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To cite this article: Ray Tui & Satyesh Chandra Roy (2008) Physical localization of highly nutritional protein coding *AmA1* gene in amaranths through molecular cytogenetic tools, *Caryologia*, 61:3, 216-224, DOI: [10.1080/00087114.2008.10589633](https://doi.org/10.1080/00087114.2008.10589633)

To link to this article: <https://doi.org/10.1080/00087114.2008.10589633>



Published online: 04 Feb 2014.



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# Physical localization of highly nutritional protein coding *AmA1* gene in amaranths through molecular cytogenetic tools

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**Abstract** — A highly nutritional protein coding gene *AmA1* of *Amaranthus hypochondriacus* was searched in different species of *Amaranthus* by using various molecular biological techniques. PCR, Southern hybridization, primed *in situ* labeling (PRINS) and Cycling-primed *in situ* labeling (C-PRINS) confirmed the presence of *AmA1* coding region only in *Amaranthus hypochondriacus*. The *AmA1* gene was successfully localized on interphase nuclei and also on the metaphase chromosomes. The single copy, unique *AmA1* gene was found to be present in the subtelo-meric region of two homologous chromosomes in the group of 2-2.2  $\mu\text{m}$  in length. In the present study, a rapid and reliable method for physical localization of single gene on plant chromosome was described and both the methods for *in situ* localization i.e. PRINS and C-PRINS were compared.

**Key words:** *Amaranthus*, *AmA1* gene, cycling-primed *in situ* labeling (C-PRINS), primed *in situ* labeling (PRINS).

## INTRODUCTION

Amaranths are the most important group of plants in Amaranthaceae containing many leafy vegetables and grain types. The genus *Amaranthus* is widely distributed throughout the worlds of temperate and tropical regions. Traditionally these native American crops have been utilized for its food value by people from Mexico to Peru to Nepal long before any nutritional analyses had been conducted. Though both the grain and leafy biotypes of *Amaranthus* species are very popular in India, grain amaranths have gained much importance for its high protein content (17-19% of seed dry weight) as compared to other traditional crops having an average of ~10% protein (LARKINS 1981). Since past few years amaranths have received renewed attention as alternative field crops (BRESSANI *et al.* 1987a; b; TUCKER 1986) mainly due to its essential amino acids such as lysine, tryptophan and sulfur containing amino acids rich protein (SENF 1980). A highly nutritional, 35 kDa protein *AmA1* has been reported from *Amaranthus hypochondriacus* corresponding closely to

that of World Health Organization recommended protein standard for optimum human nutrition (RAINA and DATTA 1992). There are several other popularly edible grain and leafy vegetables of amaranth, which had not been studied for identification of this 35 kDa *AmA1* protein encoding gene. Despite the increasing attention there is neither a genetic nor any cytological linkage map available in case of amaranths. In this present study, our main intention was to investigate the presence of this highly nutritional protein coding *AmA1* gene in other grain and leafy vegetables of amaranths and also to localize the *AmA1* gene physically on chromosome.

Attempts to localize specific nucleotide sequences on chromosomes were however quite limited in plants. Moreover it had been difficult to identify chromosomes objectively by morphological means in plants having small chromosomes such as amaranths measuring 1.1-2.8  $\mu\text{m}$  at mitotic metaphase. Most popular non isotopic labeling of nucleic acids, fluorescence *in situ* hybridization (FISH) has been extensively used to visualize DNA sequences in interphase nuclei (DONG and JIANG 1998), mitotic and meiotic chromosomes (NENNO *et al.* 1994; PEDERSEN *et al.* 1995) as well as on extended DNA fibres (DE JONG *et al.* 1999) and bacterial artificial chromosomes (JIANG *et al.* 1995). Plant cytogeneticists used conventional *in*

