«Запорізький національний університет»
Міністерства освіти та науки України

Збірник вправ для самостійної роботи з курсу

ПРОФЕСІЙНО-ОРІЄНТОВАНИЙ ПРАКТИКУМ ІНОЗЕМНОЮ МОВОЮ

для студентів денного та заочного відділення освітнього рівня магістр спеціальностей «Біологія» та «Генетика»

Затверджено
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Збірник вправ для самостійної роботи з курсу «Професійно-орієнтований практикум іноземною мовою» для студентів денного та заочного відділення освітнього рівня магістр спеціальностей «Біологія» та «Генетика» / Укладачі: Лях В.О., Бойка О.А. – Запоріжжя:ЗНУ, 2016. – с.

Видання складається з завдань для самостійної роботи студентів з курсу «Професійно-орієнтований практикум іноземною мовою» поділених на розділи за біологічними тематиками. Воно містить тексти для читання та переводу та завдання, які сприяють поповненню активного мовного словника з професійних термінів та слів по розділах Ботаніка та рослини, Зоологія та тварини, Людина, Екологія, Хімія та біохімія, Генетика. Подано кілька наукових статей для самостійного опрацювання студентами.

Призначено для студентів, які навчаються за спеціальностями «Біологія» та «Генетика».

Рецензент
Відповідальний за випуск *В.О. Лях*, завідувач кафедри СПГ та генетики

ЗМІСТ:

ВСТУП

Навчально-методичне видання підготовлено відповідно до навчальної робочої програми дисципліни «Професійно-орієнтований практикум іноземною мовою», яка передбачає підготовку магістрів у вищих навчальних закладах IV рівня акредитації за спеціальністю «Біологія» та магістрів за спеціальністю «Генетика». Видання розраховане на студентів біологічного факультету денної та заочної форм навчання.

Самостійна робота студентів є важливою складовою навчального процесу, яка сприяє активізації засвоєння студентом знань та їх реалізації, є основним засобом опанування навчального процесу студентом у вільний від занять час.

Завданням самостійної роботи студентів є засвоєння певних знань, умінь, навичок, закріплення та систематизація здобутих знань. В межах спеціальності «Біологія» студенти спеціалізується на більш поглибленому вивченні

Розділ 1. Ботаніка та рослини.

Завдання 1. Прочитайте та перекладіть подані нижче тексти.

WINDOWSILL MICROPROPAGATION?

After breeding *Verbascum* hybrids for a few years, we needed a different reliable method of propagation which would allow us to produce at least a dozen plants from a single specimen. When a new hybrid is bred, there is only the single plant and digging it up to make root cuttings can cause serious damage. Traditionally, clones would be produced by taking root-cuttings about 2.5 cm/l in long or even longer. Initially we used this method and found that you could grow a few extra plants quite easily, but a dozen or so plants meant chopping up to 30 cm/1 ft or more off the root. We began to wonder just how small you could make the cuttings. Pieces about 1 cm/½ in long were found to grow very easily. We then tried pieces only 5 mm/¼ in long and they gave equally good results, so we kept reducing the size of the cuttings until we discovered that pieces only 2 mm/ 1/12 in long would grow successfully.

Suddenly we discovered that some very odd things were happening. We always took care that these thin slices were planted the right way up, pressing them into the surface of the compost so that the top of the slice was visible after planting. Apparently, the thin root discs would lose their polarity and produce sprouts on the ‘wrong’ side and often the slices would split and fail to grow. It became apparent that the splitting was due to the upper surface drying out more than the lower which was in contact with the moist compost.

Since the polarity of the root slices seemed to be unimportant when they were very thin, we decided to try planting them on the edge so that both flat surfaces were equally in contact with the compost. This solved the problem of splitting and we were soon experimenting with slices only 1mm/ 1/25 in thick, most of which grew perfectly well. We were then able to obtain material for propagation by simply excavating a small hole beside a specimen plant, locating a suitable root and taking only a few centimeters from it with a sharp knife.

Although we have only used this method with *Verbascum*, it could well work with other plants which are usually propagated by root cuttings, such as oriental poppies and lupin cultivars. We would be interested to hear from readers who try.

A very fine textured compost is essential. We use a peat-based seed compost, passed through a 4 mm/ 1/6 in-mesh sieve and, for *Verbascum*, add chalk. Other types of plants may need different composts. We use trays of thimble-sized cells (20 × 20 mm/ ¾ in × ¾ in), standing on capillary matting in an unheated propagator. The cells are pre-watered and the thinly-sliced cuttings are inserted in slits made with a penknife blade in the surface of the compost. After planting, the edge of the cutting is just visible at the surface. A razor blade and some manual dexterity are needed but we have grown 800 plants this way so far this year using the kitchen and bathroom windowsills.

