Mechanisms and Controlling Factors of Electron Transport through *Geobacter sulfurreducens* PilA Protein

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Abstract

It was demonstrated that the pili of *Geobacter sulfurreducens* may be able to efficiently transfer electrons (act as a molecular conductor). Although experiments have been performed proving *Geobacter sulfurreducens* conductive properties, little quantitative estimation of the mechanisms and controlling factors of electron transfer have been performed including identification of transmission spectrum, density of states, and electron transfer paths. Two mechanisms of its conductivity have been proposed. In one, prosthetic groups associated with this protein are the main mediators of its electron transfer capabilities. In the other, the pili protein itself can be an efficient conductor. We perform electronic structure and transport calculations, on PilA, a main protein of *Geobacter sulfurreducens* pili, to estimate the conductance properties of this protein without prosthetic groups. Our results show that electron tunneling is not likely at low applied biases in part because strong transmission bands of fragments locate far from Fermi level, and because positively charged arginines and lysines in the middle of the protein form electrostatic traps, preventing efficient electron transfer. Application of high bias voltages potentially opens up the possibility for these traps to be filled out with electrons resulting in sequential electron transfer through the central region of the protein. In addition, phenylalanines and leucines in the protein form electron transfer loops that stabilize electrons, further aiding in sequential electron transfer through PilA at high applied voltages.

Objective

Identify the possibility of using *Geobacter sulfurreducens* PilA protein in biomolecular electronic devices:

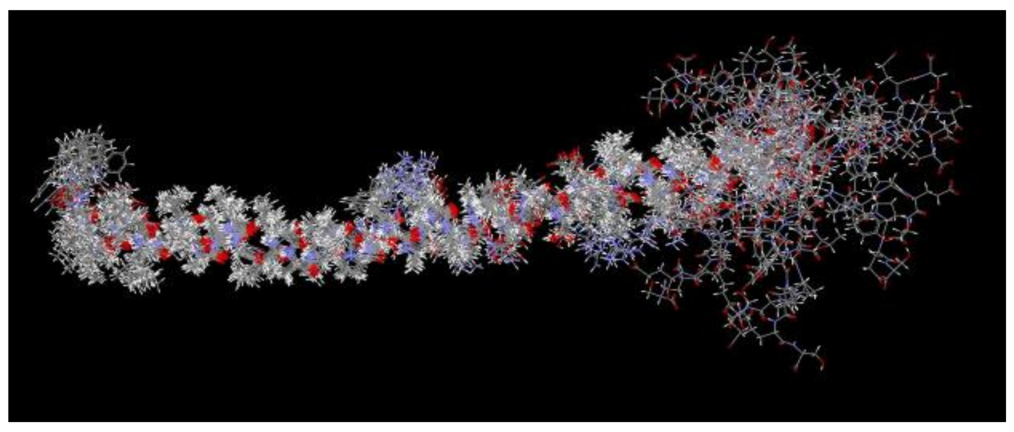
- With molecular structure and electron transport calculations performed using high performance computing , we take a step in identifying mechanisms of pili conductivity by looking at the possibilities of electron transport through specific regions of PilA, a major component of *Geobacter sulfurreducens* pili.

Methods

PilA (PDB Accession 2M7G) has three fragments that are distinguishable by their amino acid compositions.

Fragment 1 = N-terminal fragment, Fragment 2 = Central fragment, Fragment 3 = C-terminal fragment

Figure 1: (A) 3D Structure (all isomers) of PilA:



B) Central helical amino acid sequence of PilA used in our calculations in black. PilA was split into three fragments for analysis by using double alanines highlighted in red as points of separation:

