except in the cell plate. The primary septum contains β-glucan but little or no α-galactomannan. This feature appears to be directly implicated in the subsequent fission process as suggested above. The small amount of cell surface β-glucan that is still detected could be the remains of incompletely digested primary septa (fig. D).

In the budding yeast *S. cerevisiae*, it has been hypothesized that α-mannan is elaborated intracellularly and β-glucan only on the plasmalemma[2]. Our evidence indicates that in *S. pombe* both α-galactomannan and β-glucan or immunoreactive precursors are synthesized intracellularly.

Using a similar experimental approach with the budding yeasts *S. cerevisiae* and *Saccharomyces rouxii*, α-mannan and β-glucan were found to intersperse to a considerable degree in the cell wall, the septum and the bud scar. In analogy with *S. pombe*, β-glucan was overlaid by α-mannan over the whole cell surface including the bud scars where most of the chitin was present (unpublished observations).

By specifically locating β-glucan and other polysaccharides[20,21], our experiments provide a basis for a better understanding of the architecture of yeast cell walls. Although different layers have been observed in yeast cell walls using fixatives and nonspecific reagents[22], our results rather indicate areas enriched with different polysaccharides leading to a highly cohesive structure for the whole depth of the wall as suggested by Cabib and Roberts[2].

Finally, this is another example of the multiple use of the protein A-gold technique which allows the intracellular[23] as well as the cell surface localization[24] of antigens by TEM and SEM, respectively.

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A new chromosome race of *Sorex araneus* L. from Northern Poland

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Summary. G-band patterns were studied in the chromosomes of two Polish populations of the common shrew. Two chromosome races were established in Poland, differing by various combinations of chromosome arms.

Key words. Shrew; *Sorex araneus;* chromosome race.

The two chromosome races of *Sorex araneus* L. originally described by Meylan[2] have proved now to be separate sibling species. The Western European monomorphic race of the shrew was identified as *Sorex coronatus* Millet, 1828[3]. The whole range of *Sorex araneus* L. (Central and Eastern Europe together with the British Isles and Scandinavia, and Siberia up to the River Yenisei and Lake Baikal) is inhabited by the shrew populations exhibiting a polymorphic system of Robertsonian translocations. Six (pairs 3–8) of the nine pairs of autosomes in *S. araneus* are subject to polymorphism. In different parts of the range these pairs are composed of different arms. It has been recommended[4] that the term 'chromosome races' should be applied to shrews with varying combinations of arms in pairs 3–8. In this respect three chromosome races of *S. araneus* have been distinguished in Scandinavia[4,5], three races in England[6], two further chromosome races in Continental Europe; one in the Ulm region (Baden-Württemberg)[7] and a second in the Białowieża Primeval Forest (Northeastern Poland)[4,8]. This same chromosome race was also found in the River Biebrza valley about 150 km to the northwest of Białowieża[9]. Two chromosome races of *S. araneus*[10,11] were also distinguished in Siberia, and one of them, occurring in lowland areas (Novosibirsk region), has a combination of arms in four pairs of autosomes identical with the 'Białowieża' race [12].

Table 1. Material used for chromosome studies

Locality	2N	2Na	Sex	Designation of morphs	No. of animals studied
Wytyczno	23	20	♂♂	A_8–	2
near Włodawa	23	21	♀	A_8H_5–	1
	24	21	♂	A_8H_5–	1
Drużno Lake	27	25	♀♀	$A_8A_7A_6H_5$–	3
near Elbląg	28	25	♂♂	$A_8A_7A_6H_5$–	4
	28	26	♀	$A_8A_7A_6A_5$–	1

Table 2. Arm-combinations of polymorphic pairs of chromosomes in *Sorex araneus* from different geographical regions

Populations	Arm combinations of two-armed chromosomes (pairs 3–8)										Ref.
Öland, S. Sweden	l j	i h	m g								4
Ulm, W. Germany	l j	i h	m g								7
Skåne, S. Sweden	l j	i h	m g	o k	q n	r p					4
Jämtland, C. Sweden	l j	i h	m g				r n	p k			4
Jämtland, C. Sweden*	l j	i h	m g		q k		r n				4
Lapland, N. Sweden	l j		m g**		q k		n h	p i	r o		4
Kuhmo, NE. Finland	l j		m g		q k		n h	p i	r o		5
Drużno, N. Poland	l j	i h		o k							–
Białowieża, NE. Poland	l j						n h	k i	r g	p m	4, 8
Biebrza val., NE. Poland	l j						n h	k i	r g	p m	9
Wytyczno, E. Poland	l j						n h	k i	r g	p m	–
Oxford, S. England	l j	i h	m g		q k	r p			n o		6
Hermitage, S. England	l j	i h	m g	o k							6
Aberdeen, Scotland	l j	i h	m g	o k	r q				p n		6
Novosibirsk, W. Siberia	l j				r q		n h	k i	o g	p m	12
Chaldejevo, W. Siberia	l j	i h			r q		n m	k g	p o		12
Tanchoj, W. Siberia	l j	i h									12

* Only one specimen (exceptional 'hybrid'); ** Usually not fused.

