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### In vitro models for the study of osteoarthritis

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1 **Review**

2

3 **In vitro models for the study of osteoarthritis**

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17

18 **Highlights**

- 19 • No in vitro model of osteoarthritis has been validated against the native disease
- 20 • Cytokine and compression models are most commonly used
- 21 • Cytokine based models often use concentrations far greater than values measured in vivo
- 22 • Supraphysiological loads are also used often to exaggerate the response
- 23 • The development of an in vitro model might require a combinatorial, multi-modal approach

24 **Abstract**

25 Osteoarthritis (OA) is a prevalent disease of most mammalian species and is a  
26 significant cause of welfare and economic morbidity in affected individuals and populations.  
27 In vitro models of osteoarthritis are vital to advance research into the causes of the disease,  
28 and the subsequent design and testing of potential therapeutics. However, a plethora of in  
29 vitro models have been used by researchers but with no consensus on the most appropriate  
30 model. Models attempt to mimic factors and conditions which initiate OA, or dissect the  
31 pathways active in the disease. Underlying uncertainty as to the cause of OA and the different  
32 attributes of isolated cells and tissues used mean that similar models may produce differing  
33 results and can differ from the naturally occurring disease.

34 This review article assesses a selection of the in vitro models currently used in OA  
35 research, and considers the merits of each. Particular focus is placed on the more prevalent  
36 cytokine stimulation and load-based models. A brief review of the mechanism of these  
37 models is given, with their relevance to the naturally occurring disease. Most in vitro models  
38 have used supraphysiological loads or cytokine concentrations (compared with the natural  
39 disease) in order to impart a timely response from the cells or tissue assessed. Whilst models  
40 inducing OA-like pathology with a single stimulus can answer important biological questions  
41 about the behaviour of cells and tissues, the development of combinatorial models  
42 encompassing different physiological and molecular aspects of the disease should more  
43 accurately reflect the pathogenesis of the naturally occurring disease.

44

45 *Keywords:* Cytokine; In vitro; Loading; Model; Osteoarthritis

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## 46 Introduction

47 Osteoarthritis (OA) is the most common form of arthritis and is one of the leading  
48 causes of disability worldwide. Most mammalian populations are affected, including humans  
49 and domesticated animal species including sheep (Vandeweerd et al., 2013), horses (Ireland  
50 et al., 2013), cats (Clarke et al., 2005) and dogs (Clements et al., 2009). Estimates in human  
51 populations suggest that 9.6% of men and 18% of women over the age of 60 years have  
52 symptomatic OA (Woolf and Pfleger, 2010). In 2006-2007 in the United Kingdom 94% of  
53 hip and 97% of knee replacements were carried out for relief of OA, costing an estimated  
54 £809 million<sup>1</sup>. Consequently OA is a major concern, particularly in ageing populations  
55 (Nguyen et al., 2011).

56  
57 Symptoms of OA most commonly include pain, swelling and stiffness in the affected  
58 joint, resulting from the degradation of articular cartilage (Madry et al., 2012), changes in the  
59 composition of the subchondral bone (Sniekers et al., 2008; Saito et al., 2012) and synovitis  
60 (Goldhammer et al., 2010). Historically, OA was primarily observed in elderly individuals  
61 which led to the idea that OA was a ‘wear-and-tear’ type disease (Berenbaum, 2013).  
62 However, this idea is now less favoured because younger patients often display symptoms of  
63 OA secondary to injuries or because of a genetic predisposition to the disease (Da Silva et al.,  
64 2009).

65  
66 OA is a multifactorial disorder and no single aetiological mechanism has been found  
67 common to all forms of the disease (Iliopoulos et al., 2007). Large genetic studies have  
68 identified numerous genetic risks for OA (Reynard and Loughlin, 2013), although the odds  
69 ratios for most single nucleotide polymorphism (SNP) associations are low, and rarely do

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<sup>1</sup>See: <http://www.arthritisresearchuk.org/arthritis-information/data-and-statistics/osteoarthritis.aspx> (accessed 24 November, 2014)

£1 = approx. US\$1.50, €1.36 at 06 April 2015.

70 they apply to more than one form of the disease. The mechanisms which underpin genetic  
71 risks are often unidentified, and in vitro models are critical if we are to expand our  
72 understanding of their role in disease progression.

73

74 Both in vivo and in vitro models of OA have been used in the past (Goldring et al.,  
75 2008; Grenier et al., 2014; Fang and Beier, 2014). Whilst models can be broadly grouped  
76 according to the primary mechanism by which the catabolic process is stimulated, each with  
77 their own strengths and weaknesses (Table 1), subtle variations mean that an almost infinite  
78 number of variations exist for a single model (Benam et al., 2015). Similarly, whilst in vivo  
79 models may give the most accurate reflection of the naturally-occurring whole-joint disease,  
80 the ease of manipulating an in vitro system, as well as a shift towards the 3R philosophy of  
81 refining, reducing and replacing the use of animals in animal science (Madden et al., 2012)  
82 makes in vitro modelling of the disease desirable. The observation that spontaneous OA in  
83 domestic animals has a similar pathogenesis to that observed in humans (Clements et al.,  
84 2006), and the availability of naturally-occurring, early-stage diseased tissue, for example at  
85 slaughter in food animal species or following a veterinary surgical intervention in companion  
86 animals (Clements et al., 2009) makes domestic animals an important source of clinical  
87 material for such models.