PLANTS FOR GARDEN PONDS

Oxygenating plants. Oxygenating plants provide shelter for spawning fish and they fry, as well as releasing oxygen directly into the water in strong light. They also take up mineral salts from the water that would normally encourage the growth of algae. A dozen or so should be planted in a small container and allow one container to every 2 m^2 in a small pool, but as the pool enlarges relatively fewer containers are needed; a pool of over 55 m^2 would require twenty containers. If the plants become too prolific it is a simple matter to lift out a few containers to allow more space.

Deep water and marginal plants. There are many aquatic plants that grow in deep water. Their roots need soil and this is best kept in a container, allowing the plant to be lifted jut of the water for pruning, treating for pests and diseases and for feeding. The container can be a box, pot, basket or a proprietary plastic container. The soil should be plain with the addition of bonemeal; some charcoal lumps will help to keep the soil sweet.

Some plants float on the surface with trailing roots that pick up nutrients from the water and these can be easily lifted out and thinned if they spread too far.

Marginal plants in the main have their rootstocks just under the water with their leaves and flowers held well above the surface. Here again, containers should be used to allow the plant to be lifted out, thinned and stopped from talking over the pond. Many aquatic plants are invasive.

Water lilies. The water lily is justifiably the most popular of water plants. It has brilliant blooms and at the same time its leaves cover the water surface to provide both shelter to fishes and welcome shade that prevents excessive algae growth, in addition, water lilies – all species and hybrids of Nymphaea – are available in a variety of sizes to suit the size and depth of any pond, from the pygmy types that need just a shallow covering of water to the more vigorous types that would swamp a small pond completely and need deep water to prevent the leaves from standing proud of the surface.

Water lilies should be grown in containers. They will give sufficient anchorage and nutrition while stopping the plant from outgrowing the pond. They will also allow easy access to the plant for maintenance, treatment for disease or pest attack, and feeding. Containers allow a certain flexibility of position and can be adjusted to give the right depth of water over crown of the plant; this is achieved by inserting bricks or other inert material under the container to raise it.

There are two main groups of water lilies: the hardy and the tropical. In temperate zones the hardy ones are fine for outdoor ponds; the tropical lilies are only suited to indoor and outdoor ponds where the water temperature is maintained at 21^0 C throughout the year.

The best soil to grow water lilies in is a heavy loam well fortified with bonemeal (approximately 0.1 litres per 4.5 litres of soil). Animal manures are not recommended as the water becomes over rich with nutrients that will encourage algae growth. Should the loam be poor quality and low in nitrogen mix some dried blood into the soil. The roots should be well anchored by ramming the soil well

down in the container, leaving some room for a layer of shingle or gravel over the soil to prevent fish from stirring up the fine particles and making the water cloudy.

Water lilies need sun, plain soil and the right depth of water. Given these they will reward the gardener with a prolific show of flowers from early summer onwards.

Bog plants. Stretches of open water are often surrounded by wetlands, areas of constantly moist soil where the water table is just beneath the surface. A number of plants have adapted their root system to cope with this high moisture level. Many of these 'bog plants' have brightly coloured flowers and interesting leaf shapes and make fine subjects for planting near a garden pond.

RADISH

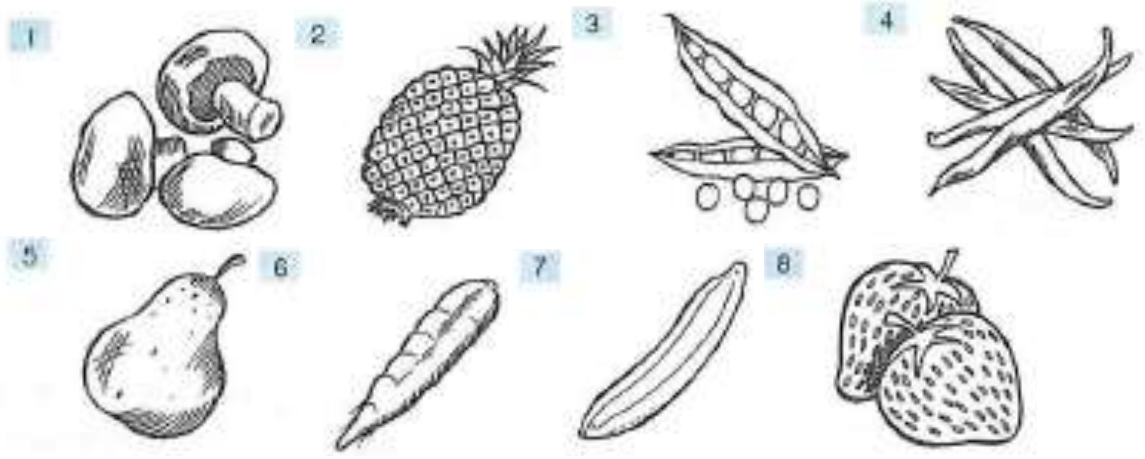
Soil facts. All gardening books will tell you that radishes require fertile, well-drained soil, rich in humus and free from stones. But radishes generally have to put up with what they are given. Despite this lowly status, they must be given some soil preparation to ensure the quick growth so necessary for tenderness and flavor. Dig in some peat or well-rotted compost. Apply a fertilizer before sowing and rake to a fine tilth.