FTLIELLIVV AIIGILAAIA IPQFSAYRVK AYNSAASSDL RNLKTALESA FADDQTYPPES

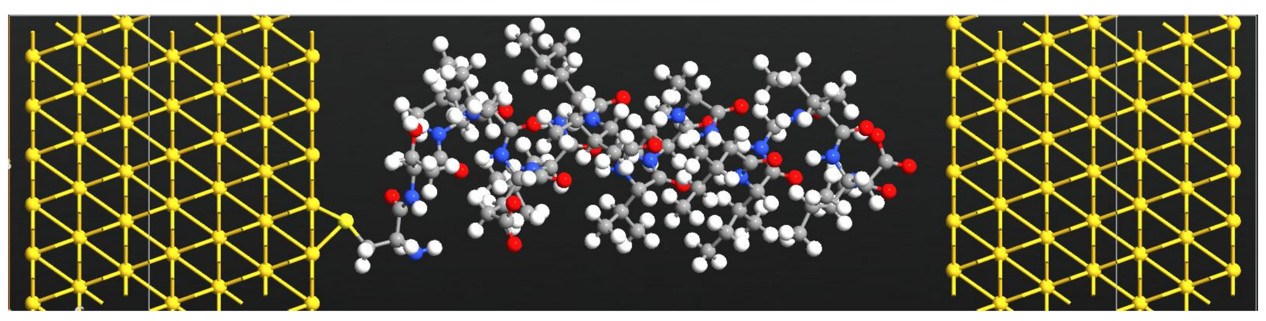
Software and Simulation Setup

Molecular orbital and energy calculations were performed on fragments using Gaussian09 software (DFT/B3LYP)

Number of HPC cores used per calculation: 64 cores

Average time of completion per calculation: 7 hours (~300 atoms)

Figure 2: Fragment Attached to Left Gold through a Thiol Group, While Right Gold is Unattached



Electron transport calculations were performed on fragments using Atomistix Toolkit software (DFT/ double-ζ basis set)

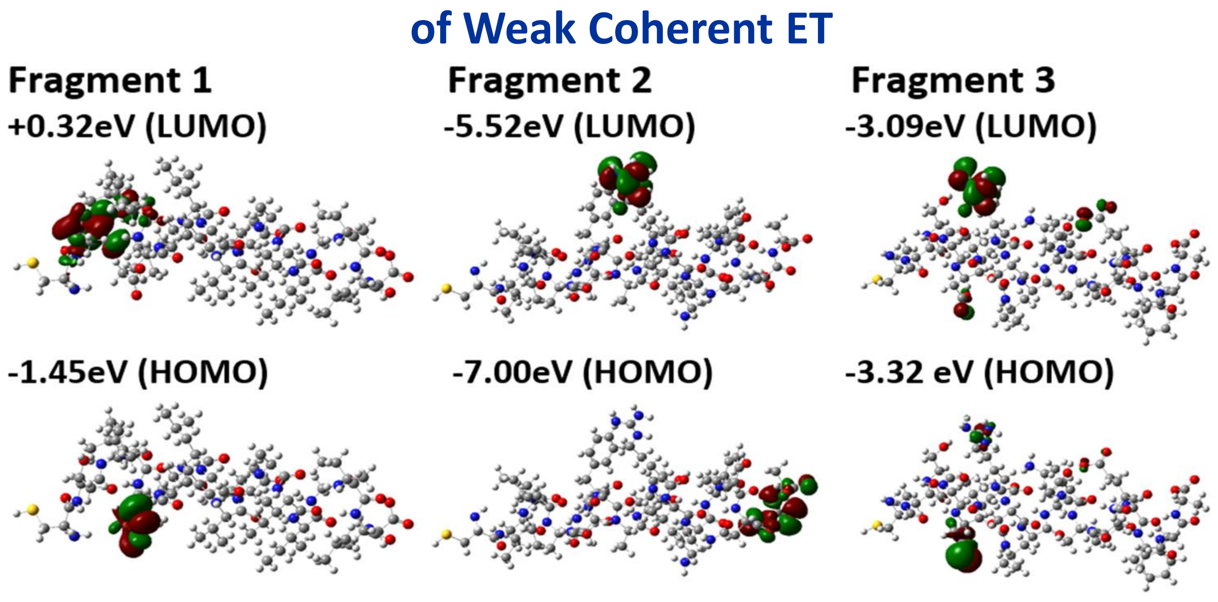
Number of HPC cores used per calculation: 64 cores

Average time of completion per calculation: 8-12 hours (~1000 atoms)

Results

Figure 3:

No Delocalization of Molecular Orbitals of Free Fragments is Indicative of Weak Coherent ET



Results

Location of Transmission Bands Far from Fermi Indicate ET Not Likely at Low Voltages

