



T-cell lineage commitment revisited

Years of controversy about the lineage relationship between $\alpha\beta$ and $\gamma\delta$ T cells may at last have been resolved: it now appears that most T cells derive from an identical T-lineage committed precursor.

Hematopoietic stem cells formed in the fetal liver and the bone marrow eventually follow one of several fates. Those that colonize the thymus eventually commit to become T lymphocytes and initiate developmental events that ultimately transform them into mature effector T cells equipped to play important roles in immune responses [1]. Maturing T cells undergo DNA rearrangements that shuffle variable (V) and constant (C) region gene segments to generate the genes coding for the T-cell antigen receptor. Surface-expressed T-cell receptors endow T lymphocytes with recognition properties allowing discrimination between self and non-self. At the population level, T-cell receptor diversity is enormous, but individual T cells express only one of these many variants consisting of an α and a β chain or, in a mutually exclusive fashion, of a γ and a δ chain. For proper assembly and function, the T-cell receptor requires further association with a set of signaling proteins collectively referred to as the CD3 complex [2].

In ontogeny, $\gamma\delta$ gene rearrangement and expression precedes the appearance of $\alpha\beta$ T cells. The first cells to don a T-cell receptor appear at about day 14 of mouse gestation and bear V γ 3 and V δ 1 chains. Shortly thereafter, T cells expressing V γ 4, also paired with V δ 1, can be detected. These early V genes are expressed only in the fetal period and are undetectable in the thymus after birth [3]. Two features endow early $\gamma\delta$ T cells with rather interesting properties not shared by most other T cells. First, their T-cell receptors exhibit no junctional diversity, creating essentially monoclonal cell populations. Second, these cells demonstrate a remarkable tissue distribution, with V γ 3 T cells populating the epidermis and V γ 4 T cells homing to the reproductive epithelium.

Considered as a whole, this information suggested that early $\gamma\delta$ T-cell populations may perform tissue-specific functions [4]. Evidence obtained in our and other laboratories previously established that these two initial T-cell waves required for their production both a stem cell population and a thymic microenvironment of fetal origin [5,6]. Furthermore, the developmental potential of this fetal stem cell population appears limited to early $\gamma\delta$ T cells [7]. In contrast, cells expressing other $\gamma\delta$ or $\alpha\beta$ T-cell receptors derive from a different stem cell population, also appearing during the fetal period but persisting well into adulthood (Fig. 1). These T cells become detectable by day 16–17 of gestation. From then on, cells having $\alpha\beta$ T-cell receptors become the predominant T-lymphocyte population in the thymus.

What is the lineage relationship between these late-appearing $\gamma\delta$ and $\alpha\beta$ T cells? In 1987, Allison, Pardoll and colleagues [8,9] proposed a sequential model for lineage commitment based on the observation that $\gamma\delta$ T cells appear before $\alpha\beta$ T cells. According to this model, if T-cell receptor γ and δ genes cannot productively rearrange, then T-cell receptor α and β genes attempt rearrangements. This scheme predicts that $\alpha\beta$ T cells originate from failed $\gamma\delta$ T cells. Alternative models proposed instead that $\gamma\delta$ and $\alpha\beta$ T cells have separate origins and predicted that rearrangement of T-cell receptor α and δ genes were mutually exclusive events. Several groups initiated molecular genetic experiments to test these models. The experiments, however, were complicated by the location of all δ T-cell receptor gene segments within the T-cell receptor α locus (Fig. 2).

