

BIODIVERSITY AND GENETICS

GENETIC DIVERSITY AND BIODIVERSITY CONSERVATION

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Biological diversity: genetic and environmental components

Biological diversity has two strictly related components, genetic and environmental, and this has made experimental studies particularly difficult. Currently research on this subject has proliferated because of its theoretic and practical implications. For example, the gene-environment interactions in man are studied: 1) in the development of cognitive, intellectual and “creative” capacities, and even in relation to sex; 2) in the predisposition to various contagious diseases, metabolic disorders, vascular and tumoural pathologies; 3) in relation to behavioural disturbances (schizophrenia, psychoses, manias, aggressivity, asociality, tendency to develop drug addiction), etc.

In some species, it is possible to compare strains with known genetic differences for a significant number of genes (very few if considered in percentages). In the past, the experimental approach which provided the best results was based on the elimination of the variability of one of the two components, either genetic or environmental. As it is much easier to eliminate the variability of the first component with respect to the second, many studies have been carried out with this last-mentioned technique. Genetically homogeneous organisms (pure lines, clones) can be obtained with different methods depending on the reproductive modality and regeneration capacity of the species to which they belong. In those of obligatory sexual reproduction, pure lines are produced via successive crossbreeding with close kindred (parent-offspring or brother-sister, inbreeding); in hermaphrodite species, self-fertilisation of successive generations is used. This is the most extreme form of inbreeding in organisms that can reproduce via vegetative reproduction; the descendents of a single individual are genetically homogeneous and constitute clones. In plants, for example, it is possible to obtain clones starting from somatically differentiated cells of a single individual, that differentiate and return totipotent, that is, capable of forming new individuals. In human beings, totipotency of staminal cells (in particular in embryonal ones, in which blastomeres can give origin to genetically identical individuals) would make reproductive cloning technically possible, which however is not acceptable for ethical rea-

sons. These studies have demonstrated that the variability of environmental origin (clonal variability) is not transmitted to the next generation (the non inheritance of acquired characteristics). Within a clone, natural selection is completely ineffective. This explains why the capacity of adaptation of populations with low genetic variability is minimal; genetic erosion in a population often preludes its extinction.

To describe the role of genes and the environment in the biological variability it is necessary to introduce several terms. The hereditary constitution (or hereditary patrimony) of an individual is the so-called *genotype*; it is the set of genes that a given individual receives from his parents and remains substantially unaltered for life. The sum of morphological, physiological, and behavioural characteristics of an individual is called *phenotype*; it is the result of the interaction between its genotype and the environment in which it develops and lives; the phenotype, unlike genotype, is continually modified during life. The sum of phenotypes which a given genotype can give origin to in various environmental contexts is called the *norm of reaction*.

Classic studies on the norms of reaction of various genotypes of a plant, the composite *Achillea lanulosa*, were conducted by CLAUSEN and his collaborators (1948) in California. Various individuals, genetically identical in that they originated via vegetative reproduction of a single plant, were cultivated at various altitudes, from sea level to more than 3,000 m. The individual progenitors of each clone were gathered at sites at different altitudes and with different microclimates. The comparison between the various plants showed that, though sharing the same genotype, they differed in appearance, growth rate, fertility, etc. owing to the different environmental conditions (Figure 2.25). On the other hand, even genetically different individuals, though cultivated in the same environmental conditions, gave rise to different genotypes. It is important to note that there is no “best” genotype in all environmental conditions: genotypes that give lush plants at sea level do not develop at 3,000 metres; vice-versa genotypes that grow well at 3,000 metres either do not develop or develop very little at sea level. The wider the norm of reaction of the genes that control a character, the broader its phenotype variation will be. Conversely, if the norm of reaction of the genes is narrow, the character will present a single phenotype, independent of the environmental conditions in which the individual grows and lives. Therefore, the gene does not necessarily determine a given character, or in any case, it

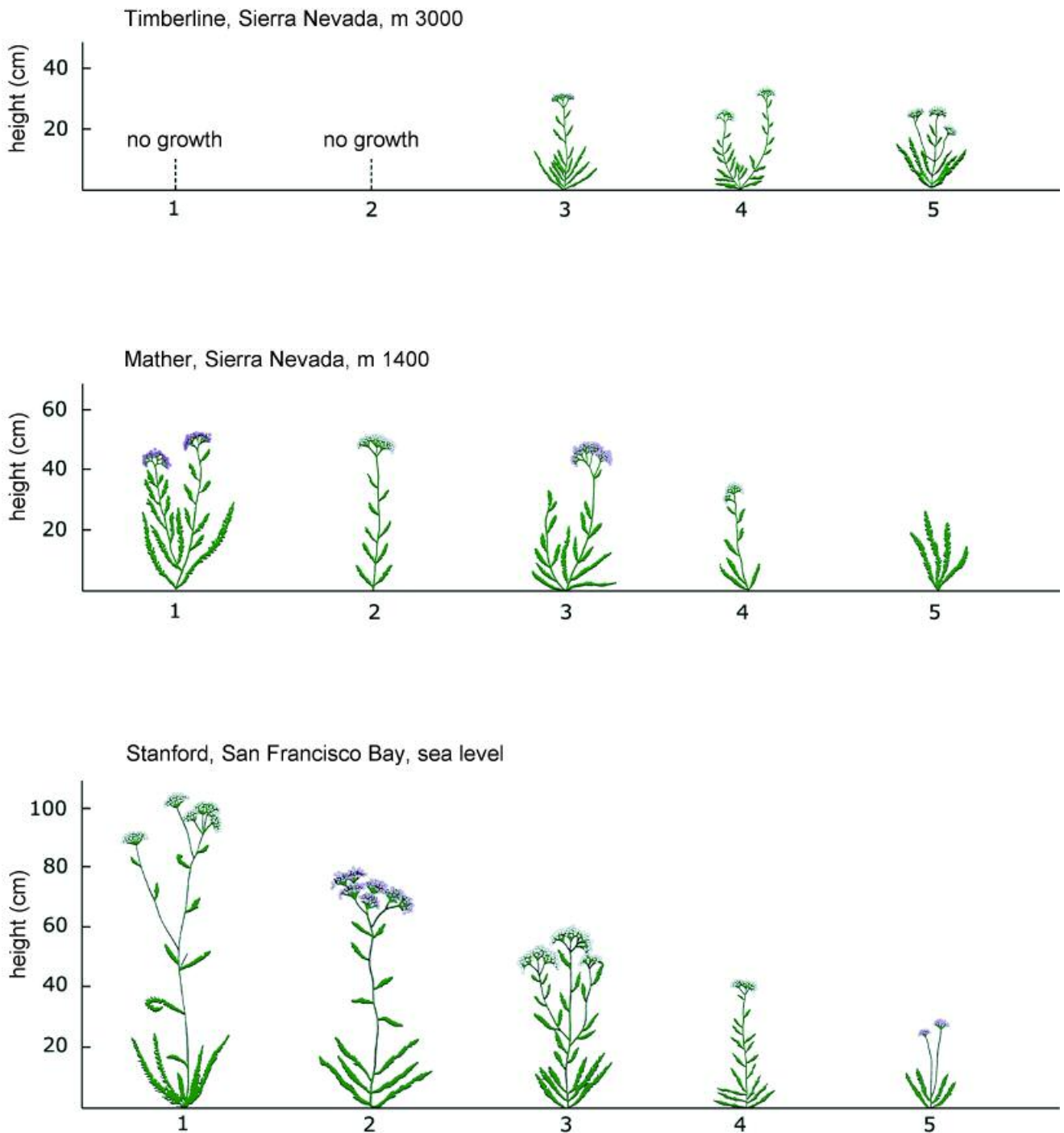


Fig. 2.25 - Phenotype variation in clones (numbered 1 to 5) of the composite *Achillea lanulosa*. Each clone was obtained through vegetative reproduction from a single plant: the progenital plants of the clones were collected in the following sites in California: San Gregorio, 300 m (clone 1), Knight's Ferry, 300 m (clone 2), Aspen Valley, 2,000 m (clone 3), Tenaya Lake, 2,400 m (clone 4) and Big Horn Lake, 3,600 m (clone 5). Individuals of the same clone were grown in botanic gardens situated at different altitudes: Stanford, San Francisco Bay (sea level); Mather, Sierra Nevada (1,400 m); Timberline, Sierra Nevada (3,000 m).

As one can observe: 1) the same genotype, placed in different environmental conditions gives rise to different phenotypes (at higher altitudes: Timberline, 3,000 m, did not develop; 2) different genotypes, developed under different environmental conditions, give rise to different phenotypes. In fact, a *norm of reaction* describes the pattern of phenotypic expression of a single genotype across a range of environments. (CLAUSEN *et al.* 1948, modified).

does not determine its maximum expression. It establishes a norm of reaction to external factors, in which the expression of the character controlled by that gene is the result of an interaction of the genetic factor with the environmental factors that exist during the development of the individual. The cowslip *Primula sinensis rubra*, cultivated at ordinary temperature, develops red flowers, instead if it is maintained in a greenhouse above 30°C, it produces white flowers. Instead, a similar cowslip *P. sinensis alba*, produces white flowers at any temperature. It is evident that the colour of the flowers in the two varieties is controlled by different genes, which have different norms of reaction. Similarly, the albinism of rabbits of the Himalayan breed is influenced by temperature. The fur that covers regions of its body that are more exposed to the cold (tips of the paws, ears and snout) are brown in colour instead of white. On the basis of this principle, it is possible to explain how a negative genetic constitution can be corrected with particular therapy (for example, with hormones and vitamins, or with other medication). Inversely, a normal constitution can be profoundly modified and made abnormal through the action of certain external factors. For example, giving thalidomide to a pregnant individual provokes a serious dysfunction in fetal development, which leads to the formation of a phocomelic individual; rubella caught by the mother during gestation can induce serious illnesses in the fetus, etc. In man, the possibility of modifying the expression of genes allows many therapeutic interventions to the “correct” pathological or mortal hereditary conditions. Hereditary thus loses the character of an ineluctable destiny. In any case, for the time being it is not always possible to correct the consequences of genetic conditions, such as chromosomal anomalies, that provoke mongolism, linked to mutations or particular meiotic events such as the non-disjunction.

Other well known cases of interactions between genotype and the environment are those of “seasonal forms” and summations, phenotype variations of genetically similar individuals, also known as *ecotypes*. For example, in the spring generation of the butterfly *Araschnia levana* the colour of the wings is light (form *levana*), while in the summer generation the wings are much darker (form *prorsa*). Moreover, it is possible to identify the different phenotypes, often between the *levana* and the *prorsa*, by subjecting them to a thermal shock at the beginning of the pupal stage (Figure 2.26). Similar results have been obtained in other butterfly species, such as *Precis octavia* (Figure 2.27) and *Inachis io* (Figure 2.28).

The origins of genetic diversity

Every organism develops both the structures and functions of the species it belongs to, as well as individual characteristics; this is due to the genetic information contained in the cell that gives origin to the organism and in the cells it is made up of. Genetic information has its physical basis in the molecules of deoxyribonucleic acid (DNA), in the most ancient forms of life, in some present-day viruses, or in those of ribonucleic acid (RNA). RNA is made up of four different bases: adenine, guanine, cytosine, and uracil. The first three are the same as those found in DNA nucleotides, but uracil replaces thymine as the base complementary to adenine, and is the same in several organisms.

Genetic diversity is present at all levels in the organisation of hereditary information: from codons, DNA sequences of three nucleotides that are able to codify aminoacids (the “bricks” of proteins) to genes, the physical and functional units of hereditary information that are able to direct the protein synthesis (housekeeping genes) or control the gene of other genes (regulatory genes), to chromosomes, the structural units of genetic information (genome), constituted by linear sequences of genes and other DNA sequences, in the genome.

At the base of genetic diversity there are *mutations*, variations at the gene, chromosome or genome level of the hereditary patrimony of an individual that are transmitted to offspring. Genetic mutations are alterations to the DNA sequence of a gene (substitution, insertion or base deletion), the most frequent being the malfunction of DNA replication, though the following elements can also lead to these mutations: a) errors during the DNA repairing process; b) exposure to various chemical mutagenic substances (yperite, aniline, etc); c) various physical agents (ultraviolet radiation, ionizing radiation etc). Chromosomal mutations modify the structure or the number of chromosomes; genomic mutations change the number of set chromosomes and/or their origin; if they come from the same species then it is called autopolyploidy, if from different species it is allopolyploidy.

Mutations that arise in an individual are usually unfavourable because they alter genes, chromosomes and/or genomes that natural selection has modified in the course of the evolutionary history of a population, adapting it to the environmental conditions in which it lives. However, if the environment changes due to natural causes or due to human activity, for example, following the



Fig. 2.26 - Seasonal morphs and summations in the *Vanessa Araschnia levana*; spring generation, forma *levana* (A-E); summer generation, *f. prorsa* (G-M); *f. porrima* (F); *f. obscura*: (N) (POZZI, 1990, modified).

massive emission into the environment of a toxic synthetic molecule for some organisms, the appearance of a mutant capable of disintoxicating it would lead to the survival of the population that lives in contact with that substance.

The presence of two or more different forms of a given character in a population is called *polymorphism*. If the character is under the control of a single gene, the polymorphic population will have two or more alternative forms of that gene, called *alleles*. With two alleles (A' and A'') one obtains three genotypes, two homozygotes ($A'A'$ and $A''A''$) and one heterozygote ($A'A''$). There are countless examples of gene polymorphism with various alleles: one of these, regarding various ladybird species is shown in Figure 2.29.

A polymorphism can be maintained in a population for an indefinite number of generations, or after a few generations it may return to monomorphism. For example, in the case of a mutation resistant to DDT in an insect population, the mutated allele will disappear in a few generations if DDT is not present in the environment in which the population lives, or else it will com-

pletely substitute the normal allele if DDT is present. In both cases the polymorphism will be maintained for only a few generations (transient polymorphism). Many biological adaptations are based on stable genetic polymorphisms (balanced polymorphisms). For example, genetic resistance to malaria of several human populations is linked to biochemical anomalies of the red blood cells, determined by mutations of distinct genes that appeared in an independent manner; in malarial regions, these genes display balanced polymorphisms to the advantage of the heterozygote genotype (Figure 2.30). Examples of balanced polymorphisms at a chromosomal level are those from inversion or translocation, which allow populations of a species to adapt to the different seasons, or to generally high altitudes, as in the case of the midge *Drosophila pseudoobscura* (Figure 2.31) and in the plant *Clarkia williamsonii* (Figure 2.32).

Even polymorphism connected to colour and banding of the shell of several snails (for example *Cepaea nemoralis*) is of the balanced type; the frequency of the various forms changes from one population to the next depending on the characteristics of the substrate and vegetation, because

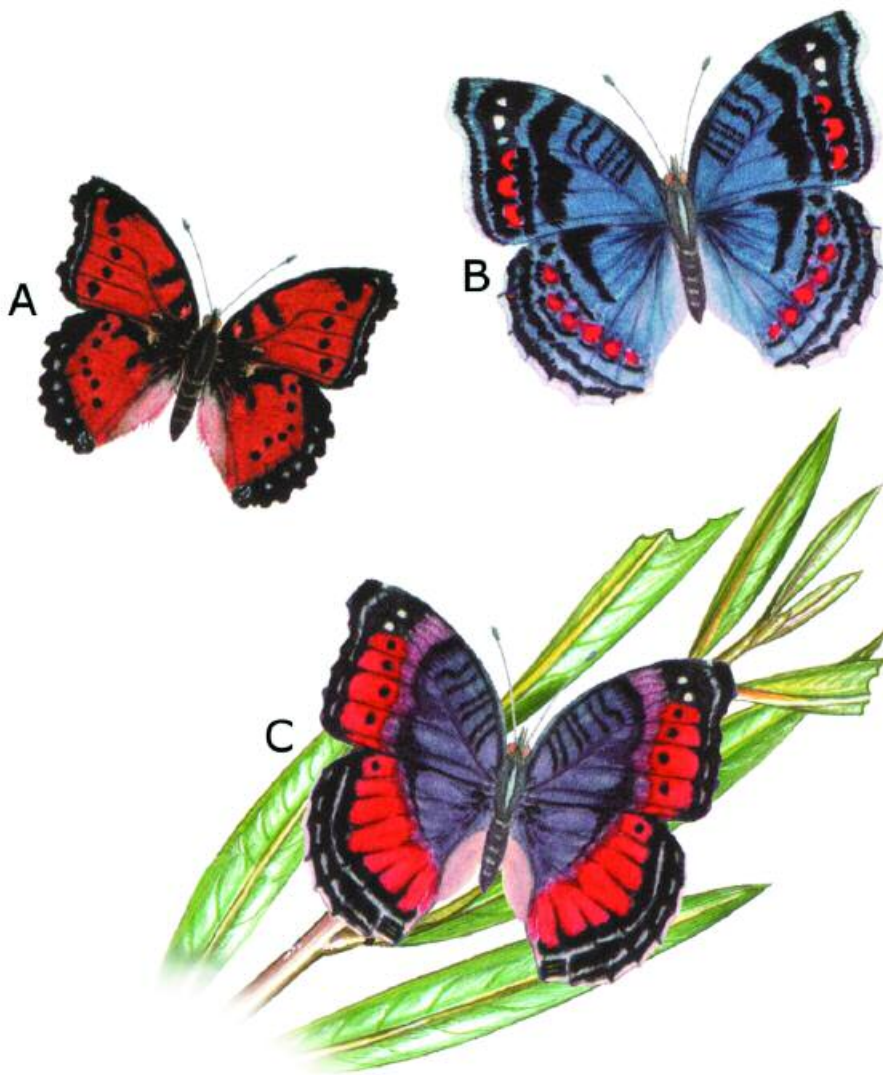


Fig. 2.27 - Seasonal morphs in the African nymphalid, *Precis octavia*; wet-season morph (A); dry-season morph (B); intermediate morph (C).

the probability of the different forms to escape being preyed upon by birds differs in different types of habitats (Figure 2.33).

