

Vetiver grass model for long term carbon sequestration and development of designer genotypes for implementation



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To reduce atmospheric carbon it is desirable that carbon is blocked into subsoil horizon to minimize its recycling back to atmosphere

This can be best achieved either by

- (a) Locking of carbon in basalt rocks as carbonate**
 - (b) Photosynthetic capture converted into bio-char**
 - (c) Photosynthetic capture locked deep into the soil**
-
- Deep rooted forest trees are most suitable to realize this objective**
 - In the absence of above Vetiver is the suitable alternative option**

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Vetiver is the most suitable alternative option

It has deep penetrating high biomass producing root system

Its roots offer a growth potential of 3 cms. per day reaching upto 2.5 meters just in six months

Root degradation is minimal in deep sub-soil horizon facilitating long-term carbon sequestration

Degradation could be further minimized by selecting casparian strip thick genotypes

Vetiver is the most suitable alternative option

India being the native home of Vetiver offers repertoire of genetic diversity to select / develop designer genotype

However, the seed forming genotypes that offer such an opportunity are not suitable for ecological plantations



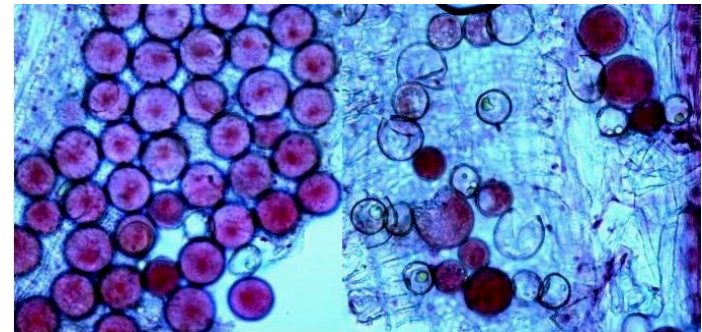
Vetiver is the most suitable alternative option

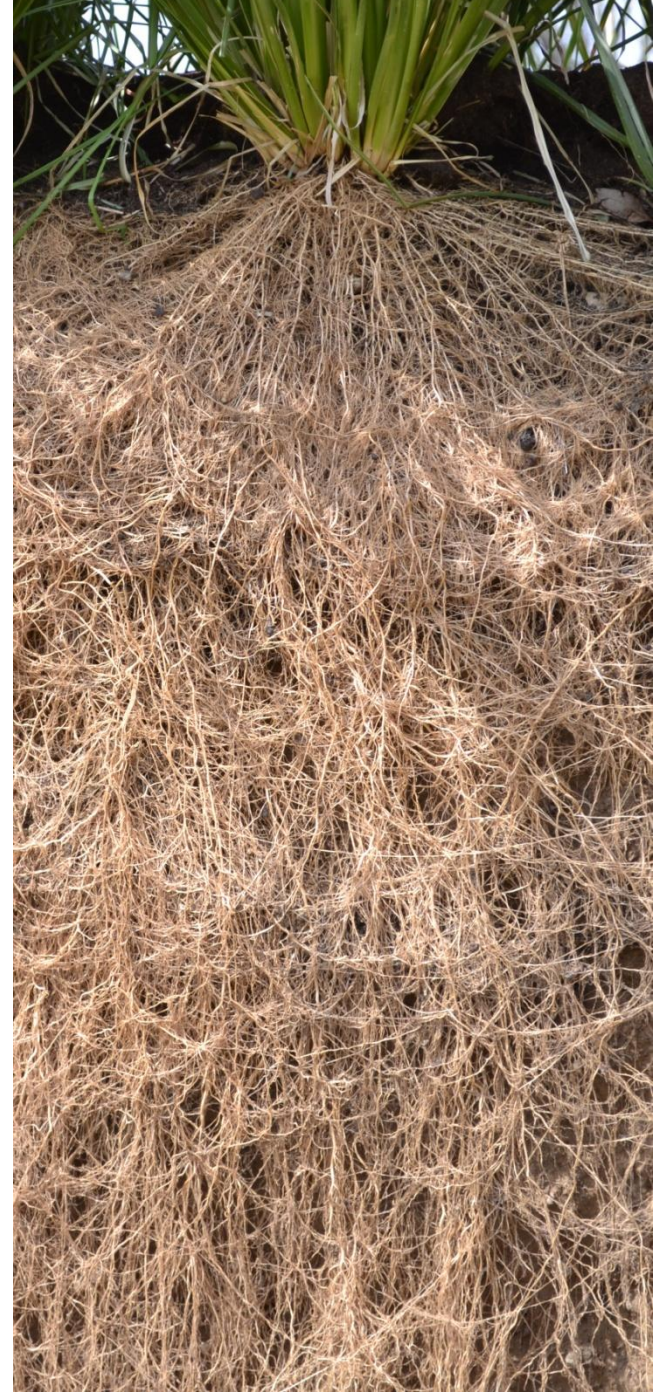
Development of designer genotypes for implementation

