concern, the geographic distribution of authors suggests underinvestment in rural institutions.

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Mechanisms of exosome-mediated immunosuppression in IDH mutant gliomas*

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OBJECTIVES/GOALS: We aim to identify how IDH mutant (IDHm) gliomas use exosomes to modulate the local and systemic immune system. We will do so by characterizing differential miRNA expression between IDHm and IDH wild type (IDHwt) exosomes and identifying the specific immune cell population targeted by exosomes in vivo. METHODS/STUDY POPULATION: Exosome RNA will be isolated from cultured patient glioma samples and perform small RNA sequencing to investigate differential expression of miRNA between IDHwt and IDHm exosomes. We will then utilize miRNA target databases in conjunction with bioinformatic pathway analysis to generate potential target regulatory pathways. To identify the in vivo effect of tumor exosomes, we will generate a novel glioma mouse model that has been genetically engineered to release labeled exosomes using the RCAS retroviral system. We will collect peripheral blood and tumor tissue for flow cytometric immune profiling and single-cell RNA sequencing. The transcriptomic data will be analyzed to identify subsets of immune populations that have taken up the labeled exosomes and assess the resulting expression changes in those cells. RESULTS/ANTICIPATED RESULTS: From the small RNA sequencing and bioinformatics analysis, we expect to find several unique miRNA expressed in IDHm exosomes that induce immunosuppressive pathways in local and systemic immune cell populations when compared to IDHwt exosomes. Furthermore, using our novel murine model, we expect to be able to track endogenously released exosomes in the local tumor microenvironment and in the circulating blood. We hypothesize that IDHm exosomes specifically target precursor myeloid cells within the local and peripheral circulating immune populations and induce the expansion of monocytes, M2 macrophages, and mono-MDSCs. DISCUSSION/SIGNIFICANCE OF IMPACT: Immunosuppression in IDHm glioma has hindered the development of adequate therapies to treat this fatal disease. Our study will illuminate the mechanism by which tumor exosomes can suppress immune surveillance. These results will help identify new therapeutic targets to sensitize the immune system against glioma cells.

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Harnessing computational tools to rank vaccine targets in *Plasmodium falciparum* candidate antigens*

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OBJECTIVES/GOALS: We aim to predict and rank conserved, immunogenic targets within key malaria proteins using computational tools. These tools incorporate parasite protein diversity and regional HLA allele frequencies to prioritize antigens for further validation and inclusion in a malaria vaccine targeting circulating strains. METHODS/STUDY POPULATION: We identified 42 conserved malaria proteins with nonredundant functions for *P. falciparum* invasion and transmission as vaccine targets. Protein sequence datasets were constructed from samples collected in highly endemic areas. We predicted targets most likely to be presented to CD4+ and CD8+ T cells. We designed and used heuristic-based and AI-weighting models that integrated predicted binding affinities to HLA alleles, HLA allele frequency data, and sequence conservation to score and rank targets. We validated our model by comparing predicted epitope distributions with published in vitro and in vivo immunogenicity data available in the Immune Epitope Database and Tools repository. RESULTS/ANTICIPATED RESULTS: We successfully predicted and ranked targets within the vaccine candidate proteins, identifying conserved and HLA-nonspecific targets that correspond to positive immunogenicity data, validating our approach. We are currently analyzing model performance by comparing predictions to over 5,800 experimentally validated *P. falciparum* targets from clinical trials and immune assays. We will evaluate each models' accuracy and ability to prioritize targets and compare their performances as measured quantitatively by precision and area under the curve metrics. We expect the AI-based model to significantly outperform the heuristic approach, improving the identification of effective vaccine targets. DISCUSSION/SIGNIFICANCE OF IMPACT: By incorporating parasite diversity and regional HLA allele frequencies, our approach addresses the challenge of directing the human immune response against genetically diverse *P. falciparum* strains in highly endemic areas. This strategy could significantly enhance malaria vaccine efficacy and can be adapted for use against other pathogens.

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The role of artificial intelligence in translational science in oncology: A systematic review and meta-analysis

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OBJECTIVES/GOALS: This study aimed to investigate the role of artificial intelligence (AI) in translational science, including personalization of interventions and drug development. METHODS/STUDY POPULATION: A comprehensive literature search was conducted via PubMed, the Cumulative Index for Nursing and Allied Health Literature (CINAHL), Cochrane Library, Medline, and Web of Science. The risk of bias in the eligible studies was assessed using the risk of bias in nonrandomized studies. Data were systematically extracted and analyzed. RESULTS/ANTICIPATED RESULTS: The literature search yielded 2129 records, from which 20 studies that met the eligibility criteria were included. Meta-analysis demonstrated the high specificity of AI-based diagnostics,

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