-oncology, the methods seek to improve patient outcomes by optimizing therapy approaches, improving diagnostic accuracy, and utilizing real-time biomarker monitoring and sophisticated data modeling.

Keywords: Medulloblastoma, Liquid Biopsy, AI-Driven Precision Medicine, Circulating Tumor DNA (ctDNA), Circulating Tumor Cells (CTCs), Extracellular Vesicles (EVs), MicroRNAs (miRNAs), Biomarkers, Tumor Dynamics, Non-Invasive Monitoring, Molecular Subtyping, Risk Stratification, Minimal Residual Disease (MRD), Multi-Omics Integration, Machine Learning, Deep Learning, Radiomics, Personalized Therapy, Treatment Optimization, Pediatric Neuro-Oncology

INTRODUCTION

Medulloblastoma is a very aggressive embryonal tumor of the central nervous system (CNS) that mostly affects children, accounting for 20% of all pediatric brain tumors (Northcott et al., 2017). These tumors are high-grade and have a tendency to spread inside the central nervous system and, less commonly, outside the neuraxis (Cassie et al., 2017). The current standard of treatment is a combination of maximally safe surgical resection, craniospinal irradiation, and multi-agent chemotherapy (Gajjar et al., 2019). Despite advancements in treatment, major obstacles persist, including high recurrence rates, therapy-induced toxicities, and long-term neurocognitive deficits, particularly in younger patients (Ramaswamy et al., 2016). A major obstacle in the treatment of medulloblastoma is the difficulty of collecting recurring tumor samples to track the course of the illness and the effectiveness of treatment. Conventional tumor samples necessitate risky, invasive neurosurgical techniques that are impractical for long-term surveillance (Taylor et al., 2019). As a result, liquid biopsy is becoming increasingly popular as a non-invasive option for real-time tumor dynamics monitoring. Liquid biopsy is the process of identifying and analyzing tumor-derived biomarkers from biofluids, including blood and cerebrospinal fluid (CSF), such as circulating tumor DNA (ctDNA), extracellular vesicles (EVs), and microRNAs (miRNAs) (Wang et al., 2021). This method has a lot of potential for improving diagnosis, risk assessment, and directing individualized treatment. The use of artificial intelligence (AI) in precision medicine is another game-changing advance in medulloblastoma treatment. AI generates insights by leveraging powerful computing and inference, allowing the system to think and learn, and using enhanced intelligence to boost clinical decision-making (Johnson K.B. et al., 2021). AI improves decision-making across several fields, including medicinal chemistry, molecular and cell biology, pharmacology,

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pathology, and clinical practices, even to the extent AI aids in the classification and selection of patient populations (Carini, Seyhan., 2024). Humans differ greatly on a genetic, biochemical, physiological, exposure, and behavioral level, particularly in relation to disease processes and response to therapy, according to research investigations using data-intensive biomedical technology (Schork N.J., 2019). AI, particularly machine learning (ML) and deep learning (DL) algorithms, has shown great promise in improving tumor categorization, predicting therapy responses, and discovering new biomarkers (Fathi Kazerooni et al., 2022). AI-driven precision medicine can offer customized treatment plans that maximize patient outcomes while reducing toxicity by utilizing multi-omics datasets, imaging modalities, and longitudinal patient data with tumors (Bzdok et al., 2020). Furthermore, AI can help detect early relapses using predictive modeling, enabling earlier therapies (Wang et al., 2023). This study will look at the synergistic potential of liquid biopsy and AI-powered precision medicine in medulloblastoma, including recent advances, clinical uses, present difficulties, and future possibilities.