Therefore,
We looked for strategic solutions that minimizes seed fertility

Selected a suitable genotype with fast growth potential and minimum fertility

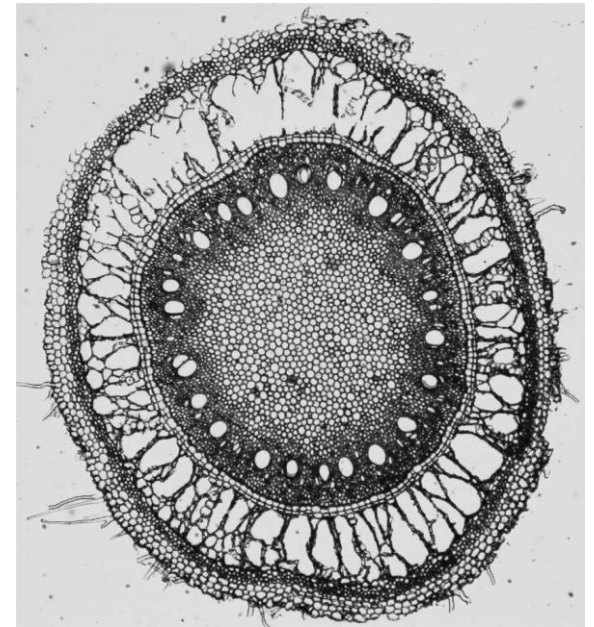
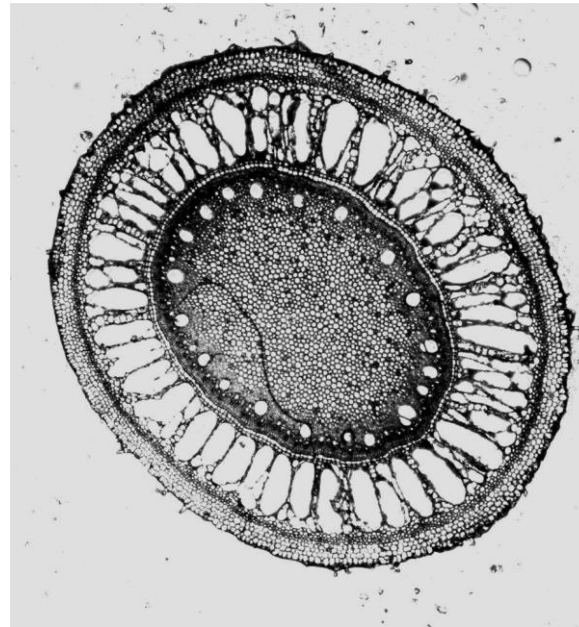
Changed to polyploid to realize seed infertile designer genotype