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*in situ* hybridization technique to distinguish between different genomes and for physical mapping of repeated sequences (HESLOP-HARRISON 1991). The detection of low copy sequences, such as the secalin gene cluster in rye (GUSTAFSON *et al.* 1990) and a number of unique sequences have also been reported in plants (AMBROS *et al.* 1986; SIMPSON *et al.* 1988; GUSTAFSON and DILLÉ 1992). However efforts to detect reliably unique sequences on plant chromosomes by using labeled DNA probes have a low success rate. It has been reported that localization of DNA sequences shorter than 10 kb on plant chromosomes using ISH or FISH is still very difficult (JIANG and GILL 1994). The occurrence of cell wall fragments and cellular debris reduce the access of DNA probes to the target sites on plant chromosomes decreasing the sensitivity of *in situ* detection. Furthermore detection of certain sequences may be hindered by the presence of highly condensed chromatin, as seen in human and plant chromosome preparations (HOOVERS *et al.* 1992; SHEN *et al.* 1987). Alternative to FISH, primed *in situ* labeling (PRINS) and Cycling-PRINS has several advantages. For PRINS, short oligonucleotide primers can be designed and synthesized with a minimum of sequence information, which hybridize to homologous targets within densely structured chromatin both easier and faster than the larger probes usually used for FISH. The use of an oligonucleotide as annealed primer also allows better penetration of debris and condensed chromatin, thus increasing the efficiency of hybridization and sensitivity of detection. In C-PRINS, sequence of thermal cycles analogous to polymerase chain reaction are involved (GOSDEN *et al.* 1991; TERKELSEN *et al.* 1993a; b) in which 20% increase in labeled DNA after each cycle of C-PRINS has been reported (TERKELSEN *et al.* 1993a). Because of its speed and sensitivity, the number of application of PRINS and C-PRINS in human cytogenetics is rapidly increasing (KOCH *et al.* 1995a; b; TERKELSEN *et al.* 1995; PELLESTOR *et al.* 1996). However C-PRINS was used to detect DNA sequences shorter than 2 kb on human chromosomes (GOSDEN and LAWSON 1994a; b). Direct PRINS and C-PRINS have been reported for the rapid physical mapping of several types of repetitive DNA sequences on the mitotic chromosomes of *Vicia faba*, *Pisum sativum*, and *Secale cereale* (KUBALÁKOVÁ *et al.* 1997). Both the techniques have already been used successfully for the detection of unique transgene on rice chromosomes (SAHA *et al.* 2006).

In this communication an attempt has been made to standardize a protocol for reliable and

rapid physical localization of the unique gene on plant chromosomes. Moreover to study the distribution of *AmA1* gene in other amaranths, PCR, Southern blot analyses and physical localization of gene on chromosome by PRINS and C-PRINS techniques have been employed. In addition, potential applications of both the techniques, PRINS and C-PRINS were compared.

## MATERIALS AND METHODS

*Plant Materials* - Plant materials used in this study are listed in Table 1. Seeds of three grain amaranths, *A. hypochondriacus*, *A. caudatus* and *A. cruentus* of different accessions were obtained from National Bureau of Plant Genetic Research (NBPGR), Simla, India and seven leafy vegetables of amaranths, *A. gangeticus* (syn. *tricolor*), *A. paniculatus*, *A. viridis*, *A. blitum*, *A. lividus*, *A. tristis* and *A. polygamus* were collected from different localities of West Bengal and other parts of India and were identified by Botanical Survey of India (BSI), Kolkata, India.

*cDNA of AmA1* - *E. coli* strain DH-5 $\alpha$  harboring the plasmid pTZ18U containing *AmA1* cDNA (pAmA1.3) was obtained from National Institute for Plant Genome Research (NIPGR), Jawaharlal Nehru University, New Delhi, India.

*Isolation of genomic DNA* - Genomic DNA was isolated from young leaves of both leafy vegetables and grain amaranths using a protocol modified from DELLAPORTA *et al.* (1983). Briefly tissues were ground to fine powder and extracted for 20 min at 65° C using extraction buffer (50 mM Tris-Cl pH 8.0, 10 mM EDTA pH 8.0, 100 mM NaCl, 1% SDS and 10 mM 2-mercaptoethanol). The supernatant was extracted twice with phenol: chloroform (1:1), 1/10<sup>th</sup> volume of 3 M ammonium acetate and equal volume of pre-chilled isopropanol were added, stored at -20° C for overnight and centrifuged at 10000 g for 10 min. The pellet was suspended in TE buffer (10 mM Tris and 1 mM EDTA pH 8.0) after washing with 70% ethanol. To remove co-precipitated RNA, RNase treatment was done. Polyethylene glycol (PEG 8000) treatment was done to remove proteins and polysaccharides from DNA following DIXIT (1998). Concentration of DNA sample was determined by comparing band intensity with known concentration of lambda DNA digest after 0.8% agarose gel electrophoresis and ethidium bromide staining and also by spectrophotometric measurement of the OD reading at 260 and 280 nm against TE buffer in Beckman DU 530 spectrophotometer.