88

89 Additionally, models of OA offer the opportunity to study early features of the  
90 development of the disease, prior to the development of a fulminant catabolic process, which  
91 have been difficult to dissect because of the lack of available tissue from early disease and the  
92 limited molecular changes associated with it (Aigner et al., 2006). No consensus on the most  
93 appropriate model for the representation of particular features of OA has been made, as each  
94 model has its own mechanisms for the induction of a general catabolic process. Furthermore,

95 the molecular phenotypes of different forms of OA also show distinct differences (Xu et al.,  
96 2012), and such subtleties can be considered when designing models of OA rather than  
97 ignoring them when using more general in vitro models.

98

99 The relevance of in vitro models to clinical disease always needs to be interpreted  
100 with caution. For example, numerous publications report the chondroprotective effects of  
101 glucosamine and chondroitin sulphate on in vitro models (Dechant et al., 2005; Chan et al.,  
102 2007), but clinical trials have failed to show such effects in vivo (Wandel et al., 2010;  
103 Sawitzke et al., 2010). Whilst some effects of the differences can be ascribed to delivery,  
104 complexity, duration and variation of the phenotype, ultimately in vitro models should be  
105 designed to better reflect the natural in vivo disease. This particularly applies to the disease  
106 state, where almost all models are designed to replicate the symptoms of end-stage OA with  
107 little or no regard to the early disease where chondroprotection is likely to yield greater  
108 benefits.

109

110 This review summarises the two most commonly used in vitro models of OA, namely,  
111 cytokine-based models and load-based models, and then discusses their various merits and  
112 how they reflect the naturally-occurring processes.

113

#### 114 **Cytokine induction of OA-like processes**

115 Classic research on OA has focused on cartilage, but other tissues such as bone,  
116 synovium, ligament, infrapatellar fat (Maccoux et al., 2007) and periarticular muscles (Geyer  
117 et al., 2009) are also involved (Fig. 1). The changes seen in these tissues are attributed to  
118 diffusible factors, including proteolytic enzymes, such as matrix metalloproteinases (MMPs)  
119 and members of the ‘a disintegrin and metalloproteinase with thrombospondin-motif’



120 (ADAMTS) family that are present in the joint environment during the disease (Little et al.,  
121 2005; Clements et al., 2006).

122

### 123 *Cytokines in OA*

124 During OA, synoviocytes, mononuclear cells or chondrocytes may increase their  
125 expression of catabolic proteins (Fernandes et al., 2002) following stimuli such as cytokine or  
126 chemokine exposure, including interleukin (IL)-1 $\beta$  and tumour necrosis factor (TNF)- $\alpha$ ,  
127 which are present in the joint following synovial inflammation (Sohn et al., 2012). Pro-  
128 inflammatory cytokines make ideal candidates for the induction of OA-like biological  
129 changes in articular cells or tissues in culture, in which temporal and concentration effects  
130 can be explored.

131

132 Models of OA where cytokines are the primary method of induction are very common  
133 and are generally well understood. The model is usually inexpensive and is very easily  
134 manipulated. The ability to expand cells in vitro also means that many replicates are possible,  
135 allowing multiple hypotheses to be tested from single sources of tissue. Nevertheless, cells in  
136 culture (particularly chondrocytes) are prone to dedifferentiate to fibroblasts after only a  
137 small number of passages (Caron et al., 2012; Minegishi et al., 2013), and isolating cells from  
138 their matrix removes possible matrix-effects. Additionally, inter-tissue crosstalk is difficult to  
139 characterise in vitro and both time- and concentration-dependent effects are not well  
140 understood (Table 1).

141

142 Evidence for a role of IL-1 $\beta$  in OA is well established, and it has been used as a  
143 potential therapeutic target, for example through the design of vectors activated by IL-1 that  
144 protect against its catabolic effect (Campbell et al., 2005) or through the antagonism of the

145 IL-1 receptor (IL-1R) (Chevalier et al., 2009). Exposure to IL-1 $\beta$  stimulates chondrocytes and  
146 synovial cells to produce catabolic proteases (Maccoux et al., 2007) with apocrine signalling  
147 further enhancing MMP release and the resulting degradative cascade. The catabolic response  
148 can be blocked by the inhibition of IL-1 $\beta$  through antagonism with the IL1-R antagonist (IL-  
149 1Ra) (Bujak and Frangogiannis, 2009).

150

151 Inflammatory molecules produced by chondrocytes in response to IL-1 $\beta$ , include  
152 prostaglandin (PG)E<sub>2</sub>, cyclooxygenase (COX)-2, IL-6, IL-8 and leukaemia inhibitory factor  
153 (LIF). IL-1 $\beta$  also leads to the accumulation of reactive oxygen species, through expression of  
154 inducible nitric oxide synthase (iNOS) by the transcription factor nuclear factor kappa B (NF-  
155  $\kappa$ B), ultimately leading to apoptosis (Fig. 2a). This mechanism can also be accelerated by IL-  
156 1 $\beta$ -mediated damage to mitochondrial DNA, leading to a further release of reactive oxygen  
157 species and enhancing apoptosis (Loeser, 2011).