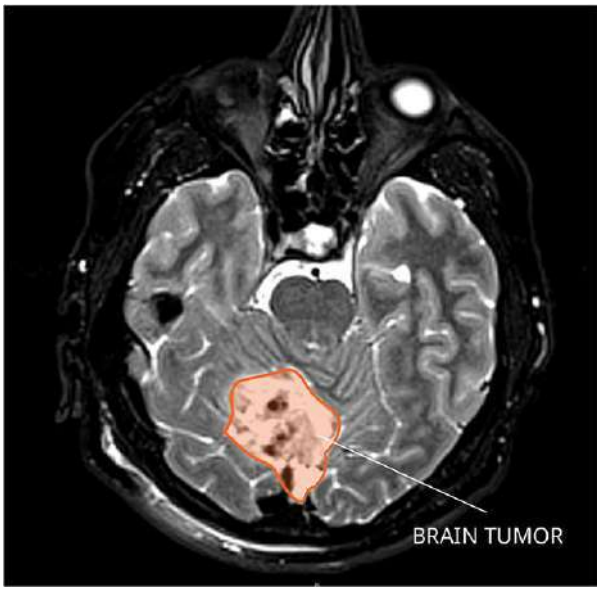

Fig. 1: MRI of medullosblastoma in the brain. Credit: NRI-CONNECT staff

Histopathology of Medulloblastoma

Histopathologically, medulloblastoma is made up of tiny, spherical, blue cells that have strong mitotic activity and hyperchromatic nuclei. The most frequent histological type, classic medulloblastoma, has tightly packed cells with Homer-Wright rosettes, indicating neuroblastic differentiation. A good prognosis and substantial nodularity with reticulin-free pale islands are characteristics of the desmoplastic/nodular variation, which is frequently linked to malignancies driven by SHH. Medulloblastoma histogenesis has been debatable for a long time. According to some writers, the germinal matrix surrounding the ventricle contains primitive neuroectodermal cells that are the primary source of it (Alessandra Rossi et al., 2008). The pleomorphic cells with big nuclei, prominent nucleoli, and abundant apoptotic bodies are characteristics of the extremely aggressive large cell/anaplastic (LC/A) variety, which is frequently associated with Group 3 tumors that have MYC amplification. Medulloblastoma with extensive nodularity (MBEN), an uncommon form, has widespread nodularity and is most commonly encountered in newborns with SHH activation, with a good prognosis (Louis et al., 2021; Roussel and Robinson, 2013). About 10% of cases are molecularly classified as the WNT subgroup, which is caused by CTNNB1 mutations that result in the accumulation of nuclear β-catenin. With a 90% survival rate, these tumors, which originate from the lower rhombic lip, have a good prognosis. SHH-driven medulloblastomas have age-dependent prognoses, are linked to PTCH1, SUFU, and SMO mutations and develop from cerebellar granule neuron progenitors. Group 3 tumors, which are frequently associated with MYC amplification, are the most aggressive with a high metastatic potential and low survival rates. The most prevalent grouping, Group 4 tumors, have isochromosome 17q and have intermediate clinical outcomes; however, their molecular causes are not well understood (Taylor et al., 2012; Ramaswamy et al., 2016). Genetic and epigenetic alterations play a crucial role in medulloblastoma pathogenesis. Mutations in CTNNB1 are commonly seen in WNT tumors, whereas SHH cancers show changes in the genes PTCH1 and SUFU involved in the hedgehog signaling pathway. Patients with MBWNT and MBSHH should undergo genetic testing as a routine of treatment since they have the greatest incidence of harmful germline mutations in the known cancer risk genes (Waszak SM et al., 2018). While Group 4 cancers usually have structural changes such as isochromosome 17q, Group 3 tumors typically display MYC amplification. Subgroup categorization has been further improved by DNA methylation

analysis, which has further improved risk stratification and revealed new treatment targets. Next-generation sequencing developments have made it possible to comprehend tumor heterogeneity more thoroughly, highlighting the role that epigenetic factor plays in the biology of medulloblastoma (Jones et al., 2012; Schwalbe et al., 2017). Optimizing the long-term prognosis, therapeutic treatments, and diagnostic accuracy for patients with medulloblastoma require a thorough understanding of the disease's histopathological and molecular landscape (Northcott et al., 2011; Eberhart et al., 2002).

