

Linum, flax

Klaus Ammann, February 10 2007

For feedbacks email klaus.ammann@ips.unibe.ch

1. Taxonomy

1.1. General taxonomy

(Muravenko et al., 2003) undertook genome comparisons with chromosomal and molecular markers for three closely related flax species and their hybrids.

The genus *Linum* L. comprises more than 200 species, including commercially valuable cultivated *Linum usitatissimum* L.

Taxonomy of the genus is complex and questionable (Flora USSR, 1949; Tsvelev, 1996; Tutin et al., 1978). Karyotypic analysis of *Linum* L. species started more than half century ago and allowed several flax species to be recognized (Chennaveeraiah & Joshi, 1983; Harris, 1968; Lewis, 1964; Ray, 1944). It has been observed that chromosome number ranges from 12 to 72 in the genus, and that chromosomes are small (1–4 μ m) and morphologically similar. Although monochrome staining reveals only general karyotypic differences, the results obtained with this method have made it possible to construct a putative phylogenetic tree both for the Old World and for New World species of the genus *Linum* (Chennaveeraiah & Joshi, 1983; Harris, 1968). In addition, intra- and interspecific genetic diversity has been characterized with molecular (RAPD) (Fu, 2005; Fu et al., 2002a; Fu et al., 2003a; Fu et al., 2002b; Fu et al., 2003b; Lemesh et al., 2001; Lemesh et al., 1999a; Lemesh et al., 1999b) and protein (Kutuzova et al., 1999; Mansby et al., 2000) markers, allowing certain taxonomic relationships to be assumed for several flax species. Notwithstanding, there are still numerous questionable issues in taxonomy and phylogeny of the genus *Linum*.

First and foremost, this is true for cultivated *L. usitatissimum* and its close or distant wild relatives, which are commonly assigned to the section *Linum* (Davis, 1967; Flora USSR, 1949; Tutin et al., 1978).

1.2. Taxonomy of *Linum usitatissimum* and related species

Taxonomy of cultivated *L. usitatissimum* and closely related species is rather complex and equivocal. It is believed that *L. usitatissimum* L. was domesticated approximately 6000 years ago (Lay & Dybing, 1989; Zohary & Hopf, 1988), and yet this species is still able to cross with its putative wild ancestor, *Linum angustifolium* Huds. (Gill & Yermanos, 1967a, b; Seetharam, 1972; Seetharam & Srinivas, 1972). The two species

each have 30 chromosomes in the karyotype. The same chromosome number is characteristic of *Linum bienne* Mill., which is also thought to have contributed to the origin of *L. usitatissimum* L. (Lay & Dybing, 1989). However, some authors consider *L. bienne* as a subspecies of *L. angustifolium* Huds., and some others even equate these two species (Flora USSR, 1949; Tutin et al., 1978). On the other hand, there is an opinion that *L. bienne* Mill. is a subspecies of *L. usitatissimum* L. (Chernomorskaya & Ctankevich, 1987). Hence, to eliminate this disagreement, it is necessary to employ modern molecular and cytogenetic techniques. Genetic polymorphism of the above three species has been assessed preliminarily by RAPD analysis [10]. Yet complex genome comparisons with the use of chromosome and molecular markers have not been carried out so far in order to clarify the taxonomic status and phylogenetic relationships of the three closely related flax species.

