Fundamental aspects of the embryonic and post-natal development and maintenance of the mammalian female germline are still unknown. Here we employ a retrospective, phylogenetic-based method for reconstructing cell lineage trees from somatic mutations accumulated in microsatellites, to study female germline dynamics in mice. Reconstructed cell lineage trees can be used to estimate lineage relationships between different cell types, as well as cell depth (number of cell divisions since the zygote). We show that in the reconstructed mouse cell lineage trees, oocytes form a cluster that is separate from hematopoietic and mesenchymal stem cells, both in young and old mice, indicating that these populations belong to distinct lineages. Furthermore, while cumulus cells sampled from different follicles are distinctly clustered on the reconstructed tree, oocytes from the left and right ovaries are not. Clustering of subsamples of oocytes suggests that the number of progenitors of this population is between 3 and 10. We also observed an increase in oocyte depth with mouse age, which can be explained by either depth-guided selection of oocytes for ovulation or by post-natal renewal. Overall, our study sheds light on substantial novel aspects of female germline preservation and development.

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