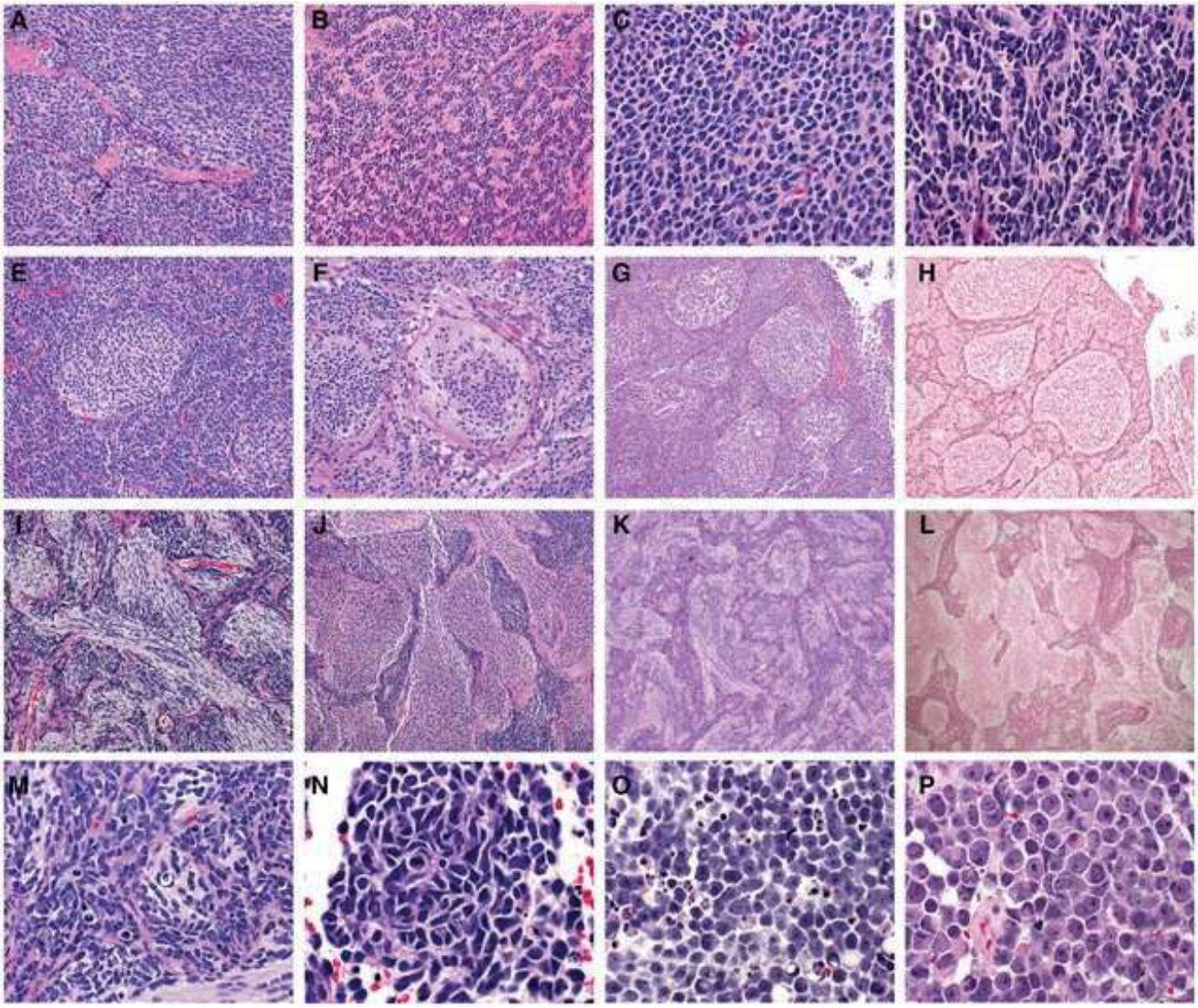

Fig. 2. There are four histologic varieties of medulloblastoma, which are histologically defined groupings. The classic variety (A-D) is characterized by tiny cells with round to oval nuclei, according to Brent A. Orr from brain pathology in 2020 (A) , frequent Homer Wright rosettes (B) , and no significant cytologic pleomorphism or cell molding (C). A slight increase in cell size and cytologic pleomorphism (D) are still within the spectrum of histologies in the classic variant. The desmoplastic/nodular variant (E-H) is characterized by nodules of neurocytic differentiation surrounded by more primitive internodular areas (E and G). The differentiated nodules show desmoplasia surrounding the nodules, which can be detected by pericellular reticulin deposition (H). Medulloblastoma with extensive nodularity (MBEN) (I-L) is characterized by a high proportion of differentiated elements compared to primitive internodular elements (F-J). The nodules in the MBEN variant often coalesce together, forming irregular patterns accompanied by a pattern of linear "streaming" between nodules. Similar to other desmoplastic nodular tumors, MBENs show reticulin deposition in the internodular regions (L). The large cell/anaplastic variant (LCA) is a combination of two variants, the anaplastic variant and the large cell variant (M-P). The anaplastic variant is characterized by increased cell size, cytologic pleomorphism, cell molding and

wrapping, frequent mitotic activity, and apoptotic bodies (M and N). The large cell variant is characterized by large discohesive cells with prominent nucleoli (O and P).

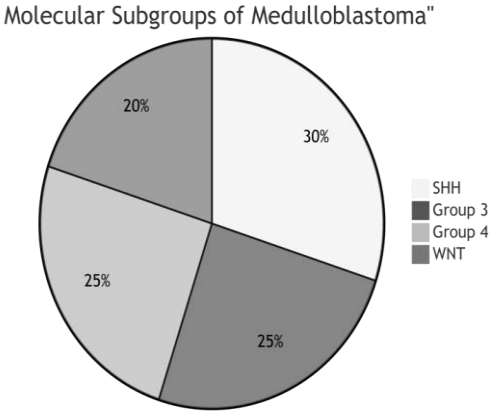

Fig. 3. Piechart representing the four molecular subgroups (WNT, SHH, Group 3, Group 4). Created in Draw io

