

the clavine group of alkaloids both in sclerotial as well as the honeydew stages, whereas, the pathogen *C. purpurea* responsible for ergot of rye produces the ergotoxine-ergotamine group of alkaloids. Thus based on morphological and chemotaxonomic characters it is clear the pathogen that leads to ergot of pearl millet in India is *Claviceps fusiformis* Loveless.

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#### CHLORAMPHENICOL RESISTANCE IN GENUS *BACILLUS*

CHLORAMPHENICOL resistant bacteria such as *Escherichia coli*<sup>1, 2, 3</sup>; *Pseudomonas aeruginosa*<sup>1</sup>; *Pseudomonas fluorescens*<sup>4</sup>; *Proteus mirabilis*<sup>1</sup> and *Staphylococcus aureus*<sup>5, 6</sup> have been reported and the mechanism of the resistance has been studied. S. Osawa isolated a number of chloramphenicol resistant mutants from *Bacillus subtilis* ATCC 6633 which are resistant to 5 µg of chloramphenicol<sup>7</sup>. However, there has been no report on naturally occurring strain of *Bacillus* which is resistant to chloramphenicol. The author has isolated several chloramphenicol-resistant strains of *Bacillus* from soil. One of the isolates, showing similar bacteriological properties as *Bacillus megaterium*, was used throughout the experiment (Strain 7). It was gram positive spore forming bacilli, giving typical large, round, opaque whitish colony on nutrient agar, produces acid only from mannitol, sucrose, glucose, arabinose and xylose. Lactose was variable. Isolates were identified following the scheme of *Bergey's Manual of Determinative Bacteriology*, 7th Ed. and *A Guide Book to the Identification of Genera of Bacteria* (V.B.D. Skerman, 1967). *Bacillus megaterium* strain 7, could grow in the presence of 10 µg/ml and was trained to grow by subculture in increasing concentrations of chloramphenicol (50 µg/ml chloramphenicol). *Bacillus megaterium* KM and *Bacillus*

*cereus* T, used as standard, could not grow at the concentration of 10 µg/ml. In order to measure chloramphenicol activity, the cells of chloramphenicol-sensitive and resistant strains of *Bacillus megaterium* were incubated in the nutrient broth containing 250 and 500 µg/ml of chloramphenicol for 0, 8 and 20 h at 37°C with shaking. [Nutrient broth consisted of meat extract (Kyokuto Seiyaku Co., Tokyo) 10.0 g.; polypeptone (Daigo Eiyo Kahaku Co., Osaka) 10.0 g.; sodium chloride 5.0 g; deionized water 1000 ml pH 7.3]. The amount of chloramphenicol in the medium was bio-assayed using the cup-plate method. Only a weak inactivation was observed when the resistant strain was used. To increase the sensitivity of the test, the cells of either the resistant strain (*Bacillus megaterium* strain 7) or the sensitive strain (*Bacillus megaterium* KM obtained from the collection of this laboratory) was incubated with <sup>14</sup>C-chloramphenicol in nutrient broth and the degradation products of <sup>14</sup>C-chloramphenicol in the supernatant were analyzed by chromatography and autoradiography. Degradation products of <sup>14</sup>C-chloramphenicol were detected only when the resistant strain was used (uninduced condition). The amounts of degradation products were markedly increased when the cells of the resistant strain, which were pre-grown in the presence of 10 µg/ml of chloramphenicol, were incubated for 20 h with <sup>14</sup>C-chloramphenicol (induced condition). No degradation products, however, were detected when the cells of *Bacillus megaterium* KM were incubated with <sup>14</sup>C-chloramphenicol under similar uninduced or induced conditions. Degradation of <sup>14</sup>C-chloramphenicol was also demonstrated when the cell-free extract of *Bacillus megaterium* strain 7 was incubated with <sup>14</sup>C chloramphenicol, acetyl-CoA and Mg<sup>++</sup> ion, while no degradation was observed with the cell-free extract of *Bacillus megaterium* KM. Thus, chloramphenicol decomposing enzyme in *Bacillus megaterium* strain 7 may partly be responsible for the chloramphenicol resistance of this organism. Further work on the study of mechanism of the resistance is in progress.

