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**PHYLOGENETIC AND PHYLOCLIMATIC INFERENCE OF
THE EVOLUTION OF POTENTILLEAE (ROSACEAE)**

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DOCTORAL THESIS



UNIVERSITY OF GOTHENBURG

This thesis will be defended in public at 13.00 A.M on the Juni 11th, 2010 in the Lecture Hall,
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ABSTRACT

Polyploidization has occurred many times during the evolution of angiosperms. Allopolyploidization is believed to be the process behind many of these genome duplications, and has resulted in a genetically diverse angiosperm flora. I have investigated the patterns of allopolyploidization in the tribe Potentilleae (Rosaceae), where many species have been proposed to have an allopolyploid origin. I have assessed the extent of allopolyploidization in the group, with special emphasis on genus *Potentilla*, by comparing a topology based on nuclear data to one based on plastid data. This led to the identification of several incongruences that supports the notion of a reticulated evolution of the group. However, this has to be confirmed as not all incongruences identified with this method have to be the result of hybridization. Instead, further phylogenetic inference of relationships among the proposed allopolyploid species has to utilise low-copy nuclear genes.

For future prospects, I have therefore evaluated Temperature Gradient Gel Electrophoresis (TGGE) for separating paralogues of low-copy nuclear genes. The method was found to require fewer PCR and sequencing reactions, compared to bacterial subcloning, a method routinely used to separate heterogeneous DNA samples. TGGE was therefore found to be an efficient and applicable method for separating gene copies for phylogenetic investigations of allopolyploid species.

The work presented in this thesis has also provided new insights into the evolution of Potentilleae. The phylogenetic analysis show that the ivesioid Potentilleae, a morphologically aberrant and diverse group comprising the three North American genera *Ivesia*, *Horkelia* and *Horkeliella*, form a well-supported clade nested within the *Potentilla* clade. Furthermore, a dated phylogeny of the family Rosaceae finds this clade to have originated approximately 25 Ma, a time when climate change is believed to have reshaped the flora of western North America. The analysis using phyloclimatic modeling of the evolution of the group reveals a close connection to climate change. The results indicate Great Basin as the area of origin and a westward range expansion to Sierra Nevada during Miocene. Several lineages were found to have crossed the mountain range after a Mediterranean type of climate had established in California.

The analysis of microsatellite and AFLP data propose that climate change also have influenced the genetic diversity in Arctic populations. Geographical patterns of this diversity corroborate the hypothesis that Beringia served as a refugium for plants during the Wisconsinan glaciation. Evidence of additional refugia on Banks, Prince Patrick and Melville Islands was also found and further supported by geological data on ice expansion at the last glacial maximum.

From the results of the investigations conducted during my thesis work I therefore conclude that allopolyploidization and climate change have had a great influence on the evolution of Potentilleae.

Keywords: *Potentilla*, *Ivesia*, *Horkelia*, allopolyploidization, TGGE, Beringia

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