**PCR amplification of *AmA1*** - The *AmA1* coding region was amplified by PCR using forward primer F51 (5'-CACCATGGCGGGATTACCAGTG-3') and reverse primer R1044 (5'-CAAGGAA-GAACCTCTTGTTC-3') as reported by CHAKRABORTY *et al.* (2000). PCR amplification was carried out with 20 pmol each of *AmA1* gene specific primers F51 and R1044, 0.3 mM dNTP mix (MBI Fermentus, Hanover, MD, USA), 2.5  $\mu$ l of 10 X PCR buffer (MBI Fermentus), 2.5 U *Taq* DNA polymerase (MBI Fermentus), 2 mM  $MgCl_2$  (MBI Fermentus) and 1  $\mu$ g template DNA in 25  $\mu$ l reaction volume. Amplification reactions were performed in a PerkinElmer model 2400 thermocycler (Perkin Elmer, Waltham, MA, USA) as follows: initial denaturation at 94°C for 5 min followed by 30 cycles of 94°C for 1 min, 60°C for 1 min and 72°C for 1 min and final elongation at 72°C for 7 min. The amplified products were separated by 1% agarose gel electrophoresis (AGE), stained with ethidium bromide (Sigma, USA) and visualized under UV illumination.

**Southern blot hybridization** - Southern blot analysis was done according to the methods of SAMBROOK *et al.* (1989) with slight modifications. Approximately 10  $\mu$ g of genomic DNA from all the species of *Amaranthus* (Table 1) were digested with *EcoRI* (Roche Diagnostics, GmbH, Mannheim, Germany) and DNA from *A. hypochondriacus* was digested with *BamHI* (Roche), *BglII* (Roche), *HindIII* (Roche) and *EcoRI* respectively, followed by separation in 0.8% (w/v) agarose gel. After complete denaturation and renaturation, the gel was blotted onto positively charged Hybond-N<sup>+</sup> nylon membrane (Amersham Biosciences, Buckinghamshire, UK).

The 1.2 kb *AmA1* sequence was digested out from pAmA1.3 plasmid using *EcoRI* restriction enzyme according to the map provided by CHAKRABORTY *et al.* (2000), gel was eluted using Qiagen gel elution kit (Qiagen, Valencia, CA, USA) and labeled with [ $\alpha$ -32P] dCTP (Perkin Elmer) using "Ready Prime" random labeling system (Amersham Biosciences). The membranes were hybridized with radiolabeled *AmA1* gene probe for overnight at 68°C, followed by washing twice in buffer 1 (2 X SSC and 0.1% SDS) at room temperature and twice in buffer 2 (0.1 X SSC and 0.1% SDS) at 68°C for 30 min per wash. The membranes were then exposed to Kodak X-ray film for 7 days at -80°C and thereafter the films were developed.

**Chromosome preparation and karyogram analyses** - About 2–4 mm long root tips were excised and put in ice cold water for 20–24 h, followed by fix-

ation in ethanol:acetic acid (3:1, v/v) at 14–18°C for overnight. Fixed root tips were washed thoroughly with 0.01 M citrate buffer (sodium citrate/citric acid, pH 4.8) and digested with 1% (w/v) cellulase (Sigma) for 1 h and 2% (w/v) pectinase (Sigma) for 30 min at 37°C. After careful removal of enzymes from the softened material by washing with distilled water for 30 min with three changes each after 10 min, the root tips were transferred on Amplisides. Finally, the treated root tips were squashed, air dried and stored at -20°C. Karyogram of metaphase chromosome was performed using IKAROS Metasystem (v.3.4.0) karyotyping software.