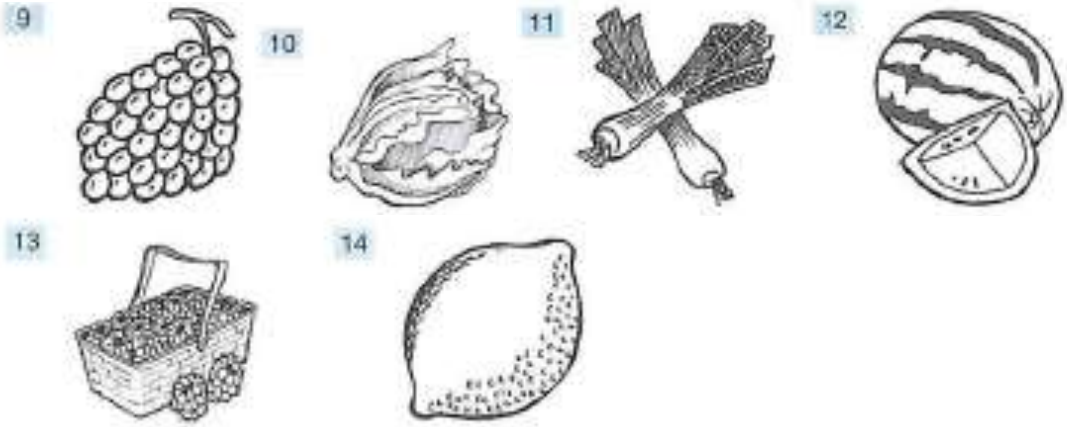
Looking after the crop. With the Summer varieties little or no thinning should be necessary. If there is any overcrowding then thin immediately so that the plants are 1-2 in. apart. Protect the crop against birds. Spray with Derris or Crop Saver if Flea Beetle begin to perforate leaves. Hoe to keep down weeds. Water if the soil is dry; rapid growth must not be checked.

Harvesting. Pull the Summer varieties when the globular ones are penny-sized and the intermediates are no longer than you thumb. They can, of course, grow much longer, but these overgrown specimens would be hot, woody and hollow. The winter varieties can be left in the soil and lifted as required during the winter. But it is better to lift them in November and store as for carrots.

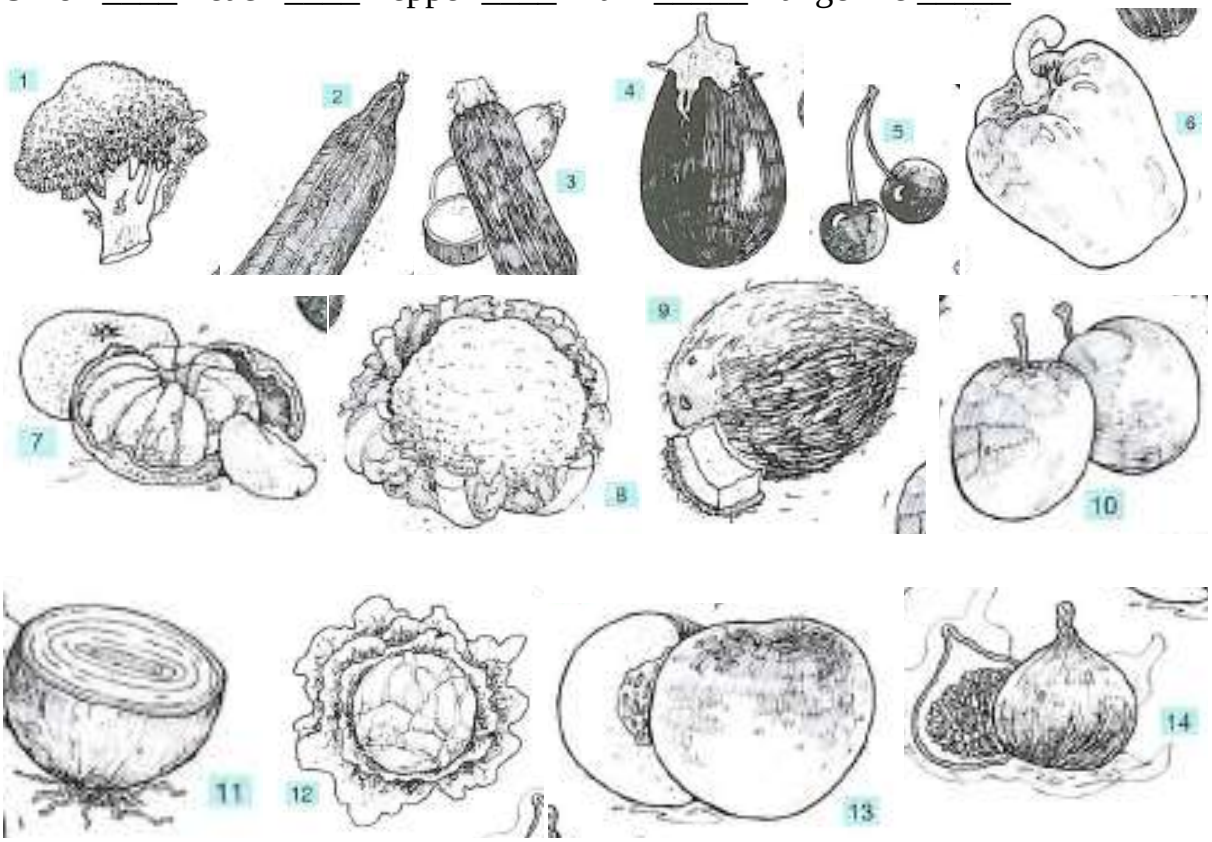
Завдання 2. Впишіть номери відповідних малюнків назв рослин.