158

159 IL-1 plays a role in bone pathophysiology relevant to OA, particularly IL-1 $\alpha$  which is  
160 also known as osteoclast activating factor (Lee et al., 2010). In bone, there is an increase in  
161 the activity of PGE<sub>2</sub> in osteoblasts and stromal cells, as well as an increase in the expression  
162 of receptor activator of NF- $\kappa$ B Ligand (RANKL). RANKL is critically involved in the  
163 activation, maturation and survival of osteoclasts (Tanaka et al., 2005). IL-1 has also been  
164 shown to induce multinucleation of osteoclasts, thus potentiating the function of the cells. In  
165 vivo, when adult rats were injected with a moderate amount of IL-1 $\beta$  (1  $\mu$ g/kg bodyweight),  
166 an increase in serum and urinary Ca<sup>2+</sup> concentration was noted, as well as an increase in  
167 osteoclast number, implying an increase in bone resorption (Nguyen et al., 1991)

168

169 TNF- $\alpha$  has also been used to induce OA-like changes in in vitro experiments, because  
170 it is found in diseased synovial fluid (Horiuchi et al., 1999; Fujita et al., 2005), and is able to  
171 induce catabolism and inhibit anabolic pathways in joint tissues and cartilage cells (Liacini et  
172 al., 2003). While IL-1 $\beta$  and TNF- $\alpha$  are the most commonly used cytokines in modelling OA,  
173 other cytokines may also play important roles. Concentrations of IL-6, IL-8, vascular  
174 endothelial growth factor (VEGF) and monocyte chemoattractant protein-1 (MCP-1) are all  
175 increased in the synovial fluid of OA joints (Sohn et al., 2012). Osteoclasts are recruited by  
176 IL-6, and thus it may be an important modular of the bone remodelling observed in OA  
177 (Silfverswård et al., 2004). However, in model designs, these cytokines are rarely considered,  
178 possibly because they are characterised as chondrocyte-derived and thus they can be induced  
179 by other cytokines such as IL-1 $\beta$  or TNF- $\alpha$  (Bunning et al., 1990). Using cytokines in  
180 combination may allow for the induction of OA-like cell and tissue responses that more  
181 closely replicate the natural disease, particularly in lieu of synovial effects in the model  
182 design.

183

#### 184 *In vivo determination of cytokine concentrations*

185 Cytokine-based models use a wide variety of concentrations and durations of cytokine  
186 stimulation, namely those which produce a measurable downstream effect, rather than a  
187 concentration that reflects that in naturally occurring disease. Besides, OA is a slowly-  
188 progressing disease, and relatively small increases in cytokine concentrations have been  
189 identified in naturally-affected joints.

190

191 When OA synovial fluid is assayed, the quantities of IL-1 (< 2 ng/mL) and TNF  
192 (almost 3 ng/mL) are highly variable between experiments, but are low in comparison with  
193 those used to exert an effect in vitro (Table 2). The variation in physiological concentrations

194 is evident and may be the result of several factors, including the method used to quantify the  
195 cytokines, or the phenotype of the disease. In contrast, the concentrations used in models are  
196 typically much higher at up to 100 ng/mL of IL-1 $\beta$  (Macrory et al., 2009), and up to 50  
197 ng/mL of TNF- $\alpha$  (Gabriel et al., 2010).

198

### 199 *Explant-based models of cytokine stimulation*

200         Explant-based models are simple and easy to produce, and have the major advantage  
201 that they can be used to examine the response of cells in their natural extracellular matrix  
202 and, once removed from their extracellular matrix, the cell phenotype is altered (Zien et al.,  
203 2001). Using explanted tissue also allows features such as matrix degradation to be observed.  
204 However, the use of tissue explants creates new problems; for example, cells at the explant  
205 edge die (Hunziker and Quinn, 2003; Gilbert et al., 2009), there are limitations to the number  
206 of samples which can be obtained from the same source and more than one tissue might be  
207 required to maintain viability (Amin et al., 2009).

208

209         Cartilage is highly sensitive to TNF- $\alpha$  and physiologically relevant concentrations as  
210 low as 0.25 ng/mL (Westacott et al., 1990) are sufficient to increase the release of  
211 glycosaminoglycans (GAGs) from OA cartilage (human) when compared with healthy  
212 cartilage in a 14 day period (Westacott et al., 2000). Species-specific differences may exist in  
213 the stimulation required to elicit a particular response (such as GAG release); thus, GAG  
214 release from feline cartilage explants requires stimulation with both recombinant human IL-  
215 1 $\beta$  and oncostatin-M (OSM) in combination (Gabriel et al., 2010), although a feline-specific  
216 stimulus may have elicited a different response.

217

218 A possible autocrine network has been suggested because both IL- $\beta$  and TNF- $\alpha$  show  
219 strong positive protein staining in the superficial zone of cartilage as well as in the synovial  
220 fluid in late-stage OA. Meanwhile, deep zone cells only demonstrate marginal staining in the  
221 most severe cases (Tetlow et al., 2001), illustrating the differential responses of chondrocytes  
222 in disease. Notably, the early stages of disease rarely demonstrate any chondrocyte  
223 expression of cytokines, implying that any inflammatory cytokines present in the joint at the  
224 early stage of the disease are most likely to be synovial in origin (Tetlow et al., 2001).