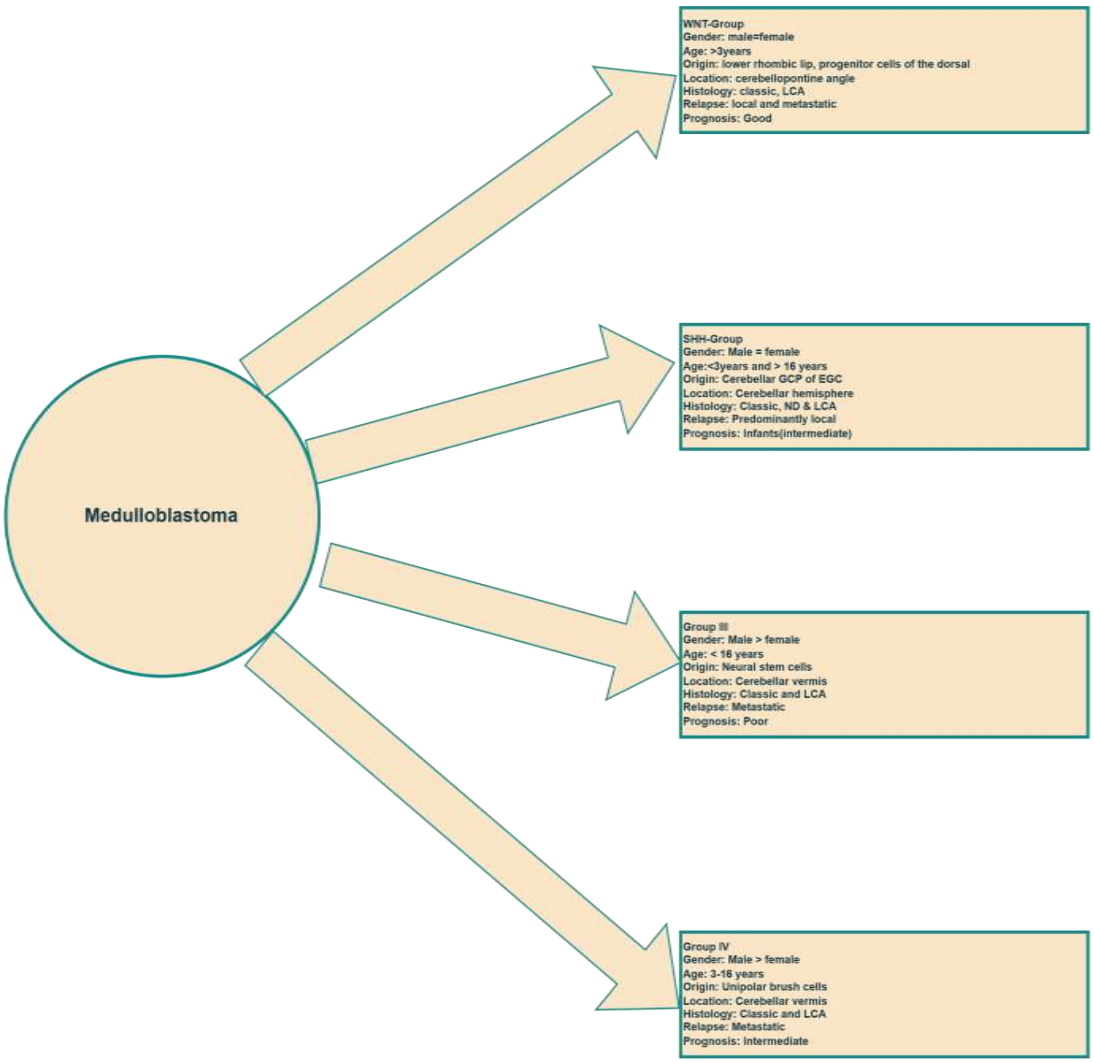

Fig. 4. Different subgroups of medulloblastoma are represented graphically. Four distinct medulloblastoma subgroups are depicted, including gender, age of diagnosis, location, histology, cellular origin, relapse pattern, and prognosis. Created in Draw io.

Liquid Biopsy in Medulloblastoma

Liquid biopsy is a new minimally invasive technique that has great potential for medulloblastoma diagnosis, prognosis, and monitoring. Liquid biopsies examine circulating tumor-derived components from bodily fluids like blood and cerebrospinal fluid (CSF), including circulating tumor DNA (ctDNA), circulating tumor cells (CTCs), extracellular vesicles, and microRNAs (miRNAs). This is in contrast to traditional tissue biopsies, which necessitate invasive neurosurgical procedures. It is possible to differentiate between pseudo-progression and real progression using liquid biopsy. It could potentially improve informed decision-making when it comes to therapeutic planning in cases with unclear MRI results (Stepein, N. et al., 2023; Greuter, L. et al., 2022). By offering real-time molecular insights into tumor heterogeneity, therapy response, and disease progression, this strategy has the potential to completely transform the management of medulloblastoma (Dang et al., 2021; Liu et al., 2020).