A well known case of adaptive balanced polymorphism is found in heterostylous plants, that is, the presence in the flowers of individuals of the same species with styles of different length (plants with either longistylous flowers or brevistylous flowers); this adaptation, present in various species of the genus *Primula*, prevents self-fertilisation (Figure 2.34).

Another mechanism which keeps polymorphism stable is selection that is dependent on frequency. In this case, the fitness of a genotype varies depending on changes of its frequency within a population; examples of this

phenomenon are seen in *Batesian Mimicry* and *Müllerian mimicry*. For example, the female of the butterfly *Papilio dardanus*, which is palatable and not protected from predators has a marked polymorphism connected to colour, pattern and wing shape. Several forms of this butterfly, that have a peculiar geographic distribution in sub-Saharan Africa, mimic different species of unpalatable butterflies protected from predation, present with different frequencies in the regions where *P. dardanus* lives. Batesian mimicry is where a member of a palatable species acquires a deceptive resemblance in appearance and behaviour to a harmful, toxic unrelated variety and is then more likely to escape predators, thereby furthering its success in survival.

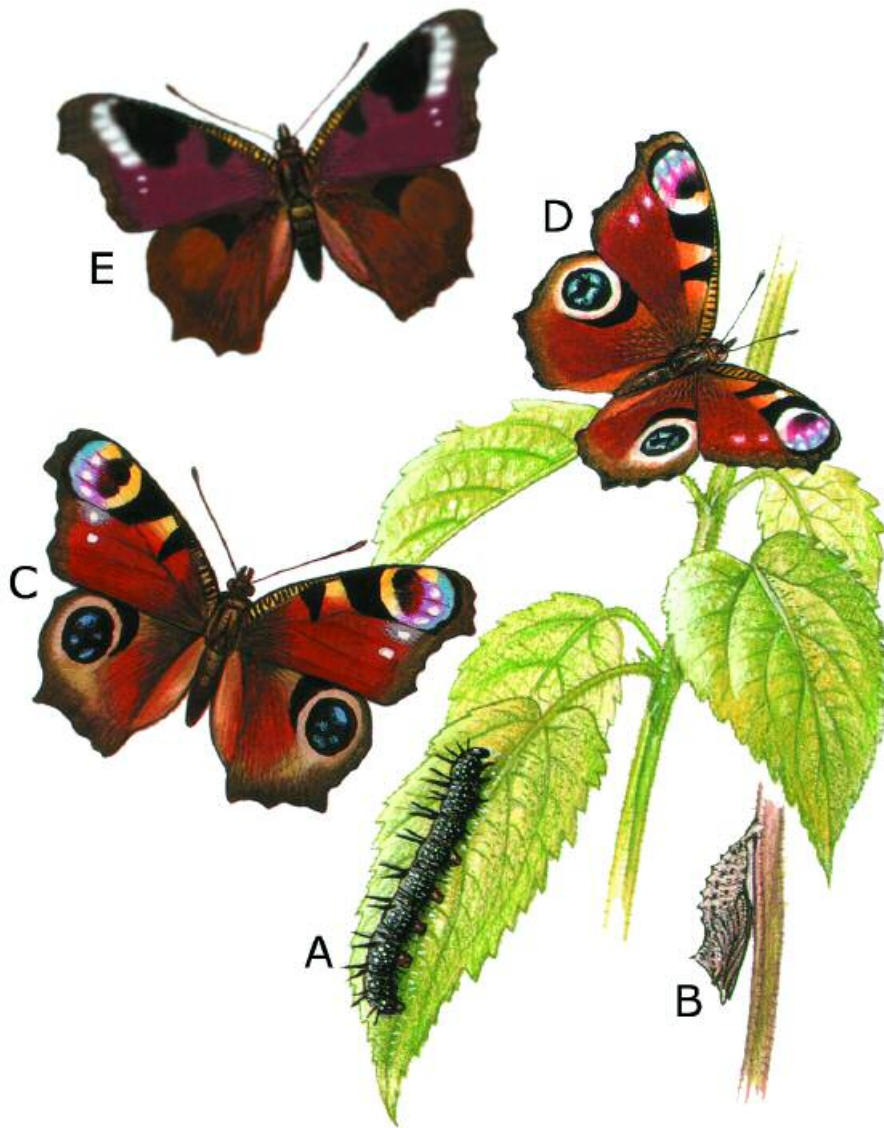


Fig. 2.28 - The *Vanessa Inachis io* in various stages of its life cycle; larva (A); chrysalis or "chrysalid" (B); typical adult morphs (C, D) and a summation (E) obtained through thermal shock (24 hours at -10°C at the beginning of the pupa stage).

Instead, Müllerian mimicry refers to two unpalatable species that are mimics of each other with similar warning signals such as conspicuous warning coloration (also known as aposematic coloration). Thus, all mimics share the benefits of the coloration since the predator will recognise the coloration of an unpalatable group after a few bad experiences. Since several species have the same appearance to the predator, the loss of life will be spread out over several species, reducing the impact on each individual species. For example, *Zygaena ephialtes* (Figure 2.35) with its aposematic coloration, that has a range which includes a large part of the Palearctic region, mimics two distinct aposematic models, one with a red

and black pattern, the other with a white, black and yellow pattern. The first of these models is by far the most frequent in continental Europe and in central Asia, while the second is particularly abundant in the Italian peninsula and in the Balkans, principally due to the great number of unpalatable species of the genus *Syntomis*.

Mutations are at the basis of gene and chromosomal polymorphisms, which as already mentioned, are the primary source of genetic diversity. The rate of mutation, however, is low and does not generate a sufficiently great genetic variability to allow populations to adapt via natural selection to changes in space and time of environmental conditions (a partial exception are microorganisms

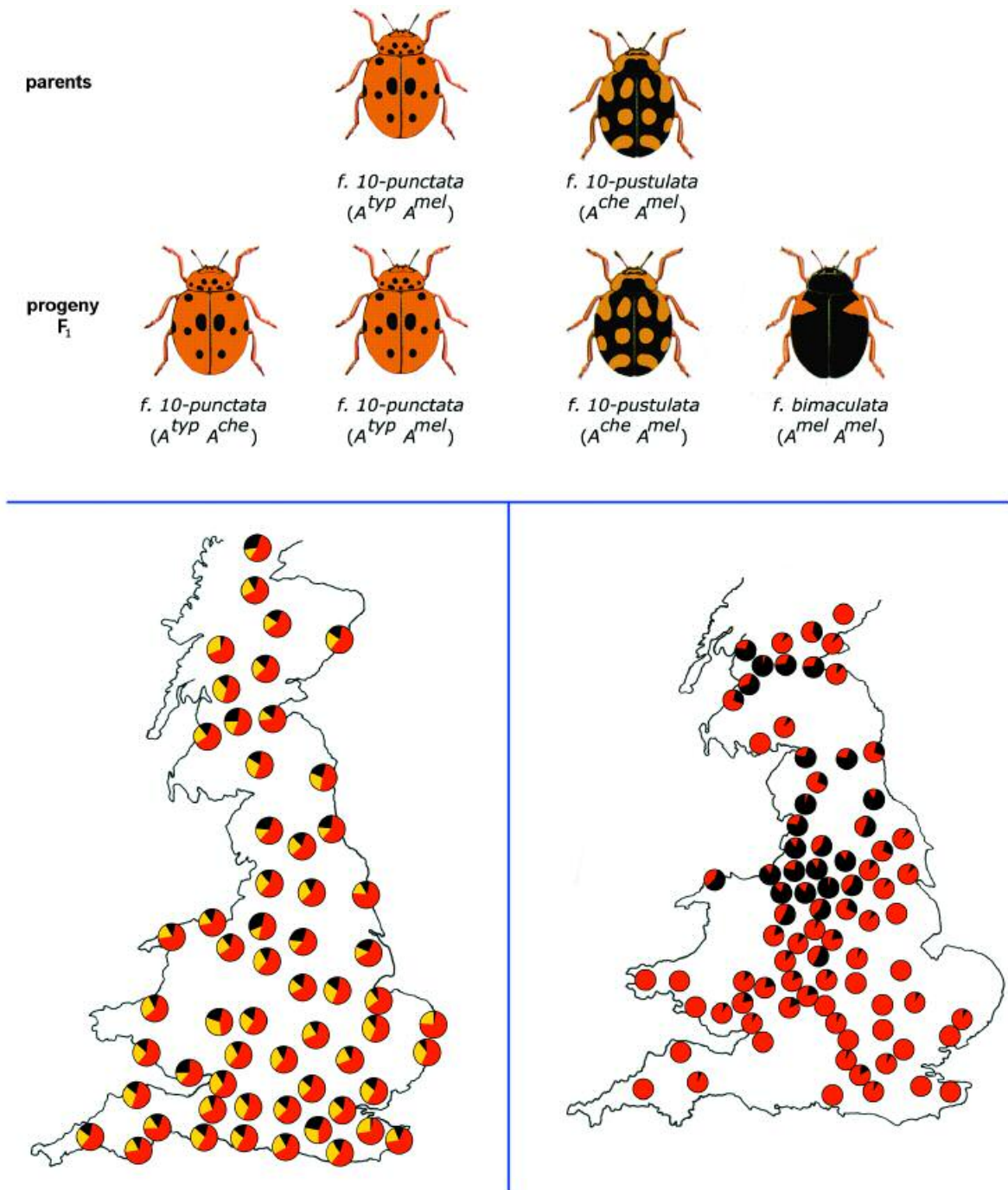


Fig. 2.29 - Genetic basis of the chromatic polymorphism of two ladybirds of the genus *Adalia*.

Top: Chromatic polymorphism of the ladybird *Adalia decempunctata* (Coleoptera, Coccinellidae). Gene *A* is polymorphic with three alleles: A^{typ} (dominant over A^{che} and A^{mel}), A^{che} (dominant over A^{mel} , though recessive with respect to A^{typ}), A^{mel} (recessive with respect to A^{typ} , as well as A^{che}). An outline is provided of the crossing-over between an individual of the *10-punctata* form (genotype $A^{typ} A^{mel}$) and one of the *10-pustulata* form (genotype $A^{che} A^{mel}$); in the progenies of F_1 50% of the individuals have the *10-punctata* form (25% with genotype $A^{typ} A^{che}$ and 25% with genotype $A^{typ} A^{mel}$), 25% have the *10-pustulata* form (genotype $A^{che} A^{mel}$) and the remaining 25% have the *bimaculata* form (genotype $A^{mel} A^{mel}$) (MAJERUS, 1994, modified).

Bottom left: Frequency relative to forms *10-punctata* (in red), *10-pustulata* (in yellow) e *bimaculata* (in black) of *A. decempunctata* in Great Britain (MAJERUS, 1998, modified).

Bottom right: Frequency relative to melanic forms (in black) and non-melanic (in red) of *A. bipunctata* in Great Britain (LEES, 1981, modified).

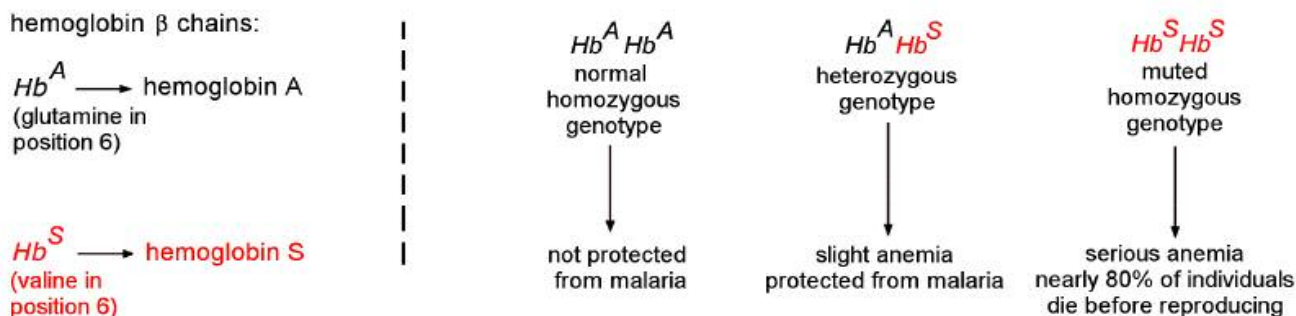


Fig. 2.30 - Balanced polymorphism of gene *Hb* in human populations that have adapted to malaria; heterozygote individuals $Hb_A Hb_S$ are protected from the disease.

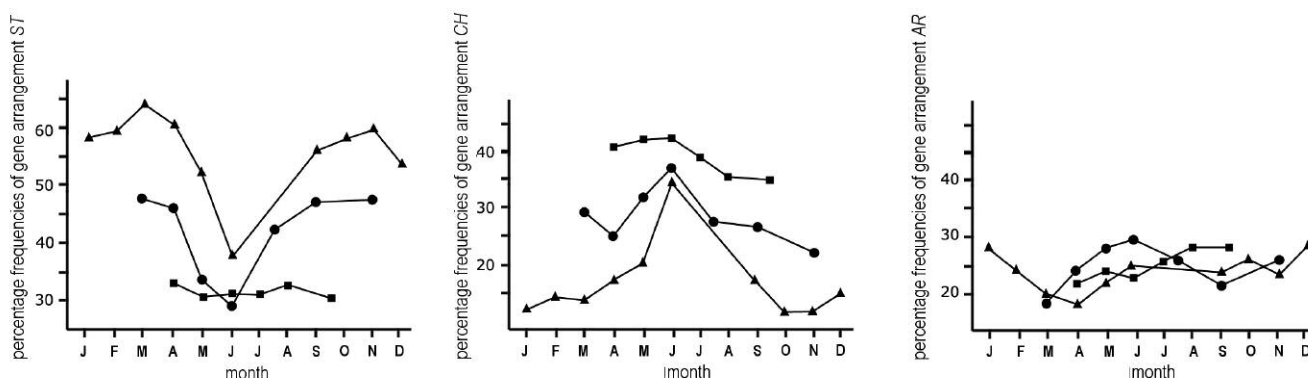


Fig. 2.31 - Temporal frequency changes of three polymorphic chromosomal rearrangements (inversions) in the California fruitfly *Drosophila pseudoobscura* populations. The chromosomal rearrangements considered are: Standard (*ST*), Chiricahua (*CH*) and Arrowhead (*AR*). Each figure shows the frequency of each particular chromosomal rearrangement over one year in the three localities: Andreas Camp ▲, Pinon Flats ●, Keen Camp ■. The frequency of the inversions *ST* and *CH* change dramatically in the first two populations that live at lower altitudes, reaching the minimum and the maximum respectively at the beginning of summer, while it remains relatively constant at Keen Camp. The frequency of *AR* remains relatively constant throughout the year in all locations (WRIGHT and DOBZHANSKY, 1946, modified).