225

#### 226 *Chondrocyte culture-based cytokine models*

227 The choice of whether to use a monolayer, a cell scaffold or intact tissue will  
228 influence the cells' response to the cytokine stimulus applied. The sensitivity of chondrocytes  
229 to their molecular and loading environment dictates that ideally they should not be isolated  
230 from their matrix, or if they are, the matrix in which they are embedded should closely match  
231 the behaviour of normal, healthy tissue. However, the low cellularity of cartilage tissue  
232 necessitates the demand for large explants, thereby reducing the number of replicates which  
233 can be obtained from a single tissue source. Monolayer cultures allow the expansion of the  
234 cellular resource, although this is finite for tissues such as cartilage (Nicholson et al., 2007),  
235 as the cell phenotype changes in monolayer culture (Zien et al., 2001).

236

237 The ease of using chondrocytes in monolayer combined with their rapid response to  
238 cytokine stimulation has resulted in this being the most widely used model. Numerous  
239 models that use cytokines added to cell or tissue culture medium have been shown to produce  
240 OA-like responses in chondrocytes in monolayer, such as a decrease in the expression of type  
241 2 collagen and aggrecan, and an increase in the expression of MMP-13, across multiple  
242 species (Miyaki et al., 2009; Novakofski et al., 2012; Yang et al., 2014).

243

244           Alternatively, stimulating chondrocytes with the synovial fluid from OA patients  
245 (Hoff et al., 2013), a more physiologically-relevant stimulus, produces similar results,  
246 including the expression of the pro-inflammatory cytokines IL-6, IL-8, IFN- $\gamma$ , MCP-1,  
247 granulocyte-colony stimulating factor (G-CSF) and VEGF. However, this method of  
248 stimulation is also limited by the imprecise understanding of the relative contribution of  
249 different mediators which are driving catabolism in this model, and the lack of repeatability  
250 because of the limited synovial fluid volume that can be obtained from a single source.

251

#### 252 *Co-culture-based cytokine models*

253           Recognising that OA is a disease that affects and involves the interaction between  
254 multiple tissues are co-culture experiments that permit the study of these interactions in vitro.  
255 Cytokine or osmotic pressure stimuli can be easily applied to co-culture models, though the  
256 tissues might require different culture conditions, necessitating some compromise on the  
257 culture conditions used when cultured together. The co-culture of synovial membrane with  
258 chondrocytes is one method by which the complexity of the pro-inflammatory cascade can be  
259 reproduced in vitro, because synovium is the primary source of these mediators (Ushiyama et  
260 al., 2003).

261

262           Co-culturing synovium from OA patients with healthy cartilage explants produces an  
263 increase in the expression of IL-1, IL-4, IL-7, IL-8, IL-10, IL-13 and osteoprotegerin (OPG),  
264 similar to synovial fluid from OA joints, as well as reducing GAG production in the cartilage  
265 (Beekhuizen et al., 2011). Whilst it may be desirable to use synovium to model OA in vitro, it  
266 is composed of two different, but interacting, cell types and shows highly variable lesion  
267 patterns both across different OA joints, and within a single joint with clinical OA (Rhodes et

268 al., 2005; Goldhammer et al., 2010; Smith, 2011). Consequently, deconstructing the effects  
269 within the synovial co-culture model is complex, although characterisation of the factors  
270 responsible for the response will help to standardise across experiments. The use of bone in  
271 co-culture experiments is also important, because it appears to have a role in maintaining the  
272 long-term viability of chondrocytes in the superficial zone of articular cartilage (Amin et al.,  
273 2009).

274

#### 275 *Bone cytokine models*

276 Evaluation of the response of bone to cytokine stimulation in models of OA is scarce,  
277 which is unsurprising because it is difficult to ascertain the precise cytokine environment to  
278 which bone cells are exposed to in OA. Most data on cytokine roles in bone focus on the  
279 specific roles of TNF- $\alpha$ , IL-6 and IL-1 release during osteocyte injury (Komori, 2013).  
280 Further, generation of RANKL is induced by IL-6 and IL-1, and mice lacking RANKL  
281 completely lack osteoclasts (Kong et al., 1999). Osteoclasts driven to apoptosis release  
282 soluble RANKL, and conditioned media from these cells further induce osteoclastogenesis  
283 (Al-Dujaili et al., 2011). Notably, bone plays a larger role than previously considered in  
284 cartilage health, and removal of cartilage explants from the underlying bone tissue leads to a  
285 higher percentage of cell death in chondrocytes than if chondrocytes were left attached to the  
286 bone (Amin et al., 2009).

287

288 Mouse calvarial cultures incubated with IL-1 showed bone resorption, demonstrating  
289 that cytokines act on cultured bone (Gowen et al., 1983), and cultured osteoblasts actively  
290 synthesised NO in response to IL-1 $\alpha$  in a dose-dependent fashion, although IL-1 $\beta$ , TNF- $\alpha$  and  
291 IFN- $\gamma$  failed to elicit a response (Ake et al., 1994). Evidently, cytokines play a role in bone  
292 turnover, and bone is responsive to inflammatory stimuli. IL-1 $\beta$  has been shown to induce the

293 release of PGE<sub>2</sub>, MMP-3 and MMP-13 from osteoblasts (Pecchi et al., 2012), although this  
294 can be inhibited with chondroitin sulphate.

