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KARYOTYPE ANALYSIS IN *PHASEOLUS VULGARIS* L. CULTIVARS

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Key words: *Phaseolus vulgaris*, cultivars, karyotype

Abstract: Chromosome's number were 2n=22 on all *Phaseolus* cultivars. All chromosomes were found morphological uniform, without satellites, and submetacentrics.

INTRODUCTION

Beans are one of the most ancient crops of the world. Together with maize and cassava, they have been a dominant staple in the low to mid-altitudes of the Americas for millennia. Beans (*Phaseolus spp*. L) are extremely diverse crops in terms of cultivation methods, uses, the range of environments to which they have been adapted, and morphological variability. They are found from sea level up to 3,000 metres above sea level, are cultivated in monoculture, in associations, or in rotations. Beans are consumed as mature grain, as immature seed, as well as a vegetable (both leaves and pods). Their genetic resources exist as a complex array of major and minor gene pools, races and intermediate types, with occasional introgression between wild ancestors and domesticated types. Beans are thus a crop that is adapted to many niches, both in agronomic and consumer preference terms. As fruit (pods) can be obtained in as little as two months, rotations are possible with other crops during short growing seasons. Short bush growth habits offer minimal competition and permit inter-planting with other species, for example, in reforestation projects or among fruit trees or coffee plantations during the early years until the main crop can be exploited. At the other extreme are aggressive climbers found at higher altitudes on subsistence farms where a few plants are maintained as a sort of insurance and are continually harvested for about six months. Over the past twenty years, beans have also been increasingly cultivated on a commercial scale, and are now offered in national, regional and international markets (1).

Diets of subsistence level farmers in Africa and Latin America often contain sufficient carbohydrates (through cassava, corn/maize, rice, wheat, etc), but are poor in proteins. Dietary proteins can take the form of scarce animal products (eggs, milk, meat, etc), but are usually derived from legumes (plants of the bean and pea family). Legumes are vital in agriculture as they form associations with bacteria that "fix-nitrogen" from the air. Effectively this amounts to internal fertilisation and is the main reason that legumes are richer in proteins than all other plants. Thousands of legume species exist but more common beans (*Phaseolus vulgaris* L.) are eaten than any other. In some countries such as Mexico and Brazil, and those around the Great Lakes in eastern Africa (Burundi, Rwanda, Kenya, Tanzania), beans are the primary source of protein in human diets. As half the grain legumes consumed worldwide are common beans, they represent the species of choice for the study of grain legume nutrition.

Phaseolus is the genus to which the common bean, *Phaseolus vulgaris* belongs. The genus *Phaseolus* contains 55 species, 5 of which have been domesticated. All *Phaseolus* species originate in Meso America and have been cultivated for thousands of years by pre-Columbian civilizations.

Previous classifications placed in this genus a number of other well known species that have now been removed to genus *Vigna*, sometimes necessitating a change of species name. For example, older literature refers to the Mung bean as *Phaseolus aureus*, whereas more modern sources classify it as *Vigna radiata* (1, 2, 4, 5).

MATERIALS AND METHODS

The investigated plants were *Phaseolus vulgaris* L. cultivars from Siret area: Seminole, Clujana, Saxa and Prelude.

Germination of the seeds was performed into Petri dishes, on filter paper moistured with distilled water, at 22 ± 2°C. When roots were reached 5 – 10mm in length, these were treated with 0.2% colchicines for 2 hours, at room temperature. Roots were kept for other two hours in distilled water. Fixation was done for about 16 hours in ethylic alcohol / acetic acid (3:1) mixture, at room temperature. For hydrolysis of vegetal material was used HCl 50% for 10min, at room temperature. The staining was realized with Carr reactive, according literature (1, 2, 3). The slides were prepared according squash method. Microscopy was carrying out using 100x objectives, with a Nikon Eclipse 600 light microscope. Photos were taken with a Nikon CoolPix 950 digital camera, at 1600x1200 dpi resolution. All images were processed with Adobe Photoshop software.

Homologous chromosome groups were settled in accordance with the rapport between long arm and short arm, the difference between arms and with the relative length of the chromosomes.

RESULTS AND DISCUSSIONS

Seminole cultivar karyotype

In all investigated cultivars we found a chromosomal number of 2n=22. In Seminole cultivar (Fig. 1) there are three morphological types: pairs I – III metacentrics, pair IV subtelocentrics and submetacentrics – pairs V – XI. The longest chromosomes were found to be chromosomes from first pair (3,84 µm and 3,76 µm), and the shortest the eleventh pair (1,96 µm and 1,94 µm).

