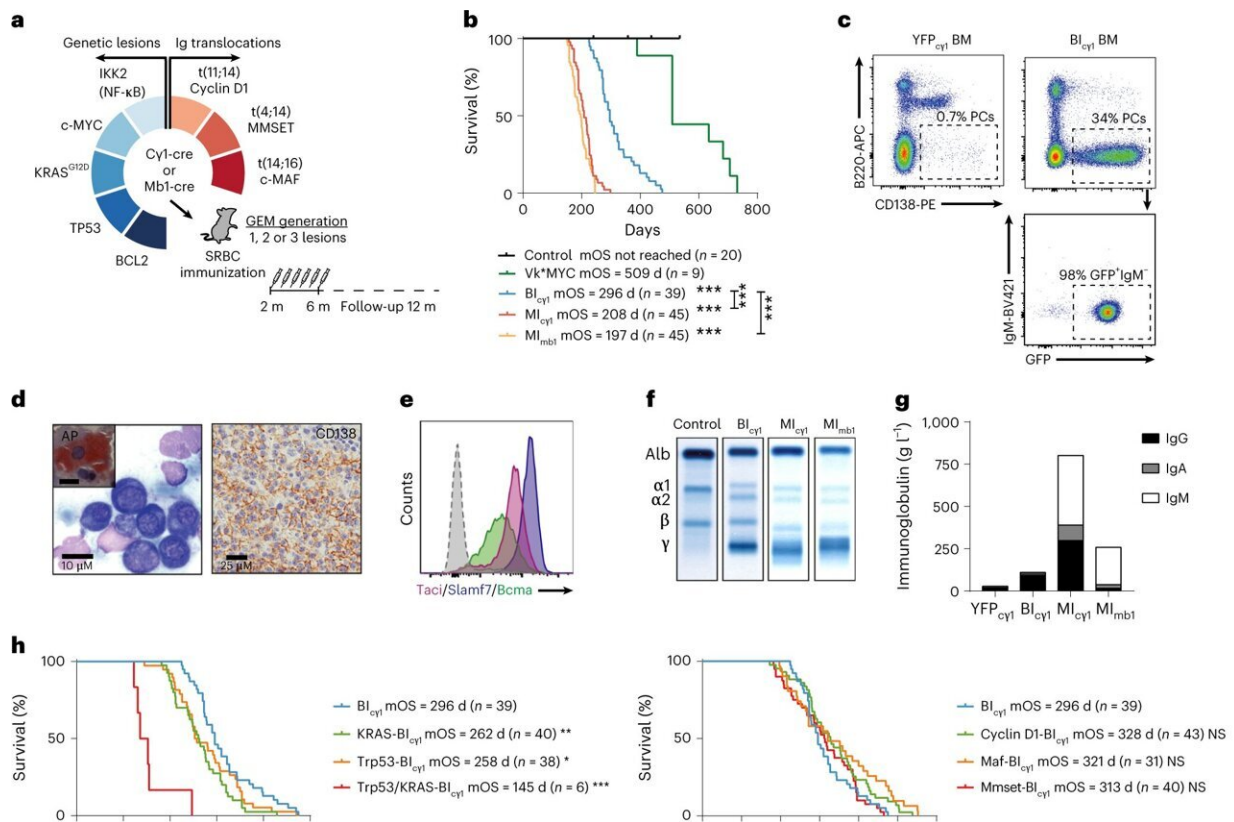


Scientists create mouse avatars to treat multiple myeloma

March 29 2023



Genetically heterogeneous mouse models of human-like multiple myeloma. **a**, Schematic of the genetic screen strategy, whereby transgenic mice were crossed with *cy1-cre* or *mb1-cre* mice. Among 31 genetically heterogeneous mouse lines generated, MI_{mb1}, MI_{cy1} and BI_{cy1} strains developed MM. GEM, genetically engineered mice; m, months. **b**, Kaplan–Meier OS curves of MI_{mb1}, MI_{cy1}, BI_{cy1}, control (YFP_{cy1} and YFP_{mb1}) and Vk*MYC mice. **c**, Representative flow cytometry analysis in the BM of BI_{cy1} mice at the time of death, which shows an increased number of GFP⁺CD138⁺B220⁻sIgM⁻ MM cells. **d**, Giemsa staining of

a representative BM sample in BI_{cy1} mice revealed human-like PCs with expression of acid phosphatase (AP; left). On the right, immunohistochemical examination in BI_{cy1} mice revealed CD138 surface expression by MM cells. **e**, MM cells show increased surface expression of *Bcma*, *Slamf7* and *Taci* according to flow cytometry analyses. **f**, Representative electrophoresis of immunoglobulin secretion in serum samples from MI_{mb1}, MI_{cy1} and BI_{cy1} mice shows M spikes corresponding to the gamma fraction. **g**, Quantification of immunoglobulin isotypes in serum samples by ELISA in MI_{mb1} ($n = 3$), MI_{cy1} ($n = 2$), BI_{cy1} ($n = 4$) and YFP_{cy1} control ($n = 9$) mice. **h**, Kaplan–Meier survival curves of mouse lines that develop MM derived from the BI_{cy1} strain with additional *KRAS*^{G12D} mutation, heterozygous *Trp53* deletion, or expression of cyclin D1, c-MAF or MMSET. **i**, Kaplan–Meier survival curves of mouse lines that develop MM derived from MI_{cy1} mice with additional *KRAS*^{G12D} mutation, heterozygous *Trp53* deletion, c-MAF expression or BCL2 expression. **j**, Kaplan–Meier survival curves in mice with MMSET/NSD2 expression crossed with lines carrying either *IKK2*^{NF-κB} activation or c-MYC expression, which developed MM at old ages. **k**, Flow cytometry analyses in BI_{cy1} and MI_{cy1} mice revealed that precursor states precede clinically evident MM in genetically heterogeneous mice. **l**, Analysis of *Igh* clonality according to RNA-seq of immunoglobulin gene loci and classification by the presence of explicit clonotypes for each sample. B cell receptor (BCR) repertoires and the most expanded clone groups in control, MGUS and MM samples. Log-rank (Mantel–Cox) test was used. **P*

Citation: Scientists create mouse avatars to treat multiple myeloma (2023, March 29) retrieved 4 July 2023 from <https://medicalxpress.com/news/2023-03-scientists-mouse-avatars-multiple-myeloma.html>

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