295

### 296 **Load-based models of inducing OA**

297 Chondrocytes are sensitive to load, and must always be under sufficient force to  
298 maintain extracellular matrix homeostasis, yet below that which induces apoptosis or  
299 stimulates an inflammatory cascade within the tissue (Henrotin et al., 2012). Subchondral  
300 bone is also mechanosensing, and responds in vivo by changing its thickness and reducing its  
301 resorption when loading is increased (Murray et al., 2001). Identifying the load thresholds  
302 that alter the balance from maintenance of homeostasis to injury is important to our  
303 understanding of the magnitude of a beneficial or deleterious load.

304

305 Load models are easily manipulated and, as a result, high throughput experiments can  
306 be performed. Signalling pathways associated with mechanotransduction are becoming well  
307 understood (Millward-Sadler and Salter, 2004; Mobasheri et al., 2005), allowing better  
308 appreciation of the processes associated with this model. Removing cells from their native  
309 matrix and embedding them into an artificial scaffold alters, at least theoretically, the native  
310 signalling network, and the force used in the experiment is innately dependent on the ability  
311 of the scaffold to withstand that force.

312

313 Cell loading models require high cell numbers that might not be available from some  
314 sources. Using entire tissues overcomes this problem, and allows cells to use natural cell-  
315 matrix interactions and cross-tissue communication as well as much greater forces.  
316 Conversely, native tissue experiments are limited to larger species and lower numbers of  
317 replicates. Additionally, cells have been shown to undergo substantial cell death at the cut



318 edge (Huntley et al., 2005; Huntley et al., 2005a) so distorting observations at these sites  
319 (Table 1).

320

### 321 *In vivo determination of cartilage load*

322 Several in vivo studies have attempted to determine the physiological pressures  
323 experienced by articular cartilage during loading. The pressure passing through the load-  
324 bearing region of a human acetabular prosthesis has been determined to be approximately 3.5  
325 MPa during locomotion (Hodge et al. 1989), and the articular contact pressure of the human  
326 knee does not exceed 8 MPa, even when the menisci have been removed (Fukubayashi and  
327 Kurosawa, 1980). Loads of a similar magnitude have been reported in both the medial and  
328 lateral compartments of canine elbow joints, with mean contact pressures between 3.0 and 4.0  
329 MPa and peak pressures between 6.6 and 9.1 MPa (Cuddy et al., 2012). These data suggest  
330 that the articular loading experienced by different joints in different species are  
331 physiologically comparable, and concurs with estimates of the articular cartilage compressive  
332 stress in different mammalian species, which only vary within one order of magnitude from  
333 mice to cows (Simon, 1970).

334

335 Chondrocytes sense the loading of their environment through integrin receptors  
336 (Bader et al., 2011). When activated, the integrins stimulate stress pathways leading to  
337 cytoskeletal disruption and release of inflammatory cytokines, such as IL-1 $\beta$  and TNF- $\alpha$   
338 (Valhmu et al., 1998; Durrant et al., 1999; Bader et al., 2011). Cytokine-induced proteolytic  
339 enzyme release is mediated by nitric oxide, PGE<sub>2</sub> and reactive oxygen species. The  
340 extracellular proteins cleaved by the activated proteases are then capable of further induction  
341 of both proinflammatory cytokines and matrix proteases, though the receptors activated by  
342 collagen fragments remain elusive (Klatt et al., 2009).

343

344 The signalling pathways induced by static loading and cytokine induction are similar  
345 and the mechanism that governs both is similar in both models (Fig. 2b). The compression  
346 pathway, however, appears reliant on the magnitude and duration of the stress (Fanning et al.,  
347 2003).

348

#### 349 *Explant based models of cartilage loading*

350 The use of tissue explants, assessing the response of cells embedded in the natural  
351 matrix, is the simplest method for assessing the effects of load. Load is applied to tissue  
352 explants through various methods, based on the variable in question. Most typically, ‘drop  
353 towers’ in which a free weight is released from a predetermined height onto the tissue are  
354 used to impart a single impact load. This is believed to replicate the development of ‘post  
355 traumatic’ OA, which occurs following an injurious articular load. Load can also be applied  
356 in a cyclical manner with devices such as pneumatic or hydraulic loading chambers.

357

358 Static loading can induce similar deleterious changes in cartilage explants when  
359 applied at an appropriate magnitude. For example a compressive strain of 50% applied to a  
360 cartilage explant results in a decrease in the synthesis of collagen type II and proteoglycans  
361 (Chen et al., 2001). Static compression of calf patellofemoral cartilage to 25% or 50% strain  
362 for 24 h produces deleterious changes in cartilage metabolism, resulting in an increase in  
363 expression of *MMP3*, *9* and *13* mRNA and decrease in *COL2A1* and aggrecan (*ACAN*) within  
364 1-2 h post loading (Fitzgerald et al., 2004). IL-1 receptor activation and activation of the  
365 extracellular-signal related kinase 1/2 (ERK1/2), p38, mitogen-associated protein kinase  
366 (MAPK) family member pathways in a time-dependent manner mediate these changes  
367 (Fanning et al. 2003).