**Primed *in situ* DNA labeling and cycling-primed *in situ* labeling** - The procedures of primed *in situ* DNA labeling (PRINS) and cycling-primed *in situ* labeling (C-PRINS) were modified from the method of ABBO *et al.* (1993) and KUBALÁKOVÁ *et al.* (2001). Slides without any pretreatment were used directly for reaction and/or alternatively, the slides were washed three times in 2 X SSC for 5 min at room temperature followed by an RNase (50  $\mu$ g ml<sup>-1</sup>, Sigma) treatment in reaction buffer (1 mM Tris-HCl, 1.5 mM NaCl, pH 7.5) at 37°C for 60 min and proteinaseK (2  $\mu$ g ml<sup>-1</sup>, Sigma) treatment at room temperature for 1 min or gradual dehydration with 70–90% ethanol. After pretreatment the slides were rinsed in 1 X PCR buffer (10 mM Tris-HCl, pH 8.4, 50 mM KCl, 1.5 mM  $MgCl_2$ ) for 5 min and used for reaction. For direct PRINS, the labeling reactions were performed in 50  $\mu$ l volume containing 1 X PCR buffer (Ampli Taq, Applied Biosystem), 2.5 mM  $MgCl_2$ , 200  $\mu$ M of each primers, 100  $\mu$ M of each dATP, dCTP, dGTP, 17  $\mu$ M of dTTP and 8  $\mu$ M of fluorescein-11-dUTP (Roche) and 3 U of Amplitaq gold DNA polymerase. Reaction mixture was sealed under Amplicover discs with Amplicover clips. Thermal cycle comprised of 18 min at 95°C to activate the Amplitaq gold DNA polymerase, then 94°C for 2 min, 60°C for 15 min and extended at 72°C for 45 min. Reaction mixture for C-PRINS was same as PRINS except 2 mM  $MgCl_2$ , 34  $\mu$ M of dTTP, 2  $\mu$ M of fluorescein-11-dUTP and 5 U of Amplitaq gold DNA polymerase were used. C-PRINS reaction was carried out following an initial cycle of 18 min at 95°C, 1 min at 94°C, 5 min at 60°C, 10 min at 72°C, followed by 30 cycles each of 1 min at 94°C, 1 min at 60°C and 2 min at 72°C with a final extension for 7 min at 72°C. The reactions were carried out using GeneAmp *in situ* PCR system 1000 (Applied Biosystems, Foster City, CA, USA) and the experiments were repeated at least thrice to establish the reproducibility of the results.

**Chromosome staining, signal detection and fluorescence microscopy** - Both PRINS and C-PRINS reactions were terminated with stop buffer (0.5 M NaCl, 0.05 M EDTA, pH 8.0) for 5 min at 65° C and washed with wash buffer (0.1 M maleic acid, 0.15 M NaCl, 0.05% Tween 20, pH 7.5) at room temperature, for 5 min. The cover slips were immediately mounted and counter stained with Vectashield antifade solution (Vector Laboratories, Burlingame, CA, USA) containing 4',6'-diamidino-2-phenylindole (DAPI, 0.2 µg ml<sup>-1</sup>). Amplislide were examined with a Zeiss Axioskop 2 fluorescence microscope equipped with filter sets for the detection of fluorescein isothiocyanate (FITC) and DAPI, 100 W HBO and HAL illuminator. Filter set 1 and set 9 were used for the visualization of fluorescein and DAPI fluorescence, respectively. Signals were recorded by CCD camera and analyzed by FISH Imager™ (v.1.0) software.