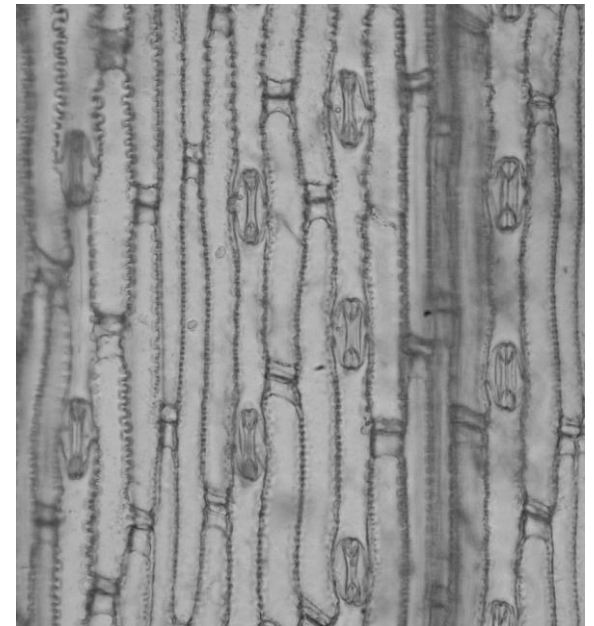
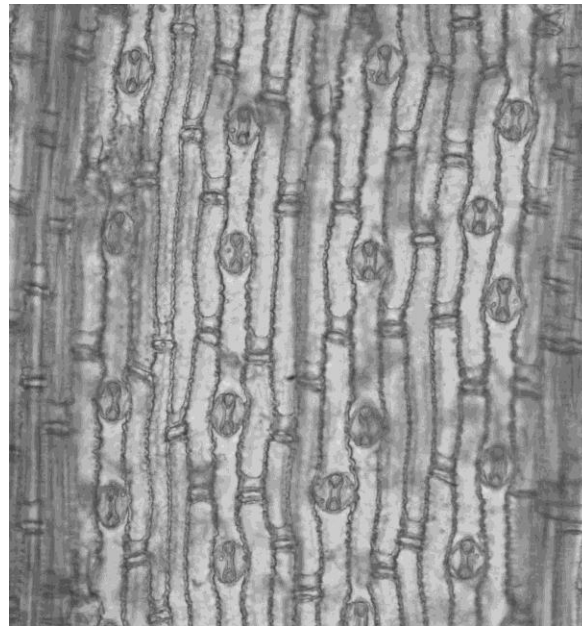




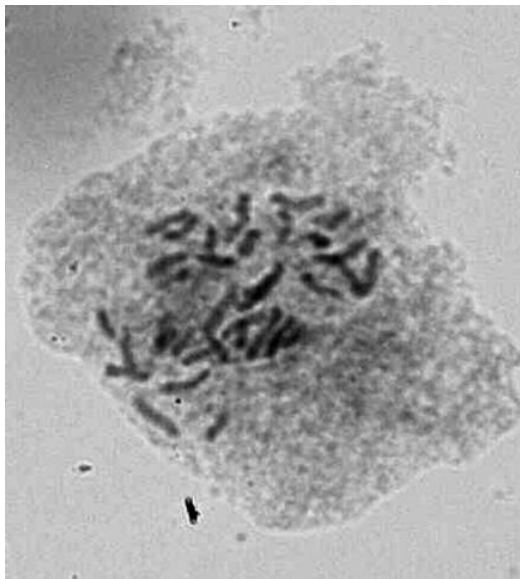
**Root
anatomy and
Stomatal
features
in the diploid
vs
tetraploid
clone of
Vetiver**



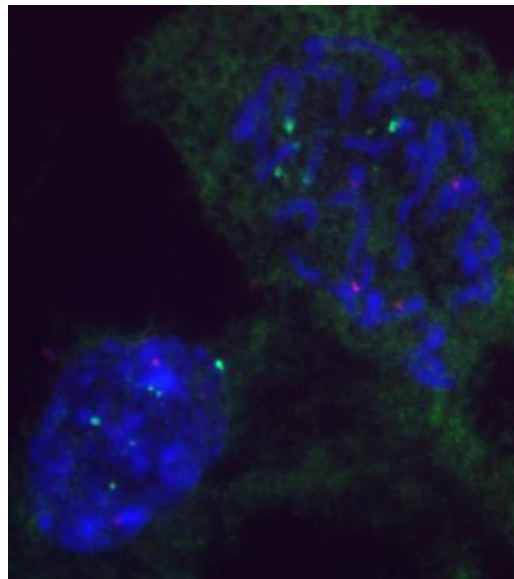
**Note: Higher
Vascular
cylinder vs.
cortex ratio
in the
tetraploid**