Beans ___ Carrot ___ Cucumber ___ Grapes ____ Leeks ___ Lemon ___
Lettuce ___ Mushrooms ____ Pear ___ Peas ____ Pineapple _____
Raspberries _____ Strawberries _____ Watermelon _____

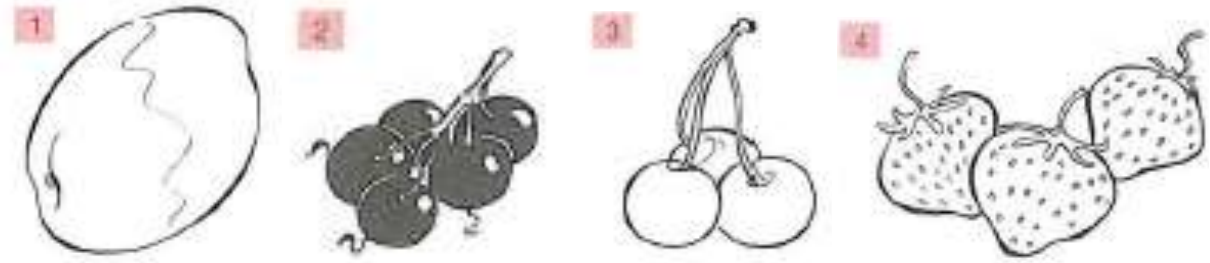




Завдання 3. Впишіть номери відповідних малюнків назв рослин.
Aubergine ___ Broccoli ____ Cabbage _____ Cauliflower ____
Cherry ____ Coconut ___ Courgette ____ Cucumber ____ Fig ___
Onion ____ Peach ____ Pepper ____ Plum _____ Tangerine _____



Завдання 4. Напишіть назву фруктів під кожним малюнком обираючи з запропонованих назв: bleckberries, blackcurrents, cherries, kiwi fruit, mango, melon, strawberries.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Розділ 2. Зоологія та тварини.

Завдання 1. Прочитайте та перекладіть подані нижче тексти.

POND LIVESTOCK

Fishes for garden ponds. One of the most exciting aspects of the garden pond is the livestock that it can support. Of these, the most spectacular and interesting are the fishes, which provide a continuous movement and sparkle that people of all ages find fascinating. The golden varieties of fish are the most easily seen and appreciated; the dark green varieties are well camouflaged and need patience to see them and watch their movements. The brighter fish are more vulnerable to predators, and a sufficient cover of plant life in the pond is necessary for their protection.

Fishes are important to the pond environment, as they take in oxygen from the water and then expel carbon dioxide through their gills; the carbon dioxide is then absorbed into the plant tissues along the water. Carbon, hydrogen and oxygen are processed within the plant with sun's rays, a process called photosynthesis, giving off surplus oxygen into the water for the fishes to take up again and repeat the cycle for the benefit of both fishes and plants. At night the process is reversed, with the plants taking up oxygen and releasing carbon dioxide. This can cause a low level of oxygen in the morning making the fishes sluggish. As soon as the sun rays start working on the plant life the oxygen starts moving again.

Some fishes are scavengers, acting as unwitting cleaners in the pond by taking up debris from the pond floor and water as food. It is advisable to cover all soil with a layer of stones or gravel to prevent the soil being stirred up and clouding the water, stopping the fishes from being seen clearly in the pond.

For describing each individual species of fish, there is a detailed terminology for the various fins and points; this is very useful to know about in order to read the literature supplied by fish fanciers and dealers, and books on the subject.

Other pond livestock. Apart from the livestock deliberately introduced into the water, other forms creep in uninvited, but most of these are beneficial, either keeping the pond clean or providing a ready meal for the fishes. Other are more trouble, however, causing damage to fish and plant life, especially the small fry and the young fresh growth; it is important to keep an eye on the health of the pond life and spot any damage to fishes or plants that may have been caused by an unwanted guest. Among the vast amount of livestock it is quite difficult to determine which is friend and which is foe, and it is impossible to keep an outdoor pond free from the visitations of insects and other life forms.

Snails. One of the few animals that needs to be introduced into the pond is the snail. There are a number of aquatic snails that will happily feed on debris and help to keep the pond clean without feeding on the plant life.