## RESULTS AND DISCUSSION

**PCR Analysis** - For identification of *AmA1* gene in other amaranths, PCR was performed in all the plant materials as listed in Table 1 such as leafy vegetables, *A. gangeticus* (syn. *tricolor*), *A. paniculatus*, *A. viridis*, *A. blitum*, *A. lividus*, *A. tristis* and *A. polygamous* and all the grain amaranths, *A. hypochondriacus*, *A. caudatus* and *A. cruentus* using the *AmA1* specific primer pairs. A single band was detected in all the accessions of *A. hypochondriacus* by PCR amplification (Fig. 1), but no other leafy vegetables or grain amaranths produced the

same band. To check the reproducibility, the PCR reaction was repeated several times. The *AmA1* specific primer pair consistently produced the same sized band only in *A. hypochondriacus*, suggesting the specificity of *AmA1* coding nucleotide sequence in *A. hypochondriacus*.

**Southern hybridization** - Southern hybridization was done to confirm the occurrence of *AmA1* among all the amaranths of the present study (Table 1). After hybridization of the radiolabelled *AmA1* specific probe with the genomic DNA digested with *EcoRI*, single hybridized band was observed in the lanes of *A. hypochondriacus* (Fig. 2a). Other amaranths of both the biotypes did not produce any hybridization signals. Absence of any non-specific band confirmed the absence of any homologous sequence in other species of *Amaranthus* of this study. For further confirmation of the presence of *AmA1* in *A. hypochondriacus*, *BamHI*, *BglII*, *HindIII* and *EcoRI* digested DNA of different accessions of *A. hypochondriacus* were separately hybridized with radiolabeled *AmA1* gene specific probe. In all cases it produced strong signals (Fig. 2b) confirming that highly nutritional protein coding single gene *AmA1* is present only in *A. hypochondriacus*.

**PRINS and C-PRINS detection** - PRINS and C-PRINS reactions were performed in all the materials as listed in Table 1. Previously, the specificity of the primers had been established by PCR analysis with an annealing step of 60° C. In both the *in situ* detection methods, optimized protocols resulted in clear signals only in *A. hypochondriacus* with negligible non specific labeling (Fig. 3), but strong signals were obtained after C-PRINS

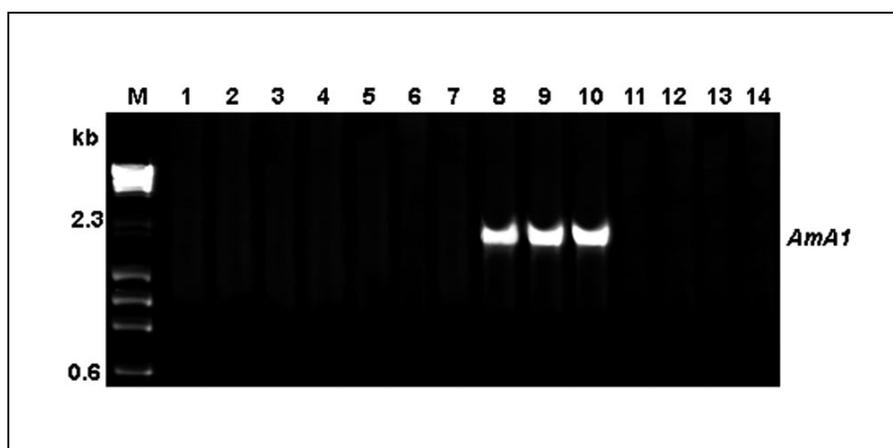


Fig. 1 — PCR amplification of genomic DNA with *AmA1* specific primer producing single band of *AmA1* gene. Lane M: λ DNA *Hind* III digest and ΦX 174 DNA *Hae* III digest marker. Lane 1 -14: AG1, AP1, AV1, AB, AL, ATR, APL, AH1, AH2, AH3, ACD1, ACD2, ACR1 and ACR2 in a sequence as mentioned in Table 1.

Table 1 — Members of amaranths used in the present study.

