

JOR Consensus Obesity and OA Q17: Can/should we determine whether obesity accelerates aging using OA as a model - structurally, molecularly, and functionally?

Christopher B. Little¹, Kelsey H. Collins², Tim M. Griffin³, Brian O Diekman^{4,5}, Richard F. Loeser⁵, Beatriz Caramés⁶, Carla R. Scanzello⁷, Matlock A Jeffries⁸, Sarah J Rice⁹

¹ Raymond Purves Bone & Joint Research Lab, Kolling Institute, Faculty of Medicine and Health, University of Sydney, NSW, Australia

² Department of Orthopedic Surgery and Anatomy, University of California San Francisco, CA, USA

³ Aging and Metabolism Research Program, Oklahoma Medical Research Foundation, Oklahoma City, OK, USA

⁴ Lample Joint Department of Biomedical Engineering, University of North Carolina at Chapel Hill and North Carolina State University, Raleigh, NC, USA

⁵ Thurston Arthritis Research Center, The University of North Carolina, Chapel Hill, NC, USA

⁶ Unidad de Biología del Cartílago Grupo de Investigación en Reumatología, Instituto de Investigación Biomédica de A Coruña, SPAIN

⁷ CReATE Motion Center, Philadelphia VA Medical Center, & Division of Rheumatology, Univ. of Pennsylvania, Philadelphia, PA, USA

⁸ Arthritis Research Unit, Oklahoma Medical Research Foundation; Oklahoma City VA Medical Center, Oklahoma City, OK, USA

⁹ Centre for Genetics and Genomics, Musculoskeletal and Dermatological Sciences, The University of Manchester, Oxford Road, Manchester, M13 9LJ

Response/Recommendation: YES

Chronological age/aging and overweight/obesity are both well recognized risk factors for structural and symptomatic OA in humans and in rodents. Biological aging (measured by telomere shortening, DNA methylation, transcriptomic clocks, cell senescence, mitochondrial dysfunction, etc.) is also associated with worsening obesity and OA structural and symptomatic disease. Chronic low-grade inflammation is characteristic of both aging (inflammaging) and obesity (metabolic syndrome) and has direct impacts on structural and symptomatic OA onset and progression. Pre-clinical models commonly used to study the effects of chronological age on different diseases including OA are confounded by increasing adiposity and obesity in older/aged animals (particularly in rodents) that is both strain- and sex-dependent. Using pre-clinical models to explore the isolated effects on OA of chronological aging, biological aging and obesity (as well as the potential bi-directional effects of OA on obesity and biological aging) requires deliberate experimental planning and data interpretation. However, while the necessary methods, resources and pre-clinical models (including specific genetically modified mouse strains) to conduct such detailed studies are available, many gaps in knowledge persist. Importantly from a translational perspective, over two-thirds of individuals with OA have one or more additional chronic conditions, this co/multi-morbidity increases with age and obesity, and the concept of differential organ-aging is an emerging paradigm in human disease and global patient well-being. Research to define the mechanisms driving the interaction between OA and obesity, chronological aging, and systemic and joint-tissue biological aging is needed and will have high translational significance by increasing the likelihood of identifying and validating disease-modifying therapies for OA and its common co-morbid conditions.

Level of evidence for the response/recommendation: **Strong** that the question has translational relevance to the human/clinical condition (i.e. “we should”) **Moderate-Strong** that the tools and methods are available to address the question (i.e. “we can”).

Delegate Vote: Agree: Disagree: Abstain:

Rationale: *Aging, obesity and OA risk - clinical evidence.* The most consistently cited risk factors for OA, both structural and symptomatic disease, are aging (years lived), overweight and obesity (including measures such as increased body mass index (BMI), height-waist-ratio (HWR), adiposity, dyslipidemia), joint injury (both destabilizing and chronic repetitive loading), and female sex¹⁻¹⁸. There are complex mediating and moderating inter-relationships between these (and other) OA risk factors, as well as specificity for which play greater or lesser roles in OA in particular joints (e.g. hip, knee, ankle). Critically, the precise mechano-biological mechanisms driving OA risk associated with the different risk factors, and the inter-relationships between these, remains incompletely defined necessitating ongoing research to identify potential diagnostic and therapeutic targets.

