

SAS MACRO for Generation of Partial Tetra-allele Cross Design using MOLS

Developed By

Mohd Harun¹, Cini Varghese¹, Seema Jaggi¹ and Eldho Varghese²

¹Division of Design of Experiments, CAR-Indian Agricultural Statistics Research Institute

² Fisheries Resources Assessment Division, ICAR-Central Marine Fisheries Research Institute

Email ID: harun.agribhu@gmail.com; cini.varghese@icar.gov.in; seema.jaggi@icar.gov.in and eldho.varghese@icar.gov.in

Tetra-allele cross often referred as four-way cross or double cross or four-line cross are those type of mating designs in which every cross is obtained by mating amongst four inbred lines. A tetra-allele cross can be obtained by crossing the resultant of two unrelated diallel crosses. A common triallel cross involving four inbred lines A, B, C and D can be symbolically represented as (A×B)×(C×D) or (A, B, C, D) or (A B C D) *etc.* Tetra-allele cross can be broadly categorized as Complete Tetra-allele Cross (CTaC) and Partial Tetra-allele Crosses (PTaC).

Rawlings and Cockerham (1962) firstly introduced and gave the method of analysis for tetra-allele cross hybrids using the analysis method of single cross hybrids under the assumption of no linkage.

The set of all possible four-way mating between several genotypes (individuals, clones, homozygous lines, *etc.*) leads to a CTaC. If there are N number of inbred lines involved in a CTaC, the the total number of crosses, $T = \frac{N(N-1)(N-2)(N-3)}{8}$. Here is an example of complete tetra-allele cross consisting of 15 crosses that can be made for 5 lines (1, 2, 3, 4 and 5).

(1×2)×(3×4)	(1×3)×(4×5)	(1×4)×(2×5)	(1×5)×(3×4)	(2×5)×(3×4)
(1×2)×(3×5)	(1×3)×(2×5)	(1×4)×(3×5)	(1×5)×(2×3)	(4×5)×(2×3)
(1×2)×(4×5)	(1×3)×(2×4)	(1×4)×(2×3)	(1×5)×(2×4)	(2×4)×(3×5)

When more number of lines are to be considered, the total number of crosses in CT_aC also increases. Thus, it is almost impossible for the investigator to carry out the experimentation with limited available resource material. This situation lies in taking a fraction of CT_aC with certain underlying properties, known as PT_aC. Here, a SAS macro has been developed to generate a series of universally optimal family of designs using MOLS. The method starts with selecting any of the $\frac{(N-1)}{2}$ MOLS of a given order N (*the number of lines*) and retaining the first four rows and making crosses with the lines

occurring in each column. The parameters of the developed class of design is $T = \frac{N(N-1)}{2}$, $b = \frac{(N-1)}{2}$, $r, k = N$ and $f = \frac{4}{(N-2)(N-3)}$.

Example: For $N = 7$, considering 3 MOLS of order 7 chosen at random out of the total 6 possible MOLS of order 7, and retaining only first 4 rows of each, based on the symbols 1, 2, 3, 4, 5, 6 and 7 as given below.

MOLS I						
1	2	3	4	5	6	7
2	3	4	5	6	7	1
3	4	5	6	7	1	2
4	5	6	7	1	2	3

MOLS II						
1	2	3	4	5	6	7
3	4	5	6	7	1	2
5	6	7	1	2	3	4
7	1	2	3	4	5	6

MOLS III						
1	2	3	4	5	6	7
4	5	6	7	1	2	3
7	1	2	3	4	5	6
3	4	5	6	7	1	2

Now, considering the seven symbols as lines, from each LS a tetra-allele crosses can be made by taking the four lines of each column. The crosses made from each LS will be constituting a block.

The layout of the design can be obtained as generated using the developed SAS macro by just entering the number of lines.

SAS OUTPUT

The SAS System

Partial Tetra-allele Cross Design using MOLS

PTaC_Design		
Block1	Block2	Block3
(1x 2)x(3x 4)	(1x 3)x(5x 7)	(1x 4)x(7x 3)
(2x 3)x(4x 5)	(3x 5)x(7x 2)	(4x 7)x(3x 6)
(3x 4)x(5x 6)	(5x 7)x(2x 4)	(7x 3)x(6x 2)
(4x 5)x(6x 7)	(7x 2)x(4x 6)	(3x 6)x(2x 5)
(5x 6)x(7x 1)	(5x 6)x(7x 1)	(5x 6)x(7x 1)
(6x 7)x(1x 2)	(6x 7)x(1x 2)	(6x 7)x(1x 2)
(7x 1)x(2x 3)	(7x 1)x(2x 3)	(7x 1)x(2x 3)

Parameters of the design are

N	T	b	k	f
7	21	3	7	0.2

References

Parsad, R., Gupta, V.K. and Gupta, S.C. (2005). Optimal designs for experiments on two-line and four-line crosses. *Utilitas Mathematica*, **68**, 11-32.

Rawlings, J.O. and Cockerham, C.C. (1962 b). Analysis of double cross hybrid populations, *Biometrika*, **18**, 229-244.

SAS MACRO

*/*Developed by- Mohd. Harun, Cini Varghese, Seema Jaggi and Eldho Varghese*/*

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VERSION 1.0: 10-01-2020/*

*/*Features: */*

*/*It provides generation of Partial Tetra Allele Cross design using MOLS */*

*/*******/*

ods html;

%let n=7; */*Enter the number of lines (n must be prime number)*/*

proc iml;

pp1=1;

do i=2 to &n-1;

pp=mod(&n,i);

if pp=0 then pp1=0;

end;

if pp1=0 then do;

print 'Entered number is not a prime number';

end;

if pp1^=0 then do;

Square=j(4,&n,0);

do i=1 to 4;

do j=1 to &n;

Square[i,j]=mod((i-1)+(j-1),&n)+1;

end;

end;

**print square;*

do k=1 to (&n-1)/2;

if k=1 then do;

NBD1=Square;

end;

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else do;
do i=1 to 4;
do j=1 to ncol(square);
NBD1[i,j]=mod(Square[i,j]+(j-1)+(i-1),&n);
if NBD1[i,j]=0 then NBD1[i,j]=&n;
end;
end;
end;
Square=t(NBD1);
*print Square;
ww1=char(Square[ ,1],4,0);
ww2=char(Square[ ,2],4,0);
ww3=char(Square[ ,3],4,0);
ww4=char(Square[ ,4],4,0);
*print ww1 ww2 ww3 ww4;
www1=j(nrow(ww1),ncol(ww1),'C');
www2=j(nrow(ww1),ncol(ww1),'');
www3=j(nrow(ww1),ncol(ww1),'x');
*print www1 www2 www3;

Block=www1+ww1+www3+ww2+www2+www3+www1+ww3+www3+ww4+www2;
PTaC_Design=PTaC_Design||Block;
end;
T=(&n*(&n-1))/2;
b=(&n-1)/2;
k=&n;
N=&n;
f=4/((&n-2)*(&n-3));
varNames = "Block1":"Block&n"; /*since n is the maximum which is greater than k*/

print "Partial Tetra-allele Cross Design using MOLS";
print PTaC_Design [colname= varNames];
print "Parameters of the design are" ;
print N T b k f;
end;
run;

ods html close;

quit;

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