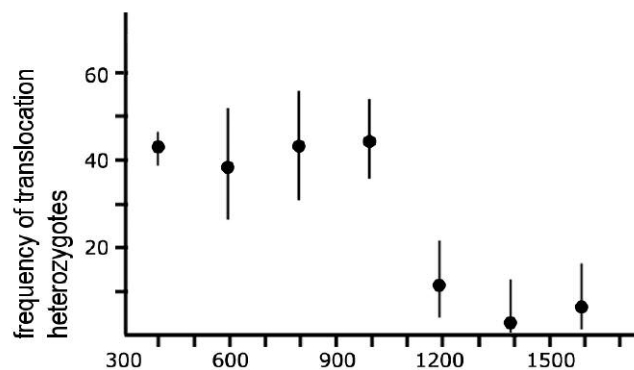


Fig. 2.32 - Chromosome polymorphism by means of translocation in the plant *Clarkia williamsoni*; the frequencies of the translocation heterozygotes in populations at different altitudes, from 300 m to 1,600 m are shown: the black dot gives the mean value in the population, the lines indicate the 95% confidence limits (WEDBERG *et al.*, 1968, modified).

with extremely brief generation times). Starting from mutations, sexual reproduction multiplies the number of genetic combinations practically to infinity. In this reproduction manner, the formation of new individuals comes about via two specialised cells, the *gametes*. Unlike somatic cells that have two sets of homologous chromosomes, one of paternal origin and the other maternal (diploid), gametes have only one complete set of chromosomes (haploid, symbol: *n*). *Meiosis* is the process of cellular division that leads to the formation of gametes and forms the basis in sexual reproduction. When two gametes unite, they form a *zygote*; a cell with two complete sets of chromosomes and therefore diploid. The zygote cell receives one set of chromosomes from each of the two gametes involved in the union. Each homo-

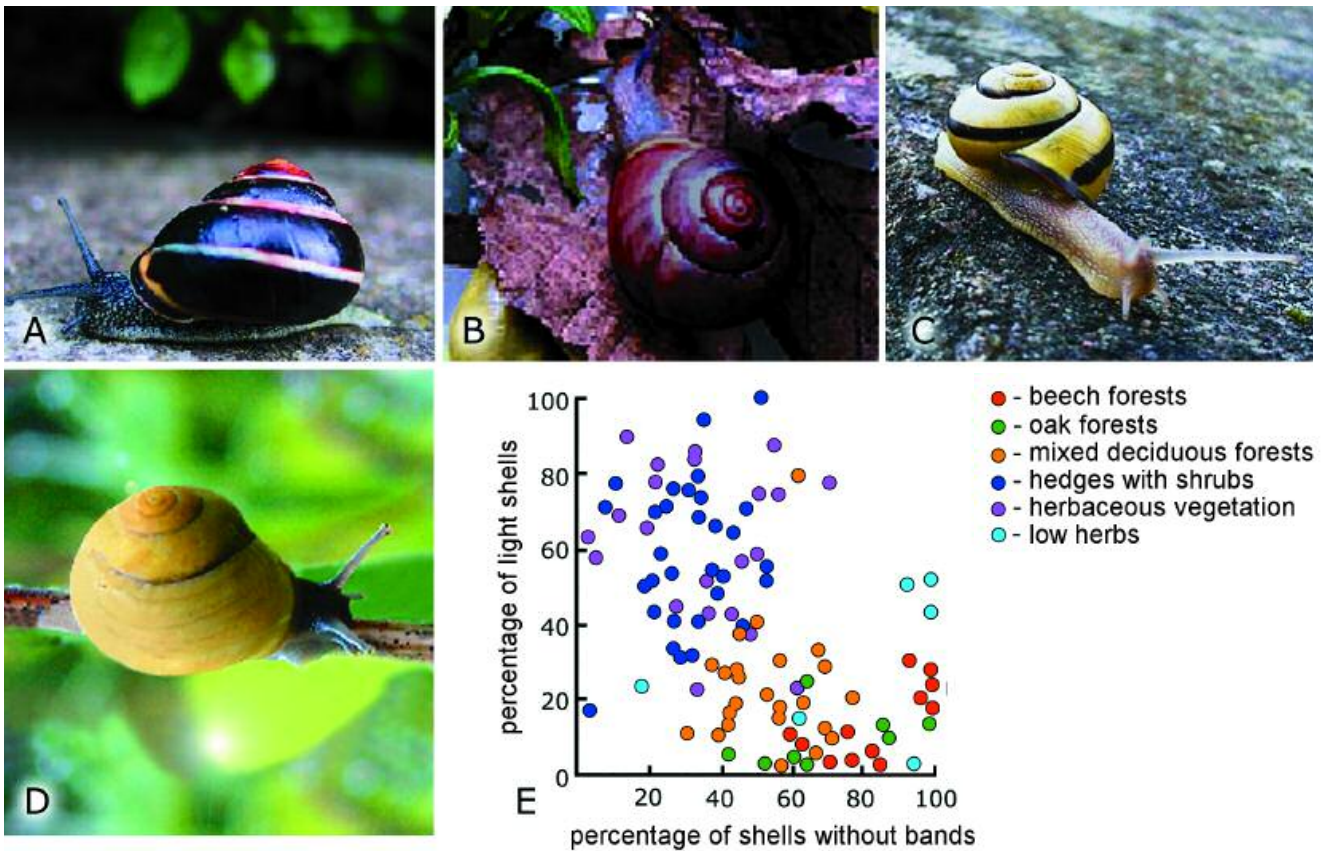


Fig. 2.33 - Visible polymorphism in shell colour and banding in the snail *Cepaea nemoralis*. A: dark shell with bands; B: dark shell without bands; C: light shell with bands; D: light shell without bands; E: Frequency of the character shell with or without bands (on the x axis) and dark or light coloured shell (on the y axis); the frequency of the various morphs differs from one population to the next, depending on the characteristics of the habitat (type of substrate and vegetation); every circle corresponds to a *C. nemoralis* population; the colour of the circle indicates the type of vegetation at the site where the population was observed. The genetic base of the chromatic polymorphism of *C. nemoralis* is relatively complex and is based on the variation of a supergene (CAIN and SHEPPARD, 1954, modified).

gous chromosome now contains two identical sister chromatids joined together. The first round of division (Meiosis I) separates homologous chromosomes. Meiosis II, the second round of division, separates sister chromatids. There are four haploid cells produced at the conclusion of meiosis. More precisely, meiosis produces haploid gametes in animals, while it produces spores in plants; from these gametophytes are produced (haploid) which produce the gametes). Meiosis derives from *mitosis*, the duplication process of somatic cells.

Gametes are genetically varied, containing a mix of both paternal and maternal genetic information. This is accomplished in two processes. During meiosis I, genetic information is distributed through independent assortment. Homologous chromosomes will eventually part

ways into separate cells. However, homologous chromosomes are oriented independently of their companions. That means that each daughter cell has a fifty-fifty chance of receiving the maternal chromosome or the paternal chromosome. The number of combinations generated by independent assortment of the homologous chromosomes depends on how many chromosomal pairs there are (Figure 2.36). In human beings, in which $n = 23$, the number of combinations is 223; hence in the gametes of a human being there are almost ten million genetic combinations. An even more important mechanism in creating new genetic combinations is recombination or crossing-over, that is, the exchange of segments of a chromosome with corresponding segments of its homologous chromosome, which occurs during the first

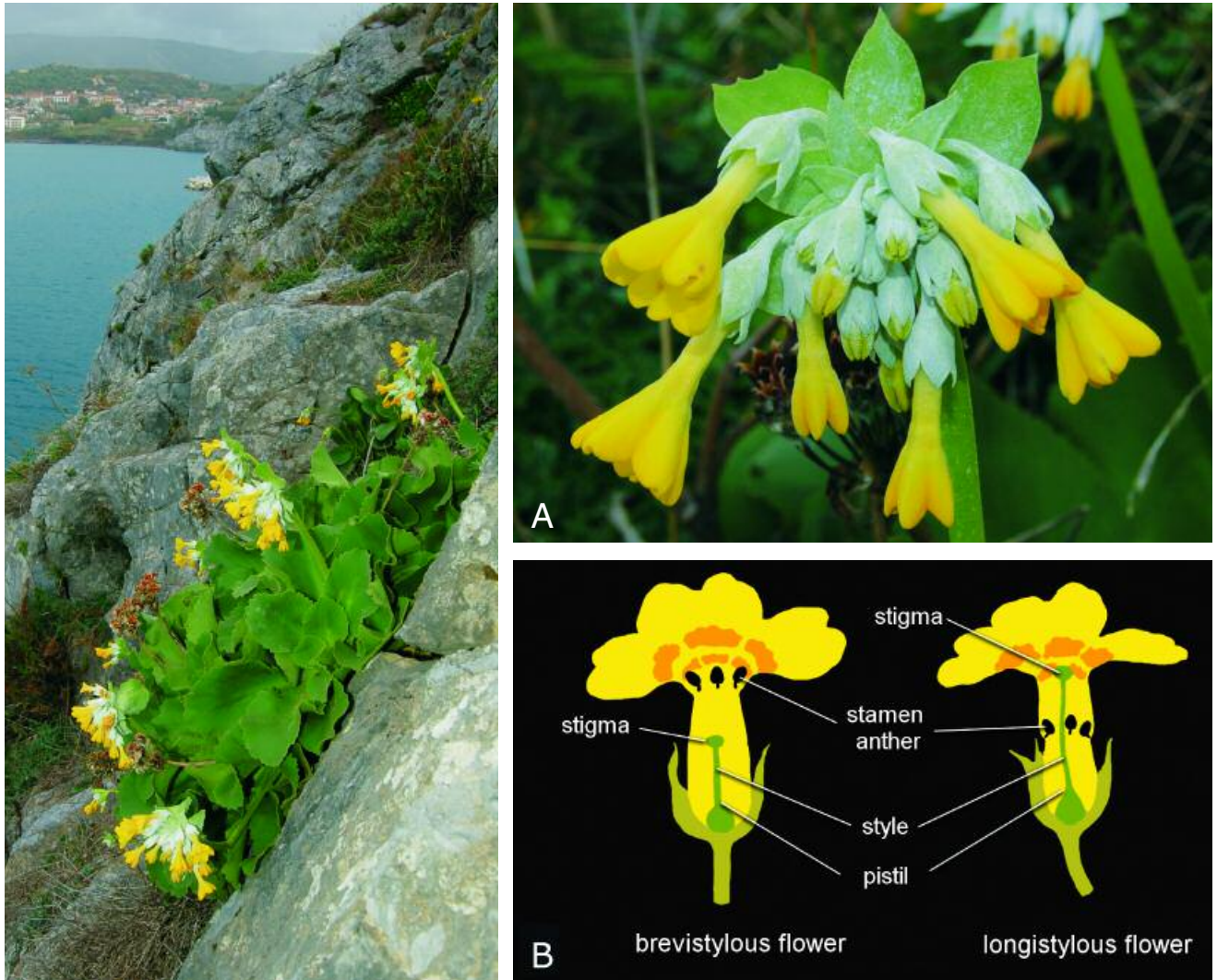
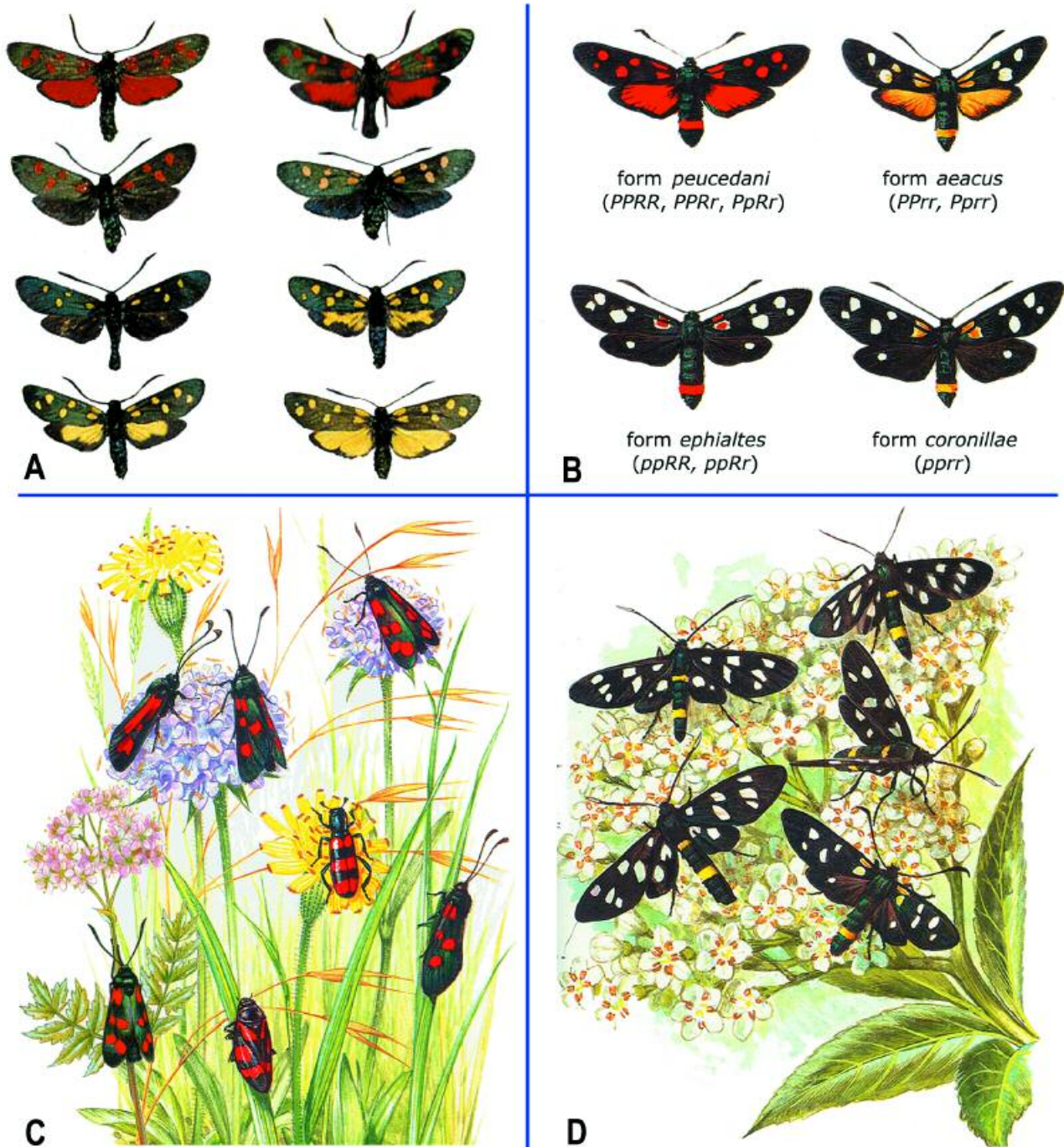


Fig. 2.34 - Heterostyly in the genus *Primula*. Like many other angiosperms, cowslips are *hermaphrodite* flowers, that is, with stamen and pistil in the same flower; however they rarely self-pollinate. Various mechanisms favour cross-fertilisation which is the union of male and female gametes produced by different individuals, conspecific but genetically differentiated (*allogamy*). The figure illustrates the out-breeding mechanism of heterostyly, a polymorphism that produces two types of flowers in a population: *longistylous* flowers, with long styles, stigma at the upper end of the corolla tube, stamens halfway up the tube, and *brevistylous* flowers, with short styles, stigma halfway up the corolla tube, stamens at the upper end of the corolla tube. The plant can have either brevistylous flowers or longistylous flowers, but not both. Many populations of almost all the species belonging to the genus *Primula* have plants with both longistylous and brevistylous flowers, with a similar frequency. An inflorescence of brevistylous flowers of the Cowslip *P. veris* is illustrated in A, in B a brevistylous flower (on the left) and a longistylous one; in C and in D sections of brevistylous flowers (on the left) and longistylous ones (on the right) are shown. Pollinating insects penetrate deeply into the corolla-tube picking up the pollen grains from the anthers of plants with longistylous flowers; other pollinators visit the upper part of flowers and gather pollen grains from plants with brevistylous flowers which they then transfer to the stigma of longistylous flowers and vice-versa. Heterostyly impedes self-pollination, thus favouring negative assortative mating (not accidental) among plants that are phenotypically different. Polymorphism connected to heterostyly is controlled by at least three closely-associated (*loci linked*) genes, which constitute the *supergene* for heterostyly.

Fig. 2.35 - Müllerian mimicry and polymorphism in lepidopterans of the genus *Zygaena*.

A - Polymorphism connected to the coloration and pattern of the butterfly *Zygaena transalpina* (Lepidoptera, Zygaenidae), unpalatable for almost all its potential predators; non-melanic red morphs in the first rows from the top, widespread in northern Italy and the Alps, displaying Müllerian mimicry with a red and black pattern illustrated in Fig. C; in the second row red morphs of the subspecies *xanthographa* that occur in central-southern Italy; in the third row yellow morphs generally melanic of the subspecies *tilaventa*, widespread in Friuli and Venezia Giulia.



B - Polymorphism in the butterfly *Zygaena ephialtes*: top left, a red peucedanoid morph (*peucedani*) displaying Müllerian mimicry with the red and black pattern illustrated in Fig. 3; top right, a yellow peucedanoid morph (*aeacus*); bottom left a red ephialtoid morph (*ephialtes*); bottom right a yellow ephialtoid morph (*coronillae*), displaying Müllerian mimicry with a black, yellow and white pattern, including the species of the genus *Syntomis* (Lepidoptera, Ctenuchidae), illustrated in Fig. D.

C - Müllerian mimicry displayed in various species in the genus *Zygaena*, coleopterans of the genus *Trichodes* and hemipterans of the genus *Cercopis*. This type of mimicry that is widespread in Europe is also displayed in non-melanic red morphs of *Z. transalpina* and the red peucedanoid morph of *Zygaena ephialtes* (SBORDONI and FORESTIERO, 1984, modified).

D - Müllerian mimicry displayed in the species *Syntomis* and in the yellow ephialtoid morph of *Zygaena ephialtes*; top left a specimen of *S. ragazzii*, top right and below are three specimens of *S. phegea*, bottom right a specimen of the yellow ephialtoid morph *Z. ephialtes*; this mimicry complex is widespread in the Italian peninsular and in the central Balkans (SBORDONI and FORESTIERO, 1984, modified).

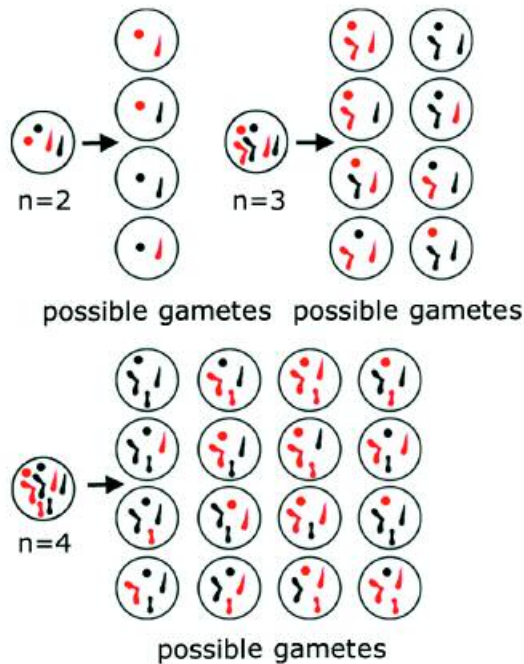


Fig. 2.36 - Independent assortment of homologous chromosomes during the first meiotic division (CURTIS and BARNES, 1985).

meiotic division when the homologous chromosomes are strictly paired (Figure 2.37).

