

SWEET POTATO BREEDING IN INDIA – PROBLEMS AND PROSPECTS

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SUMMARY

A new, comprehensive breeding programme has so far produced six new high yielding sweet potato cultivars using Japanese, American and Indian parental material. Cytological studies based on pachytene analysis have elucidated the degree of chromosome homeology among three genomes of hexaploid sweet potatoes. Tetraploid *Ipomoea biloba*, which appears to be a segmental allotetraploid may be a bridging form between diploid taxa and the sweet potato. Diploid *Ipomoea biloba* shows a high level of homeology with diploid *Ipomoea crassicaulis*.

RESUME

Un vaste nouveau programme de sélection et d'amélioration a permis d'obtenir six nouveaux cultivars de patate douce aux rendements élevés à partir de matériel parental japonais, américain et indien. Des études cytologiques basées sur l'analyse pachytène ont permis de clarifier le degré d'homéologie des chromosomes entre trois génomes de patate douce hexaploïde. *Ipomoea biloba* tétraploïde qui semble être un allotétraploïde doit être une forme intermédiaire entre les diploïdes et la patate douce. *Ipomoea biloba* diploïde révèle un niveau élevé d'homéologie avec *Ipomoea crassicaulis* diploïde.

RESUMEN

Un nuevo y amplio programa de mejoramiento genético ha producido hasta ahora seis nuevos cultivares de camote de alto rendimiento usando material parental japonés, americano e hindú. Los estudios citológicos basados en análisis en fase de paquiteno han permitido elucidar el grado de homología cromosómica entre tres genomas de papa dulce hexaploide. El tetraploide *Ipomoea biloba*, que parece ser un alotetraploide segmental, puede ser un puente entre la forma diploide y el camote. El diploide *Ipomoea biloba* muestra un alto nivel de homología con el diploide *Ipomoea crassicaulis*.

INTRODUCTION

Sweet potato (*Ipomoea batatas*) has a long history of cultivation in India and its present area of cultivation is about 160,000 hectares. Bihar and Uttar Pradesh states account for nearly 60 percent of the total area under this crop in India. Sweet potatoes contain useful quantities of carotene or provitamin A, Vitamin C, calcium and phosphorous as well as starch. The nutritive value of sweet potato proteins compares well with other vegetable proteins⁴.

Little genetic improvement of this crop has been attempted in India⁵. The average yield is only 8 tons per hectare. A few high yielding clones of sweet potato were identified amongst introductions and have given increased yields in certain parts of the country¹⁵.

Most of the introductions made so far, as well as indigenous sweet potato cultivars, flower little and seed set is rare. Recently, however, the induction of flowering has engaged the attention of research workers and treatments such as girdling, training of vines over trellises, varying photo-period, applying growth hormones and grafting on root stocks of related ornamental plants have been successfully tried^{10,11}.

There is a new, multi-disciplined, problem-and-production oriented research programme at the Central Tuber Crops Research Institute, Trivandrum, with sub-centres elsewhere in the country. Year-round cultivation of sweet potato is possible at Trivandrum, and a germplasm collection is maintained at the Institute. A high percentage of accessions produce flowers.

BREEDING OBJECTIVES

Objectives are higher tuber yield, responsiveness to fertilizers, low sugar and high starch content of tubers for industrial use, high sugar and carotene content for tubers for human consumption, resistance to diseases and to the sweet potato weevil, (*Cylas formicarius* Fab), drought resistance, wider adaptability and insensitivity to photo-period.

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GERMPLASM COLLECTION AND UTILIZATION

Many sweet potato clones, including many promising exotic cultivars and the related *Ipomoea* species have been assembled. These collections have been screened and critically studied for several desirable attributes including disease and pest resistance. Apart from evaluation for direct utilization, the genetic diversity in the germplasm has been exploited by hybridization and mutation breeding programmes. The mutation breeding programme has been primarily concerned with attempting to rectify defects in otherwise desirable cultivars. As an aid to the interspecific hybridization programme, the ploidy status, crossability relationships and chromosomal inter-relationships of *Ipomoea* species were also investigated.

