thus behaves as reciprocal translocation between a small supernumerary and a metacentric.

The view that telocentrics are unstable in nature[11,12] does not seem to apply necessarily to all telocentrics. Stable telocentrics by centric fission were reported by several workers[13-15].

As far as our case of *A. sapidus* ssp. *sapidus*, $2n = 41$, is concerned, the animal had to be sacrificed to make the bone marrow and testes analyses. Consequently, we were not able to study more closely the behaviour and heredity of these particular telocentrics originated by centric fission.

1 P. Renaud, Rev. Suisse Zool. *45*, 349 (1938).
2 R. Matthey, Rev. Suisse Zool. *62*, 163 (1955).
3 K. Fredga, Chromosoma (Berlin) *25*, 75 (1968).
4 W. Schmidt and H. Leppert, Experientia *24*, 277 (1968).
5 T.C. Hsu and J.L. Patton, in: Comparative Mammalian Cytogenetics. Springer, Berlin 1969.
6 E.P. Evans, G. Breckon and C.E. Ford, Cytogenetics *3*, 289 (1964).
7 J.H. Tjio and A. Levan, Hereditas *42*, 1 (1956).
8 M. Seabright, Chromosoma (Berlin) *36*, 204 (1972).
9 W.R. B. Robertson, J. Morph. *27*, 179 (1916).
10 G.E. Marks, Am. Naturalist *91*, 223 (1957).
11 M.J.D. White, Animal Cytology and Evolution, 3rd ed. Cambr. Univ. Press, 1973.
12 C.D. Darlington, J. Genet. *37*, 341 (1939).
13 H. Kato, Chromosoma *40*, 183 (1973).
14 P.S.R.L. Narasinga Rao, M.V. Subba and I. Narayana Rao, Experientia *33*, 308 (1977).
15 G.S. Kush and C.M. Rick, Cytologia *33*, 137 (1968).

Chromosomal translocations in 2 Italian populations of *Reticulitermes lucifugus* (Rossi) (Insecta, Isoptera: Rhinotermitidae)

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Summary. The chromosomes of 2 Italian populations of *Reticulitermes lucifugus* (Rossi) were studied in both spermatogonial and oogonial divisions. The diploid chromosome complement is $2 = 42$. All the first meiotic metaphases in Sardinian males show a complex translocation arranged in chains of 4 bivalents. The Apulian males show either 21 bivalents or 19 bivalents and a chain of 2.

Reticulitermes lucifugus (Rossi) is ubiquitous over the Mediterranean area, and it is found in almost all regions of Italy[2]. Differences were found among samples collected in Italy, France and Portugal, both in chaetotaxis[3] and in quantitative traits[4]. *R. lucifugus* can be subdivided in geographically isolated subspecies[4]. In the Italian populations primary royal pairs were never found. The colonies are formed by budding or fragmentation of the mother colonies[5], and inbred local populations are very likely. Breeding experiments are difficult with these insects; therefore, we hoped to gain significant information through a cytogenetic approach. In this paper the first results of a cytogenetic investigation on *R. lucifugus* Italian populations are reported.

Material and methods. The Sardinian insects were collected in 1968 and those from Apulia, southern Italy, in 1974 and maintained in the laboratory in wood sticks steeped in moist ground. Supplementary royal individuals were collected as soon as they appeared. Cytological analyses were made on 4 supplementary kings, 2 of which were of 2nd form and 2 of 3rd, and 4 supplementary reproductive queens from Sardinian colonies, and on 6 supplementary kings of 2nd form and 2 supplementary reproductive queens from Apulian colonies. The gonads were dissected

Mitotic and meiotic chromosomes of *R. lucifugus*. *a* Spermatogonial metaphase plate of a Sardinian male. *b* First meiotic metaphase with a linearly orientated chain of 4 bivalents of a Sardinian male. *c* First meiotic metaphase with 21 bivalents in an Apulian male. *d* First meiotic metaphase with a linearly oriented chain of 2 bivalents in an Apulian male.

and kept in colchicine-hypotonic solution for 20 min, fixed in acetic-ethanol, and permanent preparations were made according to the Imai squash method[6]. The staining has been performed by Feulgen reaction.

Results. The spermatogonial and oogonial metaphases of all reproductives from Sardinian and Apulian populations show a diploid complement of 42 chromosomes formed of 10 pairs of biarmed and 11 pairs of acrocentric chromosomes. No unequal pair to be regarded as heteromorphic chromosomes was found (figure, a). In about 2000 late diplotene and first meiotic metaphases of 6 males of Sardinian strain, the pairing configurations of chromosomes of all the meiotic figures show 17 bivalents and 4 bivalents linked in chain (figure, b). The chain should be a consequence of heterozygous reciprocal translocations between 4 pairs of chromosomes, 3 medium sized meta- or submetacentrics and 1, at the end of the chain, probably acro- or telocentric. The simplest interpretation of the observed meiotic association of 4 is obtained when the following sequence is assumed: $4 - 2^4 - 2 - 1^2 - 1\text{-}3^1 - 3 - 4^3$. In 6 out of 2000 first meiotic metaphases a ring was observed; the frequency is of the same order as that of a crossing-over in a short chromosomal segment. The ring is thus most likely the consequence of a chiasma at the short arms of the chromosome 4. About 1500 first meiotic metaphases of 6 males of Apulian strain were analyzed: 3 males show a set of 21 bivalents (figure, c); the other 3 show 19 bivalents plus an association of 2 bivalents aligned in chains (figure, d). The suggested sequence would be: $2^1 - 1 - 1^2 - 2$.