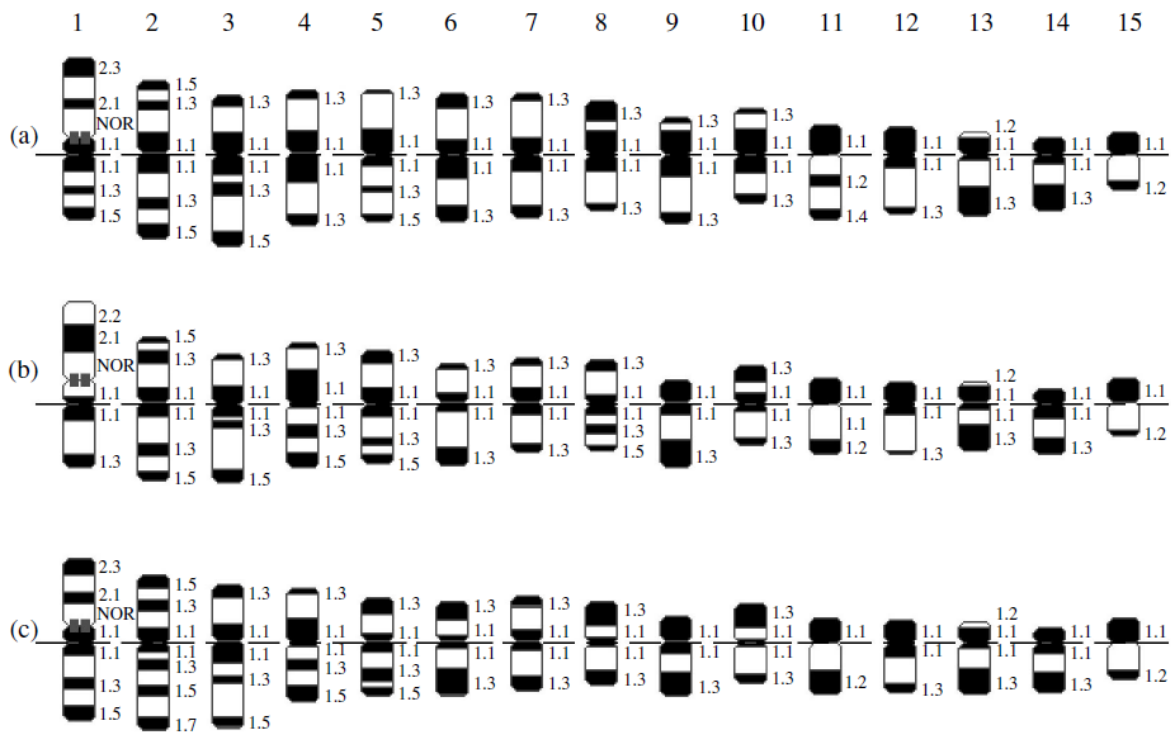


Fig. 1 Ideograms of C-banded chromosomes of (a) *L. angustifolium*, (b) *L. bienne*, and (c) *L. usitatissimum* cultivar Orshanskii 2. From (Muravenko et al., 2003)

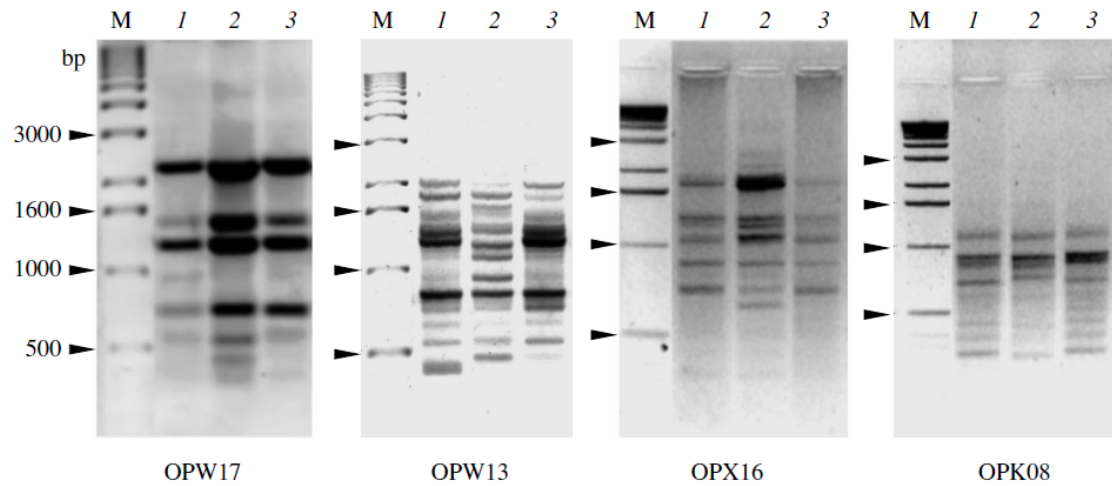


Fig. 2 RAPD patterns obtained with primers OPW17, OPW13, OPX16, and OPK08 for (1) *L. angustifolium*, (2) *L. bienne*, and (3) *L. usitatissimum*. M, molecular weight marker. From (Muravenko et al., 2003)

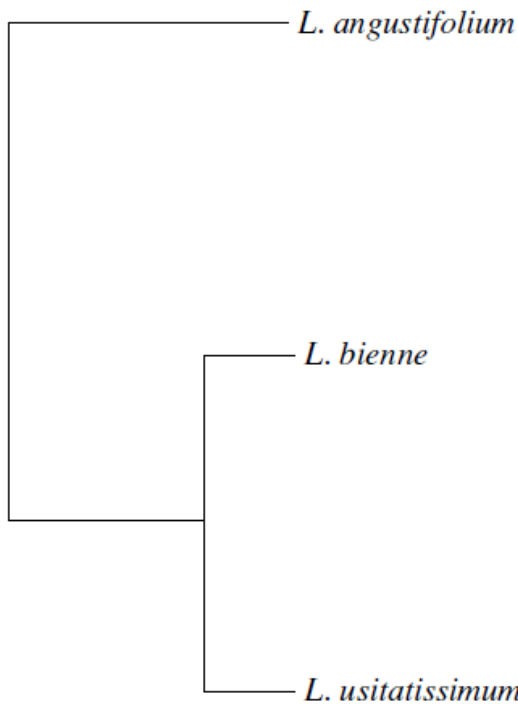


Fig. 3 Dendrogram of phylogenetic relationships of the three flax species, as inferred from analysis of genetic distances. From (Muravenko et al., 2003).

The RAPD patterns were used to construct a dendrogram of genetic similarity between the three flax species (Fig. 5). The genotypes under study formed two clusters, one including *L. usitatissimum* and *L. bienne* and the other combining these species with *L. angustifolium*. Genetic distance was 0.226 between *L. usitatissimum* and *L. bienne* and