Planorbis corneus (the Ramshorn Snail) can be put into the pool to clean up unwanted rubbish. It is easily recognized by its handsome flat coiled shell, and breeds well. It will not damage useful vegetation, and is readily available from aquatic dealers.

Viviparus viviparous (the Freshwater Winkle) delights in feeding on dead and decaying vegetation, and is popular with fishkeepers. If disturbed it will cling very tightly to whatever it is attached to, resisting any attempt to pull it off, no matter how hard.

Viviparus fasciatus is very similar to *V. viviparous*, and also eats decaying plant life; but it is also completely different, in that it releases itself the moment it is touched.

Most of the other snails that are found in the pond introduce themselves and can be left to populate the water unless they are seen to feed on your prize aquatics. Some are small and insignificant, others are larger. Some of the bigger snails are from the Lymnaea family, which includes the Great Pond Snail (*Lymnaea staginalis*), a snail that through indiscriminate feeding can cause a lot of damage and should be removed.

Amphibians. Amphibians visit the pond to lay their eggs or spawn; some fishkeepers find the spawn unsightly and remove it, but the young are beneficial to the balance of life in the water. Young tadpoles are excellent scavengers, starting off by eating vegetable matter and progressing to animal foods. Frogs, toads and newts should all be welcome because they do so much good in the garden, removing unwanted pests such as insects.

Beetles and other insects. There are well over 200 different species of aquatic beetle; some of these are savage and carnivorous, attacking fish and other water animals, but most are happy scavenging among the debris and keeping the pond clean. Unless attacks are seen, it is best to leave most beetles alone.

Surface walkers are often seen traversing the water relying on the surface tension to stop themselves sinking. The best-known of these is *Gerris najas* (the Pond Skater), which literally walks across the water on the lookout for dead or dying insects.

There are a large number of flies that leave their eggs in or close to water, from the humble midges and gnats to the larger caddis flies and dragonflies. Their eggs turn into larvae that prey on lower water creatures, other larvae and tiny fishes, and they in turn become food for larger fishes. There are over 160 different kinds of caddis fly. One of the commonest is *Phryganea grandis* with pale grey-brown wings and yellow-ringed antennae; it folds its wings along its body when at rest, like all the caddis flies. Their larvae form cases or tubes from fine particles of vegetation, stones, sand or shell to live in until the next stage in their development into flying insects.

The dragonflies form a large group of insects well-known for their spectacular colouring and erratic flight pattern. Their eggs are laid on the water surface and then sink to the bottom. When the larvae are hatched they form burrows in which they lie low, preying on small aquatic animal life; then they gradually change until they eventually become flying insects. Dragonfly larvae (nymphs) can be considered a pest. Among the other flies are *Culex pipiens* (the Common Gnat) and *Chaoborus* sp. (the Midge). The larvae of these are a good food for fishes, and anyone who fails to keep fishes in the garden pond is likely to

become aware of a subsequent noticeable increase in the gnat and midge population.

BASIL BRUSHLESS

He can flick is flamboyantly, curl it up coyly or simply twirl it around toes.

But the sparseness of this squirrel's tail will ensure he won't be snuggling up with a mate in winter.

Bright, bushy tails are a major part of squirrel courtship rituals, leaving Basil, as he is known, at a distinct disadvantage.

When he first appeared in Vicki Walker's garden in Portchester, Hampshire, she thought he was a rat. Other squirrels, it seems, will think the same. 'It's not a case of "I've got the best brush look at me", but the tail does play a very important part in the courtship process,' said Richard Grogan, wildlife officer for Hampshire and Isle of Wight Wildlife Trust.

"Without that, the squirrel's chances of finding a mare are severely hampered.' Mr Grogan believes Basil's sparse tail is probably a genetic defect.

'Alternatively, the hairs could have been pulled off by another animal but you would expect hair to have been removed from other parts of the body as well,' he said.

Basil, pictured above enjoying a snack and getting to know a collared dove, is now a favorite in Mrs Walker's garden.

'When I first saw him I was ready to call in pest control,' she said.

'But despite his odd appearance he is more than welcome and has become one of my regular visitors.'

HOW CAN ANIMALS LIVE IN A DESERT?

There is almost no water in a desert, but many animals can live in deserts. How do these animals get water and stay alive?

Everything is hot and dry in the daytime, but the nights are cold. Plants often have dew on them in the early morning. This is because cold air can't hold as much water as hot air. Small insects can drink the dew, and bigger animals eat the plants with the dew on them.