Discussion. The diploid complement of Italian populations of *R. lucifugus* is 2n = 42 for both males and females. The same complement was found in French populations, also for *R. santonensis* (Feytaud)[7]. No heteromorphic pair was found in either sex; however, mitotic chromosomes are tiny and small differences might have escaped observation. The analysis of male meiotic complements shows interchange complexes, different between and within populations. The Sardinian population displays a translocation heterozygosity involving 4 pairs of chromosomes. Among the analyzed Apulian males, 3 showed 21 bivalents and no translocation, 3 showed 19 bivalents plus an interchange complex of 2 pairs of chromosomes.

Translocation heterozygosities are common in plants[8] but rare in animals[9]. In animals they are believed to be associated with inbreeding as in roaches[10], or parthenogenesis as in some aphids species[11], or a balanced polymorphism as in certain marine snails[12]. Recently permanent segmental interchange complexes were discovered in males of *Incisitermes schwarzi* (Banks), *Kalotermes approximatus* Snyder and *Neotermes castaneus* (Burmeister), Kalotermitidae of Florida[13]; the authors suggest that the interchange complexes are related to sex chromosomes (neo Y). In *R. lucifugus* sex chromosomes in males were not discovered so far and the reciprocal translocations are probably autosomic. The differences of interchange complexes among Italian populations suggest a possible implication of this chromosomic mechanism in the geographic evolution also in relation to the budding mechanism of founding colonies[5], which increases the inbreeding. In this condition, reciprocal translocations may assure a balanced system with greater adaptive value.

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2 C. Jucci, Boll. Ist. Patol. Libro *15*, 70 (1956).
3 R. W. Lamb, personal communication.
4 J. L. A. Clement, Proc. VIII Int. Congr. Union Study Social Insects, Wageningen 1977.
5 P. P. Grassé, in: Traité de Zoologie, vol. 9, p. 408. Masson, Paris 1949.
6 H. T. Imai and M. Kubota, Chromosoma, Berl. *37*, 193 (1972).
7 J. L. A. Clement, C. r. Acad. Sci., Paris *284*, 2355 (1977).
8 C. D. Darlington and L. F. La Cour, Heredity *4*, 217 (1950).
9 M. J. D. White, Animal cytology and evolution. Cambridge Univ. Press, Cambridge 1973.
10 K. R. Lewis and B. John, Heredity *11*, 11 (1957).
11 R. L. Blackman and H. Takada, J. Ent. (A) *50*, 147 (1975).
12 H. Staiger, Chromosoma *7*, 181 (1955).
13 R. M. Syren and P. Luykx, Nature *266*, 167 (1977).

Chlorpyrifos (Dursban®) resistance in *Culex pipiens pipiens* L. from Southern France: Inheritance and linkage

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Summary. In *Culex pipiens* mosquitos from Southern France, resistance to the organophosphorus insecticide chlorpyrifos is due to the dominant allele (Chl^R) of an autosomal gene. The *Chl* gene is localized between the *a-Gpd* and *Est-2* loci at 26.8 and 5.8 units of crossing-over respectively.

Pasteur and Sinègre[1] have described a very significant correlation between the frequency of an aliesterase isozyme, $Est\text{-}2^{0.64}$, and the degree of chlorpyrifos resistance in the natural populations of *Culex pipiens pipiens* from Southern France[2,3]. The present investigation was undertaken in order to determine whether $Est\text{-}2^{0.64}$ allele is itself responsible for the resistance, or whether these 2 factors are associated because of some linkage relationships.

Material and methods. 3 autogenous strains of *Culex pipiens* were used to perform the various crosses: SG, S7 and S5. The genetics of chlorpyrifos resistance was accomplished by mass crossing some 50 males with 50 virgin females of the desired genotypes, while the linkage relationships between resistance and the *Est-2* and *a-Gpd* loci were analyzed on the offspring of individual crosses. Chlorpyrifos resistance was tested on 3rd instar larvae[1] and *Est-2* and *a-Gpd* genotypes were analyzed by starch electrophoresis[4,5].

Results. 1. Heredity of chlorpyrifos resistance. The larvae of the SG and S7 strains (or their hybrids) are all killed by chlorpyrifos concentrations equal or higher than 0.0015 ppm, while those of the S5 strain are not affected by chlorpyrifos concentrations below 0.0030 ppm (table 1 and figure, A). The log-probit regression lines do not overlap and they are both very steep: the slope has a value of 11.9 for the susceptible S7 or SG strains and of 12.1 for the resistant S5 strain. The resistance ratio (LD_{50} resistant/LD_{50} susceptible) can be estimated to 0.0080/0.0008, i.e. 10fold. The regression lines as well as the LD_{50} of both susceptible (S7 and SG) and resistant (S5) strains have remained unchanged for more than 2 years (30 generations), suggest-