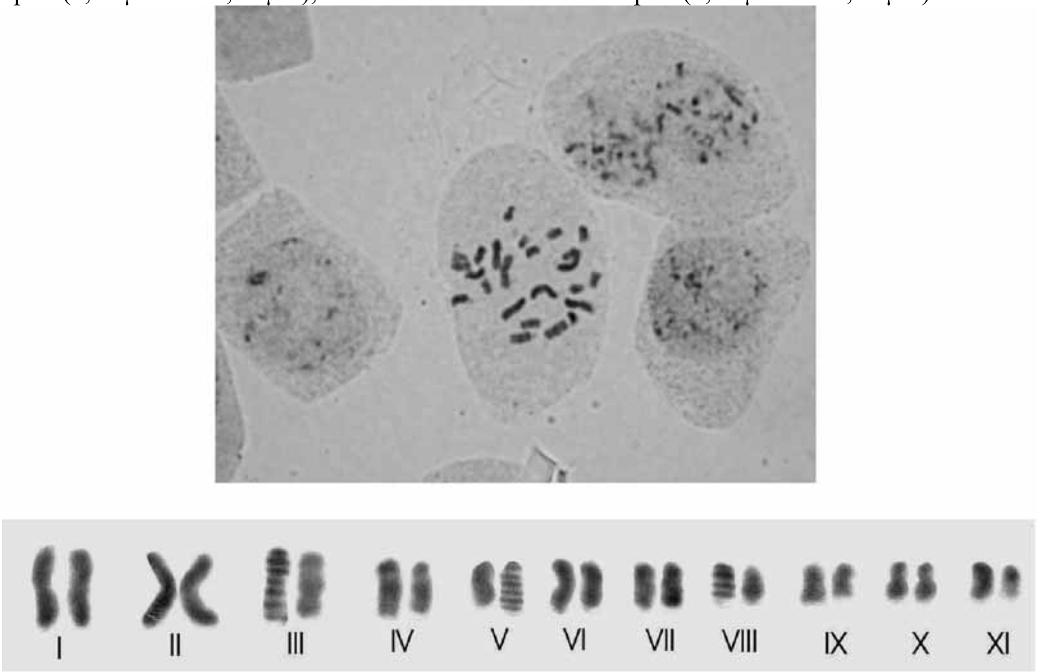

Fig. 1 Metaphase (up) and karyotype (down) in *Phaseolus vulgaris* L., Seminole cultivar

Clujana cultivar karyotype

In Clujana cultivar (Fig. 2) it isn’t possible to establish morphological types prior to the uniformity and small dimensions of chromosomes. The longest chromosomes were found to be chromosomes from first pair (2µm and 1.84 µm), and the shortest the eleventh pair (1.04 µm and 0.96 µm).

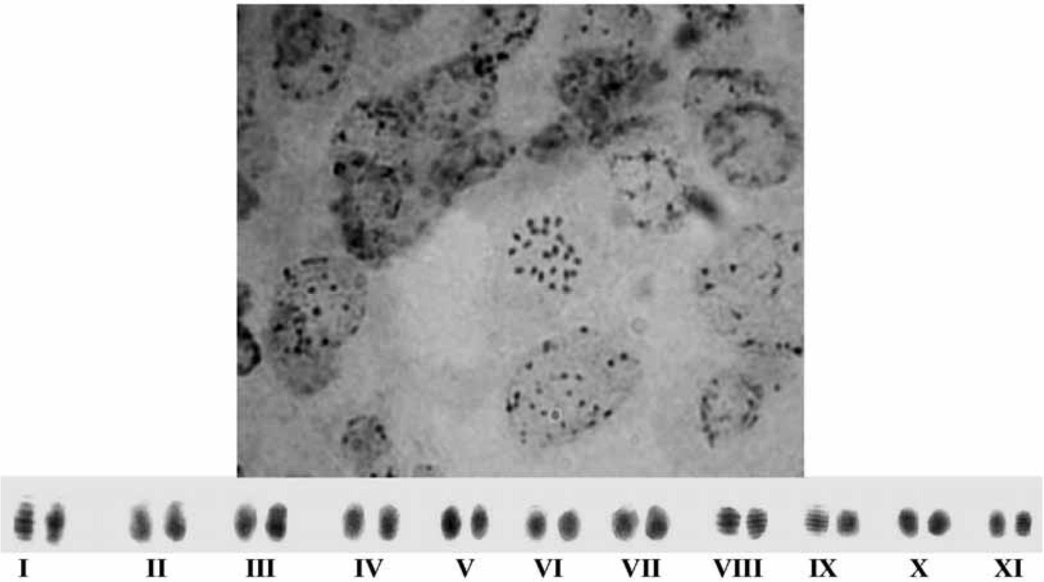

Fig. 2 Metaphase (up) and karyotype (down) in *Phaseolus vulgaris* L., Clujana cultivar

Saxa cultivar karyotype

In Saxa cultivar (Fig. 3) there are three pairs of metacentric chromosomes (I, IX and XI), and the all other pairs were found to be submetacentrics.

