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Living apart together: crosstalk between the core and supernumerary genomes in *Fusarium poae*

Eukaryotes can display remarkable genome plasticity, including the presence of supernumerary chromosomes that differ markedly from the core chromosomes. The origin of these supernumerary chromosomes, the reason for their different characteristics, and their interactions with the core genome are still largely unknown. Here we report on the supernumerary chromosomes of the prominent fungal wheat pathogen *Fusarium poae*. Using SMRT long reads, the 38 Mb core genome was assembled into four chromosomes that contain the complete genome complement of related *Fusarium* species in a highly syntenic fashion. An additional ~8 Mb of sequence was assembled into contigs that make up at least one supernumerary chromosome. Clear differences exist between the core and supernumerary genome. The core chromosomes contain 2% transposable elements (TEs) while the supernumerary genome consists of 25% TEs. The TEs on the core chromosomes show clear signs of repeat-induced point mutation (RIP), in sharp contrast no RIP was found on the

supernumerary genome. Furthermore, no gene duplications are present on the core, but many are found on the supernumerary genome. Importantly, the specific absence of RIP in the supernumerary genome accounts for the differences between the core and supernumerary genomes in *F. poae*. An exchange of genetic material occurs between the core and supernumerary genomes. Intact TEs from the supernumerary genome integrate into the core chromosomes, occasionally leading to gene disruptions. On the core chromosomes, the integrated TEs are subjected to RIP. In addition, large blocks of supernumerary sequence (>200kb) have recently been translocated to the core chromosomes. *Vice versa*, genes from the core chromosomes are duplicated to the supernumerary genome, where they may show an increase in copy number. This “living apart together” crosstalk bestows significant opportunities for adaptation and evolution on the organism, and shows that the supernumerary genome is an evolutionary cradle for novel genotypes.