

Euphytica

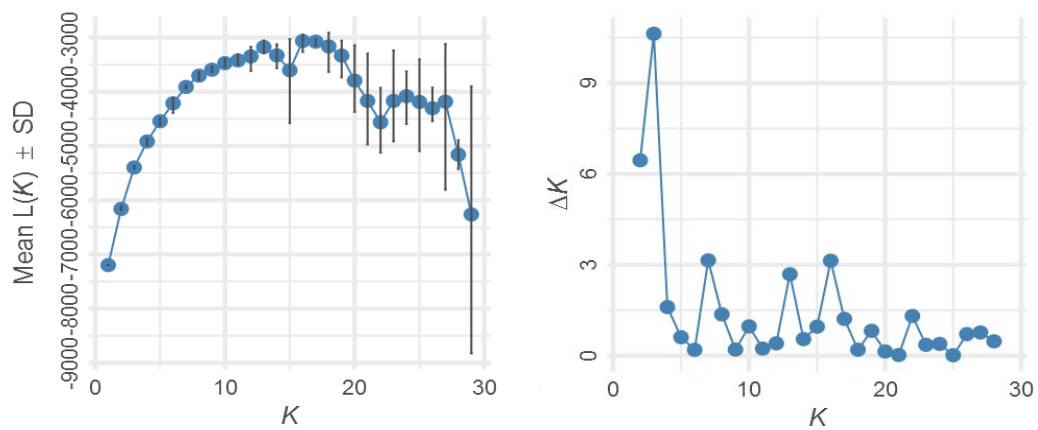
**Genetic diversity of flax accessions originating in the Alpine region – a case study for *ex situ* germplasm characterization based on molecular markers**

Eva-Maria Halbauer, Valentina Bohinec, Melanie Wittenberger, Karin Hansel-Hohl, Stephan Gaubitzer, and Eva M. Sehr\*

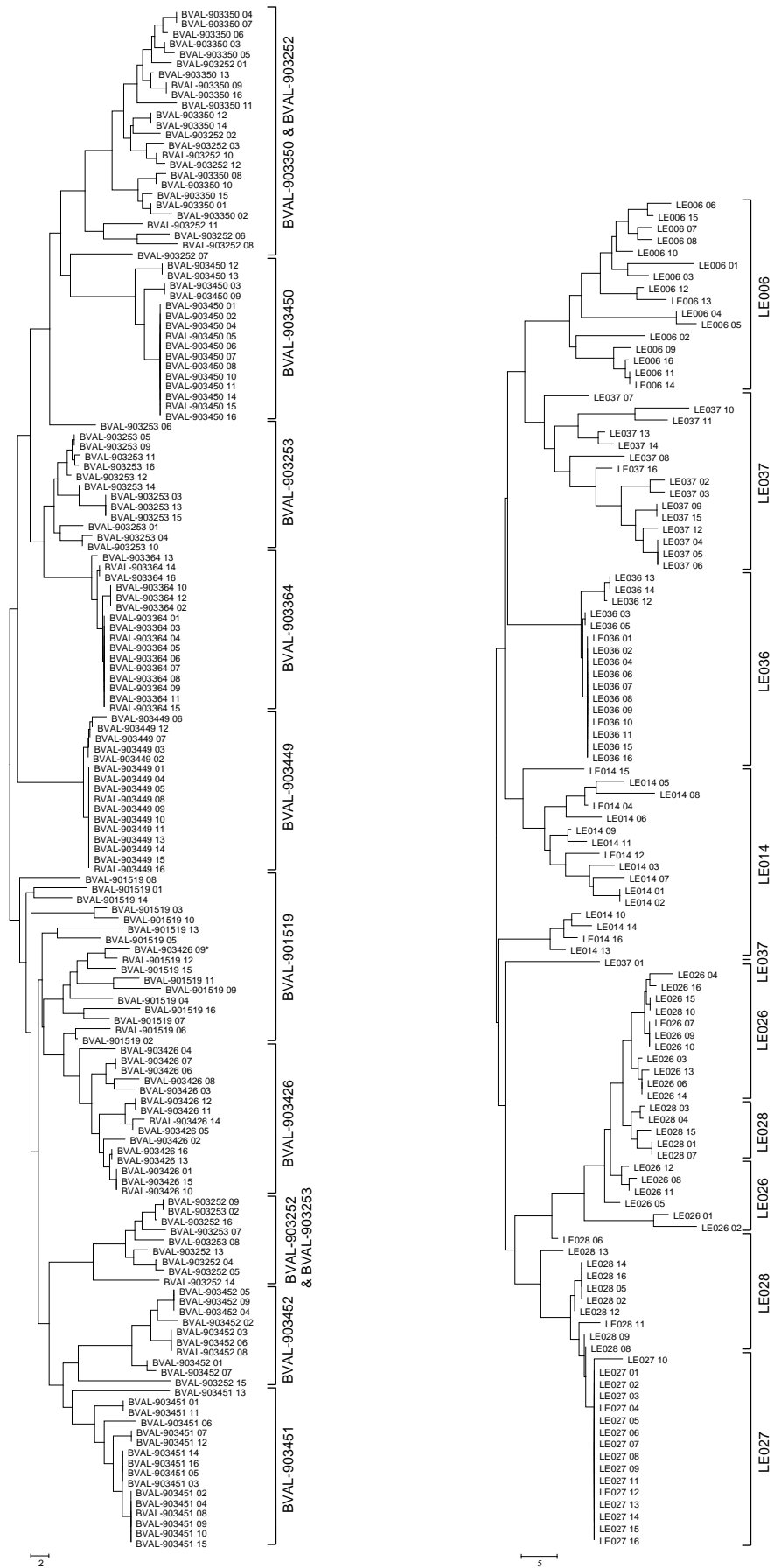
AIT Austrian Institute of Technology GmbH, Centre of Health & Environment, Konrad-Lorenz Str. 24, 3430 Tulln, Austria