Chronological vs biological age/aging. While years-lived since birth (chronological age) is a readily defined variable, not all people show equivalent age-associated disease risk, trajectory or burden^{19; 20}. The latter are features of “biological age/aging”, which encompasses a range of clinical, functional

and biological measures that may better predict individual ageing status and outcomes in longitudinal aging cohorts, including those related to chronic pain, musculoskeletal conditions and OA^{5; 19-38}. Key processes associated with and used as measures and biomarkers of biological aging, include telomere shortening, DNA methylation, transcriptomic features, cell senescence and the senescence-associated secretory phenotype (SASP), disabled autophagy, and mitochondrial dysfunction^{7; 19; 22-26; 28; 34; 38-73}. These biological-aging changes can be identified systemically (e.g. in circulating leukocytes) and in organ-specific cells, with disparity between biological-age in different organs and tissues, including those of the musculoskeletal system, increasingly recognized as part of variable human age-associated morbidity and mortality^{74; 75}. The role and importance of the different systemic and joint-tissue/cell (e.g. chondrocyte, osteoblast, synovial fibroblast) biological aging processes in the incidence and progression of OA structural and symptomatic disease, remains an area of controversy and active clinical research^{9; 22; 23; 30; 37; 38; 46; 51; 52; 55; 76}. Importantly, there is evidence of a bi-directional relationship between obesity and biological aging in different cells and organs^{5; 77}. While the mechanisms driving the obesity/aging interaction remain to be fully elucidated, the systemic and local chronic low-grade inflammation associated with both conditions is implicated, and is also associated with OA structural and symptomatic disease pathophysiology and risk^{62; 69; 77-84}.

Aging, obesity, OA and multi-morbidity. There is an enormous volume of epidemiological data from populations in many countries, on the number of people living with 2 or more chronic health conditions.^{8; 36; 85-135} The prevalence of this co- or multi-morbidity increases with both age and obesity. OA is highly associated with numerous co-morbid conditions with over two thirds of individuals having one or more additional health problems. The significant co-morbid disease associations are seen both before and after OA diagnosis suggesting bi-directional interaction. The pathobiological mechanisms driving OA co-morbid disease association and any modifying effects of age and obesity have not been determined. Further, OA therapies may be less or more effective in patients with multi-morbidity, and testing new interventions in settings where aging, obesity, OA and co-morbid conditions intersect, is critical to define efficacy in real-world patient populations.

Pre-clinical models. Many different animal models have been developed and used to study OA structural and symptomatic disease pathophysiology and treatment¹³⁶⁻¹⁴². With the diversity of models has come recognition that different OA disease phenotypes can have distinct cellular and molecular mechanisms underpinning both structural and symptomatic disease¹³⁷⁻¹⁴⁹. In particular, there has been burgeoning comparison of spontaneous age-associated OA and surgically or mechanically induced post-traumatic OA, and both of these with and without diet induced obesity^{136; 137; 142; 145; 147; 150-155}. These studies have provided novel insight into OA-associated modulation of different biological-aging processes including telomere shortening, mitochondrial dysfunction, cell senescence and inflammation, including SASP^{25; 60; 64; 65; 156-164}. Chronological aging models of spontaneous OA, however, can be confounded by sex-dependent increasing dyslipidemia, adiposity and obesity in older/aged animals¹⁶⁵⁻¹⁷⁰. Further, both spontaneous and diet-induced obesity are strain- and sex-dependent and can be modified by factors such as age, previous pregnancy etc^{151; 153; 169; 171-175}. While reflecting age-associated co-morbidity and biological aging changes in people^{75; 176; 177}, this limits dissection of the specific effects and bi-directional interactions of age, obesity and OA. However, there are implementable experimental methods/protocols (e.g. caloric restriction, appetite modifying drugs^{172; 178; 179}), and mouse strains with modified aging and adiposity (e.g. lipodystrophic (LD) mice^{180; 181}, senescence accelerated & resistant (SAM/SAMPR) mice¹⁸²⁻¹⁸⁶, and others^{159; 167; 184; 187-189}) that can enable the individual effects of age and obesity and their bi-directional cross talk with OA to be investigated, the cellular and biological mechanisms defined, and new therapies tested in more clinically and heterogenous patient relevant setting.

Summary: Age and obesity are clinically relevant risk factors for OA, which in turn can modify biological-aging and drive co-morbid disease. Using appropriate pre-clinical models and designing studies to define distinct and shared mechanisms driving this common and costly disease interaction will advance understanding of the role of OA in obesity/aging and may ultimately lead to improved therapeutic discovery and development.

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