

Exploring whole genome duplications in eukaryotes – A case study on plant pathogenic oomycetes and the impact of adaptive radiation

Whole genome duplications (WGD) followed by differential gene loss have for a long time been recognized as a major evolutionary force in eukaryotes. It has been observed that these events are often associated with important biological innovations and adaptive radiation of species. Whereas the occurrence of WGDs in vertebrates, plants and fungi have been demonstrated and are generally accepted, recent evidence for a WGD within the group of oomycetes are still controversial and final confirmation is pending.

The phylogenetic class of oomycetes contains many severe pathogens of plants and animals with huge economical and ecological impact. In the recent years, facilitated by the availability of the several genome sequences, significant knowledge in the biology of these pathogens has been acquired. These species have large genomes with a high number of expanded gene families of which many are involved in pathogenicity. It has been indicated by others and independently by our own research that *Phytophthora* might have undergone a WGD prior the speciation. This event might be responsible for the expansion of these gene families and consequently the driving force for the specialization to different hosts. Whereas intra-species synteny, i.e. co-linearity of homologous genes on two different chromosomes, has been used as a validation for WGD in other eukaryotes, the lack of long-range synteny in *Phytophthora* spp. has hampered this approach. Hence, we want to apply different, synteny-independent techniques to find additional evidence for the presence of the WGD in the evolutionary past of oomycetes. These techniques include meso-synteny, i.e. homology between two different chromosomes regardless of the linearity. To assess the performance of these methods in oomycetes we want to compare our results with data from species where the presence or absence of a WGD has been shown with high confidence. This will allow us to shed further light on the pending question whether oomycetes and in particular *P. infestans* did undergo a WGD prior to the speciation that is responsible for the adaptation to different hosts.

We're looking for a motivated and intelligent student with a background in biology, computer sciences or bioinformatics for a period of at least 4 months full time, but preferably 6 months or longer.

We offer the student an opportunity to learn bioinformatic skills and, more importantly, to do bioinformatic research in a stimulating environment. The Theoretical Biology and Bioinformatics group deals with a wide range of subjects, ranging from modeling of developmental and evolutionary processes, heart modeling, immunological bioinformatics to comparative genomics and evolutionary biology. For further information on this and also other possible research projects within the group please contact Michael Seidl (m.f.seidl@uu.nl).