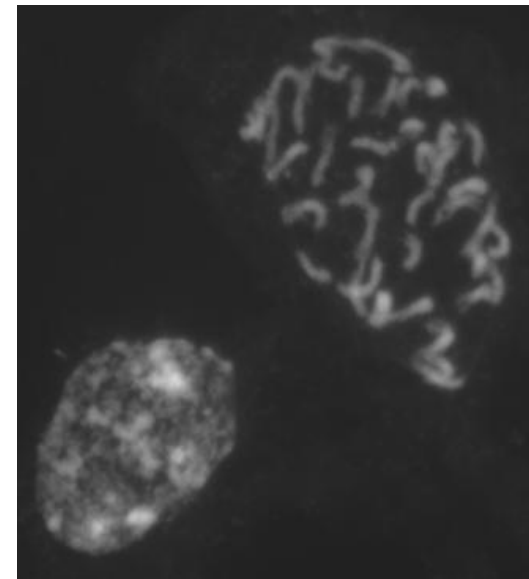
Cytological characterization of seed infertile autotetraploid clone of Vetiver



Feulgen



rDNA FISH



DAPI

DNA fingerprints of the autopolyploid clone of Vetiver

ISSR Markers :

Lane M : λ DNA / Hind III digest

Lane 1 : UBC807- AGAGAGAGAGAGAGAGT

Lane 2 : UBC810- GAGAGAGAGAGAGAGAT

Lane 3 : UBC811- GAGAGAGAGAGAGAGAC

Lane 4 : UBC812- GAGAGAGAGAGAGAGAA

Lane 5 : UBC814- CTCTCTCTCTCTCTA

Lane 6 : UBC818- CACACACACACACACAG

Lane 7 : UBC823- TCTCTCTCTCTCTCC

Lane 8 : UBC825- ACACACACACACACT

Lane 9 : UBC826- ACACACACACACACC

Lane10 : UBC828 -TGTGTGTGTGTGTGA

RAPD Markers :

Lane M : λ DNA / Hind III digest

Lane 1 : OPJ 6- TCGTCCGCA

Lane 2 :OPJ 9 - TGAGCCTCAC

Lane 3 : OPJ10- AAGCCCGAGG

Lane 4 :OPJ12 - GTCCCGTGGT

Lane 5 :OPJ13 - CCACACTACC

Lane 6 : OPJ14- CACCCGATG

Lane 7 :OPJ15 - TGTAGCAGGG

Lane 8 : OPJ16- CTGCTTAGGG

Lane 9 :OPJ17- ACGCCAGTTC

Lane10 :OPJ18- TGGTCGAGA

Internal transcribed sequence based variability in diploid (2V) and tetraploid (4V) plants of Vetivar