368

369 A load equivalent to  $1.5 \times$  bodyweight placed on a human knee joint caused only 10%  
370 strain in the patellofemoral cartilage following 10 min of static loading (Wong and Sah,  
371 2010). Similarly, intact human femoral head cartilage loaded to the equivalent of a single leg  
372 stance (less than  $2.3 \times$  bodyweight) is subject to a strain of 33% (Greaves et al., 2010).  
373 Consequently the use of higher strains in in vitro models exaggerates the maximal normal  
374 physiological load experienced by a joint in vivo, although this reflects the requirement to  
375 induce an effect within a shorter timeframe. Furthermore, the elastic (Young's) modulus  
376 varies across cartilage within a joint (Shepherd and Seedhom, 1999), and thus the load  
377 required to induce a specific strain, or strain produced from a specific load will also differ  
378 across samples from the same joint.

379

380 In vitro studies have been used to determine the critical stress thresholds of cartilage  
381 explant, in which apoptosis, collagen degradation and nitrite accumulation are observed.  
382 Values range between 4.5 MPa for cyclic loading (six compressions to a final strain of 30-  
383 50%, held for 5 min rested for 25 min, Loening et al., 2000) and 15 MPa for a single impact  
384 load (Torzilli et al., 1999) for bovine cartilage, although the results between experiments are  
385 highly variable. Notably, bovine cartilage explants subjected to a 0.5 MPa cyclic loading  
386 increase proteoglycan synthesis across various cycle lengths (Parkkinen et al., 1992)  
387 supporting the hypothesis that moderate loading is beneficial to cartilage health.

388

### 389 *Chondrocyte culture-based loading models*

390 The response of cells to load can be dissected further by isolating cells in culture,  
391 embedding them in an artificial matrix, and compressing them using a bioreactor. This has  
392 the advantage of permitting very precise changes in loading parameters, as it is highly

393 reproducible, as well as looking at the effects of different matrices on the cellular response.  
394 However, a large caveat to such experiments is that the cell response observed in vitro may  
395 not represent that observed in vivo where the interaction of the matrix is critical to the effect  
396 produced.

397

398 In vitro loading of isolated chondrocytes seeded in a 3-dimensional (3-D) culture  
399 (typically agarose) results in both an increase in cell proliferation and proteoglycan synthesis  
400 when cyclically loaded at a physiological strain of 15% (Lee and Bader, 1997). 3-D culture  
401 also allows for the application of bi-axial cyclic loading (direct compression or tension, and  
402 shear) (Pingguan-Murphy and Nawi, 2012), and addresses the observation that in vivo several  
403 loads may simultaneously impact on a joint during normal activity. When subjected to biaxial  
404 loading (10% compressive strain with 1% sheer strain) for two 12 h periods, separated by a  
405 12 h resting period, both cell proliferation and an increase in GAG production were observed,  
406 demonstrating the importance of closely representing the joint environment in in vitro  
407 experiments.

408

409 Cyclic loading of bovine chondrocyte-embedded calcium polyphosphate scaffolds at  
410 1 kPa and 1 Hz for 30 min, activates Erk1/2 and c-Jun N-terminal kinase (JNK) as seen with  
411 static loading, and causes an increase in activator protein-1 (AP-1) binding. This stimulus  
412 induces *MMP-3* and *13* expression and results in MMP-13 mediated extracellular matrix  
413 (ECM) degradation. However, following the loss of functional tissue, collagen type II and  
414 aggrecan gene expression occurs after 12 h, and synthesis occurs by 24 h post loading (Fig.  
415 2c) (De Croos et al., 2006).

416

417 *Co-culture based loading models*

418 Co-culture methods have been used to explore the effect of loading on articular  
419 tissues in parallel, although they are challenged by the necessity to use different culture  
420 conditions for each tissue, or to compromise the culture conditions. For example, alginate-  
421 embedded chondrocytes cultured on a porous filter above mechanically stretched osteoblasts  
422 become more hypertrophic during stimulation of the osteoblasts. This change was most  
423 pronounced when the osteoblasts were subjected to tensile loads, suggesting molecular  
424 ‘cross-talk’ occurs between the two cell types in response to mechanical stress in bone (Lin et  
425 al., 2010).

426

427 Co-culture of OA osteoblasts with healthy alginate bead-embedded chondrocytes  
428 result in a phenotypic shift to chondrocyte hypertrophy and matrix mineralisation, which does  
429 not occur with healthy osteoblasts stimulated with IL-1, IL-6 or OSM (Sanchez et al 2005).  
430 This demonstrates the limits of artificially stimulating cells and the phenotypic differences of  
431 naturally-diseased cells and highlights the need for better characterisation of the soluble  
432 factors released by these cells as well as better definition of the molecular stimulation  
433 required to induce the OA phenotype in healthy cells.

434

#### 435 *Bone loading models*

436 Osteocytes are the major mechanosensors of bone, although they are rarely included  
437 in models of OA because they are notoriously difficult to culture in vitro. Analysis of the  
438 osteocyte (in contrast to osteoblast) response to compression has been hindered due to this  
439 challenge (Kato et al., 1997). Osteocyte cell lines seeded into type I collagen gels layered  
440 with osteoblasts on their surface respond to mechanical loading, with co-cultured constructs  
441 increasing type I collagen expression with loading, and osteocyte embedded gels expressing  
442 PGE<sub>2</sub> after mechanical stimulation (Vazquez et al., 2014).