Biotype	Taxon	Population Code or Accession Number	Source	Chromosome Number (2n)
Vegetative	<i>Amaranthus gangeticus</i>	AG1	West Bengal, India	32
	<i>Amaranthus paniculatus</i>	AP1	West Bengal, India	32
	<i>Amaranthus viridis</i>	AV1	West Bengal, India	32
	<i>Amaranthus blitum</i>	AB	West Bengal, India	32
	<i>Amaranthus lividus</i>	AL	Tamil Nadu, India	32
	<i>Amaranthus tristis</i>	ATR	Tamil Nadu, India	32
	<i>Amaranthus polygamous</i>	APL	West Bengal, India	32
Grain type	<i>Amaranthus hypochondriacus</i>	AH1/ IC17930	NBPGR, Simla, India	32
	<i>Amaranthus hypochondriacus</i>	AH2/ IC17936	NBPGR, Simla, India	32
	<i>Amaranthus hypochondriacus</i>	AH3/ IC17938	NBPGR, Simla, India	32
	<i>Amaranthus caudatus</i>	ACD1/ IC381185	NBPGR, Simla, India	32
	<i>Amaranthus caudatus</i>	ACD2/ IC381200	NBPGR, Simla, India	32
	<i>Amaranthus cruentus</i>	ACR1/ EC277971	NBPGR, Simla, India	32
	<i>Amaranthus cruentus</i>	ACR2/ EC321563	NBPGR, Simla, India	32

in both interphase nuclei (Fig. 3b) and early metaphase chromosomes (Fig. 3d). Although the images were captured by CCD camera and processed by image analysis software, they were clearly visible through the microscope.

FITC fluorescence revealed specific labeling of a single pair of chromosomes in *A. hypochondriacus* of all the accessions (Fig. 3c, d). It suggests that single copy, unique *AmA1* gene is present in two homologous chromosomes of *A. hypochon-*

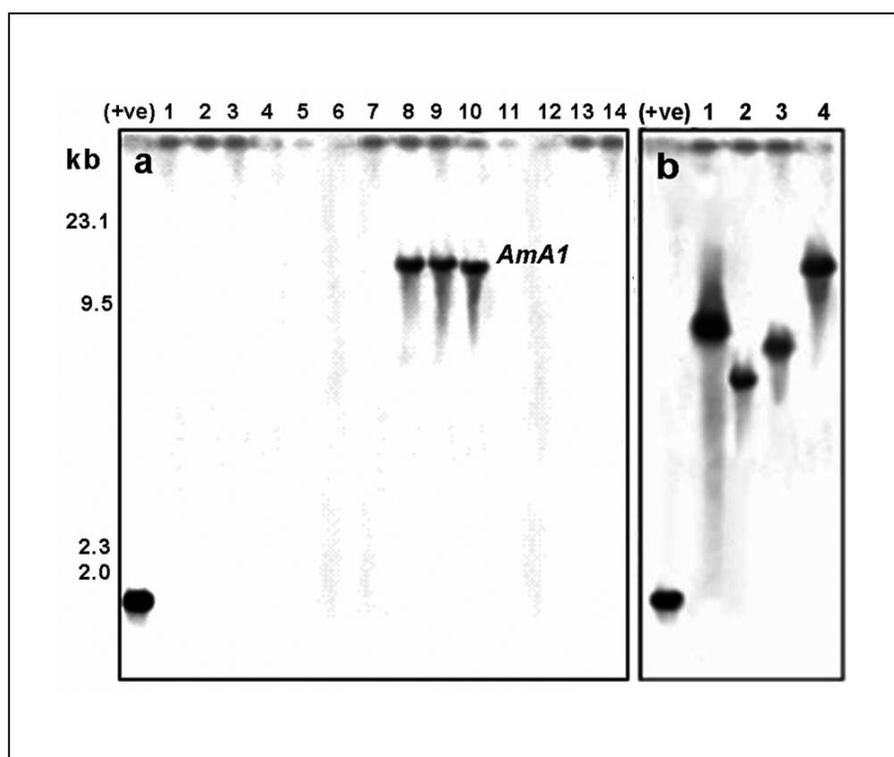


Fig. 2 — Southern blot analysis. **a** DNA was digested with *EcoRI*. Lane 1-14: AG1, AP1, AV1, AB, AL, ATR, APL, AH1, AH2, AH3, ACD1, ACD2, ACR1 and ACR2 in a sequence as mentioned in Table 1; **b** DNA of *A. hypochondriacus* (IC17930) was digested with *BamHI* (lane 1), *BglII* (lane 2), *HindIII* (lane 3) and *EcoRI* (lane 4) respectively. Lane (+ve): 1.2 kb *AmA1* gene fragment as positive control.