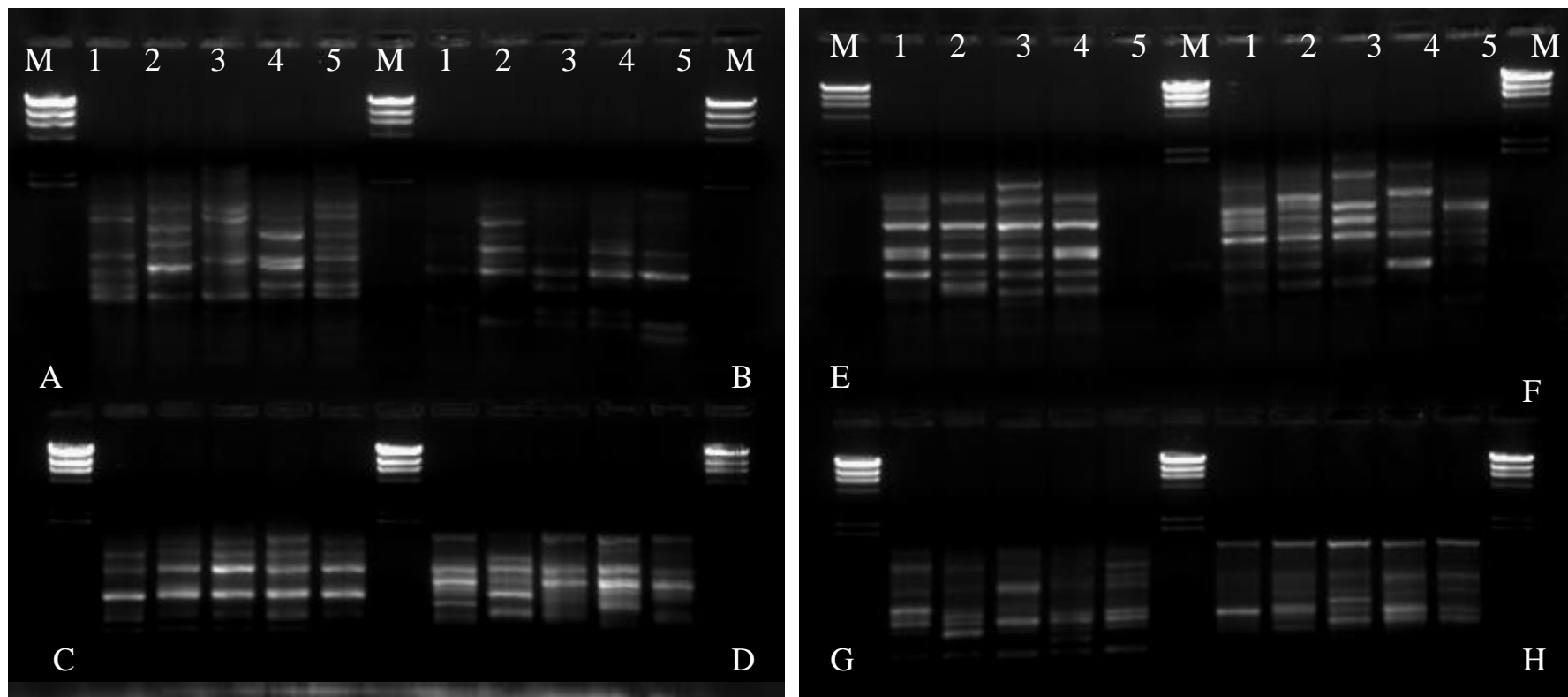
(Red colour- variation (4.63%)*, green colour - Conserved region(5.8S) and Black with red colour - ITS-1 & ITS-2 region of 45S rDNA)

