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Nataša Jonoska*, Department of Mathematics and Statistics, 4202 E. Fowler Av. CMC 342, Tampa, FL 33620, and **Masahiko Saito**. *Detecting reoccurring patterns of scrambled genes*. Preliminary report.

DNA recombination occurs at both evolutionary and developmental levels, and is often studied through model organisms such as ciliate species *Oxytricha* and *Stylonychia*. These species undergo massive genome rearrangements during their development of a somatic macronucleus from a zygotic micronucleus. We use graphs and words to represent the rearrangement process and we investigate genome-wide the range of scrambled gene architectures that describe the precursor-product relationships. We find that there are two general patterns, reoccurring genome wide, that describe over 90% of the *Oxytricha*'s scrambled genes. We further investigate the patterns of interleaving genes and find that there are specific star-like graph structures that describe most complex interleaving patterns. (Received January 17, 2016)