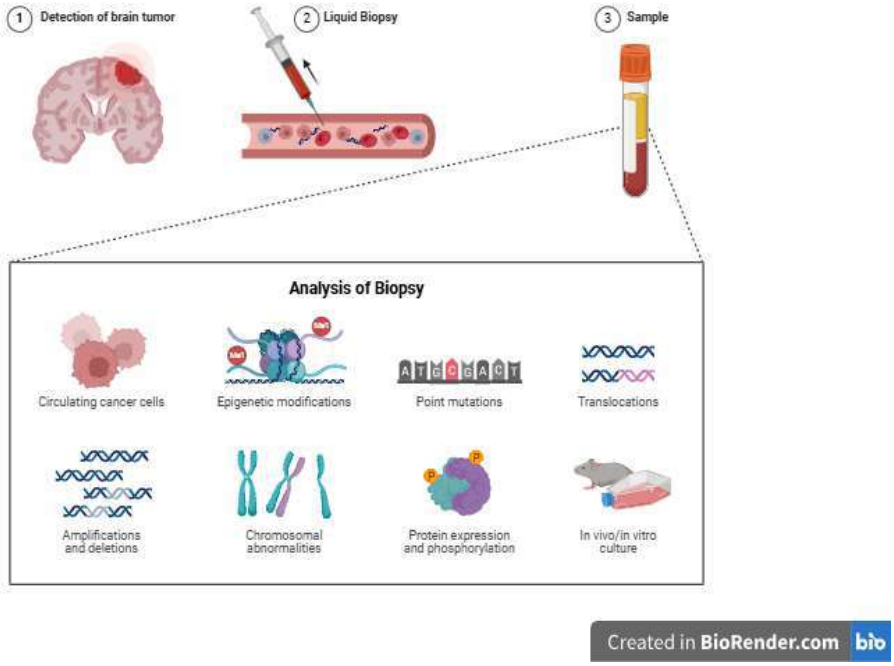

Fig. 5. Liquid biopsy technique on brain cancer

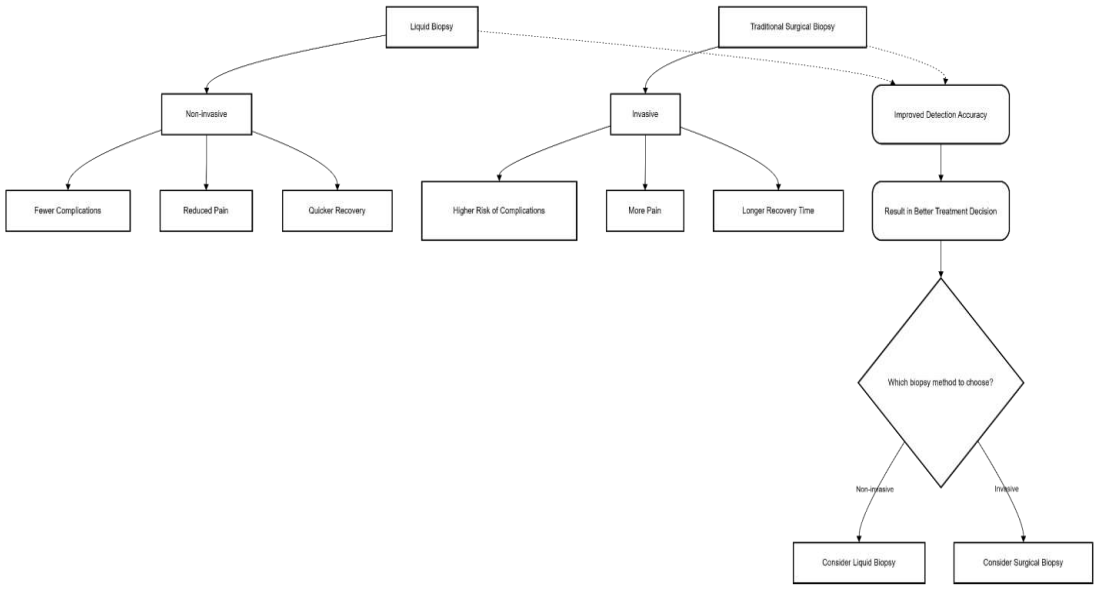

Fig. 6. Flowchart showing comparison of liquid biopsy and traditional surgical biopsy in terms of invasiveness, cost, real-time monitoring, and accuracy. Created in Draw io

(A) Circulating tumor DNA (ctDNA) in Medulloblastoma: Medulloblastoma is one of the many malignancies for which circulating tumor DNA (ctDNA) has been extensively researched as a biomarker. Mutations or methylations in ctDNA specific to tumors can be found in cDNA (Buccili, B. et al., 2024). Noninvasive genomic profiling and the identification of tumor-specific mutations are made possible by ctDNA fragments that are released into the bloodstream or CSF, which offers a snapshot of the genetic landscape of the tumor. According to studies, ctDNA levels are correlated with tumor burden, and detecting them can help with early recurrence monitoring and risk categorization (Escudero et al., 2020). Since there are several molecular subgroups of medulloblastoma (WNT, SHH, Group 3, and Group 4), ctDNA analysis may be able to identify biomarkers specific to each subgroup, which might aid in making informed treatment decisions (Pajtler et al., 2017). Furthermore, apart from subgroup categorization, ctDNA profiling allows for real-time tumor evolution tracking. Over time, tumor cells develop additional genetic mutations, especially in reaction to therapy. Clinicians can monitor the development of resistance mutations using longitudinal ctDNA analysis, which enables early intervention and treatment strategy adaptation (Ladewig et al., 2022). Additionally, studies have also demonstrated that ctDNA analysis can identify minimum residual disease (MRD), which improves patient outcomes by anticipating recurrence before clinical symptoms manifest (Shah et al., 2021).

(B) Circulating tumor cells: Another important aspect of liquid biopsy is the presence of circulating tumor cells (CTCs). These uncommon cells, which are released into the bloodstream from the original tumor, provide important information about the development of the tumor and its propensity to spread. Characterization of CTCs has been made possible by recent developments in single-cell sequencing, which have demonstrated their function in the spread of medulloblastoma (Smith et al., 2019). Given that medulloblastoma often spreads through routes in the cerebrospinal fluid, CTC identification from CSF is especially important. In addition to providing data on tumor burden, CTCs make it possible to profile individual cancer cells transcriptomically and proteomically. This can facilitate individualized treatment methods by assisting in the identification of clones that are resistant to therapy (Hong et al., 2020). Furthermore, CTCs are a valuable indicator for risk classification since their presence in CSF has been associated with a worse prognosis (Wu et al., 2021).

(C) Extra vesicles and microRNAs (miRNAs): Extracellular vesicles, like exosomes, have become recognized as possible biomarkers for medulloblastoma and are essential for intercellular communication. Tumor-derived exosomes are a desirable source of molecular information because they include proteins, lipids, and nucleic acids that are representative of their parent cells (Zhang et al., 2022). Additionally, the growth of medulloblastoma has been linked to microRNAs (miRNAs) in exosomes, with certain miRNA signatures being associated with tumor subtypes and prognosis (Riley et al., 2021). Exosomal biomarkers have been studied for their potential to predict therapeutic responses. Following chemotherapy resistance, several miRNAs exhibit upregulation, indicating a potential involvement in modulating drug resistance pathways (Kaur et al., 2021). Exosomal miRNAs from CSF may be isolated and analyzed, allowing for real-time therapy efficacy monitoring and, eventually, helping to inform therapeutic choices.

AI in Precision Medicine for Medulloblastoma

The advent of high-throughput, data-intensive biomedical research technologies and assays, like wireless health monitoring devices, imaging protocols, and DNA sequencing, has made it necessary for researchers to create methods for integrating, analyzing, and interpreting the enormous volumes of data they produce (Schork, NJ, 2019). With the use of predictive analytics, individualized treatment plans, and sophisticated data integration, artificial intelligence (AI) is revolutionizing precision medicine in medulloblastoma. Large-scale multi-omics datasets, imaging techniques, and clinical data are all used by AI-driven models to improve patient outcomes, optimize treatment approaches, and improve diagnosis. AI's incorporation into medulloblastoma research is opening up new avenues for advancements in risk stratification, molecular categorization, early identification, and treatment response prediction (Brock et al., 2021; Johnson et al., 2022; Zhuang et al., 2023; Singh et al., 2023).