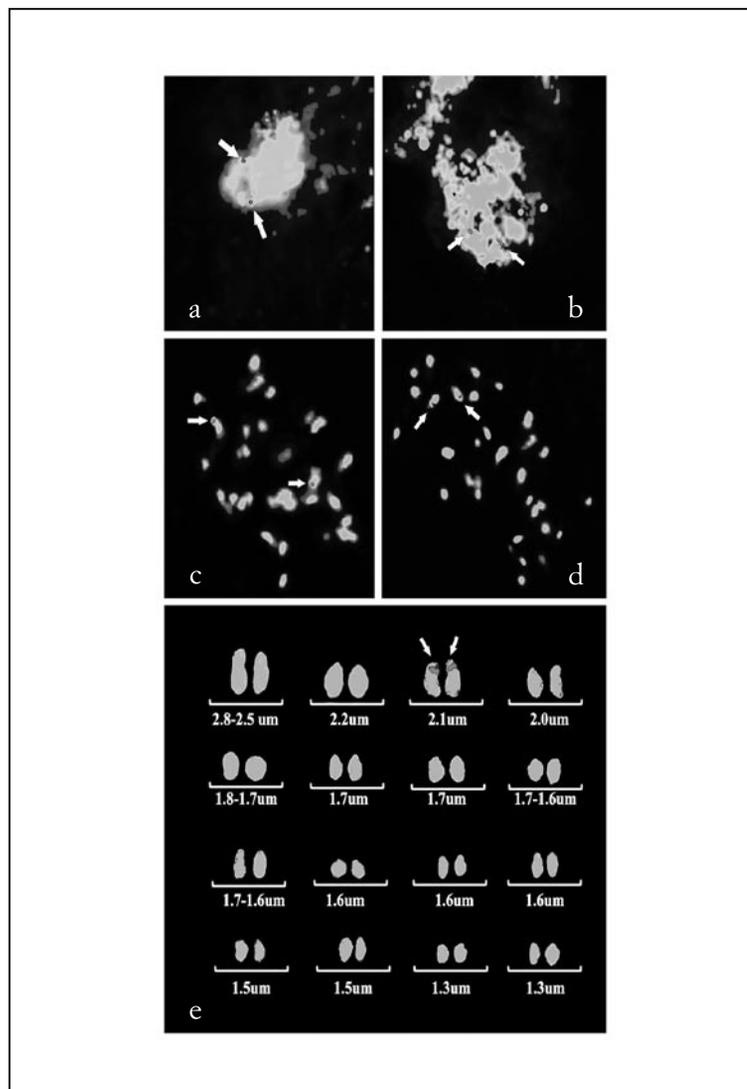


Fig. 3 — Localization of *AmA1* sequence in *A. hypochondriacus*. **a** on interphase nuclei by PRINS (ca.  $\times 1000$ ); **b** on interphase nuclei by C-PRINS (ca.  $\times 1000$ ); **c** on early metaphase chromosome by PRINS (ca.  $\times 1000$ ); **d** on early metaphase chromosome by C-PRINS (ca.  $\times 1000$ ); **e** Karyogram after localization of *AmA1* gene by C-PRINS. Arrows on the figures indicate the strong hybridization signals (yellow-green colour spot) obtained after incorporation of fluorescein-11dUTP. Chromosomes are counterstained with DAPI (blue colour).

*driacus*. After primer annealing and extension, two distinct sites were also detected on the interphase nuclei (Fig. 3a, b). The exact identification of chromosomes bearing *AmA1* gene could not be done because of its very small size with no distinct difference in chromosome morphology. However detailed chromosome morphology of *Amaranthus hypochondriacus* was studied through IKAROS software (Fig. 3e). The length of chromosomes bearing *AmA1* gene ranges from 2-2.2  $\mu\text{m}$ . As the chromosomes were in little early metaphase, determination of the exact length of chromosomes

bearing *AmA1* gene was not possible. Although it can be said that chromosomes bearing *AmA1* come in the group of 2-2.2  $\mu\text{m}$  long chromosomes. In metaphase plate, the FITC signals were found to be present at the sub-telomeric region of homologous chromosomes. The signal position at the distal part of chromosomes may be due to the fact that distal regions are the most decondensed part of cereal chromosomes and contains a large number of actively transcribed genes that are active during the cell cycle of cells that divide rapidly (JIN *et al.* 2002).

