Abstract

We discuss theoretically the force $F$ between two colloidal particles, each of them carrying one single strand DNA. The two strands are complementary only on a finite sequence of $(\ell)$ consecutive base pairs. We define an adjustment length $\kappa^{-1}$ (a few base pairs): in the adjustment regions near both ends of the paired region, the tension is still mainly on one single strand. But in the central part (for $\ell > \kappa^{-1}$) the two backbones are equally loaded. This leads to a rupture force $F_c$ increasing linearly with $\ell$ for $\ell \kappa < 1$, and saturating for $\ell \kappa > 1$.

Abstract français

Force maximum de tirage sur un ADN hybride

Deux particules colloïdales, chacune portant une chaîne greffée d’ADN, et les deux chaînes pouvant s’hybrider, peuvent se ponter. On discute théoriquement la résistance en tension de ce pontage, lorsque l’hybridyation porte sur une séquence de $\ell$ bases consécutives. Il apparaît une longueur d’ajustement $\kappa^{-1}$ (de l’ordre de quelques paires de base). Dans une région d’ajustement (de taille $\kappa^{-1}$) près de chaque extrémité, la structure est distordue. Par contre, dans la région centrale (pour $\kappa \ell > 1$) les deux chaînes supportent des tensions égales, et la structure n’est pas perturbée. Ceci conduit à une force de rupture $F_m$ qui augmente linéairement avec $\ell$ pour $\kappa \ell < 1$, et qui sature pour $\kappa \ell > 1$.

Texte court en français

Divers systèmes de reconnaissance des acides nucléiques sont fondés sur des chaînes à un brin, greffées sur une surface, et opposées à des chaînes partiellement complémentaires, greffées sur une autre surface -nanoparticule ou pointe d’un microscope de force [1], [2], [3]. Il existe une tension maximum $F_c$ que peut supporter un pontage de ce genre. Dans la présente note, nous essayons de comprendre la forme de la relation $F_c(\ell)$, et nous comparons les résultats à quelques données de la réf. [1].

Le modèle utilisé est un modèle "d’échelle souple" décrit sur la figure [1]. Bien entendu, il faut imaginer cette échelle comme torsadée pour engendrer une
double hélice, mais il semble que l’hamiltonien de base (éq. 1) garde un sens pour une forme plus réaliste.

Le résultat est une distortion, qui est importante près des deux extrémités de la zone appariée, et qui s’étend sur une longueur $\kappa^{-1}$ près des deux extrémités. On ne gagne rien sur $F_c$ à créer des structures hybrides de longueur $\ell >> 2\kappa^{-1}$. En comparant ces idées aux résultats de la référence [4], on arrive à une estimation $\kappa^{-1} \sim 6.2$ paires de bases.

1 Introduction

Hybridisation between short DNA sequences, grafted on two surfaces, can lead to useful recognition systems. In particular, one can use an AFM tip [1], [2], [3], measuring the force between tip and substrate for a single molecule. An obvious question then arises: what is the dependence of the rupture force $F_c$ on the length of the hybridized portion? Is it useful to go to long lengths?

In the present note, we try to provide a qualitative answer to this question, using a very crude ”ladder model” for the hybridized portion.

2 The ladder model

We focus our attention on fig.1, where the tension $F$ is fed on one single strand at each end. A complete description of a distorted helix is, in principle, possible but complicated. We shall use here the simpler ”ladder model” sketched on fig. 1. In the real world, the ladder is twisted into a double helix. But the distribution of forces should be qualitatively the same for both cases.

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{ladder_model.png}
\caption{Two particles linked by a single bridge}
\end{figure}

Our starting point is a set of one dimensional displacement $u_n$ and $v_n$ for the two sides of the ladder: ie for the members of a base pair ($n$). $u_n$ describes the ($\delta\epsilon$) portion (with $n$ ranging from $-\ell/2$ to $\ell/2$) and $v_n$ describes the conjugate portion ($\beta\gamma$). $u_n$ is different from $v_n$, because the ladder is distorted by the force $F$. We postulate an elastic energy:

$$H = \sum_{-\ell/2}^{\ell/2} \frac{1}{2} Q (u_{n+1} - u_n)^2 + \sum_{-\ell/2}^{\ell/2} \frac{1}{2} Q (v_{n+1} - v_n)^2 + \sum_{-\ell/2}^{\ell/2} \frac{1}{2} R (u_n - v_n)^2 \quad (1)$$

The $Q$ terms describe elongation of the backbone in one same piece: ($\alpha\gamma$) or ($\delta\omega$). The $R$ terms come from the coupling between base pairs, and we expect $R$ to be weaker than $Q$.  