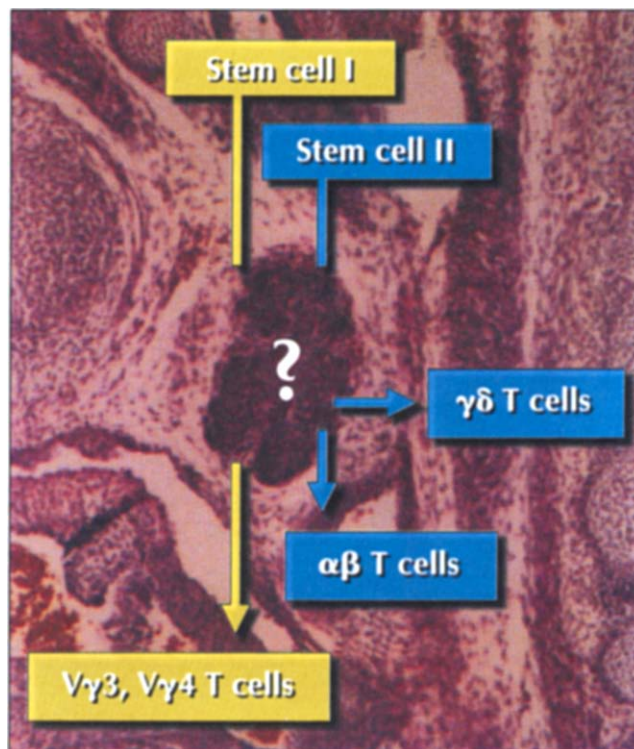


Fig. 1. Developmental fate of precursor T-cell populations in the thymus. An early fetal stem cell population can differentiate within a fetal thymus to generate T-cell receptor V γ 3- and V γ 4-bearing monoclonal T-cell populations residing in the epidermis and reproductive epithelia, respectively. A different stem cell population can reconstitute all other $\alpha\beta$ and $\gamma\delta$ T cells observed in the neonate and adult. Events leading to lineage commitment in this later-appearing precursor cell population have remained controversial (see text).

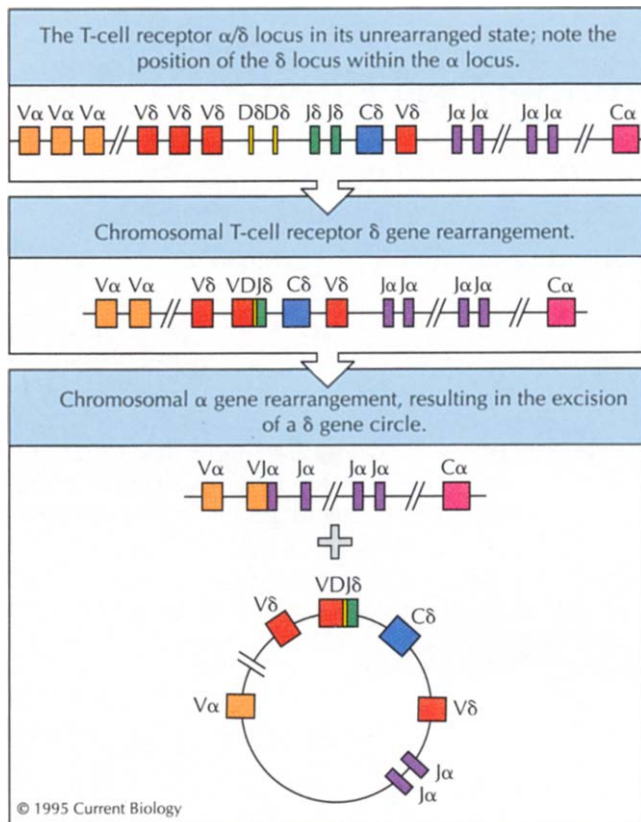


Fig. 2. Schematic depiction of T-cell receptor δ gene rearrangement, followed by T-cell receptor α gene rearrangement and concomitant excision of a T-cell receptor δ gene circle. Adapted from [14].