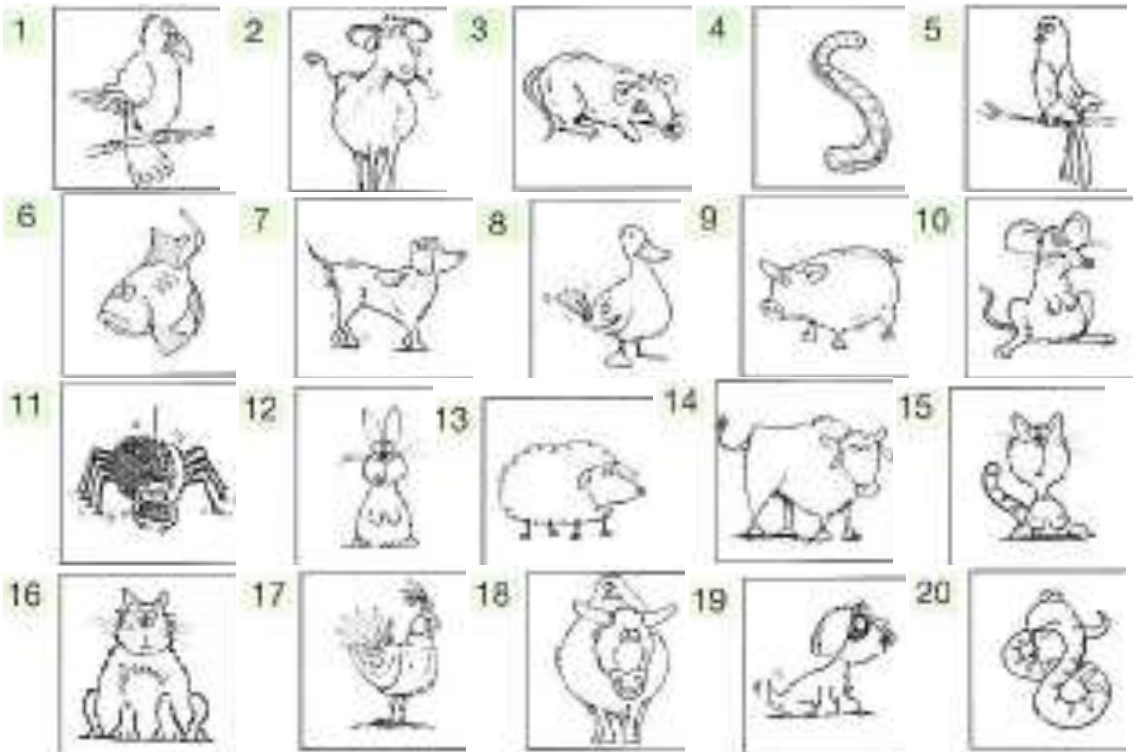
Small birds and animals get water from the bodies of insects. Bigger birds and animals get water from the bodies of small animals. The North American bird called a roadrunner runs fast and catches small snakes, lizards and scorpions.

Some animals can wait many years for water. When rain falls, baby shrimps come out of their eggs. They grow quickly and lay new eggs. Then the water dries up, and the shrimps die. But the new eggs do not die. They wait in the ground for the next rain. They can wait for 50 years!

Most big animals can't live in the desert because they need a few liters of water every day. They can't keep water in their bodies for a long time. But camels are different. They can drink 90 liters of water in ten minutes, and then drink nothing for 40 days.

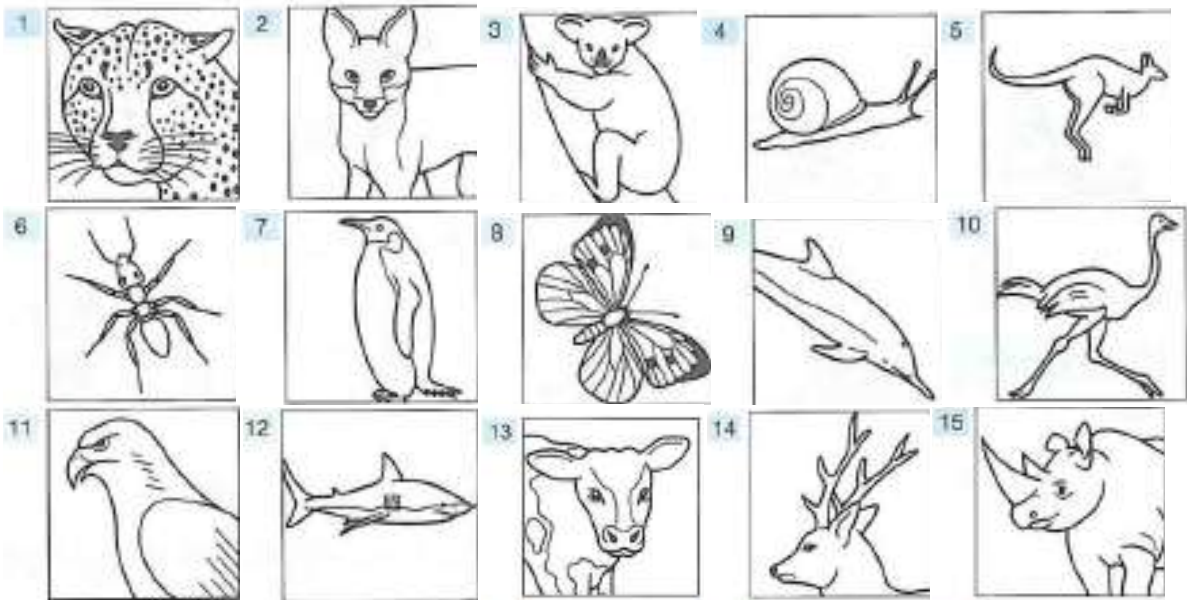
Завдання 2. Впишіть номери відповідних малюнків назв тварин.