As a consequence of the independent assortment of chromosomes and recombinant chromosomes in Meiosis I and Meiosis II, the offspring produced through sexual reproduction are genetically different individuals (monozygotic twins, genetically identical, come from a single fertilised egg). Sexual reproduction, though extremely complex has evolved independently in various groups of organisms. The loss of sexual reproduction (for example, in populations of angiosperms owing to local extinctions of pollinators) often preludes the extinction of a population. Genetic diversity of species is influenced by gene flow. This is the transfer or migration of genes from one population to another. It may result in adding new genetic material to the established gene pool of a particular species or population, thus increasing genetic variability.

If this rate of gene flow is intense and prolonged in time, it becomes an important “antievolutionary” factor. In fact, it tends to maintain the populations of a species genetically uniform, reducing the differences that arise among them with the following consequences: 1) mutations, that appear in an independent manner in various populations; 2) natural selection, that is the differential

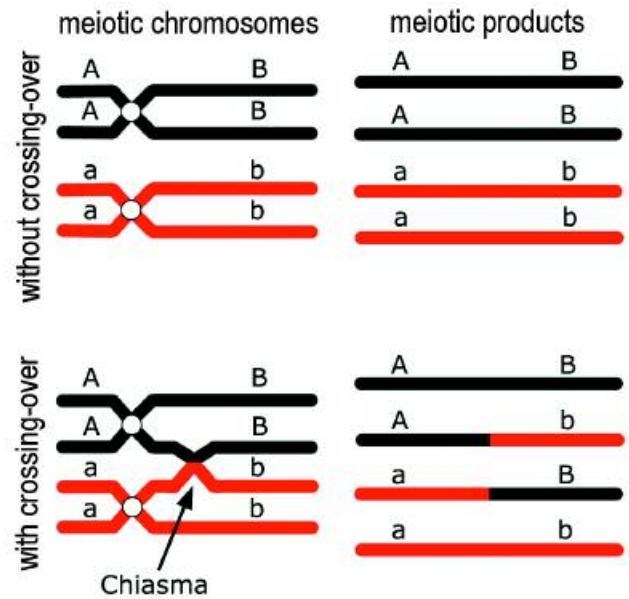


Fig. 2.37 - Pair of homologous chromosomes, each formed by two identical chromatids, linked by the centromere, at the end of prophase I; meiotic products formed without *crossing-over* (above) and with *crossing-over* (below).

reproduction (fitness) of different genotypes, which make genes and gene combinations adapt better to particular environmental conditions in which the population lives; 3) genetic phenomena, that is stochastic changes (that is, random) of genetic and chromosomal frequencies caused by variations in the number of individuals that make up a population. The prolonged interruption of gene flow among populations (caused, for example, by physical barriers) increases genetic differentiation and may culminate in the establishment of new species (allopatric speciation – Figures 2.38 and 2.39).

Genetic diversity of populations and the threat of extinction

As mentioned previously, genetic diversity, which can be studied utilising various genetic markers today, is fundamental for the survival of populations. In fact, it is the basis of adaptive processes which enables populations to successfully respond to continual changes in ecological factors (climatic conditions, competitive species, parasites, usable trophic resources, chemical composition of the medium, etc), as explained in the so-called *Red Queen Hypothesis* of VAN VALEN (1973).



Fig. 2.38 - Morphologic and genetic differentiation in diploid and autotetraploid orchids of the group *Anacamptis morio*.

A: *A. champagnouxii*, $2n=36$ (southern France; DELFORGE, 2001);

B: *A. morio morio*, $2n=36$ (northern France; BOURNÉRIAS *et al.*, 1998);

C: *A. morio* A, $2n=36$ (Trentino, Italy; PERAZZA, 1992);

D: *A. morio* A morpha *albiflora*, $2n=36$ (Italy; CRESCENTINI and KLAVER 1997);

E: *A. longicornu*, $2n=36$ (Sicily; DELFORGE, 2001);

F: *A. morio* E, $2n=36$ (Macedonia; DELFORGE, 2001).

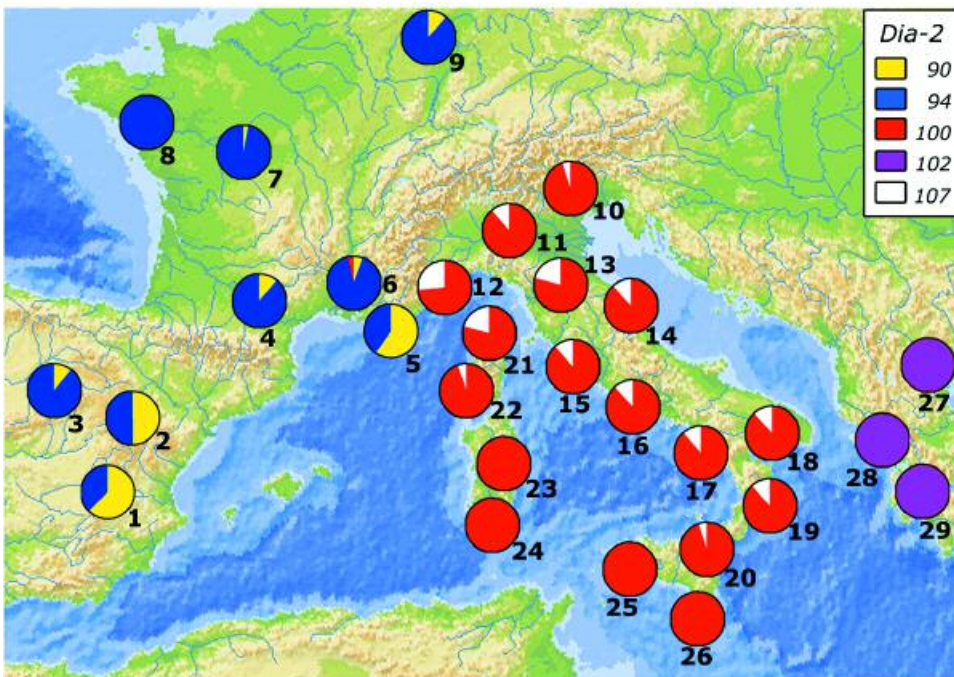


Fig. 2.39 - Allele frequency of the *Dia-2* gene coding for the enzyme diaphoresis of the *A. morio* complex ($2n$). 1, 2, 5: *A. champagnouxii* ($2n$); 3: *A. champagnouxii* ($4n$); 4, 6-9: *A. morio morio* ($2n$); 10-22: *A. morio* A ($2n$); 23-26: *A. longicornu* ($2n$); 27-29: *A. morio* E ($2n$).

For a population to maintain its genetic variability and its adaptive flexibility, it is necessary that its size remains above a certain level (concept of minimum vital population, MVP; SHAFFER, 1981). In small populations, in fact, environmental stress can provoke fluctuations in birth and death rates which could lead to the population's extinction. Moreover, small populations lose genetic variability due to inbreeding and genetic drift. Moreover, as the genetic load is present in the hereditary patrimony of each member of a population, crossbreeding among kin (and in hermaphrodite species, self-fertilisation) increases the probability that these negative or lethal alleles are present in the offspring at a homozygote level (depression through inbreeding). As a consequence, many individuals do not reach sexual maturity or, if they do, they have fewer offspring, with a lower reproduction rate or they may even be sterile. There are many mechanisms in nature to prevent inbreeding. For example, in many gregarious primates, males once reaching sexual maturity, abandon the group in which they were born and reproduce in another group, this has proved to be a form of sexual selection or advantage in many animal species. Individuals with phenotype characteristics that are different from the most frequent ones in a population have a greater probability of mating. In plants, cross-fertilisation (the pollinisation among flowers of different plants) is enhanced through various adaptations, while self-fertilisation is hindered. In plants with hermaphrodite flowers, the male and female sexual organs often mature the gametes at different times, or else are located in such a way as to make self-fertilisation improbable. When the populations become small, many of these mechanisms cease to work. However, in order to maintain the genetic variability of a population, what is important is not the total number of individuals that make up the population (N), but rather the number of individuals that reproduce (N_e = effective size of the population). In natural populations N and N_e can be very different. In insects, for example, the number of eggs and larvae in a population can be very high; most individuals however die before metamorphosis killed by infections, endoparasites, predators, or because of scarcity of trophic resources, or even due to adverse climatic conditions. In other groups, especially where parental care is absent, mortality in the first stages of life is high. In estimating the size that a population should have to maintain an elevated genetic variability in time, a distinction should be made between those that are subjected to great de-

mographic fluctuations (for example, many invertebrates and annual plants), and those in which these fluctuations are minor (for example, mammals and birds). In both cases, environmental and negative demographic events that are foreseeable in the mid-long-term should be taken into consideration.

Apart from population size, interpopulation genetic variability is greatly influenced by the presence or absence of gene flow with other conspecific populations. The loss of genetic variability in isolated populations following migration is, in fact, a phenomenon that is rarely reversible, and which can only be balanced by mutation. Hence, these populations risk extinction. At present, isolated populations are much more numerous than in the past owing to physical barriers created by man, such as vast areas dedicated to intensive agricultural practices, conurbations, industrial settlements, and extensive road networks, etc.

There are numerous examples of populations and species that currently face the risk of extinction, many of which have a greatly reduced genetic variability (genetic erosion). Worthy of note among these are: the northern elephant seal *Mirounga angustirostris*, dramatically reduced in numbers last century owing mainly to indiscriminate fishing; the cheetah *Acinonyx jubatus* which has displayed complete absence of genetic variability from marker studies; the Asiatic lion *Panthera leo persica*, that has a residual population crossbred with individuals of the African subspecies *Panthera leo leo* which has shown a rapid and significant increase in fertility; the bison *Bison bison*, which is thought to have been present before the colonisation of North America by the Europeans with 50 to 100 million individuals, and that survives today only within nature reserves and parks; the European bison *Bison bonasus*, whose current population, distributed mainly in the Bialowieza Park in Poland, derives from few individuals and which shows the effects of depression from inbreeding (increased mortality and reduced fertility, HART and PUCEK, 1994); the giant panda *Ailuropoda melanoleuca*, whose survival is threatened above all by deforestation, the fish *Hoplostetis atlanticus*, *Gadus morhua*, *Thunnus thynnus*, *Xiphias gladius*, *Salvelinus fontinalis*, whose loss of genetic variability has been documented following intensive fishing (serious infections and parasitosis recently observed in Mediterranean populations of tuna and sword fish probably as a consequence of loss of genetic variability that they have been subjected to). Among the Italian species, there is the Lady's slipper *Cypripedium calceolus*, extinct or risking extinction in several European

countries not so much due to indiscriminant gathering as once thought, but rather to fruiting failure linked to the rarefaction of insect pollinators, which has consequently led to the intensification of vegetative reproduction in many populations (Figure 2.40); the rare marsh orchid *Anacamptis palustris*, reduced to small populations owing to the rarefaction of its natural habitat (land reclamation and draining of wetlands), whose genetic variability is now much lower than a similar species *A. laxiflora*; the red deer *Cervus elaphus*, whose reduced numbers, scarce resistance to disease and very low fertility are due to inbreeding depression; the Apennine chamois *Rupicapra pyrenaica ornata*, found to be almost without variability in marker studies.

In order to protect populations and species threatened with extinction it is necessary to know their genetic structure. For example, in threatened populations where inbreeding depression is evident and the number of individuals that reproduces is diminishing generation by generation, it may be necessary to introduce individuals of different geographic origin. In any case, this practice is not without its risks and caution must be used. The genes of a population are, in fact, the result of long and extended processes of coadaptation; outbreeding might bring about a decrease in the level of genetic coadaptation (outbreeding depression).

The conservation of the genetic diversity of organisms, both within and among populations has a crucial importance for their conservation which has led to the creation of a new science: Conservation Genetics. The two principal objectives that this discipline pursues are: 1) to maintain current state of genetic biodiversity 2) to restore evolutionary processes that bring about genetic diversity. In particular, it is necessary to monitor the genetic variability of those animal and plant populations subjected to forms of exploitation by man such as hunting, indiscriminant gathering, and to establish on a case-by-case basis the entity of compatible use while maintaining genetic variability. Moreover, the genetic structure should be characterised on a geographic scale (phylogeography) in order to identify the Evolutionary Significant Units (ESU). These units are made up of genetically differentiated populations following a generally prolonged geographic isolation; each of these units merits conservation measures in that they represent a significant fraction of the genetic diversity of the species (AVISE and HAMRICK, 1996). Last of all, geographic areas that are identified as “centres of genetic diversity” owing to the presence of endemic species, or to numer-

ous and genetically variable populations of species that are not found elsewhere, or hybrid zones (that is, those contact areas between genetically differentiated populations) should be protected.

The establishment of reserves for the conservation of genetic diversity in Italy and in the rest of the world is both necessary and urgent. The traditional parks and nature reserves, in fact, often do not include these genetic diversity centres within their confines; moreover, the criteria and management methods of genetic diversity reserves are not the same as those utilised in traditional parks and nature reserves.



C. calceolus



C. californicum



C. guttatum



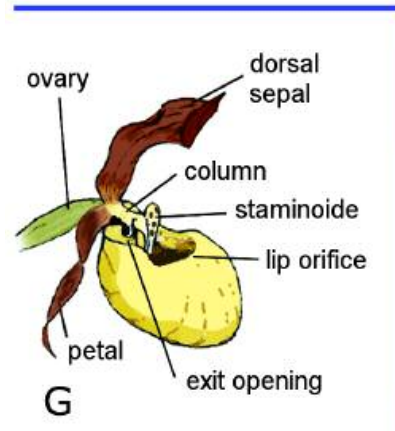
C. macranthos



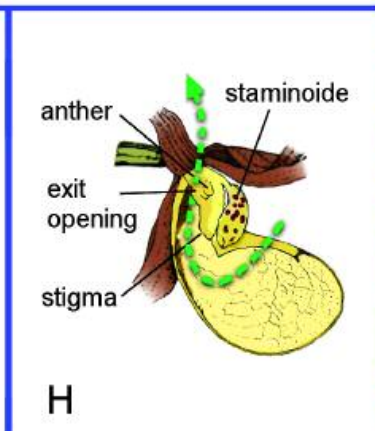
Andrena sp. on the
lip orifice of *C. calceolus*



Andrena haemorrhoa



G



H



I

C. calceolus

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Fig. 2.40 - Orchids of the genus *Cypripedium* and their pollinators.

Several species of orchid species of the genus *Cypripedium* (Figures A-E, I) are shown displaying brightly coloured large flowers with the distinctive lip and shoe-like shape of “*Lady's Slippers*”. The flowers of these orchids do not reward their pollinators and therefore rely on their ability to mislead them through some form of deception (deceptive orchids). The saccate lip of these orchids has evolved as a trap for pollinators who are lured into the pouch of the labellum through the slit in the front, attracted by the bright colour and sweet scent of the flower (Figures E, G, H). If the insect is too large, such as the honey bee (*Apis mellifera*), it can remain trapped and die; if the insect is too small, it escapes from one of the two lateral openings without soiling itself with pollen. Specific pollinators, in *C. calceolus* several averaged-sized apoids of the genus *Andrena*, in particular *A. haemorrhhoa* (Fig. F), penetrate inside the “hairy” pouch which leads to a pair of openings, one beneath each pollen mass. First, however, the insect must pass under the stigma, so if it bears any pollen from a visit to another flower, it will be deposited before picking up a fresh load, thus preventing self-pollination. The massive use of DDT and other pesticides has led to the decline of pollinators of the subfamily *Cypripediaceae*; thus, the majority European and North American flower species are not fertilised and do not produce flowers (*fruiting failure*). As natural self-fertilisation is not possible in *Cypripedium*, reproduction often occurs through hypogean rhizomes. There are high levels of inbreeding in populations where this occurs, and consequently a reduction in genetic variability (*genetic erosion*).

Figure G illustrates the morphology of a flower of *C. calceolus*, in Figure H a sagittal section shows the internal structure of the flower; an arrow indicates the path taken by the pollinator from its access through funnel-shaped orifice of the lip to its exit from one of the two side openings (Figures A and D from DELFORGE, 2001; B and C da CRIBB, 1997; E from BUTLER, 1991; F from GIBBONS 1995; G from JONG, 2002; H from PROCTOR *et al.*, 1996; I from BOURNERIAS, 1998, modified).

GENETIC DIVERSITY OF PLANT SPECIES OF AGRICULTURAL INTEREST

[Oronzo Antonio Tanzarella, Enrico Porceddu, Gian Tommaso Scarascia Mugnozza]

Biodiversity of agricultural plants is understood as those genetic resources that can be obtained from agriculture inclusive of selviculture, that is, any kind of material of plant origin, of current or potential value for agriculture and foodstuffs and non-foodstuff products, such as textiles, pharmaceutical products, biocombustibles, building material, and products for bioindustry, etc. The transition of primitive human communities from hunter-gatherer nomads to stable communities of farmers has allowed man to satisfy the food requirements for a growing number of individuals and to limit the number of members that had to search for a means of sustenance. This led to the rapid demographic increase in the Neolithic period



Fig. 2.41 - Several farm products.