Chromosomal T-cell receptor α gene rearrangement thus results in the excision of T-cell receptor δ gene segments as circular pieces of DNA. In principle, the thymus should be a rich source of such DNA circles, and indeed three groups have successfully created T-cell receptor δ circle DNA libraries, but subsequent analyses of these libraries generated conflicting data [10–12]. The reasons for the observed discrepancies remain unresolved, but may relate to differences in procedures used to purify DNA circles or an inherent lack of quantitative representation in DNA circle libraries. These difficulties notwithstanding, a different set of experiments provided strong evidence against the sequential-rearrangement model. Several studies identified DNA elements mediating transcriptional repression of T-cell receptor γ genes in $\alpha\beta$ but not $\gamma\delta$ T cells. The ability to commit to a particular T-cell lineage may thus depend on the propensity of different precursor cell populations to produce factors silencing the T-cell receptor γ locus. In 1990, following reports of additional studies in transgenic mice, it became commonly accepted that differentiation along the $\alpha\beta$ and $\gamma\delta$ T cell lineages was independently regulated [13].

Now, however, Dudley *et al.* [14] and Livak *et al.* [15] challenge this view following quantitative assessments of T-cell receptor δ gene rearrangement in mature $\alpha\beta$ T cells. These cells retain rearranged T-cell receptor δ sequences within a germ-line configured α gene or as

part of excised DNA circles, as demonstrated in these recent publications as well as in a previous study [12,14,15]. This finding is in line with observations that large numbers of $\alpha\beta$ T cells never initiate active division, an event that would inevitably result in the loss of extrachromosomal DNA circles. Both groups, then, could analyze the frequency of productive T-cell receptor δ gene rearrangement in $\alpha\beta$ T cells. If the gene rearrangements are random, in a third of cases they should preserve the translational reading frame leading to the synthesis of a functional T-cell receptor protein. Such a frequency of functional rearrangements would be expected if lineage determination occurs independently of T-cell receptor gene rearrangements.

However, a sampling of several hundred T-cell receptor δ gene rearrangements revealed a significantly reduced frequency of in-frame δ rearrangements in mature $\alpha\beta$ T cells [14,15]. This depletion of productive δ gene rearrangements in $\alpha\beta$ T cells supports the hypothesis that a proportion of cells with productive T-cell receptor δ chains are removed from the $\alpha\beta$ T-cell precursor pool and may eventually become $\gamma\delta$ T cells. Under conditions in which T-cell receptor δ chains do not reach the cell surface, the frequency of in-frame T-cell receptor δ gene rearrangement should rise to that expected for a random process.

This prediction was successfully tested by Dudley *et al.* [14] using 'knock-out' mice that had normal T-cell receptor gene rearrangement but were unable to synthesize T-cell receptor δ chains. As the observed depletion in normal mice was partial rather than total, at least one other molecule must be involved in the removal of a proportion of cells that can express δ chains from the precursor $\alpha\beta$ T-cell population. The most likely candidate was the T-cell receptor γ chain. An analysis of T-cell receptor γ gene rearrangement in $\alpha\beta$ T cells by Dudley *et al.* [14] revealed a depletion of productive rearrangements similar to that noted at the T-cell receptor δ locus. This additional finding provides further evidence that T-cell precursors first try to rearrange T-cell receptor γ and δ genes in an attempt to become $\gamma\delta$ T cells. Cells failing to express a $\gamma\delta$ T-cell receptor then try to become $\alpha\beta$ T cells (Fig. 3).

Clearly, conditions must limit the capacity of precursor cells to develop into $\gamma\delta$ T cells, as most become $\alpha\beta$ T cells. Livak *et al.* [15] propose that lineage-commitment decisions result from a competition between signals generated by expressed $\gamma\delta$ T-cell receptors and some ill-defined $\alpha\beta$ T-cell commitment events. The contemporaneous rearrangement of T-cell receptor β , γ and δ chain genes provides one level at which such competition could be waged. In the absence of a T-cell receptor α chain, the recently described pre-T-cell receptor complex is a likely candidate for being a source of signals that direct precursors to differentiate into $\alpha\beta$ T cells [16]. The pre-T-cell receptor is composed of a productively rearranged T-cell receptor β chain gene and a newly