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**FUNCTIONAL REGRESSIONS IN FISHERY RESEARCH**

In linear regression situations arising in fishery biology, Ricker<sup>1</sup> has recommended the use of a functional regression, when both the variates are subject to error of measurement or inherent variability or both. In such cases the regression line is obtained by finding the line which minimizes the sum of the products of the vertical and horizontal distances of each point from the line. Ricker refers to the estimate of the regression coefficient thus obtained as the 'GM regression'.

If, instead of sum of products, the sum of squares of both the horizontal and vertical distances of each point from the line is considered, another line with slope very close to the GM regression is obtained. Let the regression line of *y* on *x* be

$$y = a + bx. \tag{1}$$

If P be any point (*x*, *y*) such that PM and PN are the vertical and horizontal distances from the line (*x*, *a + bx*) and [(*y - a/b*), *y*] are the coordinates of M and N respectively. Obviously, the distances PM and PN are (*y - a - bx*) and [(*y - a/b*) - *x*], Minimizing *PM*<sup>2</sup> + *PN*<sup>2</sup> is same as minimizing *MN*<sup>2</sup>, *MN* being the hypotenuse of the right-angled triangle PMN. Minimization of *MN* allows the line to shift itself towards the point, which is ideally required.

Considering all such *n* points as P, the quantity

$$\sum_{i=1}^n \left\{ (y_i - a - bx_i)^2 + \left( \frac{y_i - a}{b} - x_i \right)^2 \right\} \tag{2}$$

is to be minimized with respect to *a* and *b*. Differentiating (2) with respect to *a* and equating to zero gives, after simplification,

$$\sum_{i=1}^n y_i = na + b \sum_{i=1}^n x_i \tag{3}$$

Similarly differentiation with respect to *b* leads to the simplified form

$$b(b^2 - 1) \sum_{i=1}^n y_i x_i - ab(b^2 - 1) \sum_{i=1}^n x_i - b^4 \sum_{i=1}^n x_i^2 + \sum_{i=1}^n (y_i - a)^2 = 0. \tag{4}$$

If from (3) substitutions are made for *a*, (4) simplifies to

$$b^4 \left[ \sum_{i=1}^n x_i^2 - \frac{\left( \sum_{i=1}^n x_i \right)^2}{n} \right] - b^3 \left[ \sum_{i=1}^n x_i y_i - \frac{\sum_{i=1}^n x_i \sum_{i=1}^n y_i}{n} \right] + b \left[ \sum_{i=1}^n x_i y_i - \frac{\sum_{i=1}^n x_i \sum_{i=1}^n y_i}{n} \right] - \left[ \sum_{i=1}^n y_i^2 - \frac{\left( \sum_{i=1}^n y_i \right)^2}{n} \right] = 0,$$

which may be replaced by

$$S_x^2 b^4 - S_{xy} b^3 + S_{yy} b - S_y^2 = 0, \tag{5}$$

where *S<sub>x</sub><sup>2</sup>*, *S<sub>y</sub><sup>2</sup>*, *S<sub>xy</sub>* are respectively the variances of *x* and *y* and the covariance between them.

Employing the method of iteration, starting with the estimate of GM regression as a trial value will lead to a solution of (5) which being the slope of the line under consideration.

In the case of GM regression since the estimate involves only the standard deviations of the variables, the pairing up of *x* and *y* has no effect. But, since the values come from a bivariate distribution, the association of the variables has to be given due consideration when finding the functional relationship. Here, this is guaranteed by the involvement of covariance in the estimating equation (5).

The regression of *x* on *y* is also the same, but the slope will be 1/*b* since the axes are reversed. This is obtained by interchanging the expressions for variances of *x* and *y* in the estimating equation (5) and solving.

The variance of this regression is same as that of the corresponding GM regression.

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