The present paper contains results of studies on two further Polish populations of *S. araneus*. Four shrews were caught at Wytyczno near Włodawa, East Poland, N 51°50', E 23°20'[13], and a further eight shrews near Lake Drużno near Elbląg, North Poland, N 54°10', E 19°50'[14] (fig. 1). Both these populations were polymorphic in respect of one pair of autosomes (figs 2–5). The composition of two-armed autosomes in shrews from Wytyczno is as follows: 1*c*/*b*, 2*f*/*a*, 3*k*/*i*, 4*l*/*j*, 5*r*/*g* (polymorphic pair), 6*n*/*h*, 7*p*/*m*, 8*o*, *q* (one-armed chromosomes) and 9*u*/*t* (fig. 3). The composition of the arms of autosomes 3–7 is identical with that in the Białowieża population, and these shrews thus belong to the 'Białowieża' race. Among the four animals examined two (♂♂) were homozygotes (2N = 23) possessing only four one-armed autosomes in 'pair' No. 8 (fig. 2). In the other two shrews (♀ and

Figure 1. Map of Poland showing the localities of present chromosome studies (black circles) and earlier studies (white circles).

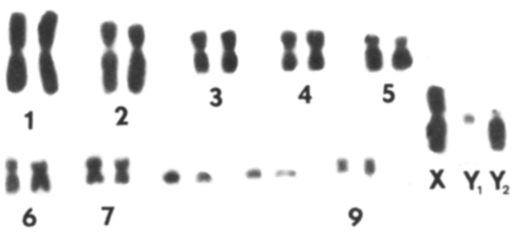

Figure 2. Karyotype of a homozygotic male (2N = 23) from the Wytyczno population.

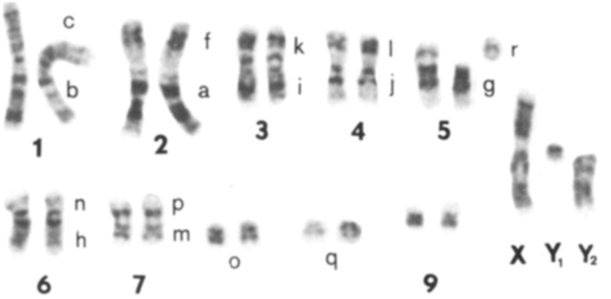

Figure 3. G-banded chromosomes of a heterozygotic male (2N = 24) from the Wytyczno population. Designation of chromosome arms by small letters in accordance with Fredga and Nawrin[4].

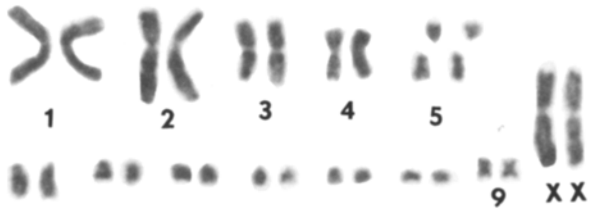

Figure 4. Karyotype of a homozygotic female (2N = 28) from the Lake Drużno population.

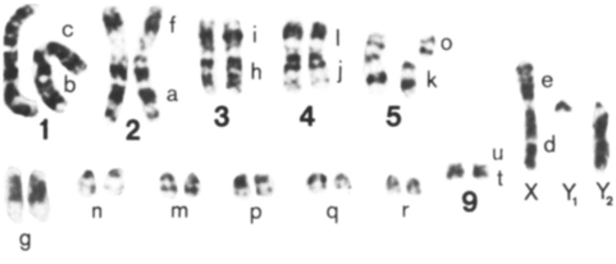

Figure 5. G-banded chromosomes of a heterozygotic male (2N = 28) from the Lake Drużno population.

♂) in addition to these four one-armed autosomes, two one-armed autosomes were found in pair No. 5 (2N = 23 and 24) (table 1, fig. 3).