| | | |
|----|---|-----|
| 2V | GATTTTGGGTATCCGACT -GAC-TGGGGTTCGCGTCCGAGCGGCGTGCCTGCGGTGCT | 58 |
| 4V | AAAAGTTGTTGTTCAA ACTTGACCTGGGGTTCGCGTCCGAGCGGCGTGCCTGCGGTGCT | 60 |
| | * * * * * ** ** * | |
| 2V | CGATGGGTTCGTAAGGGCCGATACGCCGGCCGCGTGCCGGGGCGCTGCACCGAGAACA | 118 |
| 4V | CGATGGGTTCGTAAGGGCCGATACGCCGGCCGCGTGCCGGGGCGCTGCACCGAGAACA | 120 |
| | ***** | |
| 2V | AGGTGTCGCCACCCACGCTGCTGTGCCGGCAGCATCCGCCGGCAGCCCAACTTGGGCCC | 178 |
| 4V | AGGTGTCGCCACCCACGCTGCTGTGCCGGCAGCATCCGCCGGCAGCCCAACTTGGGCCC | 180 |
| | ***** | |
| 2V | ACCGCGCCCTGCGGCGGGGAGCCAAACGCCACGTCCTCCCCACGGGTGGGTGGGAA | 238 |
| 4V | ACCGCGCCCTGCGGCGGGGAGCCAAACGCCACGTCCTCCCCACGGGTGGGTGGGAG | 240 |
| | ***** | |
| 2V | TGTCTTTTGGCGTGACGCCAGGCAGACGTGCCCTCGACCAGAAGCCTCGGGCGCAACT | 298 |
| 4V | TGTCTTTTGGCGTGACGCCAGGCAGACGTGCCCTCGACCAGAAGCCTCGGGCGCAACT | 300 |
| | ***** | |
| 2V | TGCGTTCAAAAACTCGATGGTTCCCGGGATTCTGCAATTCACACCAGGTATCGCATTTTG | 358 |
| 4V | TGCGTTCAAAAACTCGATGGTTCCCGGGATTCTGCAATTCACACCAGGTATCGCATTTTG | 360 |
| | ***** * | |
| 2V | CTACGTTCTTCATCGATGCCAAAACCGAATATCCGTTGCCGAAAGTCGTGTGGGTTAAG | 418 |
| 4V | CTACGTTCTTCATCGATGCCGAGAGCCGAGATATCCGTTGCCGAGAGTCGTGTGGGTTAAG | 420 |
| | ***** * * ** * | |
| 2V | AAATCATCGCTGCTGCGGGGAACCGAAGGCAGGCCGACCGCTCCGCCGAACAAGCAATA | 478 |
| 4V | ATATCATCGCTGCTGCGGGGAGCCGAAGGCAGGCCGACCGCTCCGCCGAGCAAGCAATA | 480 |
| | * ***** * | |
| 2V | TAAGTGTTTCCTTGACGCCTAAGGCGCCGTGGGTTCTGTTGCGGCCCTCCGCCGAAGCTC | 538 |
| 4V | TAAGTGTTTCCTTGACGCCTAAGGCGCCGTGGGTTCTGTTGCGGCCCTCCGCCGAAGCTC | 540 |
| | ***** | |
| 2V | GGGGCCCTTGGCCGAAACCGAAGCCCGGCGGCACGAGAGACTCGTTCGCGGTTCGGTTTTGT | 598 |
| 4V | GGGGCCCTTGGCCGAGCCGAAGCCCGGCGGCACGAGAGACTCGTTCGCGGTTCGGTTTTGT | 600 |
| | ***** | |
| 2V | TTAAGGTCACGACAATGATCCTTCC-GCAGGTTCACCTACGGAACCTTGTTACGATTT | 657 |
| 4V | TTAAGGTCACGACAATGATCCTTCCCGCATGT-CACCTACGGGA----- | 645 |
| | ***** ** ** * | |
| 2V | TTACTTCCCA 667 | |
| 4V | ----- | |

* estimated by Mega 4

DNA Finger prints of five diverse clones of Vetiver as amplified with 8nos. of UBC-ISSR Primers

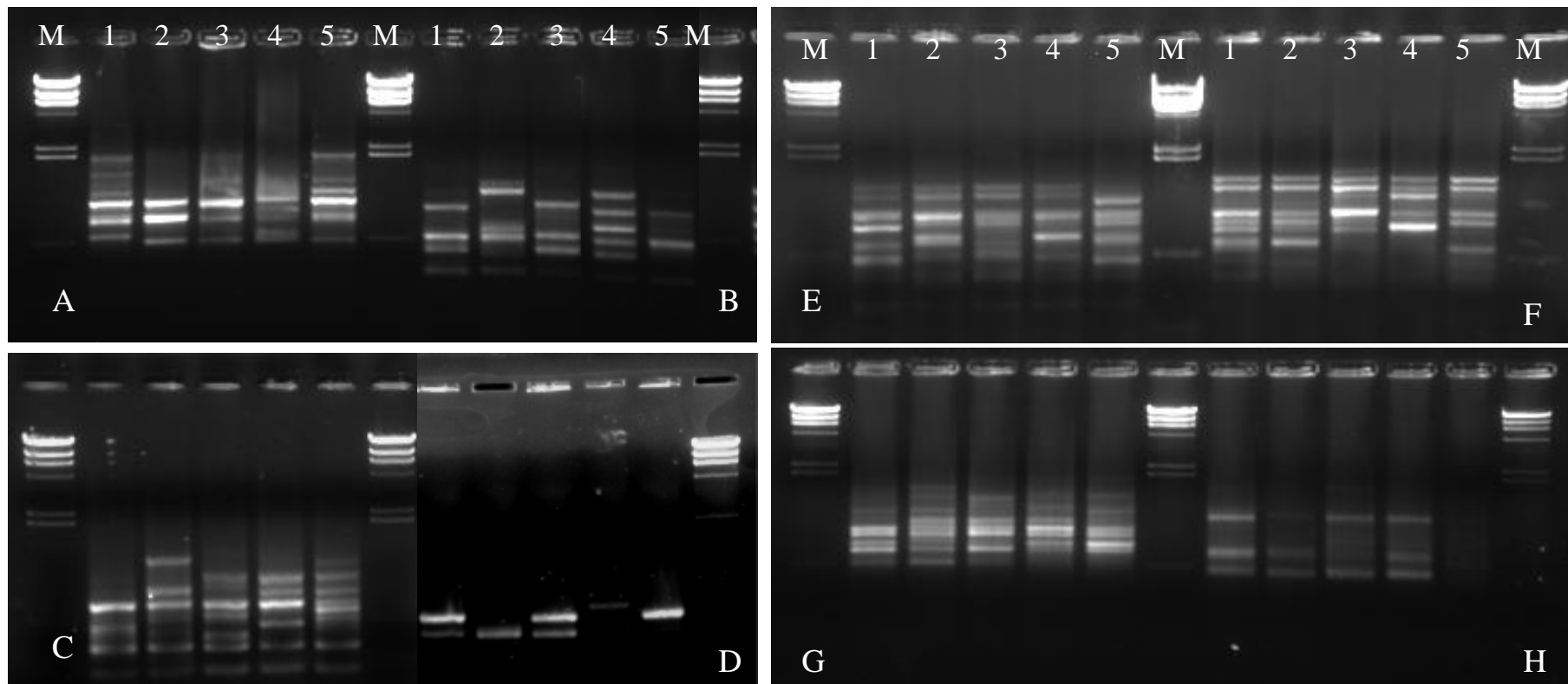
(1- Autotetraploid, 2. South Indian, 3. Dharani, 4. KS-1, 5. Thailand)