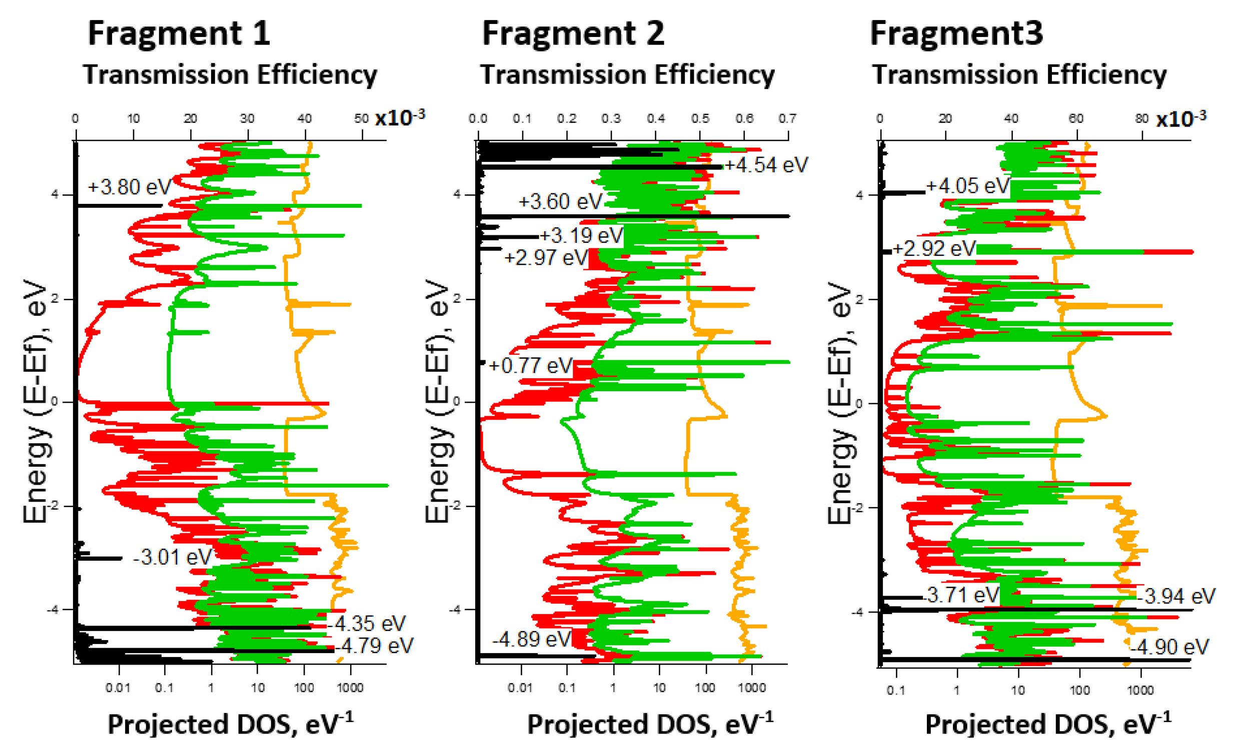


Figure 4. Electron transmission spectra (**ETS**, black) and densities of states (DOS) projected to electrodes (gold), peptide backbone including terminal groups, (green), and amino acid side groups without backbone (red) for fragments under zero bias voltage. Note: fragment 2 is ten fold more conductive than terminal fragments.

Effective Potential Drops at Charged Amino Acids Indicate Formation of Electrostatic Traps