Wheat	Sorghum
Rice	Sugar cane
Corn	Millet
Potato	Banana
Barley	Tomato
Sweet potato	Sugar beet
Tapioca	Rye
Grape	Orange
Soy	Coconut
Oat	Sunflower

Table 2.1 - The 20 main species on which human diet is based (HARLAN, 1976, modified), in descending order of importance.

and, subsequently the development of civilisation and culture thanks to the diversification of human activity. Decreased biodiversity is a consequence inherent to agricultural activity which inevitably had to choose and select the most suitable species to satisfy the food requirements for both man and domestic animals. This is demonstrated by the fact that in the history of agriculture, man has utilised about 3,000 of the 75,000 potentially edible species for crop production which, in turn, are about a quarter of all the known plant species (Figure 2.41). The species currently cultivated are 150 and human food requirements are based on 20 of these (Table 2.1), while only three species, grain, rice and maize provide 60% of the calories and 5% of the proteins consumed by man.

The history of the genetic improvement of plant species in the last one hundred years has been extraordinarily successful. With the birth of the science of genetics at the beginning of the twentieth century, it was possible to use a precise scientific approach to genetic improvement programmes which, over the years, have utilised



Fig. 2.42 - Ears of wheat in a field.

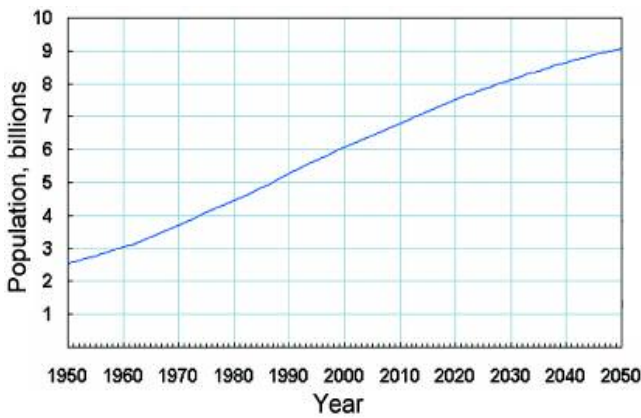


Fig. 2.43 - Growth in world population from 1950 to 2050 (Source: U.S. Census Bureau).

increasingly sophisticated instruments to modify the genetic characteristics of cultivated plants. In the 1950s and 1960s, the introduction of improved strains of cereal to underdeveloped countries, the application of modern agricultural techniques in these areas, the introduction of heavy machinery, the extensive use of chemical fertilisers and phytochemicals, led to greatly increased crop yields, giving rise to what has been defined as the

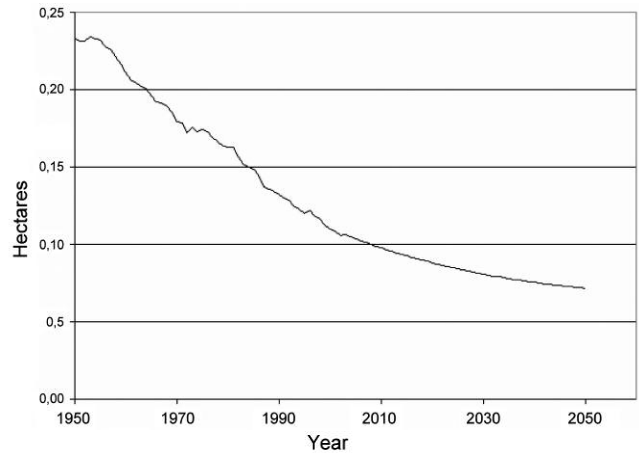


Fig. 2.44 - Variations in area of cereal crops per person from 1950 to 2050.

“Green Revolution” (Figure 2.42). The increase in crop yield was such that agriculture was now able to outstrip population growth, thus limiting the areas for further cultivation, and so reducing the rate of deforestation (Figures 2.43 and 2.44). The increased efficiency of new plant varieties also produced a more advanced quality, nutritional and technological standardisation of agricultural products, satisfying the requests of consumers and the



Fig. 2.45 - Variability among different apple varieties.

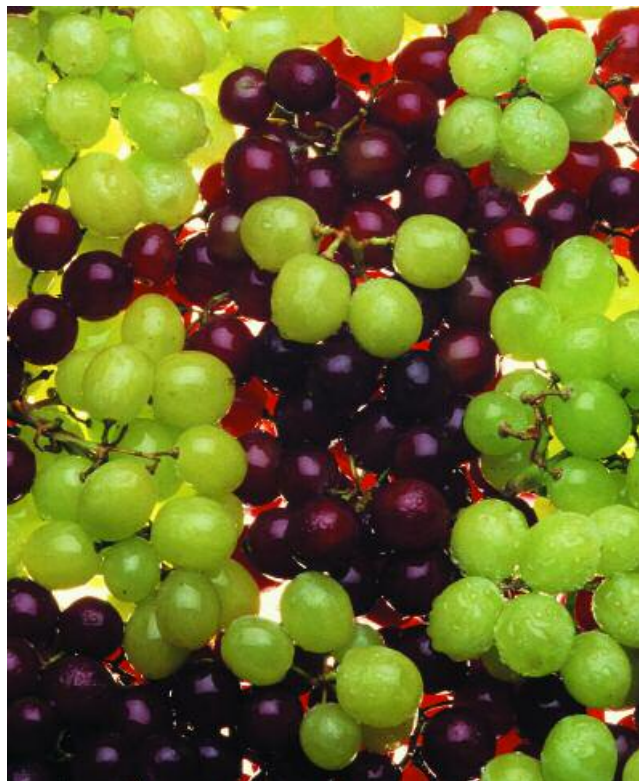


Fig. 2.46 - Grapes of different colours.



Fig. 2.47 - Variability in the colour and shape of the caryopsis and the size of maize ear.



Fig. 2.48 - Variability among wheat ears.

food transformation industry (Figures 2.45 and 2.46). As often occurs in human activity, however, even the most extraordinary results are not without their fallbacks and inconveniences. The spread of these high-yielding plant varieties, in fact, led to the severe erosion of genetic resources of cultivated species, with the disappearance of old local varieties that had high genetic variability and good adaptability to specific environments. This, in the long term, could seriously jeopardise the ability to further crops in terms of yield, quality and resistance to biotic and abiotic stress.

A part of the immense patrimony of genetic variability that exists in old local varieties cultivated in the first half of last century has been saved thanks to the collection and conservation of the germoplasm of cultivated species (Figures 2.47, 2.48, 2.49 and 2.50).

There are two possible approaches (see chapter *Conservation and monitoring of biodiversity in Italy*) to biodiversity conservation: *in situ* and *ex situ*. In situ conservation of biodiversity in agriculture was defined by BROWN (1999) as “the maintenance of the diversity present in and among populations of the many species used directly in agriculture, or used as sources of genes, in habitats where such diversity arose and continues to grow”. It encompasses entire agroecosystems, including immediately useful species, as well as their wild and weedy relatives that may be growing in nearby areas.

From the beginning of farming, wild relatives of crops have contributed to enriching the diversity and health of crop plants. Natural inbreeding between crops and wild relatives growing at the edges of farmers’ fields added to crop diversity and health. Many traits incorporated into modern crop varieties of potatoes, wheat, barley, rice, maize and oat, among other crops, which were particularly important in terms of adaptability (for example, resistance to biotic and abiotic stress) were introduced from wild relatives. Many wild crop relatives continue to exist only in domestication centres, mostly situated in developing countries. Wild relatives of crop plants constitute an increasingly important resource for improving agricultural production and maintaining sustainable agroecosystems, especially for their resilience to disease and parasites. They have contributed many useful genes to crop plants, and modern varieties of most crops now contain genes from their wild relatives. In fact, it is necessary to continually search for new pathogen-resistant genes that contrast the development of pathogen strains capable of overcoming previously introduced genes. The reduced use of phytochemicals, thanks to the use of resistant genotypes has a two-fold positive effect: it limits the environmental impact of farming activity, thus avoiding the emission of toxic substances harmful for both man and fauna, and it reduces production costs, a particularly important factor for de-



Fig. 2.49 - Variability in the size and colour of *Phaseolus coccineus* seeds.



Fig. 2.50 - Variability among the caryopsis of different rice varieties.

veloping countries. Numerous genes resistant to pathogens from wild species have been transferred to crop plants via genetic improvement programmes, for example, wheat resistant to blight and iodine from various wild species of the genera *Triticum* and *Aegilops*; rice resistant to viruses, bacteria and fungi from wild species of the genus *Oryza*, potatoes resistant to downy mildew, and tomatoes resistant to several fungi, bacte-

ria and viruses from many wild species of the genus *Solanum*, etc. It is also possible to transfer genes to improve the nutritional quality from wild species, for example, genes to increase the protein content of the caryopsis of wheat and for greater concentrations of Vitamin C in tomatoes. In many cases, unfortunately, the survival of wild plants is seriously threatened by the destruction or deterioration of their natural habitats. Numerous species of wild relatives of cultivated cereal such as wheat and millet, for example, are seriously threatened by excessive grazing and desertification processes. Other wild species used to transfer genes in potatoes, tomatoes and beans grow in mountain areas in South America and Central America; these ecosystems are extremely fragile and vulnerable to genetic erosion due to the growing anthropogenic pressure. Some wild species similar to those cultivated in agricultural ecosystems, grow on or around the farms; however with the extensive use of heavy machinery and the use of herbicides, the survival of these species seriously threatened. Increased and widespread anthropisation, even in developing countries with the consequent destruction of habitats and natural environments, makes the need to adopt adequate economic and technical measures even more urgent in order to safeguard these fundamental genetic resources in their countries of origin. In fact, these nations often do not possess the necessary economic resources to implement the opportune biodiversity conservation measures.

Naturally, *in situ* conservation, represents the ideal system of conservation of genetic plant resources because the populations can continue to evolve in their own habitat of origin, in which it is possible to reach the correct balance between conservation of pre-existing genetic variability and adaptation to environmental and climatic changes. These changes however could be too rapid, thus deteriorating the original genetic structure and the existing variability of these wild species. The ideal solution could be that of long-term seed conservation to block the genetic structure, and its regeneration in areas of origin to limit the harmful effect of selecting a different environment. For a series of reasons, there is often no alternative to *ex situ* conservation in countries and different environments from those of origin of the material conserved. For example, *ex situ* conservation becomes indispensable for old local varieties that have been abandoned by farmers. This material is an invaluable source of useful genes that can easily be transferred into modern crop-yielding varieties. As these

wild plants belong to the same species and genotypes, having been cultivated, they possess a high degree of domestication. In fact, they do not have the problems that arise from the use of wild species that require a long “cleaning” process of adverse genes introduced with hybridisation, which is carried out via repeated crossbreeding or with chromosomal engineering techniques. Another advantage of *ex situ* conservation is that the custody of the same material in several centres dislocated in various countries excludes the possibility of irrevocably destroying these irreplaceable materials. *Ex situ* conservation involves a series of activities that include the gathering, management and conservation of germoplasm collections, the regeneration of this material, the characterisation and evaluation of the accessions, and the documentation and distribution to the users. All these phases require great care and precision, but the most critical inconvenience that may arise is the regeneration of seeds to reactivate germinability. In fact, during regeneration that occurs outside the original environment, it is inevitable that modifications to the genetic structure occur, and this subsequently modifies the variability of the material in custody.

Progress made in recombinant DNA and molecular biology techniques, in particular molecular markers, has contributed in a substantial manner to make these conservation of germoplasm more efficient both *in situ* and *ex situ*. With the use of molecular markers, it is possible to make accurate evaluations of the entity and distribution of the existent genetic variability in natural populations. This makes selected targeted intervention possible in those areas where the greatest variability is present, and to take the most appropriate *in situ* conservation measures in collecting samples for *ex situ* conservation. In the next phase of conservation, molecular markers are used to monitor genetic variability, verifying that erosion has not taken place, especially during the seed regeneration. Knowledge of the existing variability in collections, and above all, the identification and elimination of possible redundancies leads to the creation of a “core collection”, that encompass the maximum genetic variability within a limited number of representative accessions of the entire collection, thus rationalising the management of material and their distribution.

Molecular techniques, in particular, the use of molecular markers, have also been used to monitor DNA sequence variation in and among species and to create new sources of genetic variation by introducing new and favourable traits from wild species. Alternative meth-

ods such as the construction of partial maps MAS (Map Assisted Selection), and combination of pedigree and marker information, have proved useful in identifying marker/trait associations. These techniques have greatly reduced the time and costs of conventional cereal breeding, hence breeders are extremely interested in new technologies that could make this procedure more efficient.

Another application of molecular markers for the genetic studies of cereals includes the detection of monogenic and quantitative trait loci (QTL) and the introduction of new characters in elite germoplasm. Knowing the location of these genes/traits and specific alleles offers the possibility to apply marker-assisted selection in cereals, because one of the main objectives of plant breeding is the introgression of one of more favourable genes from a donor parent into the background of an elite variety. Marker-assisted selection allows plant selection at the juvenile stage from an early generation, while unfavourable alleles can be eliminated or greatly reduced during these early stages of plant development. The application of particular molecular markers are also utilised in breeding for resistance to certain diseases, insects and abiotic stress.

Up to thirty years ago, the characterisation of biodiversity in Italy was limited to sporadic and fragmented initiatives by individual researchers. The turning point came in the early 1970s, with the establishment of the Germoplasm Laboratory of Bari, which subsequently became a permanent institute by the National Committee for Agrarian Sciences at the CNR (National Research Council). In the last thirty years the Germoplasm Institute has carried out an intense activity of collection, conservation and assessment of numerous cultivated species and wild progenitors of crops that are important in the Mediterranean Basin. The CNR has also promoted the creation of a national network to safeguard genetic resources of fruit trees, with the participation of CNR institutes, universities and research centres, and the Ministry for Agriculture. The establishment of the Ministry for the Environment Land and Sea Protection was another fundamental turning point for research in the environmental sector and in the management and conservation of plant and animal biodiversity in Italy. The conservation of natural ecosystems, owing to its countless implications, relationships and reciprocal interactions, cannot disregard the problems connected with agricultural activity, with sustainable and ecocompatible management, and with the plant material utilised.

Three types of initiatives can be undertaken to safeguard biodiversity which lies at the basis of Italian agriculture:

- protection of large tracts of natural ecosystems adjacent to agricultural ones that contain wild progenitors of important agricultural species, both plant and animal;
- protection and utilisation on farms of rare cultivar or threatened and/or wild progenitors, as well as breeds of critically endangered domestic animals;
- *ex situ* stocking and maintenance of the germoplasm of crop species.

As regards the first type of initiative, the first step is to identify and protect large stretches of natural habitats which, along with their populations of plant, animals and microorganisms, can contribute to the general equilibrium of nature and guarantee the conservation of genetic resources of crop species. Wild progenitors of crop plants are not always sufficiently protected in their wild habitats in nature, therefore it is opportune that this factor be taken into consideration in identifying the areas to be protected.

With regards to the second type of initiative, it is essential that this material be conserved together with the genetic variability that comes with their hybridisation.

Long-term *ex situ* stocking of genetic material belongs to the third type of initiative. Cultivars, breeds, and to a much lesser extent wild progenitors with scarce chances of survival *in situ* could be stocked by setting up gene banks.

The loss of genetic diversity in crop plants is due to adopting varieties that are characterised, among other things by rapid and uniform seed germination, almost contemporary flowering and maturation; size and form suited to mechanised cultivation and harvesting, uniformity of the product in terms of taste, size, chemical composition, and long term yielding stability. Genetic uniformity, however, encourages the rapid spread of new populations of pathogens which, following mutation, recombination or other, can manifest virulence with respect to plants and animals already utilised in agriculture that were previously tolerant or resistant.

Modern agricultural systems must use a wide mosaic of genetic diversity with regards to single crop species and among these same species in order to overcome this vulnerability. For this reason, it is important that the institutional bodies that promote and fund research programmes in the agriculture sector should sustain projects which:

- evaluate the genetic distance among varieties of a given species and determine the nature of its resistance to

pathogens and the host-parasite interaction, to be implemented together with an assessment of variations in the virulence of parasites and in the panorama of agricultural varieties under consideration;

- evaluate the genetic erosion and vulnerability and monitor the use and geographical distribution of elite germoplasm;
- establish new, alternative gene pools which act as gene reservoirs. In particular, it is necessary to identify new sources of genes and incorporate them into base material for genetic improvement.

These along with other measures could guarantee the preservation of adequate genetic variability that effectively responds to new agrotechnologies, changes in the virulence of pathogens and changes in the needs of society in general, both now and in the future.

In reaching the objectives set out in the CBD, it is vitally important to harmonise the different national programmes for biodiversity conservation. In facing these problems more effectively, which often involve the co-operation of other countries, a supranational body such as the FAO could act as coordinating body. A primary role in the conservation of genetic resources is played by the network of 16 international institutes which make up the Consultative Group on International Agricultural Research (CGIAR), almost all situated in developing countries (Table 2.2), which has a collection of more than 500,000 accessions. Many of these institutes, thanks to their location in the centres of origin where wild progenitors of crop species are found, carry out an invaluable role in the *ex situ* conservation of genetic resources.

The most significant commitment to genetic resources conservation comes from the International Plant Genetic Resources Institute (IPGRI), a direct continuator of the International Board for Plant Genetic Resources (IBPGR), promoted and established by the FAO in Roma in 1974. IPGRI, hosted in Rome by the Italian government, has the task of monitoring, safeguarding and enhancing the sustainable use of genetic resources for the well-being of mankind, through research programmes and training programmes and a series of regional centres. It carries out its statutory mission based on specific international agreements, sponsored and financed by the FAO, the World Bank, UNEP (United Nations Environment Programme), regional banks and by numerous governments, including Italy.