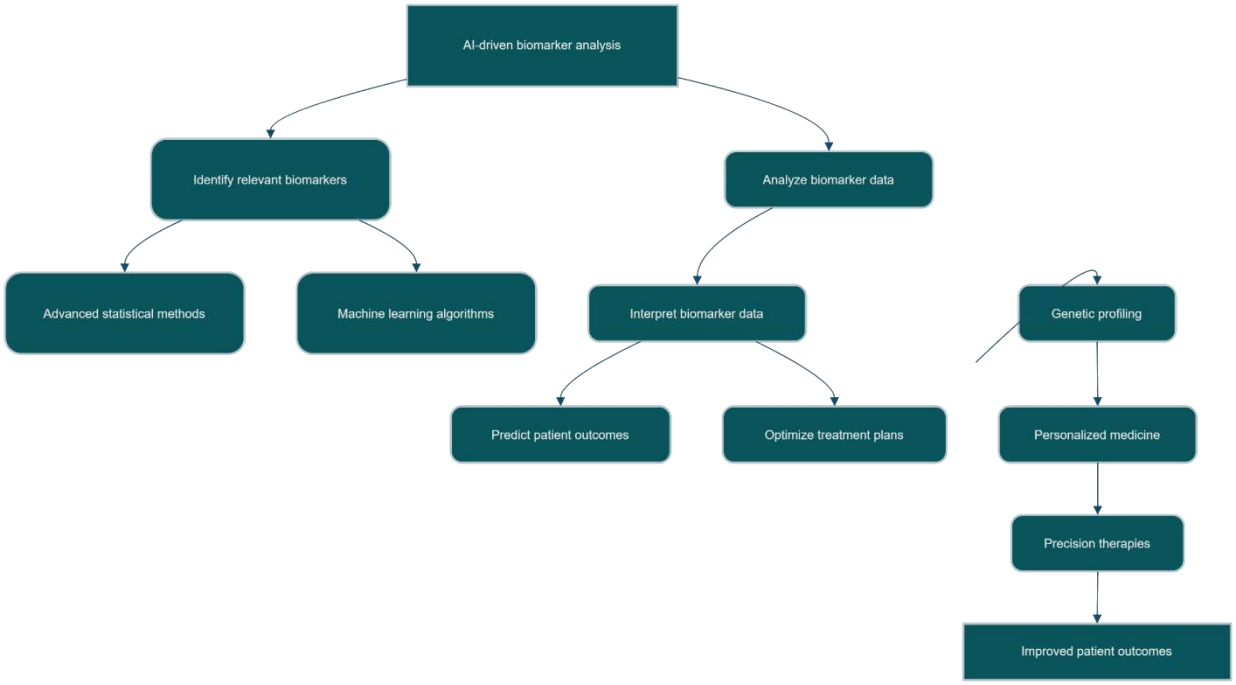

Fig. 7. AI-driven biomarker analysis in precision medicine. Created in Draw io.

(A) AI-driven molecular classification and diagnosis: Medulloblastoma is a very diverse tumor that is classified into four molecular subgroups: Group 3, Group 4, SHH, and WNT. AI-based algorithms have shown better accuracy in molecular subtyping than traditional classification techniques, which depend on immunohistochemistry and genomic sequencing. High-precision medulloblastoma classification is possible using deep learning models programmed on transcriptome and methylation data, which eliminates diagnostic ambiguity and permits treatment plans tailored to individual subgroups (Capper et al., 2018; Zhao et al., 2022). Noninvasive tumor classification has shown potential with AI-driven radiomics, which take quantitative information from imaging data. By using radiographic biomarkers to distinguish molecular subgroups, machine learning models programmed on MRI datasets provide a noninvasive substitute for tissue biopsies (Liu et al., 2020; Poon et al., 2023). This technique allows for early and accurate diagnosis, reducing the dangers associated with invasive treatments. According to Huang et al. (2023), recent developments in multimodal AI techniques have significantly increased diagnosis accuracy by combining clinical characteristics, genomes, and imaging.

(B) AI in risk stratification and prognostic modeling: For treatment intensity to be tailored to reduce toxicity and maximize therapeutic efficacy, risk stratification is essential. Prognostic models driven by AI combine clinical, radiological, and molecular data to forecast patient survival and the course of the disease. Novel prognostic indicators have been discovered using neural networks trained on patient cohorts, allowing for customized risk assessment (Patel et al., 2021; Cheng et al., 2023). Nevertheless, AI models that use data from single-cell sequencing have shed light on the heterogeneity and development of tumors. Clinicians can modify treatment plans in accordance with these models' predictions of tumor aggressiveness, resistance mechanisms, and possible therapeutic targets (Hovestadt et al., 2019; Zhang et al., 2023). Large clinical database meta-analyses driven by AI have also helped to uncover important predictive characteristics, which has improved risk stratification even further (Yoon et al., 2023).

(C) AI in treatment optimization and drug discovery: AI is transforming the process of choosing treatments by determining the best course of action for each patient. Machine learning algorithms use multi-omics information to predict drug responses and resistance patterns. AI-driven drug repurposing techniques have sped up the development of targeted therapeutics by identifying new therapeutic options for medulloblastoma (Cohen et al., 2020; Kim et al., 2023). In addition, pharmacogenomics powered by AI combines pharmacokinetic and genetic information to

customize chemotherapy treatments. Predictive models can improve dose regimens, minimizing side effects and boosting therapeutic efficacy (Smith et al., 2022; Lin et al., 2023). AI-based radiotherapy planning improves accuracy by maximizing radiation dose delivery while avoiding harm to healthy brain tissue (Hassan et al., 2023).