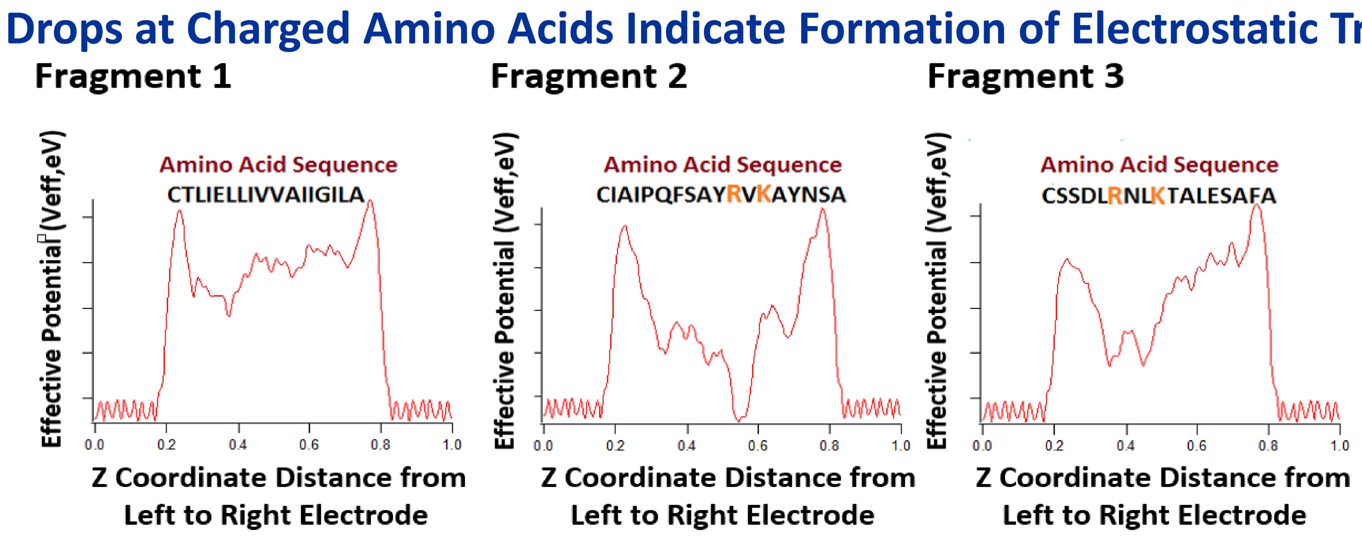


Figure 5. Electrostatic traps form at arginine(**R**) and lysine(**K**) for fragments 2 and 3 preventing efficient ET at low biases.