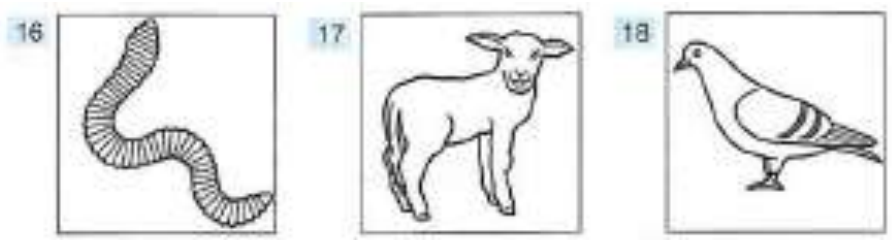
A budgie ____ A dog ____ A mouse ____ A rat ____ A bull ____ A duck ____
A parrot _____ A sheep ____ A cat ____ A goat ____ A pig ____ A snake ____
A chicken _____ A goldfish ____ A puppy ____ A spider ____ A cow _____
A kitten _____ A rabbit _____ A worm _____



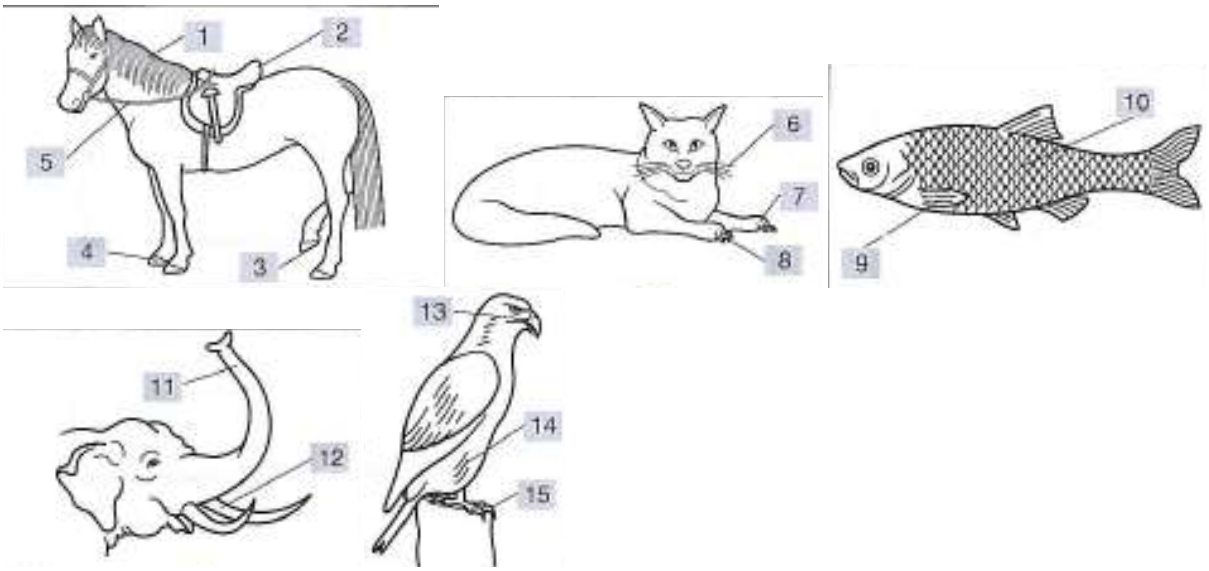
Завдання 3. Впишіть номери відповідних малюнків назв тварин.

Ant ___ Butterfly ___ Calf ____ Cheetah ____ Deer ___ Dolphin ____ Worm ___
Eagle ___ Fox ___ Kangaroo ____ Koala bear ____ Lamb ____ Ostrich ____
Penguin ____ Pigeon ____ Rhinoceros _____ Shark _____ Snail _____





Завдання 4. Впишіть назви з запропонованих нижче на відповідні місця: beak, claws, feethers, fin, hoof, mane, raw, reins, saddle, scales, shoe, talons, trunk, tusk, whiskers.



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11 _____ 12 _____ 13 _____ 14 _____ 15 _____

Розділ 3. Людина.

Завдання 1. Прочитайте та перекладіть подані нижче тексти.

UNDERSTANDING MEMORY

Remembering and forgetting are most common experiences that function daily in the life of a person. One may remember a traumatic experience that occurred in childhood and may forget what formula to use in the examination or still simpler thing what dress he wore yesterday.