A very important international agreement in harmony with the Convention on Biological Diversity is the International Treaty on Plant Genetic Resources for Food

and Agriculture, approved after seven years of negotiations by the FAO Intergovernmental Conference in November 2001.

Italy ratified the Treaty with Law April 6th 2004, No. 101. Its principal objectives are to guarantee food security through the conservation, exchange and sustainable use of the world's plant genetic resources for food and agriculture, as well as the fair and equitable benefit sharing arising from its use. The Treaty implements a multi-lateral system of access and benefit sharing for a list of 64 of the most important food and forage crops essential for food security and the interdependence for those countries that ratify the treaty.

This benefit sharing is carried out through information-exchange, access to and the transfer of technology, and capacity-building. It also foresees a funding strategy to

mobilise funds for activities, plans and programmes to help, in particular, small farmers in developing countries. This funding strategy also includes the share of the monetary benefits paid under the Multilateral System. The Treaty also recognises the enormous contribution that farmers and their communities have made and continue to make to the conservation and development of plant genetic resources. This is the basis for Farmers' Rights, which include the protection of traditional knowledge, and the right to participate equitably in benefit-sharing and in national decision-making about plant genetic resources. It also acknowledges that plant genetic resources are the raw material indispensable for crop genetic improvement and are essential in adapting to unpredictable environmental changes and future human needs.

CGIAR - Consultative Group on International Agricultural Research	http://www.cgiar.org/
CIAT - Centro Internacional de Agricultura Tropical, Colombia	http://www.ciat.cgiar.org/
CIFOR - Center for International Forestry Research, Indonesia	http://www.cifor.cgiar.org/
CIMMYT - Centro Internacional de Mejoramiento de Maiz y Trigo, Mexico	http://www.cimmyt.org/
CIP - Centro Internacional de la Papa, Perú	http://www.cipotato.org/index2.asp
ICARDA - International Center for Agricultural Research in the Dry Areas, Syria	http://www.icarda.cgiar.org/
ICRAF - International Centre for Research in Agroforestry, Kenya	http://www.worldagroforestrycentre.org/level1a.htm
ICRISAT - International Crops Research Institute for the Semi-Arid Tropics, India	http://www.icrisat.org/
IFPRI - International Food Policy Research Institute, USA	http://www.ifpri.org/
IITA - International Institute of Tropical Agriculture, Nigeria	http://www.iita.org/
ILRI - International Livestock Research Institute, Kenya	http://www.cgiar.org/ilri/
IPGRI - International Plant Genetic Resources Institute, Italia	http://www.ipgri.cgiar.org/
IRRI - International Rice Research Institute, Philippines	http://www.irri.org/
ISNAR - International Service for National Agricultural Research, Olanda	http://www.isnar.cgiar.org/
IWMI - International Water Management Institute, Sri Lanka	http://www.cgiar.org/iwmi/
WARDA - West Africa Rice Development Association, Costa d'Avorio	http://www.warda.cgiar.org/
WorldFish Center, Malesia	http://www.worldfishcenter.org/

Table 2.2 - International Research Centres of the CGIAR network.

GENETIC DIVERSITY OF FOREST TREE SPECIES

[Gabriele Bucci, Fiorella Villani, Giuseppe Scarascia Mugnozza]

Studies conducted in recent decades have shown that the genetic diversity of forest tree species in Italy, and above all, in the Mediterranean region is generally higher than in other European regions. Apart from a reasonable number of endemic species, there are specific and particular gene pools all along the Italian peninsula even for forest species that have a wide distribution range, such as *Fagus sylvatica*, *Abies alba*, *Picea abies*, *Quercus* sp.p., etc. Among the reasons at the basis of this high rate of biodiversity, there is the particular evolutionary history of the region, with the presence of

refuge-areas during the glacial eras for various species with a pan-European range. This situation requires an in-depth study on the genetic variation among and within populations of Mediterranean trees. Genetic markers and genetic maps can be of great use in the genetic study of forest populations and of the evolutionary processes of trees. Immediate applications of these studies go from forest genetic improvement to the planning and management of parks and nature reserves, as well as the elaboration of appropriate strategies for *in situ* and *ex situ* conservation of genetic resources, above all, in relation to the foreseeable changes in environmental conditions and the probable shift of favourable habitats of these aforesaid species.

INTRASPECIFIC BIODIVERSITY OF FOREST TREES

[Gabriele Bucci, Fiorella Villani, Giuseppe Scarascia Mugnozza]

The study of microevolutionary processes

An analysis of the dynamics of genetic biodiversity in populations, through the study of the microevolutionary processes that govern it, is fundamental in formulating appropriate long-term conservation strategies for genetic resources, and in adopting the correct and most effective management practices.

The limited differentiation among populations, characteristic of prevalently allogamic species such as forest trees, raises the question of how this variability is spatially organised and distributed within the single populations. Moreover, the manner in which genetic biodiversity in populations is organised may influence natural selection, the hereditary transmission of adaptive traits and/or may affect an increase of new adaptive variants in the population. For example, various studies of spatial autocorrelation of several forest tree species have highlighted significant aggregation of genotypes, with a patch size (average size of an area within which individuals show greater genetic correlation than two individuals sampled at random in the entire population) of about 20 m, for example, of *Picea Abies* and *Fagus sylvatica*.

Moreover, the actual size of natural populations has been studied (eg. *Pinus leucodermis* in Pollino, BUCCI and VENDRAMIN, 2002) along with the numerous specimens of interfertile species that possess alleles with a high adaptive value and of diversity dynamic (genus *Quercus* in Piemonte, and *Fraxinus* in the Alps and Apennines).

The genetic structure of species and biodiversity of Italian populations

Ongoing microevolutionary processes, such as genetic drift, directional selection and dispersal, combined with the characteristics of biological reproduction, evolutionary history, and heterogeneity of the colonised habitats, frequently leads to levels of genetic biodiversity that is not the same in various parts of the distribution range of the species. Macrogeographic studies of the genetic structure of the species, and in particular, estimates of the genetic diversity and divergence of populations, could lead to the identification of the gene pools and hotspots of genetic variability that are useful in elaborating appropriate conservation policies regarding the genetic resources of the species.

For example:

- the presence of unique and rare alleles with high frequency in the population of *Picea abies* in the northern Apennines indicates that it belongs to a gene pool that is different from the Alpine one, thus supporting the theory of the existence of refuge areas of species in central Italy during the last glaciation;
- through the reconstruction of the phylogenetic relationships of *Abies alba* populations it was possible to demonstrate how populations in southern and central Italy were phylogenetically similar to each other compared to the northern ones; in fact, the populations in central Italy originated from a mix of different gene pools in

the post-glacial period, that is, from the recolonisation that originated from the refuge areas situated in southern Italy during the last glaciation.

- in the case of *Pinus halepensis*, the high haplotypic variability of some hypervariable chloroplastic loci for populations situated in Gargano and in continental Greece was demonstrated, compared to other populations in the rest of the species' range, which supports a theory of possible existence of a biodiversity hotspot for species straddling the southern Adriatic;
- the theory regarding refuge-areas in southern Italy during the last glaciation was also confirmed for *Fagus sylvatica*, which then gave rise to the migratory wave of post-glaciation recolonisation of the Apennine range;
- the genetic diversity of Italian populations of *Fraxinus excelsior* was found to be greater than the remaining populations in the European range of the species; in particular, this higher level of biodiversity seems due to an eastern Alpine nucleus that has haplotypes that are not present in any other European population.

Reproductive isolation, genetic drift and habitat fragmentation

The degree of isolation in itself may constitute an important factor that can affect the genetic structure of populations. In fact, a drastic reduction in the number of reproducers within a population in conditions of isolation can determine stochastic variations of allelic frequencies leading to the fixation of specific alleles out of genetic drift, and the consequent loss of biodiversity. Moreover, this sub-

stantiates the negative effect of habitat fragmentation on biodiversity in forest trees: the greater the degree of isolation of forest tree populations due to range fragmentation, the greater the danger of loss to intrapopulation variability owing to genetic drift.

Geographic patterns of biodiversity and breeding zones

Breeding zones are those genetically homogeneous geographic regions in which adaptation of local populations to specific environmental conditions is considered optimal. Thus, the uncontrolled transfer of propagation material among different regions can pollute local gene pools and reduce the survival and growth of the material itself. Moreover, breeding zones constitute the genetic background on which it is possible to establish the number and the localisation of "biogenetic" reserves for the single forest species, in view of improved and more appropriate strategies for the long-term conservation of intraspecific biodiversity and gene pools.

For example, some studies were conducted on *Picea abies* to geographically demarcate the genetically homogeneous areas within the European range of the species: five different zones along the Alpine arc were identified. It is interesting to note that on the basis of data at our disposal, the south-western area of the Alps (the Ligurian, Maritime and Cozie Alps), included in the Apennine nucleus of the presumed refuge-area of Campoline (Pistoiese Apennines), was found to be extremely divergent compared to the rest of the Italian and European range, with high levels of intraspecific biodiversity, and therefore interesting from a conservation point of view.

BUCCI G., VENDRAMIN G.G., 2000 – *Statistiche spaziali applicate allo studio della biodiversità: identificazione di 'breeding zones' in specie forestali*. In: BUCCI G., MINOTTA G., BORGHETTI M. (a cura di) *Applicazioni e prospettive per la ricerca forestale italiana*. SISEF Atti 2. Edizioni Avenue Media, Bologna, pp. 217-224.

Local adaptations, ecotype differentiation and phylogeography

Local selective pressures can lead to adaptation to specific ecological conditions, with the creation of different ecotypes of the species that differentiate greatly one from the other. Macrogeographic selective pressures, such as those caused by climatic variables often generate clines (gradients) of changes in the species' range, in line with climatic or environmental gradients.

Population migration leave traces in the genetic patri-

mony of the organisms. For forest species, the recolonisation of favourable habitats normally occurs through the dissemination by a subgroup of individuals that are part of the original population. In the absence of selective processes, traces of the random variations in the composition or in the allelic frequency of the subgroup of colonisers can persist for a long time in populations that have settled in a given environment. In turn, the colonisers give rise to new settlements, with random variations in terms of frequency and allelic composition, and so on. This process frequently leads to a loss of genetic biodi-

versity. It is possible to reconstruct the migratory paths of forest species by analysing the path of their alleles at a macrogeographic level or by assessing the gradient of variation of the allele frequencies of the current populations, going back to the sites from which the species spread (refuge areas in the glacial period) which normally shows a high level of genetic and functional biodiversity.

In recent years, studies have been conducted on the phylogenetic relationships among forest species populations utilising neutral molecular markers that have allowed us to obtain the necessary knowledge to understand the role carried out by microevolutionary processes (historic and/or present) in establishing the current distribution of the genetic resources of a given species. Apart from reconstructing crucial events such as recolonisation processes, these studies have led to the identification of genetic biodiversity hotspots (useful in defining strategies for the conservation of genetic resources), and have provided the necessary information background which makes it possible to calculate possible migratory processes in the future, consequent to the foreseen climate changes. The results of the aforesaid activity can be summed up as follows:

1. the degree of genetic differentiation among populations varies on the basis of the reproductive strategies of the different species, in particular, on the dispersal mechanisms of seeds and pollen. Species with small seeds with easy anemophilous dispersion (e.g., *Populus tremula* - SALVINI *et al.*, 2001) have a lower degree of genetic differentiation than species with large seeds and/or zoochorous dispersion (e.g., *Fagus sylvatica*);
2. the distribution of genetic diversity among populations is strongly influenced by human activity; great anthropogenic pressures can lead to substantial changes in the genetic structure of the species, such as *Castanea sativa* in which the low genetic divergence among populations was caused by the intense exchange of genetic material in ancient Roman times;
3. most European forest species have a macrogeographic structure of genetic biodiversity, with alleles/haplotypes that are phylogenetically more similar than those generally grouped in marginal regions (BUCCI and VENDRAMIN, 2000a,b);
4. the present distribution of genetic diversity is greatly affected by events that occurred during the last glaciation and by migratory processes in the post-glacial period, starting from three main refuge areas in the three principal European peninsulas (the Iberian, Italian and Balkan peninsulas);

5. at the multispecies level, it has been observed that the forests characterised by a greater genetic divergence are situated in southern European areas where the refuge sites during the last glaciation were found, while those characterised by higher levels of genetic diversity are situated in central Europe where several migratory routes converged, leading to a genetic exchange between populations that were very divergent.

Studies conducted so far indicate that Italy is one of the principal refuges areas from which the post-glaciation recolonisation commenced. For this reason, populations of the Italian peninsula are generally characterised by high genetic richness, with the presence of rare and unique alleles/haplotypes, such as *Fagus sylvatica*, *Fraxinus excelsior*, *Quercus ilex*, *Corylus avellana*, and *Abies alba*. In the past geological periods, the proximity of the Italian peninsula with that of the Balkans encouraged the genetic exchange among populations of different origin, thus increasing the level of genetic diversity and the importance of conservation of the Italian populations, such as *Pinus halepensis* and of the multispecific complex *Quercus robur*, *Q. petraea*, *Q. pubescens* and *Q. frainetto*.

Functional biodiversity and adaptive traits

The study of the genetic basis of complex traits is the first and most important step in evaluating the relationships between functional biodiversity and the adaptive potential of populations of forest species that are capable of obtaining different ecophysiological performances which also reflect geographic diversity.

a) Adaptive biodiversity and efficient water use

Adaptation to periods of drought, particularly frequent in Mediterranean environments, may be of the structural types (cuticular thickening, waxes, trichomes, sclerophylly, prostrated epigeal structures, etc.), of the ecophysiological type (regulation of stomata movements, phenological "phase-displacement", etc.), or of the "active" type (that is, based on the interception of ground water in mild periods and deep waters in periods of drought). Several combinations or different degrees of mechanical expression mentioned are at the base of functional biodiversity and the adaptability of individual specimens, demi or populations. Very little information from literature is available on adaptive biodiversity of plant species, owing to the complexity of the research in the sector. Recent studies utilising stable carbon isotopes and other physiological techniques have pinpointed common evolutionary dynamics in species that are phylo-

genetically extremely different (*Castanea*, *Pinus*, *Quercus*, *Eucalyptus*, *Pseudotsuga* etc.), though all found in regions that have distinct seasonality (such as the Mediterranean regions) intersected by climatic gradients. The aforesaid studies indicated an inverse response in the efficiency of water use compared to what emerged in comparative experiments. Italian studies conducted on Mediterranean and eastern populations of *Castanea sativa* (LAUTERI *et al.*, 1997, 1999) discovered the physiological basis of adaptability to several types of water availability, as well as the existence of a Mediterranean ecotype and an eastern one. Origin tests indicated a great difference in the efficiency of water use, assessing the ecotypes with the use of isotopic techniques. The radical functionality and the plant-environment interactions in the soil-plant-atmosphere continuum are currently studied with oxygen stable isotopes. Progeny testing is producing the first results regarding the phenotypic plasticity and additive variance of European chestnut populations in constraining climatic sites. Parallel studies of phylogenetically distant species from the chestnut (*Quercus ilex* and *Pinus pinaster*) have confirmed analogies in the intraspecific diversity of adaptation mechanisms to water availability (TOGNETTI *et al.*, 2000) on different geographic scales.

b) Biodiversity and defence mechanisms against pathogens.

Terpenes are a class of complex secondary metabolites present in essential oils/attars and resins, that can be separated with laboratory techniques (mobile phase in gas chromatography), implicated in chemical defence processes in forest species from parasitic attacks. They are genetically controlled and are frequently utilised as biochemical markers for taxonomic characterisation in biodiversity studies among species, among populations of the same species, among families and clones. Variations in the content and nature of terpenic compounds from various parts of the range of different forest species are regarded as indications of differentiated resistance to pathogen attacks.

c) Geographic diversity of the functional characters

The morphological, structural and physiological traits of individuals concur in determining their ecophysiological performance in nature, and are at the base of functional adaptation to environmental conditions of the habitat to which they live. Variations in the above-mentioned characteristics found at the macrogeographical level (that is, different values of parameters for the aforesaid traits in populations of different origin within the species' distribution range) are indicative of the adaptive value of the traits studied, and at the same time reveal possible differential adaptations to specific climatic conditions.

DEVELOPMENTS AND PERSPECTIVES ON INTRASPECIFIC AND FUNCTIONAL GENETIC BIODIVERSITY OF FOREST TREE SPECIES

[Gabriele Bucci, Fiorella Villani, Giuseppe Scarascia Mugnozza]

In the field of forest biodiversity, it is urgent to reorder the existing genetic data, through the reorganisation of currently available information, the standardisation of work methods and the harmonisation of sampling efforts and analyses, in order to extend knowledge on the intraspecific biodiversity and to produce a "traceability map" of the existing genetic resources. Moreover, there is the need to prepare a "risk map" for intraspecific forest biodiversity, which evaluates the evolutionary response capacity of forest populations to phenomena of genetic loss via genetic drift (fragmentation, reduced extent of habitat, etc), and selection capacity with regards to altered ecological conditions of habitats (climatic fluctuations, changes in land use, etc.). National thematic maps regarding the conservation status of natural genetic resources of single forest species (with the use of GIS technology) will form the basis on which intraspecific hotspots can be identified, and they will also be useful instruments for for-

est ecologists and policy makers alike. Finally, the elaboration of response models of forest populations to foreseeable changes in environmental conditions from regional scenarios obtained with climatic models are fundamental in defining appropriate conservation policies.