Fragments Exhibit Loops of Electron Cycling Which Aids in Sequential Transfer

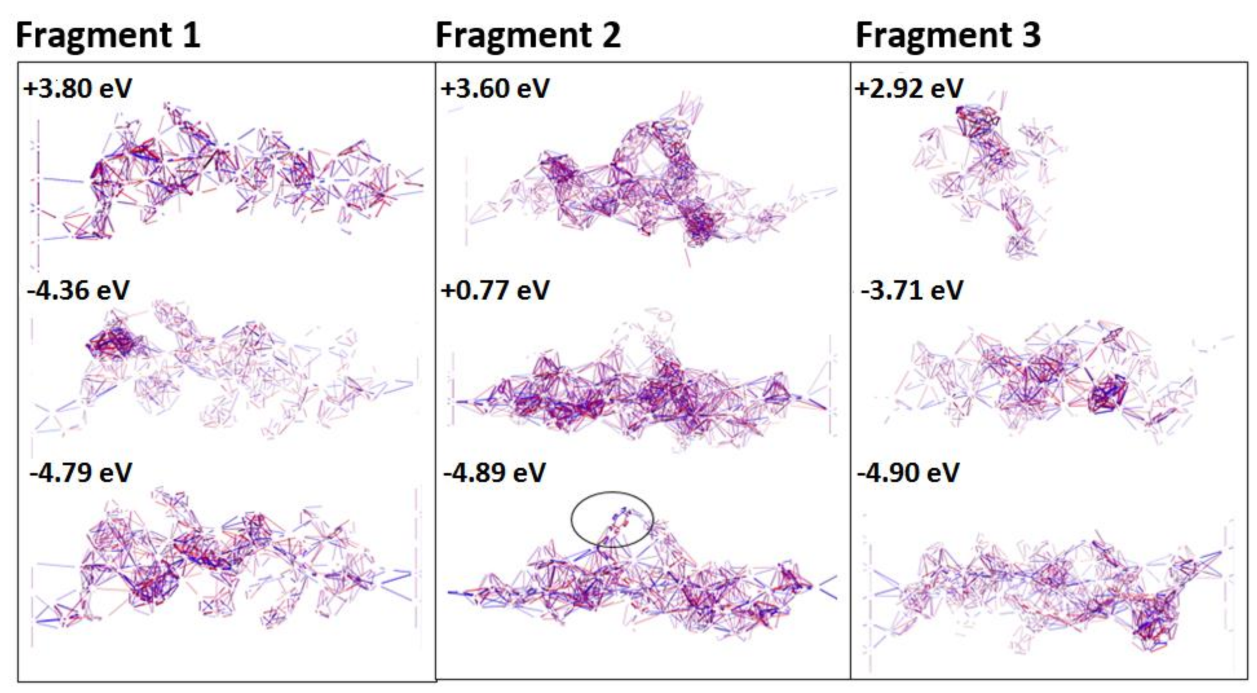
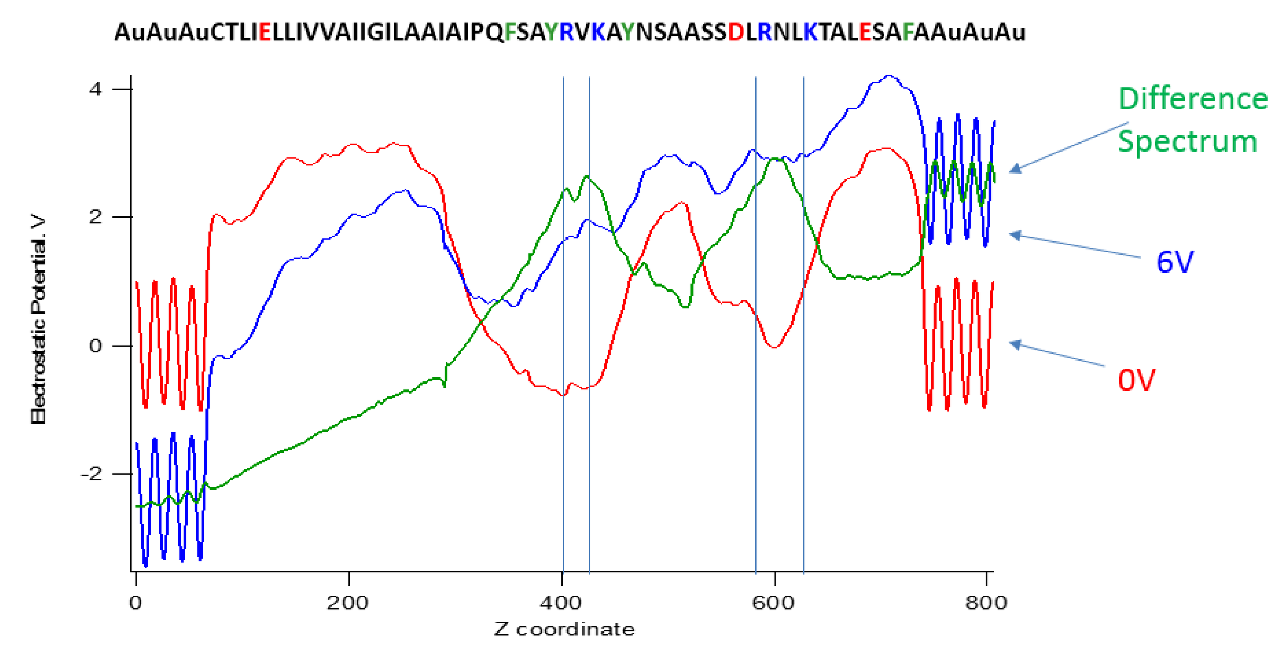


Figure 6. Electron transfer paths a zero bias show there are areas of local backwards and forwards electron cycling providing regions for electrons to reside, characteristic of sequential ET.

At High Biases, Traps are Reduced and PilA Acts as a Capacitor

Figure 7. Construction of difference spectrum between bias and unbiased electrodes indicate reduction of arginines and lysines involved in traps showing electrons escape from highly charged regions allowing ET at high biases.



Conclusions

- The lack of delocalization of frontier molecular orbitals, location of strong transmission bands far from Fermi level, weak electrode coupling, and formation electrostatic traps, indicates that at low biases, electron tunneling through PilA is unlikely.
- The tunneling through the peptide is possible after applying to the electrodes considerable bias voltages (over 6V) and only through the central peptide fragment.
  - In this case, the charged amino acids, which form electrostatic traps in the middle of the peptide, act as a capacitor.
- Leucines and phenylalanines located in various parts of the peptide form ET loops with local forward and back electron cycling preventing electrons from direct coherent tunneling, but providing additional opportunity of sequential electron transfer through the peptide at high bias voltages.
- A possible application in electronic devices may be to manipulate the protein so electron transfer goes through only fragment 2.

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