determined by shear rheology will be tuned through concentration and polymer composition to mimic vaginal mucus. We will also show the facile movement of small molecule nutrients through the SHINE-VH network via sugar-binding and permeability tests. Additionally, we anticipate that the introduction of SHINE-VH, due to their xenobiotic nature as synthetic mucins, will modulate the microbiota by diminishing inflammation, thereby reinforcing the cervicovaginal mucus and cultivating a vaginal microbiome that is more resilient to the disruptive impacts of BV. Such modulation could lead to a marked difference between the SHINE-VH-treated and untreated groups. DISCUSSION/SIGNIFICANCE OF IMPACT: BV affects ~30% of women globally and is associated with severe gynecologic and obstetric complications, representing a significant unmet need in women's health. SHINE-VH offers a novel approach to BV management, aiming to strengthen vaginal mucosal integrity, potentially reducing BV prevalence, and improving women's health outcomes.

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A comparative approach to understanding the role of oncogenic MYC signaling in the metastatic osteosarcoma tumor immune microenvironment

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OBJECTIVES/GOALS: Osteosarcoma (OS) is the most common primary bone malignancy in humans and dogs. >40% of children and >90% of dogs succumb to metastatic disease. We hypothesize MYC overexpression in metastatic canine and human OS contributes to an immunosuppressive tumor environment by driving tumor-associated macrophage influx and T lymphocyte exclusion. METHODS/STUDY POPULATION: To characterize the role of oncogenic MYC signaling in the canine metastatic tumor immune microenvironment (TIME), 42 archived FFPE lung metastatic canine OS samples were evaluated for MYC copy number variation (CNV), mRNA, and protein expression via ddPCR, nanostring analysis, and immunohistochemistry (IHC). Seven samples also underwent GeoMX spatial profiling to more specifically evaluate T cell and macrophage transcriptional profiles based on MYC status. To determine the role of MYC target modulation as a potential therapeutic option, canine and human OS cell lines were treated with a novel MYC inhibitor (MYCi975) and assessed for effects on survival, proliferation, and cytokine profiles. RESULTS/ANTICIPATED RESULTS: We demonstrate that copy number gains are not a key driver of MYC hyperactivity in canine metastatic OS. However, stratification based on MYC protein expression demonstrates that "MYC-high" tumors are associated with downregulation of cytotoxic effector T-cell associated transcripts and upregulation of tumor-associated macrophage (TAM) and extracellular matrix remodeling transcripts. We also report that MYCi975 treatment of canine and human OS cell lines results in significant inhibition of OS cell survival and proliferation at concentrations that are pharmacologically achievable in mice. Furthermore, we demonstrate MYC inhibition by MYCi975 is associated with reduced pro-inflammatory cytokine secretion in OS cell culture models. DISCUSSION/SIGNIFICANCE OF IMPACT: While MYC overactivity in metastatic canine OS may not be genomically driven, other mechanisms that lead to increased MYC protein expression are associated with transcriptomic profiles supportive of local immunosuppression. Pharmacologic targeting of MYC may serve as a strategy to bolster immunotherapeutic options in metastatic OS treatment.

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Using social network analysis to power translational research collaborations

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OBJECTIVES/GOALS: Delving into the intricate web of translational research collaborations, this study analyzed the evolving landscape of the Hispanic Alliance of Clinical and Translational Research from 2020 to 2024 using cutting-edge social network analysis (SNA). SNA is a powerful tool for visualizing, understanding, and harnessing the power of networks. METHODS/STUDY POPULATION: We conducted a systematic document review of all the Alliance IDeA-CTR Network Calls for Pilot Projects from 2020 to 2024 including key attributes of the investigators and collaborators (e.g., academic institution, highest degree, collaborator type). Scientific collaboration was defined as two or more researchers working together in a grant proposal for a pilot project application. Study data was recorded and tracked using an Excel spreadsheet. R-Statistical software was used to analyze and map the networks resulting from collaboration interactions comparing the 2020 Call and 2024 Call. Network statistics were performed including nodes, isolates, edges, components, density, diameter, average degree, and the size of the main component. RESULTS/ANTICIPATED RESULTS: Within a vibrant network comprising over 150 investigators from local and national academic institutions, clinicians (49.3%), and basic researchers (25.4%) are predominant. Initial findings showcase a remarkable surge in interdisciplinary collaborations and affiliations over time. Preliminary findings demonstrated that the number of nodes/actors increased from 16 to 75 comparing 2020 to 2024 and the edges/relationships from 12 to 66. Notably, the number of translational research clusters surged from 4 to 18, with mentorship emerging as a critical conduit bridging diverse research clusters; 16 to 78 nodes in comparison from 2020 to 2024. More extensive collaborative clusters occurred across time with over 20 researchers collaborating. A mentor was the main actor connecting these research clusters. DISCUSSION/SIGNIFICANCE OF IMPACT: This study unveils the intricacies and power of translational research dynamics, showing a palpable surge in collaboration diversity and depth. By harnessing data-driven insights, our approach catalyzes informed decision-making to amplify collaboration, diversity, and network efficacy, offering invaluable guidance for policy and practice.

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ICTR data science initiative: Empowering translational teams to better leverage data science

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OBJECTIVES/GOALS: High-performing translational teams (TTs) effectively draw knowledge from empirical data to develop health solutions. However, some TTs lack rigorous data approaches, resulting in inefficiency. The ICTR data science initiative integrates

https://doi.org/10.1017/cts.2024.1150