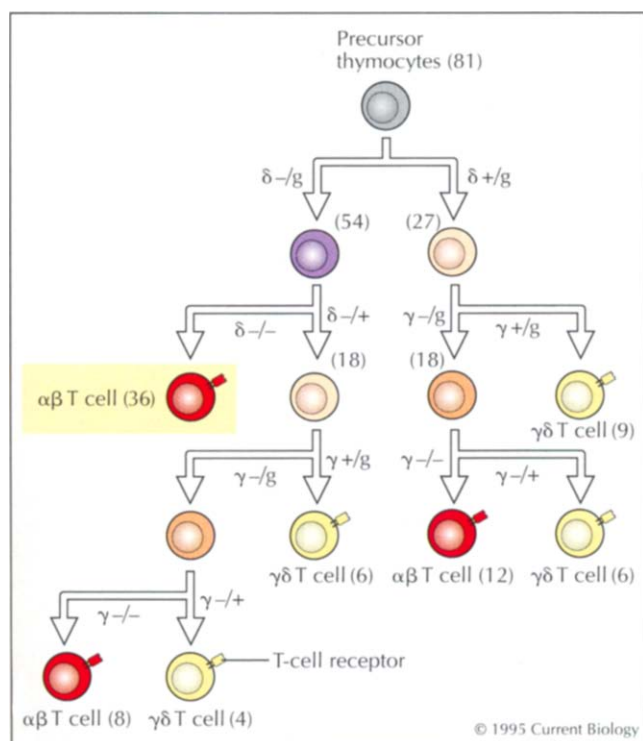


Fig. 3. The sequential-rearrangement model for T-cell development, circa 1995. As shown, 56 $\alpha\beta$ T cells (12 + 8 + 36) would derive from every 81 cells following this pathway. This would require that they have an out-of-frame rearrangement of either the δ or γ genes. The denoted $\alpha\beta$ subset (highlighted by a yellow box) is able to rearrange randomly at the γ locus, as there is no possibility of making a $\gamma\delta$ T-cell receptor. Allele states are indicated by + (in-frame), - (out-of-frame) and g (germ-line). Numbers in parentheses indicate the number of cells that would be expected to constitute a given subset, from an original 81 T-cell precursors. Adapted from [14].

cloned 33 kDa glycoprotein known as pre-T-cell receptor α (pT α). Current evidence suggests that the pre-T-cell receptor serves to signal the productive expression of a T-cell receptor β chain, thereby ensuring clonotypic expression and allowing further maturation [17].

The role that signaling through these different receptors plays in lineage commitment remains to be dissected. At a minimum, we can infer from recent experiments with transgenic mice that signaling by T-cell receptor $\gamma\delta$ or pT $\alpha\beta$ complexes can generate similar maturation signals in precursor cells [18]. However, the detection of productive T-cell receptor β rearrangement in a large proportion of mature $\gamma\delta$ T cells by Dudley *et al.* [14] argues against a strict competition model. Instead, precursor T cells would be required to remain uncommitted for some time following productive T-cell receptor β gene rearrangement. This condition could be met if signaling through the pre-T-cell receptor occurs only following ligand recognition. Alternatively, as proposed by Dudley *et al.* [14] lineage commitment may depend on the time of activation of T-cell receptor α gene rearrangement. The two models are not, of course, mutually exclusive.

The new data fulfill most predictions of the sequential-rearrangement model for T-cell lineage commitment. Revision of the Allison and Pardoll model is necessary to account for the early developmental onset of T-cell receptor β gene rearrangement. On the other hand, the new findings are inconsistent with T-cell lineage models based on the mutually exclusive rearrangement of T-cell receptor α and δ genes, or transcriptional regulation of the T-cell receptor γ locus. Indeed, recent observations indicate that transcriptional silencing may play an important role in maintaining, rather than establishing, lineage commitment [19]. A renewed interest in lineage commitment will probably surface from the developmental issues raised by the new evidence. These considerations should occupy immunologists for some time.

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