443

444 *Relevance of load: From in vivo to in vitro models*

445         The validity of a loading model depends, at least to some extent, on its relationship  
446 with the natural environment of the joint and its loading in vivo. The loading parameters of a  
447 selection of cell and tissue loading models are presented in Table 3. The use of scaffolds can  
448 impart some structure to the cells for culture-based models, and permit cyclic loading of  
449 isolated cells, albeit within ranges that are governed by the strength of the matrix in which  
450 they are embedded.

451

452         The heterogeneity of the cartilage structure means that precise reconstruction of the  
453 tissue in vitro may not be possible, and so compromises must be made when constructing a  
454 load based model (Gannon et al., 2012). The individual phenotype of each chondrocyte is  
455 related to their location in the tissue (Fujioka et al., 2013; Schuurman et al., 2015) and  
456 therefore in homogeneous tissue models, chondrocytes may not behave in the same manner.

457

#### 458 **Future directions**

459         The multifactorial nature of OA should be considered when designing a model to  
460 reproduce it, even if it is only testing a single parameter, such as the response to a load or  
461 catabolic stimulus. A deeper understanding of the pathways evoked in in vitro models, and  
462 their relevance to the changes seen in naturally-occurring OA phenotypes is important in  
463 order to improve the translational relevance of the conclusions drawn.

464

465         To date the vast majority of explant- and culture-based models have assessed cartilage  
466 in isolation. While this might reflect the ease of manipulating cartilage and the resilience of  
467 chondrocytes in cell culture, progress in tissue engineering and cell culture techniques will

468 allow for the development of more advanced models including other cell types. The  
469 responsiveness of bone to stimuli, and the cross talk that occurs between the different tissues  
470 in OA joints dictate that models should consider the role of multiple tissues when assessing  
471 the response to a given stimulus so as to enable more meaningful translation to the  
472 anticipated response in vivo.

473

474 There is no all-encompassing model that is suitable for all studies of OA, and no  
475 single model can be used to perfectly simulate naturally-occurring events. Whilst models  
476 seek to answer specific biological questions, more standardised end-points for the molecular  
477 and physiological parameters assessed are necessary, as at present it is impossible to directly  
478 compare the outcomes of the many in vitro OA models published in the scientific literature.

479

480 Other areas of articular health research, such as those looking at histological  
481 assessments of cartilage repair and damage<sup>2</sup> (Glasson et al., 2010), have developed guidelines  
482 upon which assessments should be made through the consensus of experts and the publication  
483 of their recommendations. In molecular biology, similar guidelines have been developed for  
484 performing microarray and quantitative polymerase chain reaction studies (Brazma et al.,  
485 2001; Bustin et al., 2009). Whilst the in vitro models of OA have many different functions  
486 and outcomes, guidelines could still be developed to determine the endpoints which are  
487 matrix- and chondro-protective, and the minimum number of features of a model (such as  
488 measures of matrix release and turnover, transcription changes and/or cellular morphometric  
489 changes) which are agreed to represent an 'OA-like' scenario. Similarly, models seeking to  
490 investigate the pathogenesis of OA must justify the nature of stimulatory conditions, relative  
491 to the in vivo disease, beyond simply that required to produce a response. At the very least in

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<sup>2</sup> See: [http://www.cartilage.org/files/contentmanagement/ICRS\\_evaluation.pdf](http://www.cartilage.org/files/contentmanagement/ICRS_evaluation.pdf) (accessed 7 April, 2015)

492 vitro models should be standardised to a particular disease phenotype, with reasoning for the  
493 source of the cells and/or tissues used and the outcomes to be measured, as there is no single  
494 OA phenotype which can be encompassed by all models.

495

## 496 **Conclusions**

497 The molecular pathways underpinning cytokine-stimulation and load-based in vitro  
498 models of disease are similar. The combination of different models types may permit the use  
499 of stimuli which are physiologically relevant, and which allow us to understand the  
500 development and progression of the disease, particularly the early phase, rather than simply  
501 the catastrophic downstream events after it has begun. Standardisation of the approaches,  
502 both within and between different species will allow the wider applicability of results  
503 between studies, which in turn will enhance our understanding of the disease.

504

## 505 **Conflict of interest statement**

506 None of the authors of this paper has a financial or personal relationship with other  
507 people or organisations that could inappropriately influence or bias the content of the paper.

508

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511

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885

886 **Tables**887 **Table 1**

888 Advantages and disadvantages of some of the most commonly used in vitro models

<b>Model Type</b>	<b>Variables that can be applied</b>	<b>Advantages</b>	<b>Disadvantages</b>	<b>Examples</b>
<b>Monolayer culture</b>	Cytokine stimulation, osmotic pressure	Allows expansion of cellular resource from a single sample, investigation of distinct pathways in isolation	Altered phenotype of isolated cells due to isolation from tissue and absence of normal extracellular matrix	(Sylvester et al., 2012; Novakofski et al., 2012)
<b>Co-culture</b>	Cytokine stimulation, osmotic pressure	Considers cross-talk between cell types	Altered phenotype of isolated cells  Different cell types require different culture conditions, or compromise if culture together	(Lin et al., 2010; Beekhuizen et al., 2011; Vazquez et al., 2014)
<b>3D-culture</b>	Cytokine stimulation, osmotic pressure, physical injury and loading regimens.	Affords structure and force to sensitive cells.	Magnitude of force is scaffold dependent, and may not reflect that of the normal tissue  Isolation and expansion of cell types first	(Mizuno and Ogawa, 2011; Bougault et al., 2012; Pinguan-Murphy and Nawi, 2012)
<b>Explant</b>	Cytokine stimulation, osmotic pressure, physical injury and loading regimens.	Inexpensive, easily produced, cells maintained in normal extracellular matrix.	Cell death at cut edge of tissue, few replicates available from same source, more than one tissue type may be required to maintain viability, physical attributes may change in culture	(Fitzgerald et al., 2004; Bush et al., 2005; Jeffrey and Aspden, 2006; Gabriel et al., 2010)