\*Corresponding author: eva-maria.sehr@ait.ac.at, +43 50550-3651

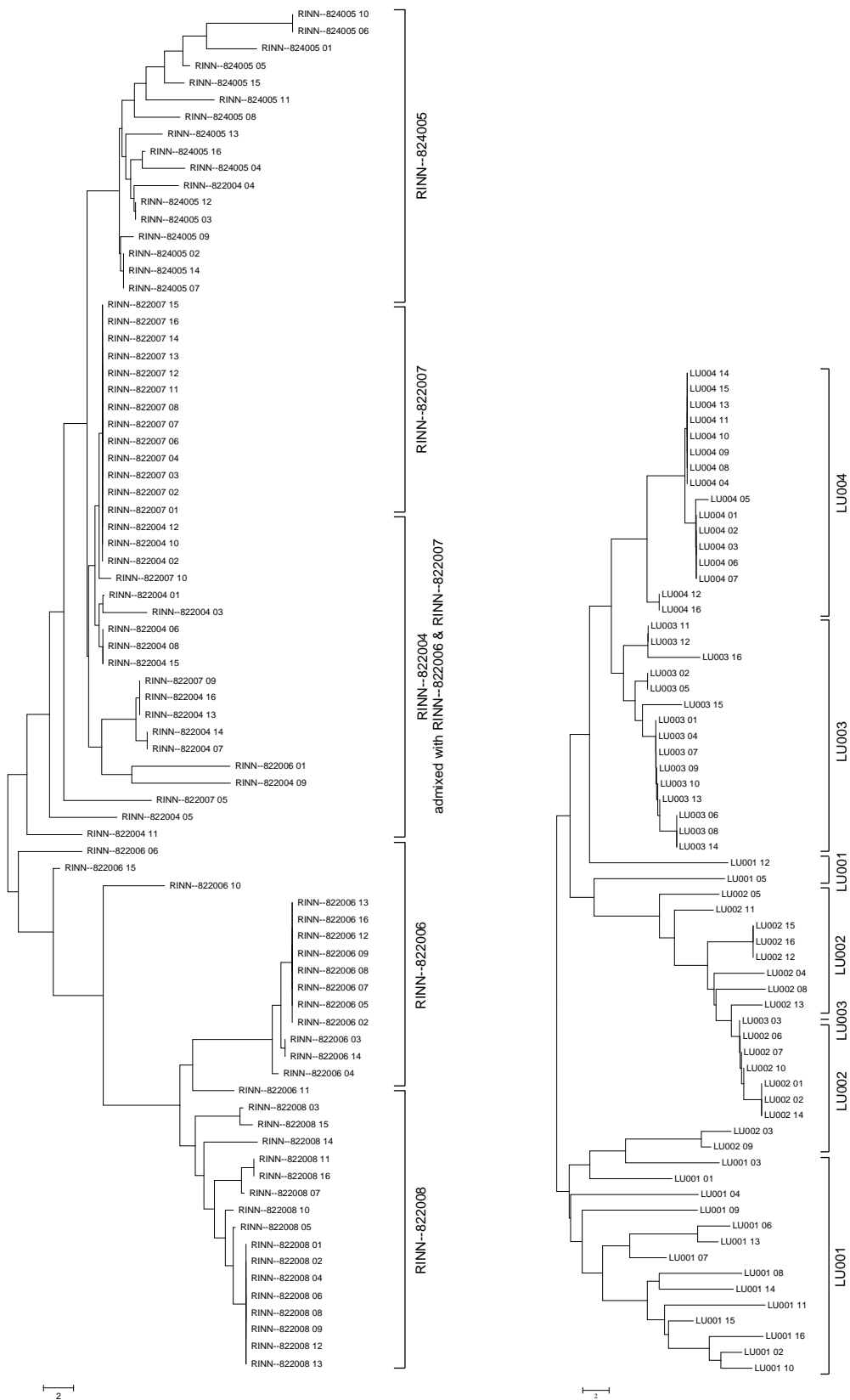
**Supplementary figures**



**Supplementary Fig. 1** For determining the number of genetic clusters, either the maximal value of  $L(K)$  – or the smallest value before the  $K$  values plateau – is taken into consideration (visually estimated as  $K = 13$ , left plot), or the highest delta  $K$  value is chosen ( $K = 3$ , right plot), depending on the biological relevance



**Supplementary Fig. 2** NJ trees based on genetic distance values of the unreduced datasets of the AGES gene bank (left) and the Arche Noah gene bank (right). Per accession, the individuals are numbered from 01 – 16. The only foreign individual (BVAL-903426 09) interfering in BVAL-901519 is marked with an asterisk. All other admixtures are indicated by the vertical labelling



**Supplementary Fig. 3** NJ trees based on genetic distance values of the unreduced datasets of the Tyrolean (left) and the Agroscope (right) gene bank. Per accession, the individuals are numbered from 01 – 16. Admixtures are indicated by the vertical labelling