According to MACAS *et al.* (1995) and KUBALÁKOVÁ *et al.* (1997), indirect PRINS increases signals as well as non specific labeling so in our study direct PRINS was used to detect the gene on chromosome. A potential of indirect C-PRINS for detection of single copy DNA sequences in plant chromosomes was demonstrated by ZHU *et al.* (1995) and SHI *et al.* (1996) who localized single copy DNA sequences as short as 1 kb in soybean. In comparison to indirect C-PRINS followed by MUKAI and APPELS (1996), the method for direct C-PRINS is faster and more sensitive (KUBALÁKOVÁ *et al.* 1997). KUBALÁKOVÁ *et al.* (2001) demonstrated the usefulness of direct PRINS and C-PRINS for localization of various types of repeated DNA sequences in plant chromosomes. In our study we also noticed better signals after C-PRINS in comparison to PRINS as observed by KUBALÁKOVÁ *et al.* (2001).

The specificity and sensitivity of PRINS and C-PRINS depends on a number of factors (KUBALÁKOVÁ *et al.* 1997; 1998; LYSÁK *et al.* 1999). The quality and age of chromosome preparation were extremely important. In our investigation, signals were best detected on fresh slides (after one or two days of squash preparation). Though KUBALÁKOVÁ *et al.* (1997) observed telomeric sequences best on 2-4 week old slides, other sequences were best detected on 1 week old slides. According to them aging may decrease non specific labeling on chromosomes. This observation differs from KOCH *et al.* (1995b) who found that the background for human chromosomes increased with the age of slides. RNase treatment is another factor which helped to reduce non specific labeling, but at the same time it resulted into less intense signal. Similar observation was also reported by KUBALÁKOVÁ *et al.* (1997). Though GODSEN and LAWSON (1994b) recommended a passage through ethanol series, it produced negatively influenced chromosome morphology, decreased signal intensity and caused additional non-specific labeling around the chromosomes. So we did not follow this treatment further. In our study, slides treated with RNase and proteinase K produced best detectable signal without non specific labeling. *In situ* detection of low- and single-copy DNA sequences has proved to be difficult for plant chromosomes. Probes above a certain size may not efficiently penetrate cell wall fragments, cellular debris and condensed chromatin to reach their target sites. Alternatively the use of short oligonucleotides as the hybridizing reagent could increase sensitivity by improving penetration of the probe DNA to target sequences. Although C-PRINS resulted in

intense signal than PRINS, both the techniques confirmed physical localization of *AmA1* gene on interphase nuclei and chromosomes. Moreover screening of specific gene in different taxa can be done rapidly by PRINS and C-PRINS than any other *in situ* hybridization methods.

In this study it was observed by PCR using *AmA1* specific primers that *AmA1* gene is present only in *A. hypochondriacus*. Further the same observation was confirmed by Southern hybridization using *AmA1* specific probe. No other popularly edible grain or leafy amaranths contain this highly nutritional protein coding *AmA1* gene. Both PRINS and C-PRINS successfully localized the single gene *AmA1* on interphase nuclei and chromosomes of all the accessions of *A. hypochondriacus*. In conclusion, these *in situ* hybridization techniques, PRINS and C-PRINS are simple, fast and efficient methods in reliable physical localization of unique gene on plant chromosome.

**Acknowledgement** — Authors are thankful to Department of Biotechnology, Government of India for providing financial support (Grant No. D.O. BT/PR/1944/AGR/08/142/2000) at CAS, Department of Botany, Calcutta University. Prof. Asis Dutta and Dr. Subhira Chakraborty, National Institute for Plant Genome Research, New Delhi, India are thankfully acknowledged for kindly providing us the *AmA1* gene.

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Received April 13<sup>th</sup> 2007; accepted May 20<sup>th</sup> 2008