(D) AI in monitoring treatment response and disease recurrence: AI-powered liquid biopsy analysis improves early recurrence diagnosis and real-time therapy response tracking. To monitor minimum residual disease (MRD) and new resistance mutations, machine learning algorithms examine extracellular vesicles and circulating tumor DNA (ctDNA) in cerebrospinal fluid (CSF) (Wang et al., 2021; Luo et al., 2023). This enhances long-term patient outcomes by enabling proactive therapy modifications. Additionally, automated examination of histological samples is made possible by AI-assisted digital pathology, which offers a quick and precise assessment of therapy response. In order to enable prompt therapy adjustments, deep learning models trained on whole-slide images can measure tumor regression and detect remaining disease (Lu et al., 2022; Takahashi et al., 2023). Monitoring quality of life and therapy impact in patients with medulloblastoma is also becoming possible with AI-driven analysis of patient-reported outcomes (Gonzalez et al., 2023).

Clinical and translational challenges in medulloblastoma

About 20% of all pediatric cancers of the central nervous system are medulloblastomas, the most prevalent malignant pediatric brain tumor (Gajjar et al., 2019). According to Ramaswamy et al. (2017), a considerable portion of patients suffer from recurrence or long-term neurological sequelae despite notable improvements in multimodal therapy, which includes surgery, radiation, and chemotherapy. Treatment resistance, genomic heterogeneity, and the difficulty of converting preclinical findings into successful clinical treatments are the main causes of medulloblastoma's complexity (Northcott et al., 2017).

(A) Clinical challenges

(i) Tumor heterogeneity and risk stratification: According to Taylor et al. (2019), there are four main molecular subgroups of medulloblastoma: WNT, SHH, Group 3, and Group 4. Each of these subgroups has unique clinical characteristics and treatment responses. Group 3 tumors, which are identified by MYC amplification, are aggressive and have low survival rates, but WNT-driven medulloblastomas have a good prognosis (Cavalli et al., 2017). Since existing methods rely on histopathological and molecular profiling, which could not accurately reflect the tumor's biological activity, risk categorization is still a major issue (Pajtler et al., 2017).

(ii) Treatment-related toxicity and long-term effects: The usual course of treatment consists of chemotherapy and craniospinal irradiation after maximum surgical resection. However, because it causes endocrinopathies, secondary cancers, and cognitive impairment, radiation-induced neurotoxicity is a serious issue, especially in young children (Merchant et al., 2016). Although continuing, efforts to lower radiation exposure in low-risk patients by proton therapy or omission need more clinical trial validation (Walter et al., 2020).

(iii) Therapy resistance and disease recurrence: There are few effective treatment options for recurrent medulloblastoma, which has a poor prognosis. Clonal development, epigenetic changes, and the protective function of the tumor microenvironment are the factors behind therapeutic resistance (Vlashi et al., 2016). The poor effectiveness of current salvage treatments, including re-irradiation or new targeted medicines, call for the creation of more potent treatment plans (Rudin et al., 2020).

(B) Translational challenges

(i) Biomaker development and early detection: The use of liquid biopsy techniques, such as extracellular vesicles and circulating tumor DNA (ctDNA), shows promise for non-invasive disease monitoring. However, technical limitations, such as poor tumor DNA shedding and a lack of defined techniques, restrict their clinical applicability (Dang et al., 2021). Integrating these biomarkers into clinical practice requires their validation in sizable cohorts (Shah et al., 2021).

(ii) Targeted therapies and precision medicine: Although precision medicine has transformed the

treatment of cancer, tumor heterogeneity and the blood-brain barrier make it difficult for targeted therapies to be used in medulloblastoma treatment (Jones et al., 2017). Vismodegib and other SHH pathway inhibitors have demonstrated potential; however, they don't work in non-SHH subgroups (Robinson et al., 2015). According to Kool et al. (2020), combination medicines are being investigated in ongoing clinical studies in an effort to improve efficacy and circumvent resistance mechanisms.

(iii) Translating preclinical findings into clinical success: Despite several promising preclinical studies, only a few innovative medicines have been effective in clinical trials. The absence of accurate in vivo models that adequately replicate medulloblastoma biology impedes therapeutic drug development (Hovestadt et al., 2019). Additionally, intertumoral and intratumoral heterogeneity hinders the interpretation of preclinical findings and their application to patient outcomes (Ladewig et al., 2022).

Impact of medulloblastoma and its treatment on nutrition

Significant nutritional problems, including weight loss, malabsorption, metabolic changes, and therapy-induced gastrointestinal issues, can result from medulloblastoma and its treatment (Patel et al., 2023). Treatment-induced malnutrition is a common occurrence in which chemotherapy and radiation produce nausea, vomiting, mucositis, and dysphagia, resulting in decreased oral intake and malnutrition (Guan et al., 2018). Another side effect is endocrine dysfunction, which occurs when radiation therapy, particularly craniospinal irradiation, disrupts the hypothalamic-pituitary axis, altering growth hormone production, metabolism, and appetite regulation (Merchant et al., 2016). In addition, gut microbiota changes occur, which play an important role in metabolism, immunity, and general nutritional health. Treatments for medulloblastoma can change the gut microbiota, causing dysbiosis and impaired nutritional absorption (Wu et al., 2021). In order to improve patient resilience, lessen treatment adverse effects, and encourage recovery, nutrition is crucial. A balanced diet rich in proteins, healthy fats, and vital vitamins (such as Vitamin D, B-complex, and antioxidants) can aid in the therapy of nutritional deficiencies (Northcott et al., 2017). Diets high in fiber, polyphenols, and omega-3 fatty acids may help decrease inflammation and improve the efficacy of treatment, according to anti-inflammatory diets (Hovestadt et al., 2019). Additionally, the ketogenic diet has been investigated as a possible treatment approach. According to preclinical and clinical research, ketogenic diets, which are low in carbs and rich in fat, may help treat brain cancers like medulloblastoma by changing the metabolism of the tumor and slowing its development (Shah et al., 2021). However, novel approaches to tailored dietary therapy have been made possible by recent developments in liquid biopsy-based metabolic monitoring and AI-powered precision nutrition. Using circulating biomarkers such as ctDNA, miRNAs, and extracellular vesicles, liquid biopsy for metabolic and nutritional monitoring offers valuable information on metabolic changes brought on by medulloblastoma and its therapy (Dang et al., 2021). AI-driven prediction models using machine learning algorithms may access patient data to detect risk factors for malnutrition, medication tolerance, and metabolic imbalances, ensuring accuracy in nutritional interventions (Liu et al., 2020).