2
We shall supplement the elastic description of eq. (1) by a breaking condition: whenever the forces inside a base pair \((n)\) are larger than a certain threshold \(f_c\), the bond will break. This corresponds to:

\[
R |v_n - u_n| > f_c
\]  

(2)

The equilibrium conditions derived from eq. (2) are:

\[
\frac{\partial H}{\partial v_n} \equiv Q (v_{n+1} - 2v_n + v_{n-1}) + R (u_n - v_n) = 0
\]

(3)

for all indices \(n\) in the interval \((-\ell/2 \leq n \leq \ell/2\)). Outside of the interval, the \(R\) term drops out. We shall be concerned, in practice, with \(\ell\) values significantly larger than one, and go to the continuum limit:

\[
Q \frac{d^2 v}{dn^2} + R (u - v) = 0
\]

(4)

There are similar equations for the other sequence:

\[
Q \frac{d^2 u}{dn^2} + R (v - u) = 0
\]

(5)

Adding (4) and (5), we find:

\[
Q \frac{d^2 (u + v)}{dn^2} = 0
\]

(6)

and this imposes a conservation of the total tension:

\[
Q \frac{d}{dn} (u + v) = F = constant \quad (n \leq \ell/2)
\]

\[
\{ u_n + v_n = nF/Q \}
\]

(7)

We then turn to a discussion of the difference \(\delta_n \equiv u_n - v_n\), which is ruled by:

\[
Q \frac{d^2 \delta}{dn^2} - 2R\delta = 0 \quad (|n| < \ell/2)
\]

(8)

The solution is a combination of exponentials: for the problem at hand, the right combination is symmetric upon the exchange \((n \rightarrow -n)\): all the base pairs are distorted in the same direction:

\[
\delta_n = \delta_0 \cosh(\kappa n)
\]

(9)

\[
\kappa^2 = 2R/Q
\]

(10)
If $R << Q$, the "adjustment length" $\kappa^{-1}$ is larger than unity.

The overall solution derived from eqs (8) and (10) is:

$$
\begin{align*}
\begin{aligned}
u_n &= nF/2Q + \frac{1}{2}\delta_0 \cosh(\kappa n) \\
v_n &= nF/2Q - \frac{1}{2}\delta_0 \cosh(\kappa n)
\end{aligned}
\end{align*}
$$

(11)

The relation between $\delta_0$ and $F$ is derived from the boundary condition at $n = \ell/2$. Here, we must have:

$$
F = Q(u_n - u_{n-1}) + R(u_n - v_n)
$$

giving:

$$
F = \delta_0 \left\{ Q\kappa \sinh \left( \kappa \frac{\ell}{2} \right) + 2R \cosh \left( \kappa \frac{\ell}{2} \right) \right\} 
$$

(12)

The force on the last hydrogen bond ($n = \ell/2$) is $R\delta_0$: when we reach the threshold $f_1$, this corresponds to:

$$
R\delta_0 \cosh(\kappa\ell/2) = f_1
$$

(13)

Eq. (12) then gives a global tension at threshold:

$$
F_c = 2f_1 \left\{ \kappa^{-1} \tanh \left( \kappa \frac{\ell}{2} \right) + 1 \right\}
$$

(14)

Two limits are of interest:

a) short strands ($\kappa\ell < 1$), correspond to:

$$
F_c = f_1(\ell + 2)
$$

(15)

$F_c$ increases linearly with $\ell$.

b) infinitely long strands: the rupture force reaches a maximum:

$$
F_c \rightarrow F_m = 2f_1(\kappa^{-1} + 1)
$$

(16)

The force $F_m$ is much larger than $2f_1$, because a number $\kappa^{-1}$ of base pairs work in parallel, near each end.

Just below this maximum, we can write from eq. (14):

$$
\frac{F_c}{2f_1} = \kappa^{-1}(1 - 2e^{-\kappa\ell}) + 1
$$

(17)

All the base pairs in the adjustment regions (of length $\kappa^{-1}$) participate to the resistance, while the center portion is at rest.

Note that, when the pairing breaks at both ends ($n = \pm\ell/2$) the other ties inside ($|n| < \ell/2$), also break (since $F_c$ is an increasing function of $\ell$).
3 Discussion

1) Clearly, we do not gain strength by choosing a long pairing sequence: the optimal pairing length is $2\kappa^{-1}$. This conclusion was achieved with a primitive "ladder model". But the existence and meaning of the length $\kappa^{-1}$ are probably more general.

2) The magnitude of $\kappa^{-1}$ is unclear. If the leading coupling between strands is due to base pairing, this should be smaller than the covalent bonds, and $\kappa^{-1}$ should be larger than unity. But we can also think that the spring constant $R$ in eq. (11) is partly controled by the stacking of base pairs: bending the base plane by an angle $\sim (\theta_n-\varphi_n)/D$ (where $D$ is the radius of the 2s DNA) may contribute another energy to $R$, and reduce $\kappa^{-1}$.

If we start from the data of ref [1], we find that the force $F_c$ was roughly equal to 1.11 nanonewton for both $\ell = 20$ and $\ell = 16$: this corresponds to the saturation regime ($F_c = F_m$ for $\kappa\ell >> 1$). On the other hand, for $\ell = 12$, $F_c = 0.83$ nN.

Using eqs (16, 17), this leads us to $\kappa^{-1} = 6.2$ base pairs. Thus, at least for this particular example, the adjustment length seems to be much larger than unity. The corresponding force $f_1$ is 17 pN.

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