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Processivity of helicase-induced DNA strand separation M. D. BETTERTON, University of Colorado, F. JULICHER, Max Planck Institute for the Physics of Complex Systems — Helicases are molecular motors which unwind double-stranded nucleic acids (dsNA) in cells. Many helicases move with directional bias on single-stranded nucleic acids (ssNA), and couple their directional translocation to strand separation. A simple model of the coupling between translocation and unwinding uses an interaction potential between the helicase and the ss-ds junction which can capture both ‘passive’ and ‘active’ mechanisms of NA unwinding. A passive helicase relies on fluctuations which open the dsNA base pairs to advance while its presence on the strand inhibits NA closing. An active helicase directly destabilizes dsNA base pairs where it is bound, thus accelerating the opening rate. Here, we take into account the effects of helicase detachment from the NA strand corresponding to a limited processivity. The average helicase attachment time then depends on the form of the interaction potential. For a passive helicase the mean attachment time does not change between ss translocation and ds unwinding, while for an active helicase in general a decrease in attachment time occurs during unwinding as compared to ss translocation.

M. D. Betterton
University of Colorado

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