RESULTS OF THE PROGRAMME

Several high yielding hybrids such as H-41(2), H-42(1), H-42(2), H-74, H-66(2), H-72(2) have been obtained having desirable qualities. H-41(2) resulted from a cross between a Japanese cultivar and an indigenous one; H-42(1) and H-42(2) result from crosses between local cultivars and an American cultivar. In trials with six replications these had tuber yields ranging from 21.5 to 37.2 tons per hectare as compared with local control cultivars with a yield range from 6.8 to 20.8 tons per hectare. Spacing was 30cm x 45cm and N, P, and K were applied at 75, 40 and 40 kg/ha respectively. The new hybrid clones produced tubers of large to medium size of excellent quality which cook well and have good storage quality. They also possess a very high degree of field resistance to sweet potato weevil (*Cylas formicarius*), a serious and widespread pest of the crop¹³. Additional important features of these hybrids are their wide adaptability to climatic variation, and they can be grown throughout the year on an economic basis. All three hybrids have now been released for commercial cultivation.^{4,5,11}

SOME CYTOGENETICAL ASPECTS OF SWEET POTATO BREEDING

Studies of a fundamental nature and of potential value in sweet potato breeding have been carried out at some research centres in the country. Significant is the karyological analyses of diploid, tetraploid and hexaploid species of *Ipomoea*¹⁴. The small size of mitotic chromosomes in these species was a constraint until successful karyological analyses at pachytene stage were obtained with the American diploid species, *Ipomoea crassicaulis*³. In this species, all the 15 bivalents could be individually identified at pachytene, and by utilizing the criteria of total length, relative length, position of centromere, size, shape and distribution of chromomeres, lengths of dark and light-staining regions and nucleolar association, detailed diagnostic features of all the chromosomes belonging to the haploid complement could be established.

Such studies have been able to be extended to the hexaploid sweet potato despite its extremely high chromosome number, $2n = 90$. Cytological information from such studies⁸ referred not only to the karyological make-up of sweet potato but also to an understanding of genomic homology. General agreement in the gross pattern of the chromosome morphology of diploid and hexaploid *Ipomoea* species was apparent in pachytene chromosomes. Forty out of the 45 haploid chromosomes of sweet potato were identified and classified into three groups based on the position of the primary constrictions. Eight metacentric types, three sub-metacentric types and eight acrocentric types were recognized and to these 19 types all the 40 chromosomes could be assigned. Homological studies at pachytene brought out a maximum multivalent association of $1^{\text{VI}} + 2^{\text{V}} + 3^{\text{IV}}$. The multivalents were predominantly quadrivalents ranging from 1 to 4. The hexavalents never exceeded one per cell but could be assigned to two distinct types. Pentavalents were relatively rare and numbered one or two. The outstanding observation, at pachytene, in respect of chromosomal association was the discovery of hexavalent association for the first time and being able to identify the participating chromosomes. These studies provide clues to the origin and genomic interrelationships of the hexaploid sweet potato. Eight chromosomal types that are each represented by a single bivalent type in the haploid complement are apparently not common to all the three genomes. Six chromosomal types which occur in duplicate are common to two out of the three genomes and two triplicated chromosomal types are present in all the three genomes. The occurrence of hexavalents and the frequent formation of quadrivalents, reflects the prevalence of chromosomal homeology between the constituent genomes. Thus, it is suggested that (i) the three parental genomes are partly homeologous, (ii) two of the genomes show closer homeology to one another than to the third and (iii) the three genomes all differ from each other with respect to one or more of the eight chromosomal types which occur singly. This cytological information suggests a segmental allopolyploid origin for the sweet potato and that the parental genomes are from closely related taxa^{7,8}. A translocation and an interstitial inversion were also observed at pachytene. These indicate the existence of chromosomal structural changes in sweet potato. Both vegetative propagation and the high genetic buffering due to hexaploid nature are conducive to the preservation and propagation of chromosomal aberrations.

CHROMOSOMAL DIFFERENTIATION AT DIPLOID LEVEL

Investigations have been also conducted on diploid taxa of *Ipomoea*. In addition to *I. crassicaulis*, the diploid species of *I. biloba*⁹ and *I. paniculata*¹⁰ were also subjected to pachytene analyses. Comparison of the pachytene karyotypes of these species permitted the estimation of chromosomal differentiation at diploid level and its role in speciation. Comparison of the karyotypes of *I. crassicaulis* and *I. biloba* revealed homology between eight chromosomes in the two complements. Our data support those of Jones and Kobayashi² based upon metaphase studies. Of interest, phylogenetically, was the recognition of karyological differentiation between two collections of *I. paniculata* which were morphologically similar¹⁰.

ORIGIN OF TETRAPLOID IPOMOEA SPECIES

In a naturally occurring tetraploid form of *Ipomoea biloba*, data from pachytene analyses proved valuable in explaining how such forms could be bridging between many diploid species and the hexaploid sweet potato.¹⁶ Both diploids ($2n = 30$) and tetraploid ($2n = 60$) forms of *I. biloba* occur along the western coast of the country with sympatric distribution. Morphological differences between these are few, but chromosomal association studies at metaphase-I, as well as the pairing behaviour of marker chromosomes at pachytene, pointed to a segmental allopolyploid origin of the tetraploid form and confirmed the direct role played by diploid taxa in its origin.

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