889

890 **Table 2**891 Osteoarthritic synovial fluid interleukin (IL)-1 $\beta$  and tumour necrosis factor (TNF)- $\alpha$ 

892 concentrations in vivo

Condition	Cytokine	
	IL-1 $\beta$	TNF- $\alpha$
Control (human) (Kahle et al., 1992)	<20 pg/mL	2890 pg/mL
Control (canine) (Fujita et al., 2005)	490 pg/mL	105.3 pg/mL
OA (human) (Kahle et al., 1992)	21 pg/mL	80 pg/mL
OA - Hip dysplasia (canine) (Fujita et al., 2005)	2010 pg/mL	600 pg/mL
OA - Mild (porcine) (McNulty et al., 2013)	109 pg/mL	-
OA - Moderate (porcine) (McNulty et al., 2013)	122 pg/mL	-

893

894 **Table 3**

895 A summary of load-induced changes in OA models

Species studied	Regimen tested	Duration of experiment	Findings of experiment	Citation
Dog (in vivo)	20-40 km/day	15 weeks	Increased water content. Decreased collagen content. Decreased proteoglycan content.	(Kiviranta et al., 1992)
Bovine explant	Six on-off cycles of 30-50% strain	5 min compression: 25 min release	Apoptosis of cells. Degradation of collagen network. Glycosaminoglycan release.	(Loening et al., 2000)
Bovine explant	100 g, 500 g and 1 kg dropped from 2, 5, 10 and 20 cm	N/A	Linear decrease in cell viability. Increased hydration of tissue. Partial depth fissures.	(Jeffrey et al., 1995)
Canine shoulder explant	5 MPa at 0.3 Hz	20 or 120 min	Cell death increased with increased loading time. Glycosaminoglycan and NO were not significantly altered.	(Levin et al., 2001)
Canine shoulder explant	5 MPa at 0.3 Hz	0, 2, 20, 120 min	Necrosis and apoptosis of cells increased with loading time. Proteoglycan increased in 2 and 20 minute groups but decreased at 120 minutes.	(Chen et al., 2001)
Agarose embedded equine chondrocytes	15% strain either statically or cyclically (0.3-3 Hz)	48 h	Dynamic strain increased cell proliferation. Static strain decreased glycosaminoglycan content, while cyclic strain increased glycosaminoglycan.	(Lee and Bader, 1997)
Bovine explant	25-50% strain over 3 min period	Maintained for 1, 2, 4, 8 and 24 h	Relative expression of matrix genes decreased. Relative expression of proteases increased.	(Fitzgerald et al., 2004)
Human chondrocyte monolayer	1, 5 or 10 MPa hydrostatic pressure at 1 Hz	4 h per day for either 1 or 4 days	mRNA and protein expression of aggrecan and collagen type 2 upregulated after 4 days. No difference at 1 day.	(Ikenoue et al., 2003)
Full thickness human cartilage explant	Single mechanical load of 14 MPa for 500 ms	Measurements taken 96 h after injury	DNA fragmentation in 34% of loaded chondrocytes (vs. 4% of control) GAG release increased in loaded explants (1.9% vs. 0.8% total GAG content)	(D'Lima et al., 2001)

896

897

898 **Figure legends**

899

900 Fig. 1. Healthy and diseased synovial joint showing the changes in the entire joint organ.  
901 Bone weakness and wearing has been reported, as well as synovial thickening and swelling,  
902 subchondral bone thickening, osteophyte formation and cartilage degradation. In addition,  
903 tendons can become weak and inflamed and ligaments can become lax.

904

905 Fig. 2. Mechanistic pathways of in vitro models of OA. Both cytokines (a) and injurious  
906 loading (b) combine to cause the typical OA-like phenotype, showing apoptosis of cells,  
907 tissue degradation and inflammatory gene expression. In these cases, feedback loops occur  
908 either through inflammation, causing further cytokine stimulation, or abnormal loading,  
909 caused by tissue degradation. However, normal homeostatic loading is vital to tissue health,  
910 and works through similar pathways, as shown by the green line in (c), leading to tissue  
911 growth.

912

913 MAPK, mitogen-activated protein-kinase; JNK, c-Jun N-terminal kinase; AP-1, activator  
914 protein-1; NF $\kappa$ B, nuclear factor kappa B; COX2, cyclooxygenase-2; PGE<sub>2</sub>, prostaglandin-E<sub>2</sub>;  
915 MMP, matrix metalloproteinase; ADAMTS, a disintegrin and metalloproteinase with a  
916 thrombospondin motif; ROS, reactive oxygen species.