

The Role of the Notch signaling pathway in Somitogenesis

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Among other functions, the Notch signaling pathway contributes to the development of [somites](#) [4] in animals. It involves a cell signaling mechanism with a wide range of functions, including cellular [differentiation](#) [5], and the formation of the embryonic structures ([embryogenesis](#) [6]). All multicellular animals use Notch signaling, which is involved in the development, maintenance, and regeneration of a range of tissues. The Notch signaling pathways spans two cells, and consists of receptor proteins, which cross one cell's membrane and interacts with proteins on adjacent cells, called ligands. The physical interaction of receptors and ligands directs the genetic response of the first cell to produce proteins that define the type of cell it will become. One of the earliest discovered roles of the Notch signaling pathway in vertebrates is in somite formation ([somitogenesis](#) [7]). Somitogenesis is the formation of [somites](#) [4], which are sphere-like structures in early vertebrate embryos that are the first visible signs of [segmentation](#) [8]. Somites then help to define many tissues and features of the adult animal's body. The Notch signaling pathway plays at least two distinct roles during [somitogenesis](#) [7]: the first is maintenance of an oscillating protein gradient, called the segmental clock, and the second is establishing the [polarity](#) [9] of [somites](#) [4]. Mutations to [genes](#) [10] in the Notch pathway can result in [birth defects](#) [11] characterized by abnormal development of bones of the spine and ribs, like spondylocostal dysostosis. Additionally, dysfunction in the pathway linked to cancer progression, HIV-related complications, and Alzheimer's disease, among other disorders.

Somites form early in [embryogenesis](#) [6] from embryonic tissue called the presomitic [mesoderm](#) [12] (PSM), and are the cellular precursors for skeletal muscle, dermis, and vertebrae tissues. Somitogenesis begins twenty-five days post [fertilization](#) [13] in [humans](#) [14] along the dorsal side of the developing embryo. Prior to [somitogenesis](#) [7], the PSM is a physically homogenous tissue, with no distinct spatial [organization](#) [15]. During [somitogenesis](#) [7], the [somites](#) [4] form from the PSM sequentially in a head to tail (anterior to posterior) direction. Nascent [somites](#) [4] are round structures, which form in bilateral pairs on either side of the [neural tube](#) [16]. During [somitogenesis](#) [7] proteins in the Notch signaling pathway provide a mechanism for adjacent cells to interact, coordinating the formation of [somites](#) [4] between cells along the length of the embryo, and regulating the expression of [genes](#) [10] that control the formation and subsequent [differentiation](#) [5] of [somites](#) [4] into mature tissues types.

John S. Dexter made the first observation of the role of the Notch signaling pathway in development while working at Olivet College in Olivet, Michigan, in 1914. Dexter, working with the fruit fly *Drosophila melanogaster* [17], observed a notch-like indentation in the wings of mutant flies. In 1917, [Thomas Hunt Morgan](#) [18], while working at [Columbia University](#) [19] in New York City, New York, identified a genetic locus that contributes to various notched mutant phenotypes. Using heritable traits such as the *Notch* locus, Morgan confirmed the chromosomal theory of inheritance, work for which he received the [Nobel Prize in Physiology or Medicine](#) [20] in 1933. Throughout the next several decades, researchers such as Richard Poulson at the Carnegie Institute of Washington, in Baltimore, Maryland, described the range

of phenotypic abnormalities associated with mutations in the *Notch* locus. Many researchers relied on the *Notch* gene to study how mutations to [genes](#) [10] affected phenotypes in adult organisms. They began to study more [genes](#) [10] when they started to sequence DNA sequencing in the early 1970s.

In 1983 Spyros Artavanis-Tsakonas and his research group at [Yale University](#) [21] in New Haven, Connecticut, sequenced the *Notch* gene in [Drosophila](#) [22] and discovered the Notch protein was likely a molecule bound to cell membranes. In 1991, Leif Ellisen, a cancer researcher at Brigham and Women's Hospital and [Harvard Medical School](#) [23] in Boston, Massachusetts, discovered that in [humans](#) [14] with lymphoblastic leukemia, something disrupts the human *Notch* gene so that it doesn't produce its protein normally. The connection between a gene in [Drosophila](#) [22] development and in human cancer led to research on the *Notch* gene in vertebrates. In 1995 Ronald Conlon, working in the lab of Janet Rossant at the Samuel Lunenfeld Research Institute in Toronto, Ontario, discovered that the mice for which scientists had obstructed the production of the Notch protein during [embryogenesis](#) [6] develop a disorganized body plan. Conlon and his colleagues demonstrated that the *Notch* gene was expressed in the PSM and directly contributed to [somitogenesis](#) [7].

The Notch signaling pathway in mammals consists of four Notch proteins and a myriad of other proteins. The Notch receptor proteins of a cell interact with the Notch ligands of adjacent cells, a process that initiates the activity of the other proteins in the pathway. The Notch proteins span the cell membrane with a large extracellular domain (ECD) outside of the cell and a small intracellular domain (ICD). The Notch protein activates only after physical contact between the Notch receptor protein of one cell, and one of its ligands embedded in the membrane of an adjacent cell. Because the Notch protein and its ligand proteins are both membrane bound proteins, two cells must be close to each other for the pathway to activate. Once the ligand binds to the Notch receptor protein, proteins cleave the Notch protein's ICD, and they shuttle it to the [nucleus](#) [24] of the cell. The ICD then interacts with various transcription factors and accessory proteins, which form a complex that regulates the expression of target [genes](#) [10]. The pathway is a mechanism by which cells can communicate their positions to each other, and by which they can drive the expression of [genes](#) [10] that will direct the fate of cells in the proper position in the embryo.

