

1079-93-373

Karin Valencia* (karin.valencia06@imperial.ac.uk), Imperial College London, South Kensington Campus, Huxley Building, Room 640, London, SW7 2AZ, England, and **D Buck, N Jonoska** and **M Saito**. *Genome-wide rearrangements in ciliates: the genus of assembly graphs.*

Ciliated protozoa are unicellular organisms that contain two types of specialized nuclei, with functionally distinct copies of the genome: a germline *micronucleus* (MIC) consisting of genes crippled by the presence of short non-coding sequences, and a somatic *macronucleus* (MAC) consisting of gene-size DNA segments made up of subunits of the MIC genes, arranged in very precise ways. During conjugation, new MIC DNA is highly edited, via recombination and other not well understood processes, and is converted into new MAC DNA. Experimental evidence suggest many recombination events can happen simultaneously. This process was previously modelled using spatial graphs, called *assembly graphs*, which consist of 1-valent and 4-valent rigid vertices, by Angeleska, Jonoska and Saito. In this talk, we investigate the topological complexity of assembly graphs by considering the highest bound of the orientable cellular genus as a function of the number vertices n . We show that a special type of assembly graph, the *tangled cord* Γ_n , maximises the genus overall assembly graphs and we find its genus range.

$$\frac{n-2}{2} \leq \gamma(\Gamma_n) \leq n \text{ if } n \text{ is even}$$

$$\frac{n-1}{2} \leq \gamma(\Gamma_n) \leq n \text{ if } n \text{ is odd}$$

(Received January 18, 2012)