Maintenance mechanisms of biodiversity: "new" approaches and "old" ideas

The recent introduction of laboratory techniques to identify the DNA polymorphisms of individuals is a potent tool that analyses the processes that are at the base of the current distribution of genetic variability and of the mechanisms that maintain it. Selective processes (clinal, directional, disruptive, epistatic, etc.) have always been considered fundamental factors in maintaining high levels of intraspecific biodiversity in forest tree populations. The availability of polymorphisms in

the expressed regions of the genome of forest species (therefore, potentially under selection) will in the near future shed light on the importance of these processes in nature with respect to stochastic type processes (for example, genetic drift), which can be detected through neutral types of polymorphisms (like most unexpressed DNA).

Intraspecific biodiversity and stability/resistance of forest ecosystems

Forest trees are long-lived, allogamous, and generally strongly heterozygote organisms that have developed mechanisms to maintain high levels of intraspecific biodiversity. These mechanisms, combined with the high heterogeneity of the habitats in which they live, have contributed to make trees among the living organisms with the highest genetic variability. However, what has yet to be discovered is the effect of this biodiversity on the productivity and stability of forest biocoenosis. To this regard, there are three fundamental questions that need to be answered through appropriate scientific studies.

(1) In fluctuating environmental conditions (typical of forest habitats in boreal regions even in the absence of external disturbances), does a population made up of individuals that have different ecological optima display a greater productivity than homogeneous populations from a genetic viewpoint and with the same optimum? Experiments and simulations on intraspecific biodiversity have provided evidence regarding the greater productivity of highly heterogeneous communities in functional terms compared to simplified communities with reduced levels of biodiversity.

(2) How important are forest trees in natural populations with individual phenotype plasticity (which encourages acclimatisation to changed environmental conditions) and intrapopulation diversity (which provides the base material for the processes of evolutionary adaptation) on the stability of forest ecosystems? Is the stability of these two processes in present forest biocoenosis the same in optimal conditions (e.g. in the centre of the species' range) as in marginal conditions (e.g. in disjunct populations of the principal range)? Even in this case, studies in intraspecific biodiversity of grassland communities have shown that a greater biodiversity within the functional groups provides a greater stability to biocoenosis, in terms of resistance to colonisation by invasive species.

(3) As a consequence of point (2), what is the importance in various forest tree species of ecotype differentiation compared to individual phenotype plasticity, that is, up to what

point is the vast range of many forest species the consequence of genetic differentiation processes in breeds or ecotypes, and to what extent is it the result of the capacity of individuals of a given species to acclimatise to a large spectrum of different environmental conditions? This last point is vital in establishing precise biodiversity conservation policies and implementing appropriate long-term safeguard strategies. For example, if the objective is the conservation of the potential adaptability of the species, it would seem crucial to protect relict populations that have adapted to specific conditions and, along with these, specific genes codifying for functional characters, as opposed to the conservation of marginal populations of functionally homogeneous species with high phenotype plasticity.

In conclusion, does maintaining the productive stability of forest biocoenosis over time mean maintaining the resistance/resilience to environmental disturbances (such as expected climate change), and does it also mean maintaining and increasing the complexity/diversity? In order to reply to this question, a greater quantity of scientific evidence from future research on the functionality of ecosystems and on the relationship between the complexity/functional diversity and productivity/stability of forest biocoenosis is necessary.

Migration in response to climate change

Forest species are capable of facing climate change predicted by global circulation models through acclimatisation to altered climatic conditions (depending on to the phenotype plasticity of the individuals), adaptive evolution (through selection of genotypes with particular ecophysiological performance) or by population migration (through the dissemination of propagules in favourable habitats). Moreover, this last process seems to have been the primary path taken by forest species in answer to environmental changes in the past.

In the past 13,000-14,000 years (that is, since the end of the last glaciation), the climate in Europe has been subjected to a constant warming, which has provoked a progressive shift of the bioclimatic belts northwards. It is well known that biotic forest communities have followed the movement of habitats that are favourable to them through a slow process of dissemination and recolonisation of these habitats that slowly have become more suited to the settlement of forest ecosystems. This process has occurred at different speeds and over different time periods for various forest species in Europe. A calculation of the mean migration speed with which forests have recolonised the areas left free by glacial cover

varies from 0.05 to 2 km per year, depending on the dissemination capacity of the species.

Climatologic series and calculation models are in agreement in foreseeing global warming in the next few decades. This would provoke a further shift of bioclimatic belts towards the poles, and in a more accentuated manner in the boreal hemisphere. The movement of favourable habitats would in turn set off the forest migration, as has already happened in the past (and is still occurring). However, compared to the past, the speed of climate change is so much faster that it far surpasses the capacity of forests to colonise and settle in favourable habitats. This would lead to a series of negative consequences for the biodiversity patrimony of our forests: (1) the composition in species of forests could change in relation to the capacity of single species to cope with the fore-

seen changes in environmental conditions and to intraspecific competition factors; (2) in most cases there would be a reduction in the range and increased fragmentation of forest ecosystems, to a greater extent where barriers hinder natural expansion and migration (for example, the Alps); (4) areas currently delegated to biodiversity conservation could be greatly impoverished in terms of adaptive/evolutionary potential of the species present and therefore no longer functional to the scope; (5) the refuge areas located in the south of Europe (the largest "reserves" of genetic variability) are the areas most exposed to the effects of climate change (desertification or tropicalisation of the climate), and whose genetic impoverishment would constitute the greatest loss of functional and genetic biodiversity and a serious damage to the richness of the European forest patrimony.

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BIODIVERSITY AND LANDSCAPE

[Carlo Blasi]

THE EUROPEAN CONVENTION ON LANDSCAPE

In the volume entitled *Flora* of the series *Conosci l'Italia*, GIACOMINI and FENAROLI wrote that the different landscapes that make up the physiognomy of Italy are almost always distinguished by the characteristic types of vegetation: types of trees and forests, types of flowers and flowering fields, types of grasses and grasslands, at times shaped by man, at other times left to grow wild. If landscape were conceived not only from an aesthetic point of view, but also from a scientific and naturalistic one, we do not believe that the emotions we receive when looking at these unparalleled elements of our planet would be limited or impoverished. Instead, we believe that new sources of knowledge would only inspire new reasons for admiration and interest in nature.

In the 1960s, Henry A. GLEASON and Arthur CRONQUIST, both curators of the New York Botanic Gardens respectively, went further in signalling the close relationship between vegetation and landscape, "Plants and the landscape. Perhaps we would do well to change one word in that phrase and write plants are the landscape" (GLEASON and CRONQUIST, 1968).

Successively, the meaning given to the term *landscape* was modified till reaching the present definition found in Article 1 of the European Landscape Convention which intends to integrate the naturalistic component with the historical, social, cultural and aesthetic ones: "Landscape" is defined as "an area, as perceived by people, whose character is the result of the action and interaction of natural and/or human factors".

From this brief premise, it is possible to understand how landscape, the result of a complex and systematic interaction of natural, historic, cultural and social factors, is the patrimony of naturalistic and humanistic sciences. For this reason, landscape is considered by the European Convention as synonymous with territory, and it becomes the fundamental nature ecosystem reference for the biological diversity conservation linked, not only to characteristics of nature, but to the more complex evolution of nature, history and culture. This is in line with the objectives and the priority habitats lists of the Habitats Directive in which many of these habitats are connected to the presence of agro-silvo-pastoral activities, and with the general objective of the Directive regarding consideration to be given to all the territory and not only the well-conserved sites.

In a recent convention organised in Rome by the *International Association for Environmental Design* (IAED), various issues connected to the current interpretation of landscape were faced. In particular, the new meaning given to the perception understood as the "recognition" of the identity of an area and not as the emotional state of an individual. As TURRI (2002) rightly affirms, landscape should be considered the visible face of the territory that moves, lives and ages with man, the perception of landscape should not be an emotional or private fact, but rather the acknowledgement of this complex interaction of history, nature and culture. Attributing the meaning of acknowledgment to perception means placing landscape in the context of actions that characterise the planning and management of the territory (BLASI *et al.*, 2005).

Fragmentation of ecosystems due to anthropogenic activity leads to new types of land cover and alters natural systems creating very evident variations in landscape, habitat, flora and faunal composition in functional and structural terms. Landscape follows the history of man and feels the effects of the cultural and social evolution of local populations. All this however within a physical and biological system that evolves and is transformed with its own timing and with different norms from the rapid transformation brought on by man. It is suffice to think of changes made in agricultural production systems, in the space of a decade, which have led to great changes in landscape. In fact, one of the most significant causes for biodiversity loss is connected to the changes in land use (see following section).

For this reasons, in describing the biodiversity status of species and communities in Italy, it is also important to briefly mention the principal landscape systems that have been obtained from integrating typological models and cartographic models (phytoclimate, lithomorphological units and vegetation series) in the vast programme "Completion of Naturalistic Knowledge" promoted by the Nature Protection Directorate of the Italian Ministry for the Environment Land and Sea Protection (see chapter *Synthesis on the main national and international monitoring plans and programmes*).

THE LANDSCAPES OF ITALY

To classify and understand landscapes in structural and functional terms it is necessary to know the physical and biological potential of a territory, and environmental heterogeneity determined principally by physical causes (cli-

mate, lithology and morphology) in typological and cartographic terms. Man's creativity combined with knowledge of environmental peculiarities has often created landscapes which contain both farmed portions of territory together with portions of wilderness, where man's activity is integrated in a compatible manner with nature to such an extent that it is almost impossible to discern the social, cultural and economic element from the natural one (cultural landscapes).

Therefore, the hierarchical land classification (BLASI *et al.*, 2000, 2001, 2003) becomes the essential methodological base to identify and map potential homogenous contexts (environmental unit) and heterogeneous contexts that are functional and morphologically homogeneous (landscape unit). All this becomes the essential knowledge reference for the territorial ecological network that is created by integrating potential heterogeneity with actual mapped heterogeneity according to the CORINE Land Cover legend (BLASI *et al.*, 2005).

This integrated vision of landscape that gives meaning to this new dynamic and active conception of biodiversity conservation, is in line with concepts expressed in the CBD and in the Habitats Directive, in particular.

This is the reason why efforts have been made in recent years to highlight potential heterogeneity through the application of an integrated and deductive process, which overlaps physical "information strata" (climate, lithological and morphological data) and biological "information strata" (vegetation, flora and fauna). In this manner, it is possible to extract models which identify the relative distribution. This process (BLASI *et al.*, 2000) integrated with traditional phytosociological findings (inductive process) has allowed us to identify heterogeneity (on a scale of 1:250,000) even in terms of "vegetation series". These series are the collection of communities that tend towards the same maturity phase within a specific territorial context that is homogeneous for its physical and biological characteristics and variable even in scale.

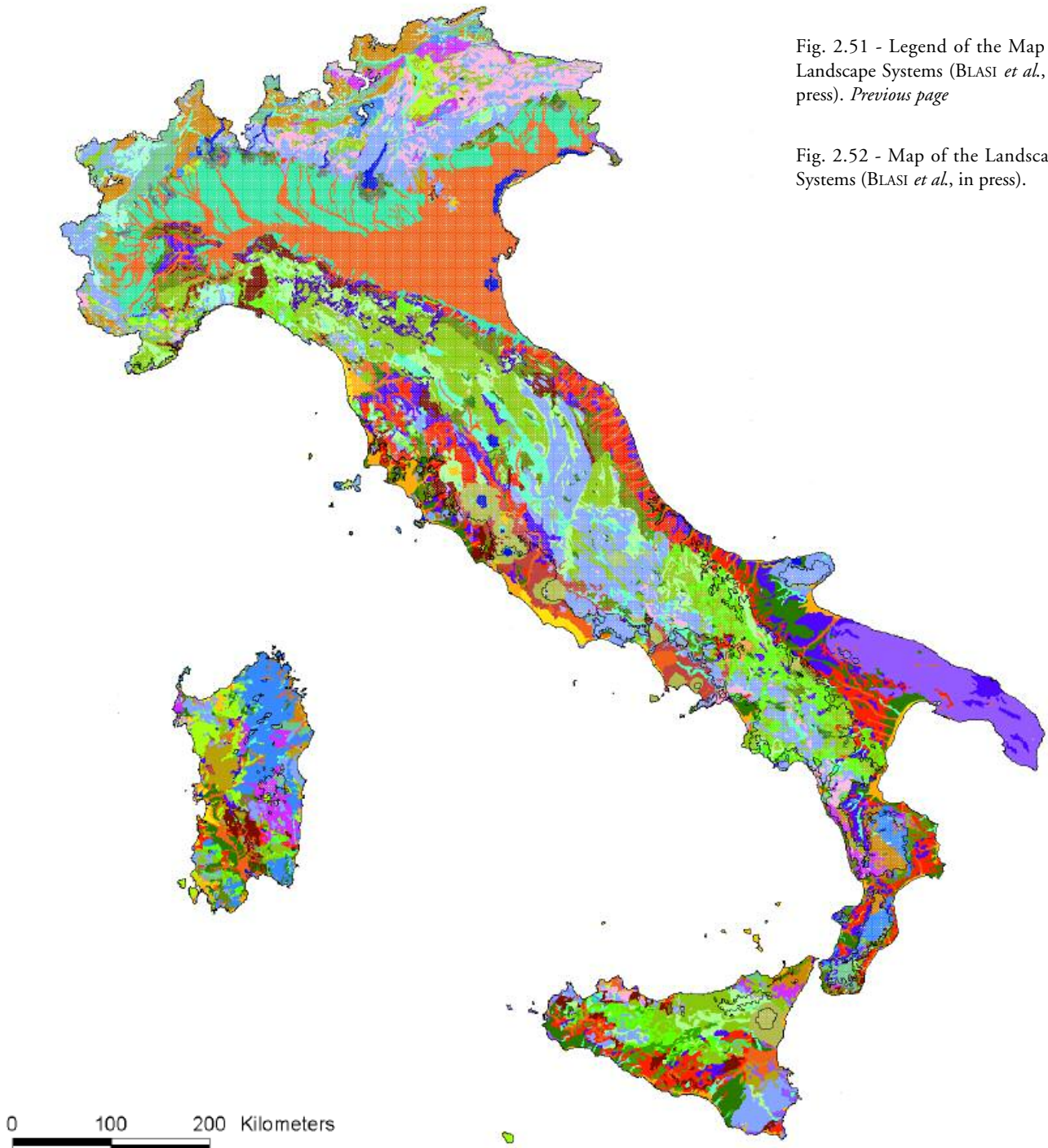
Mediterranean Region	
102	Lakes and lagoons
105	Ancient and recent coastal dune systems
106	Coastal plains and fluvial deltas
107	Recent alluvial plains
108	Ancient alluvial plains
109	Intramountain alluvial plains
110	Ancient marine and alluvial terraces
111	Travertinous plateaux
112	Carbonatic plateaux
113	Intramountain, pedemountain or coastal sandy-conglomeratic hills
114	Intramountain, pedemountain or coastal clayey hills
115	Intramountain, pedemountain or coastal marly hills
116	Intramountain, pedemountain or coastal evaporitic hills
117	Intramountain, pedemountain or coastal arenaceous-conglomeratic hills
118	Intra-apennine fluvio-lacustrine hollows
119	Tufaceous reliefs, hills and plateaux
120	Acid volcanos
121	Basic and intermediate volcanos
122	Mainly sandy-conglomeratic reliefs
123	Mainly arenaceous-conglomeratic compact reliefs
124	Mainly clayey and clayey-schistose reliefs
125	Marly rocks reliefs
126	Ophiolitic and serpentine-schistose reliefs
127	Mainly scaly clay reliefs
128	Mainly dolostones reliefs
129	Mainly calcareous rocks reliefs
130	Acid volcanic rocks reliefs
131	Basic volcanic rocks reliefs
132	Phyllites reliefs
133	Mainly micaschists and paragneiss reliefs
134	Mainly migmatic-gneisses reliefs
135	Crystalline rocks reliefs
Temperate Region	
201	Glaciers
202	Lakes and lagoons
203	Valley morainic hills
204	Morainic amphitheatre
205	Ancient and recent coastal dune systems
206	Coastal plains and fluvial deltas
207	Recent alluvial plains
208	Ancient alluvial plains
209	Intramountain alluvial plains
210	Ancient marine and alluvial terraces
211	Travertinous plateaux
212	Carbonatic plateaux
213	Intramountain, pedemountain or coastal sandy-conglomeratic hills
214	Intramountain, pedemountain or coastal clayey hills
215	Intramountain, pedemountain or coastal marly hills
216	Intramountain, pedemountain or coastal evaporitic hills
217	Intramountain, pedemountain or coastal arenaceous-conglomeratic hills
218	Intra-apennine fluvio-lacustrine hollows
219	Tufaceous reliefs, hills and plateaux
220	Acid volcanos
221	Basic and intermediate volcanos
222	Mainly sandy-conglomeratic reliefs
223	Mainly arenaceous-conglomeratic compact reliefs
224	Mainly clayey and clayey-schistose reliefs
225	Marly rocks reliefs
226	Ophiolitic and serpentine-schistose reliefs
227	Mainly scaly clay reliefs
228	Mainly dolostones reliefs
229	Mainly calcareous rocks reliefs
230	Acid volcanic rocks reliefs
231	Basic volcanic rocks reliefs
232	Phyllites reliefs
233	Mainly micaschists and paragneiss reliefs
234	Mainly migmatic-gneisses reliefs
235	Crystalline rocks reliefs

In an attempt to provide a synthesis of the principal landscapes in Italy, given that the climatic heterogeneity and lithomorphological heterogeneity on a national and regional scale is well known (BRONDI, 2001), the choice was made to integrate GIS with only two of these basic information layers, thus obtaining some 67 land-

scape systems (Figures 2.51 and 2.52). What emerged from this synthesis was the high level of heterogeneity but also the “discreet” landscape structure of Italy. Only a few areas tend to be homogeneous (such as the Padana Plain, the hilly belt of Umbria, the Marche, and the Salentino peninsula), given the great spatial integration

Fig. 2.51 - Legend of the Map of Landscape Systems (BLASI *et al.*, in press). *Previous page*

Fig. 2.52 - Map of the Landscape Systems (BLASI *et al.*, in press).