Shrews from the Lake Drużno area have completely different karyotypes. The number of chromosomes in the eight individuals examined varies between 27 and 28 (table 1, figs 4 and 5). In addition to pairs Nos 1, 2 and 9 (always two-armed) two-armed autosomes occur only in pairs 3–5 and consist of the following elements: 3*i*/*h*, 4*l*/*j*, 5*o*/*k*, while elements *g*, *m*, *n*, *p*, *q* and *r* remain one-armed (fig. 5). Pair No. 5 consists of either four one-armed (fig. 4) or one two-armed and two one-armed chromosomes (fig. 5).

The two-armed chromosomes of pairs 1, 2 and 9 and X chromosomes are composed in all the *S. araneus* populations so far examined of the same one-armed elements. The metacentric pair No. 3, on the other hand, composed of arms *i* and *h*, is typical of the Northwestern European populations: chromosomes *i*/*h* have been identified in all three British races[6], three Scandinavian[4] and in the 'Ulm' race[7], metacentrics *i*/*h* also occur in the 'Altaj' race (Chaldejevo)[12]. In the 'Białowieża' race, however, element *i* is connected with element *k*, and element *h* with element *n*. The heterozygotic pair No. 5 in populations from the Lake Drużno area is formed of *o*/*k* elements. This combination occurs in two British race ('Hermitage' and 'Aberdeen'), and in the 'Skåne' race, whereas in the 'Białowieża' race element *o* remains one-armed ('pair' No. 8) (table 2).

The 'Drużno' race is most similar to the following races: South Sweden ('Skåne) and two British races ('Hermitage' and 'Aberdeen'); two-armed *i*/*h* and *o*/*k* chromosomes occur in all these races. It differs from these races, however, by the absence of two-armed chromosomes *m*/*g* (table 2). The fusion of elements *m* and *g* is typical of all the West European, British and Scandinavian populations so far examined. In shrews from the most northern parts of Sweden (Lapland) elements *m* and *g* are usually not fused, while a Robertsonian polymorphism is present in shrews of the same race in NE Finland[4,5].

Siberian shrews from the Novosibirsk district are most similar to the 'Białowieża' race. The similarity applies to four pairs of autosomes with combinations of arms *l*/*j*, *k*/*i*, *p*/*m* and *n*/*h*; while the differences are the fusion of elements *r*/*g* and elements *o* and *q* remaining one-armed in the 'Białowieża' race, and fusion of *r*/*q* in the 'Novosibirsk' race, with elements *o* and *g* remaining one-armed (table 2).

The boundary line between shrews of the 'Drużno' and 'Białowieża' races is at present unknown. It must be assumed that these two chromosome races originate from different refuges from the Ice Age. Most probably shrews of the 'Drużno' race had a common origin with West European shrews, as is indicated by the similarity to the 'Ulm', British and Scandinavian races (with the exception of these shrews from Lapland). On the other hand the 'Białowieża' race probably had a common ancestry with some Siberian shrew populations ('Novosibirsk' race).

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Enzyme polymorphism in the Sicilian honeybee[1]

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Summary. In Sicily we can identify two genetically differentiated groups of local honeybee populations, on the basis of the only two polymorphic loci, *Mdh-1* and *Est;* the western one, whose genetic characteristics are probably those of the native honeybee (*Apis mellifera sicula*) and the eastern one affected by recent large-scale importation of Italian bees from northern Italy.

Key words. Honey bee, local population; *Apis mellifera ligustica;* enzyme polymorphism; genetic variability; genetic marker; *Est*-S allele.

Since the early 19th century, honeybees whose morphological and behavioral characteristics were distinct from those of the Italian bee (*Apis mellifera ligustica* Spinola, 1806), were known to occur in Sicily[2]. The first systematic investigations confirmed that they were a peculiar taxon[3] which was later called *A. m. sicula* Montagano, 1911[4]. The workers of the Sicilian bee have a dark abdomen[3–5], and both tongue length and cubital index are different from those of *A. m. ligustica* and *A. m. mellifera* Linnaeus, 1758[6]. Although Sicilian beekeepers have occasionally imported the more productive Italian bee ever since the last century[7], stocks of *A. m. ligustica* from northern Italy have been introduced on a large scale only during the last 10 years and only in the eastern part of the island; from there they are now spreading into other parts, thus hybridizing with the local bee.

This work aims to investigate the genetic variability of the Sicilian honeybee and its relationships with neighbouring populations, by using two gene-enzyme polymorphic systems, *Mdh-1* and *Est*. Also the eventual effects on its gene pool due to the *A. m. ligustica* introduction will be taken into account.

During 1983 and 1984, worker bees were randomly sampled in