The Notch signaling pathway plays a role in at least two key aspects of [somitogenesis](#) [7]: the oscillating pattern of gene expression known as the segmental clock, and the establishment of anterior-posterior [polarity](#) [9] of [somites](#) [4]. Somites develop sequentially beginning in the anterior of the embryo and progress towards the extending tail bud. Some [genes](#) [10] that help form the boundaries between developing [somites](#) [4] also control the development of the [somites](#) [4] themselves. These [genes](#) [10] turn on and off in a wave-like pattern, with each wave corresponding to the formation of a new somite. The timing of these oscillations is critical for proper somite formation and [segmentation](#) [8] of the embryo, and is called the segmental clock. An example of a segmental clock in mice embryos can be seen in [this video](#) [25] (Supporting Movie 1), in which the oscillations represent the expression of the [mouse](#) [26] gene *Hes7*, a transcription factor that is part of the Notch signaling pathway. Each wave corresponds to the development of one pair of [somites](#) [4] in the [mouse](#) [26] (*Mus musculus* [27]) embryo, and somite boundaries can be seen forming caudally on the embryo (right of image, top). Two other developmental signaling pathways, Wnt and FGF, also exhibit oscillations in gene expression in [somites](#) [4], and help regulate [somitogenesis](#) [7] and the segmental clock.

At least two molecules interact in a negative feedback circuit that controls the oscillations of

gene expression. The first molecule is a receptor of Notch proteins, and the second is a cytoplasmic protein called Lunatic Fringe (Lfng), which is expressed via the activated Notch signal. The activated Notch signal drives the transcription of the *Lfng* gene, which in turn produces a protein that reduces the affinity of the Notch receptors for their ligands, dampening the activation of the pathway. As Lfng proteins degrade shortly after binding to their target [genes](#) [10] on the DNA, they inhibit Notch proteins for a finite period, after which Notch receptors can reactivate and resume signal transduction. This is one mechanism by which the Notch signal moves through cells in a synchronized, rhythmic pattern, turning gene expression on and off. Because the Notch signal originates in the extending tail bud of an embryo, is transduced via adjacent cells, and contains a transient negative feedback mechanism, the signal oscillates anteriorly to where nascent [somites](#) [4] arise. Mice that have Notch [genes](#) [10] experimentally silenced or knocked out still develop [somites](#) [4], but the boundaries are chaotic and somite size varies from normal embryos significantly. Furthermore, mutations in [genes](#) [10] such as *Lfng* and *Hes7* involved in the Notch pathway can cause congenital spinal [birth defects](#) [11] such as spondylocostal dysostosis.

The second role of Notch signaling is to establish anterior-posterior [polarity](#) [9] of [somites](#) [4] through interactions with proteins that belong to the fibroblast growth factor (FGF) signaling pathway. In contrast to Notch, FGF proteins secreted from cells form a concentration gradient along the embryo with the highest levels in the extending tail bud. The Notch signal starts in the tail bud and moves through the presomitic [mesoderm](#) [12] until it reaches a region where there is little FGF protein. At this position in the embryo, the Notch signal ceases to oscillate, which causes some cells to form a somite. The position where the Notch signal terminates marks the front, or anterior half of the new somite, and initiates the expression of [genes](#) [10] that form the boundary between [somites](#) [4]. When the anterior boundary of the somite forms, different [genes](#) [10] begin to make their products that will define the anterior or posterior halves of the somite. Thus, not only do [somites](#) [4] distinguish themselves from neighboring [somites](#) [4] in what tissues they are the precursors of, but the poles within individual [somites](#) [4] also form distinct tissues.

The mechanism by which Notch and FGF initiate [somitogenesis](#) [7], define somite [polarity](#) [9], and direct cell fate is called the [differentiation](#) [5] wavefront model. Mice that have *Notch* [genes](#) [10] knocked out exhibit [somites](#) [4] with reversed [polarity](#) [9], resulting in tissues derived from [somites](#) [4] being upside-down in regards to their normal position in the embryo. Researchers argue that such reversals are caused by the disorientation of [genes](#) [10] such as *Mesp2* that are normally expressed in conjunction with *Notch* in the anterior portion of [somites](#) [4] at the front of the FGF signal.

Researchers work to describe the functions of Notch signaling. Based on evidence from [chick](#) [28] embryos, one proposed function of the pathway was that it helped furrow the PSM and form the border between [somites](#) [4]. However, in the late 2000s, researchers observed the presence of somite boundaries in both zebrafish and in mice for which the researchers had knocked out the *Nothch* [genes](#) [10], a result that challenged hypothesis of Notch signaling as the sole cause of somite border formation. Furthermore, researchers showed that the Notch signaling pathway operates exclusively from FGF and Wnt signaling pathways throughout [somitogenesis](#) [7], a result that confounded models that described Notch signaling as driving the [segmentation](#) [8] clock and the [differentiation](#) [5] wavefront through interactions with FGF and Wnt signaling pathways.

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