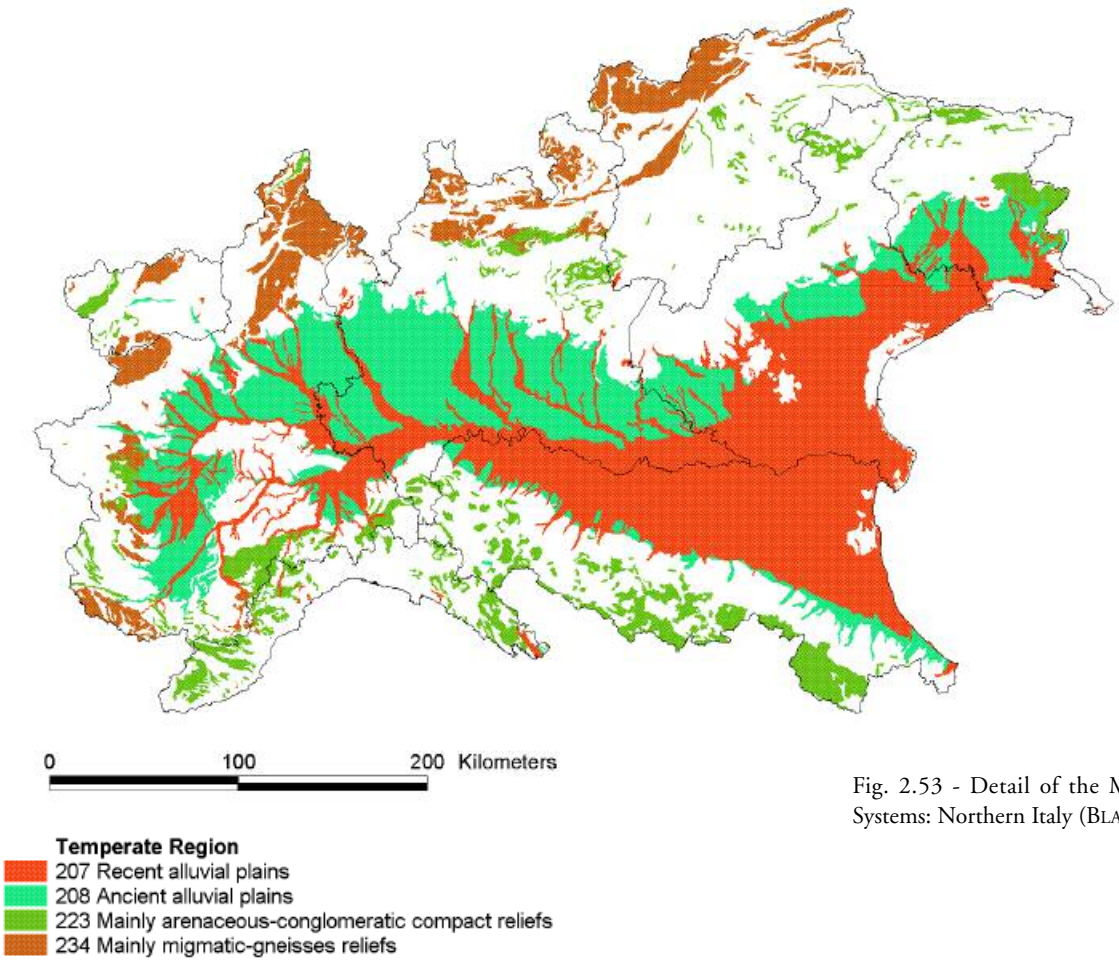


Fig. 2.53 - Detail of the Map of Landscape Systems: Northern Italy (BLASI *et al.*, in press).

among landscape systems. Among the more complex areas there is the central Alpine complex, Toscana, Calabria and Sicilia. From what has already been mentioned in the section that outlines the reasons behind biodiversity, it could be possible to extract important information to define the contexts of potentially elevated biodiversity. The polygons that identify the landscape systems are structural, that is, they are not connected to anthropogenic activity, but to the macroclimate and to

lithomorphological characteristics. Hence, it is necessary to examine a more detailed climatic and morphologic reference data for studies on a regional scale.

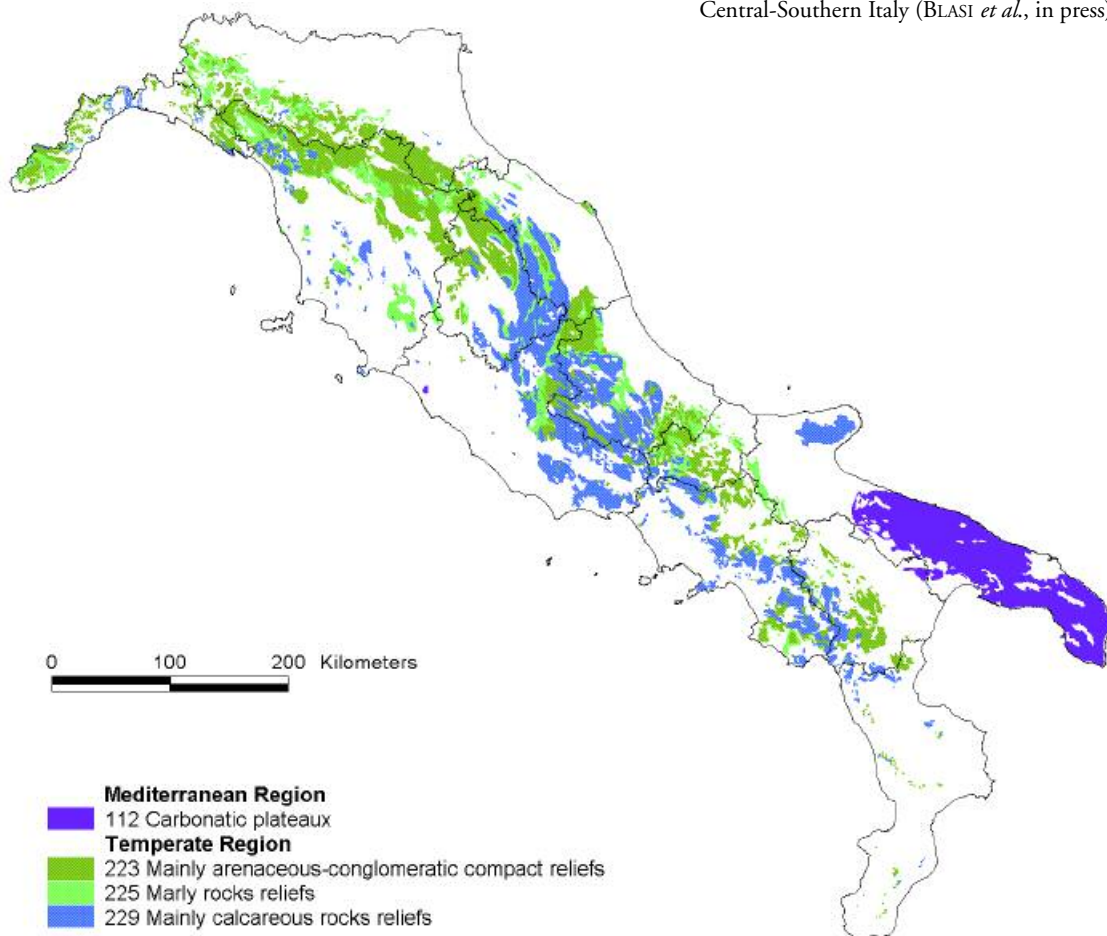
To better highlight the character of Italian landscape, we decided to separately analyse the north (including Emilia-Romagna), the centre-north and the centre-south together, Sicilia and Sardegna.

Northern Italy (Figure 2.53, Table 2.3) is strongly characterised by landscape systems of the temperate re-

	hectares	%
207 Recent alluvial plains	2,693,905.44	22.54
208 Ancient alluvial plains	1,924,980.19	16.10
223 Mostly compact arenaceous conglomerate ranges	837,740.82	7.01
234 Mostly compact ranges of gneiss-magmatic rocks	718,189.78	6.01
	6,174,816.23	51.66

Table 2.3 - Main landscape types of northern Italy (BLASI *et al.*, in press).

Fig. 2.54 - Detail of the Map of Landscape Systems: Central-Southern Italy (BLASI *et al.*, in press).



gion. There is a prevalence of sandstone-conglomeratic reliefs, composed mainly of gneiss-magmatic rock. Landscapes connected to the Mediterranean bioclimate are very sporadic, but in terms of biodiversity conservation, these small portions of the territory represent islands of extraordinary conservation interest.

Central-northern and central-southern areas of the Italian peninsula (Figure 2.54, Table 2.4) Temperate bioclimate prevails, including reliefs composed of lime-

stone, compact sandstone-conglomeratic rock, and marly rock. In areas with a Mediterranean bioclimate, there is a high percentage of limestone terraces and sandy or clayey intermontane hills.

In Sicilia (Figure 2.55, Table 2.5), landscapes with a Mediterranean bioclimate naturally prevail, and among these there are sandstone, limestone and clayey reliefs. Besides the clayey and marly hilly systems, there are those composed of evaporitic substrates and sea and alluvial terraces.

	hectares	%
112 Carbonatic platforms	949,318.43	7.22
223 Mostly compact arenaceous conglomerate ranges	1,475,249.99	11.22
225 Ranges constituted <i>in toto</i> or in part by marly rocks	696,667.31	5.30
229 Ranges constituted <i>in toto</i> or in part by calcareous rocks	1,683,638.88	12.81
	4,804,874.61	36.55

Table 2.4 - Main landscape types of central and southern Italy (BLASI *et al.*, in press).

Fig. 2.55 - Detail of the Map of Landscape Systems: Sicilia (BLASI *et al.*, in press).

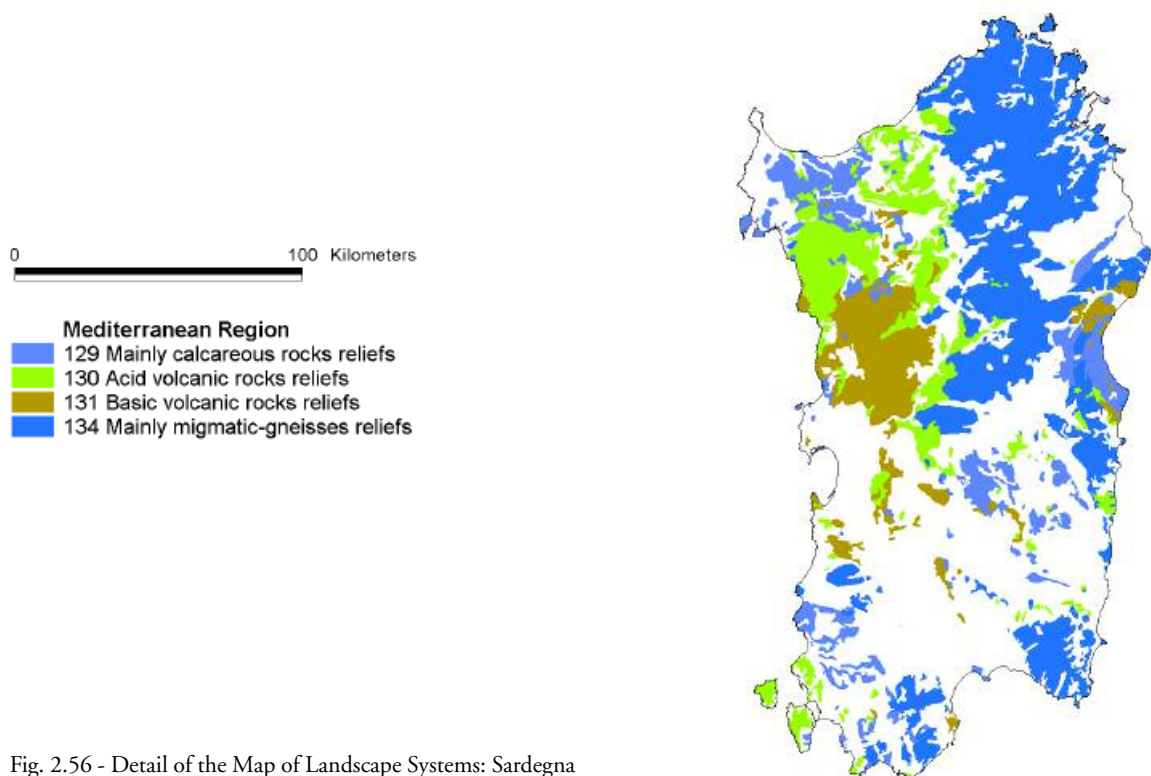
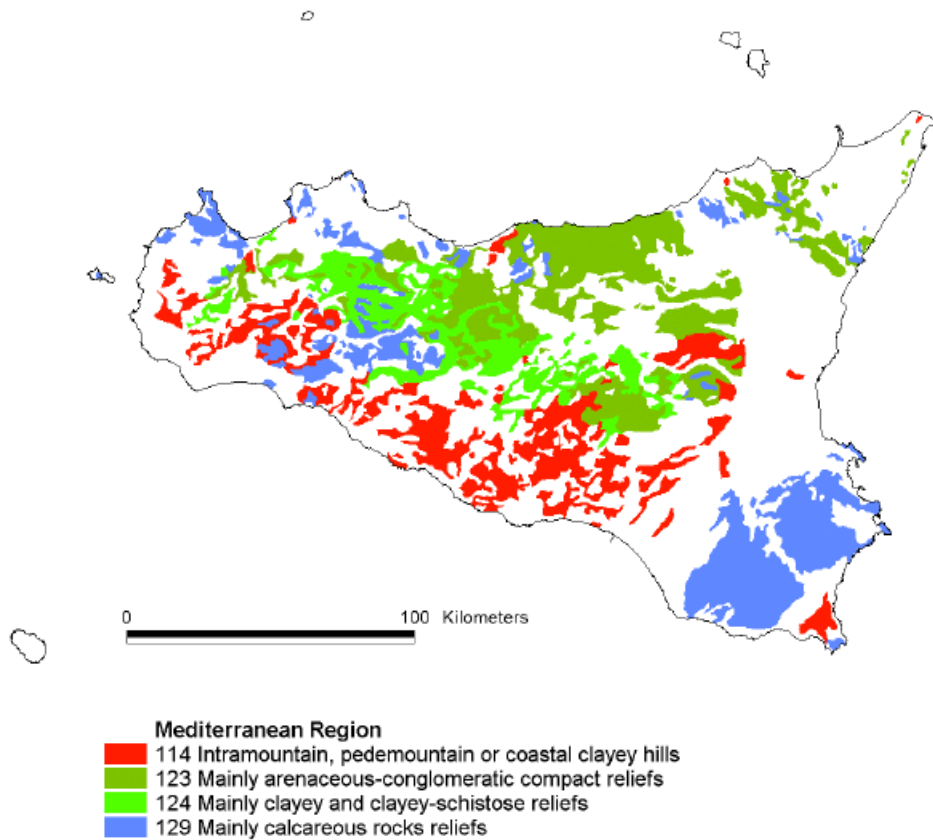


Fig. 2.56 - Detail of the Map of Landscape Systems: Sardegna (BLASI *et al.*, in press).

	hectares	%
114 Inframontane, piedmontane or coastal clay hills	282,708.20	10.99
123 Mostly compact arenaceous conglomerate ranges	349,994.32	13.61
124 Mostly clay and clay shists ranges	190,262.49	7.40
129 Ranges constituted <i>in toto</i> or in part by calcareous rocks	305,297.70	11.87
	1,128,262.71	43.87

Table 2.5 - Main landscape types of Sicilia (BLASI *et al.*, in press).

	hectares	%
129 Ranges constituted <i>in toto</i> or in part by calcareous rocks	195,559.61	8.17
130 Ranges constituted by acid volcanic rocks	234,119.05	9.78
131 Ranges constituted <i>in toto</i> or in part by basic volcanic rocks	181,996.02	7.60
135 Ranges constituted by crystalline rocks	591,741.27	24.71
	1,203,415.95	50.26

Table 2.6 - Main landscape types of Sardegna (BLASI *et al.*, in press).

Particular importance should be given to the landscapes with a temperate bioclimate in Sicilia, such as those on Etna and more generally speaking those on marly reliefs.

Mediterranean bioclimate landscapes also prevail in Sardegna (Figure 2.56, Table 2.6) including crystalline rocks reliefs, limestone reliefs and acid or basic volcanites reliefs. Marine terraces and alluvial plains are also important elements.

Typological and cartographic knowledge of Italian landscape systems will be an excellent territorial reference for the 2010 National Strategy for Biodiversity Conservation, especially in terms of territorial knowledge regarding the distribution of *alien species*, of the *old-growth forests*, and more generally speaking, in *assessing the conservation status* of homogeneous land units and in identifying the *Important Plant Areas* (IPAs).

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