The longest chromosomes were found to be chromosomes from first pair (2.84 μm and 2.38μm), and the shortest the eleventh pair (1.22μm and 1.21μm).

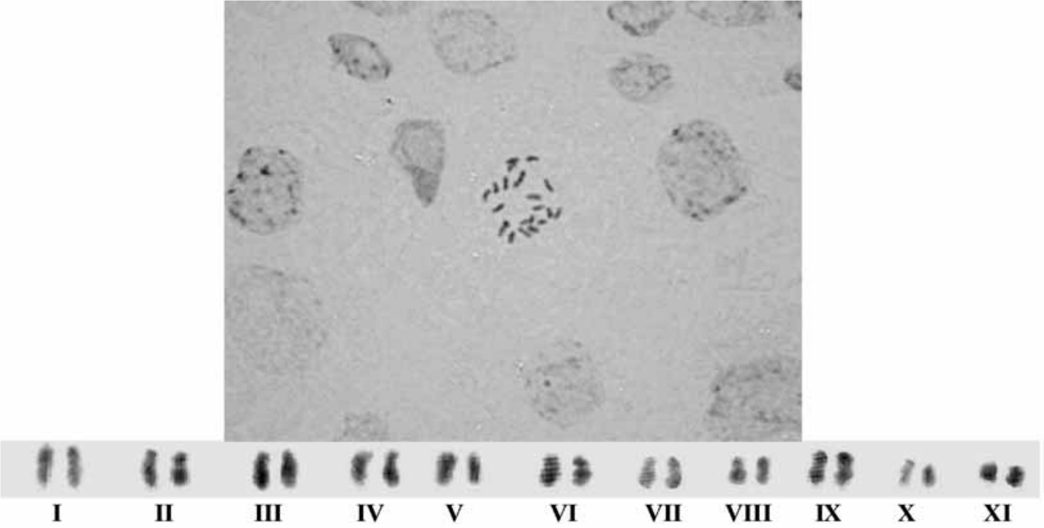

Fig. 3 Metaphase (up) and karyotype (down) in *Phaseolus vulgaris* L., Saxa cultivar

Prelude cultivar karyotype

In Prelude cultivar (Fig. 4) all chromosomes pairs were found to be extremely short, uniform, without satellites.

The longest chromosomes were found to be chromosomes from first pair (1.68µm and 1.64µm), and the shortest the eleventh pair (1.18µm and 1.14µm).

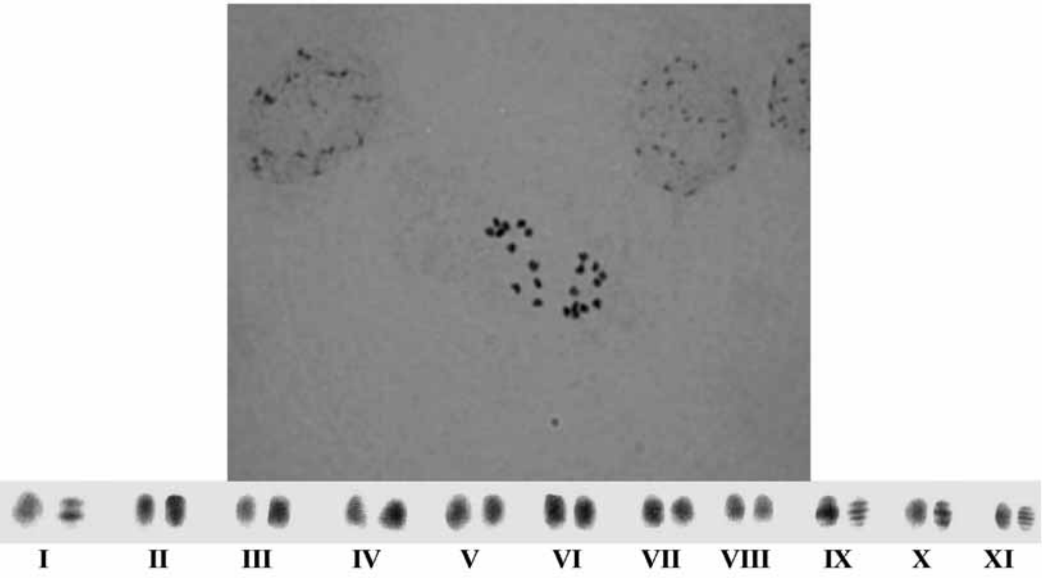

Fig. 4 Metaphase (up) and karyotype (down) in *Phaseolus vulgaris* L., Prelude cultivar

CONCLUSIONS

Chromosome number in all *Phaseolus vulgaris* L. cultivars investigated were 2n=22 (4).
In Seminole cultivar, the main morphological type is submetacentric.
In Clujana and Prelude cultivars we found very short chromosomes, morphological uniform.
In Saxa cultivar, the main morphological type is submetacentric.
All investigated karyotypes were found to be not evolved.

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