

A computer model of X-inactivation

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Motivation

Dosage compensation of X linked genes in female cells is a crucial process to survival and is achieved by the transcriptional silencing of one of their two X chromosomes, in many cases chosen at random. As many genetic and molecular aspects involved in X-inactivation are known, the very starting mechanism whereby cells count and chooses between two equivalent X chromosomes and randomly make a differentiating mark on only one of them is still not understood. The important scientific and medical implications of such a regulation mechanism have focused, in fact, substantial interest on its elusive origin.

Methods

We introduce a Statistical Mechanics inspired model of a “controlling factors” theory of X inactivation, which is investigated by computer simulations and checked against existing experimental evidence.

Results

Our model describes how the “blocking factor” complex is formed and how the symmetry in the binding of the complex to the equivalent X chromosomes is broken. In this way, it reconciles within a single framework the existing experimental evidences and points out that “counting” and “choice” are regulated by a single unifying mechanism. The simplicity and robustness of the regulation mechanism we illustrate for X-inactivation suggest it can underlay many cell processes involving allelic exclusion as well.

Availability: <http://people.na.infn.it/~nicodem/>

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