Lane M : λ DNA / Hind III digest

A : UBC807- AGAGAGAGAGAGAGAGT ; B : UBC810- GAGAGAGAGAGAGAGAT ; C : UBC811- GAGAGAGAGAGAGAGAC ; D : UBC812- GAGAGAGAGAGAGAGAA
 E : UBC814- CTCTCTCTCTCTCTCTA ; F : UBC818- CACACACACACACACAG ; G : UBC823- TCTCTCTCTCTCTCTCC ; H : UBC825- ACACACACACACACACT

DNA Finger prints of five diverse clones of Vetiver as amplified with 8nos. : 04 OPO + 04 OPJ of RAPD Primers
 (1- Autotetraploid, 2. South Indian, 3. Dharani, 4. KS-1, 5. Thailand)



Lane M : λ DNA / Hind III digest

A: OPJ 9 - TGAGCCTCAC ; B : OPJ10- AAGCCCGAGG; C: OPJ12 – GTCCCGTGGT; D: OPJ13 – CCACACTACC ;

E: OPO-4- AAGTCCGCTC; F: OPO-5 – CCCAGTCACT; G: OPO-6- CCACGGGAAG; H: OPO-7- CAGCACTGAC

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The Vetiver autoploid clone christened as “CIMAP-40” is characterized by:

- **Somatic chromosome number of $4x=40$ (compared to $2n=20$ found in progenitor / natural source)**
- **Presence of one site each of 45S and 5S ribosomal DNA represented four times in its somatic cell as delineated by FISH**
- **larger stomata, larger root vascular cylinder, genetically distinguished by unique ISSR and RAPD profiles that serve as DNA fingerprints**

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The autopolyploid clone :

- **Owing to its fast growing deep penetrating root system could potentially sequester 900 g of atmospheric carbon per year from one meter square surface area deep into sub-soil horizons likened to forest trees, with least risk of carbon being recycled into atmosphere.**
- **Seed infertile suitable for ecological plantations that does not pose any problem of becoming weedy**
- **Sports dense mesh forming root system that can withstand landslide disaster and facilitate soil conservation**
- **Strategic plantation of this autotetraploid clone in crop fields tree lines, river, road and rail-line embankments as hedgerows could potentially contribute to carbon sequestration vis-à-vis eco-technological management of land and soil, and as a resource for biomass and bioenergy with no threat of becoming weedy in unattended plantations**