Challenges and future directions

To successfully apply AI-driven technologies and liquid biopsy in the treatment of medulloblastoma, a number of issues must be resolved. For uniform and repeatable outcomes in various clinical contexts, standardizing liquid biopsy procedures is essential. The accuracy of diagnostic and prognostic evaluations can be strongly impacted by variation in sample collection, processing, and analysis (Merchant et al., 2016). Future studies must concentrate on improving these procedures in order to create generally recognized standards that support the reliable use of liquid biopsy in clinical procedures. Validating AI models across a range of demographics is another significant obstacle. Large datasets are necessary for training predictive models in AI-driven precision medicine; however, many of the datasets currently in use do not adequately cover a variety of demographic groups. According to Patel et al. (2023), this restriction may lead to biases that compromise the precision and efficacy of AI-based decision-making systems. The creation and validation of AI models should prioritize the inclusion of various patient groups in order to improve generalizability. To

guarantee that AI-powered diagnoses and treatment suggestions are relevant to all patients, irrespective of genetic, ethnic, or socioeconomic variations, rigorous clinical trials and multi-institutional cooperation will be crucial (Hovestadt et al., 2019). Nevertheless, to maximize patient results, precision nutrition therapies also need clear guidelines. Although AI-powered dietary assessment tools have the potential to customize dietary plans for specific patients, standardized procedures are required to successfully incorporate these treatments into clinical practice. To provide evidence-based dietary recommendations for pediatric brain tumor patients, further study is required due to the complicated link between nutrition, metabolism, and treatment response (Zhang et al., 2022). Furthermore, in order to make precision nutrition a cornerstone of medulloblastoma therapy, future research should examine the effects of customized diet on treatment effectiveness and general well-being. In addition to technological and clinical problems, AI-driven medical decision-making must address ethical concerns in order to promote openness, accountability, and justice. Building explainable AI models is essential to winning both patients' and doctors' trust. Clinical adoption may be hampered by black-box AI algorithms, which offer suggestions without providing thorough justifications (Northcott et al., 2017). Maintaining patient trust in these technologies while assisting medical practitioners in making defensible judgments based on AI-driven insights requires that AI models be accessible and interpretable. Furthermore, the ethical application of AI in pediatric oncology care requires strong regulatory frameworks to avoid possible biases and assure fair access to modern diagnostic and therapeutic alternatives. Disparities in healthcare accessibility can exacerbate the divide between patients who can benefit from AI-driven technologies and those who do not have access to them. To ensure that AI and liquid biopsy technologies serve all patients, regardless of their location or socioeconomic status, policymakers and healthcare organizations should collaborate to create policies that support equitable deployment (Liu et al., 2020). In order to revolutionize medulloblastoma treatment using AI and liquid biopsy, these issues must be resolved. Researchers and clinicians may make sure that these improvements result in better patient outcomes, more individualized therapy, and increased diagnostic accuracy by concentrating on standardization, validation, accessibility, and ethical issues. Future initiatives must prioritize regulatory supervision, multidisciplinary cooperation, and ongoing development of AI-driven technologies in order to fully realize their effectiveness in pediatric neuro-oncology.

CONCLUSION

Liquid biopsies and AI-powered precision medicine are transforming the clinical care of medulloblastoma by solving long-standing problems with diagnosis, risk classification, and therapy tailoring. By detecting circulating tumor DNA, extracellular vesicles, and microRNAs, this paradigm shift overcomes the drawbacks of traditional tissue samples that necessitate invasive procedures and allows for non-invasive, real-time monitoring of tumor dynamics. This strategy is further improved by the use of AI algorithms, which analyze imaging, clinical data, and complicated multi-omics datasets to forecast treatment outcomes, find new therapeutic methods, and optimize customized treatment plans. When taken as a whole, these developments hold the potential to increase survival rates, lessen toxicities brought on by medication, and enhance the quality of life for young children with this severe illness. Despite the great potential, a number of important issues need to be resolved before these technologies can reach their full potential. A smooth clinical integration requires standardizing liquid biopsy procedures, evaluating AI models on a range of patient demographics, and putting strong ethical and legal frameworks in place. Future studies must prioritize multidisciplinary cooperation, thorough clinical testing, and ongoing technical development to guarantee that these cutting-edge instruments are both widely available and efficient. All things considered, the combined use of liquid biopsy and AI-powered precision medicine marks a substantial advancement in the individualized treatment of medulloblastoma. They have the potential to drastically change the therapeutic landscape of pediatric neuro-oncology as these technologies develop and are incorporated into standard clinical workflows, providing fresh hope for increased diagnostic precision, focused therapy, and eventually better patient outcomes.

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