One may remember throughout his life that India attained independence in 1947, but can forget his father's birthday. The very act of speaking means that we are remembering and recalling the words of our language in grammatical sequence and we have also to keep track with our conversation, i.e. what we said just now; otherwise our conversation will be senseless.

In most cases memory means retaining information which we have learnt or heard. Some people can remember more of what they have done or seen or heard than others and so they are said to have better memories. The capacities of remembering vary from one another in certain aspects. But they have some elements in common.

Like in each case, the present experience or the present behavior of an individual is determined by something that has happened in the past. Memory consists of learning, retaining, recalling or recognizing. For example, when we remember the name of a person, we demonstrate that we have learnt the name earlier and that we have retained it during the intervening period and are still able to recall the name at any time.

A distinction is often made between two kinds of memory: rote memory and logical memory. Rote learning results from the mechanical process of repeating it by heart, without understanding the meaning. A small child who sings a nursery rhyme is demonstrating rote memory without any comprehension, while logical memory is the remembering / retention of the material with its meaning.

According to Atkinson-Shiffrin's psychological theory, memory is divided into two: one is short term memory (STM) and the second is long term memory (LTM). If an individual has to reproduce what he has learnt immediately after learning it, he employs, what is referred to as short-term memory or immediate memory, where it is held only for 20-30 seconds.

For example, you asked a phone number from the telephone operator and did not write but thought that you have learnt it, if the telephone line is busy, and if you have to wait for a minute or two, before dialing again, you may forgot the number by then. This is the case, when material is stored in STM. Our STM has a very limited capacity; it is believed. Miller, another psychologist, in 1956, found that the capacity of STM is (7-2=5) or (7+2=9). This means that a person can retain in STM not more 9 bits of information. This is a reason why telephone numbers or vehicle numbers are never more than 9 digits or numbers.

While the material in LTM may retain for days, weeks, months or years. The long term memory has no limits to its capacity, some theorists believe there is no forgetting from this.

In contrast to memory comes forgetting, i.e. the apparent loss of information already encoded and stored in long-term memory. The question arises, why do we forget? There is no single or simple answer to it.

The oldest explanation to forgetting is misuse, because it is often seen that driving, swimming, riding a bicycle, are such skills, which are never forgotten, although they might be use seldom. Another reason is distortion. For example, if a person is asked to recall something like a story after different intervals of time, it will be noticed that his memory of the learned material undergoes distortions. There might be distortions due to loss of information or even the other way round, i.e. addition of details. As a result, the actual contents of the story is thus forgotten.

SCIENCE OF THE HEART

It is the most widely prescribed medical test in the United States. And no wonder. The electrocardiogram tells the inside story of how that most vital of organs, the heart, goes about its work of pumping the nourishing blood of life throughout the body.

Ninety-one years have passed since Willem Einthoven, a Dutch physician-physiologist invented the first practical way to measure what happens when the heart beats. By graphically tracing the electrical impulses that spark the heart's action, he opened the field of electrocardiography. In the decades since, many pioneers have improved on Einthoven's invention, and today an electrocardiogram offers detailed and precise information on the condition and performance of the heart.

This year, Wyeth-Ayerst pays special tribute to the medical heroes who made this possible. Twelve of them are pictured in a special 1992 calendar distributed to cardiologists. The calendar is part of the company's marketing program for a trio of drugs to treat the arrhythmias that electrocardiography detects. Arrhythmias are variations from the normal heart beat and are the principal reason a physician orders an electrocardiogram, or ECG.

"The ECG is a simple test for a patient" said Marc W. Deltch, M.D., Vice President of Medical Affairs and Medical Director of Wyeth-Ayerst Laboratories. "It's quick, painless, and there is little risk. Because it identifies otherwise invisible heart conditions, the ECG has become an irreplaceable part of medical diagnosis."

Sometimes variations in heart rhythm are normal, and may be caused by exercise, caffeine, alcohol, drugs, or congenital defects. Everyone experiences these to some degree. But when arrhythmias occur frequently, they put a strain on the heart by making it work harder to maintain normal blood flow.

Electrocardiograms help to detect these problems, antiarrhythmic drugs work to correct them. Wyeth-Ayerst offers three such medications. In fact, "Wyeth-Ayerst is market leader in the antiarrhythmic arena", said Bob Czenszak, Group Product Director for the antiarrhythmic brands.

SLEEPING SICKNESS

Folks who snore and feel drowsy the next day –even after eight hours of sleep – may have problems more serious than just getting a good night's rest. A study finds that snoring sleepyheads are twice as likely to suffer a stroke as ordinary snoozers. How come? The odd sleep patterns may be a sign of sleep apnea, a condition in which breathing briefly stops throughout the night – possibly disrupting blood flow to the brain.

Завдання 2. Впишіть номери відповідних частин тіла людини позначених на рисунку 1.

Arm ___ Back ___ Bottom ___ Ear ____ Eye ___ Foot ____ Hair ____ Hand ____ Head ___ Knee ____ Leg ___ Mouth ____ Neck ____ Nose ____ Teeth ____

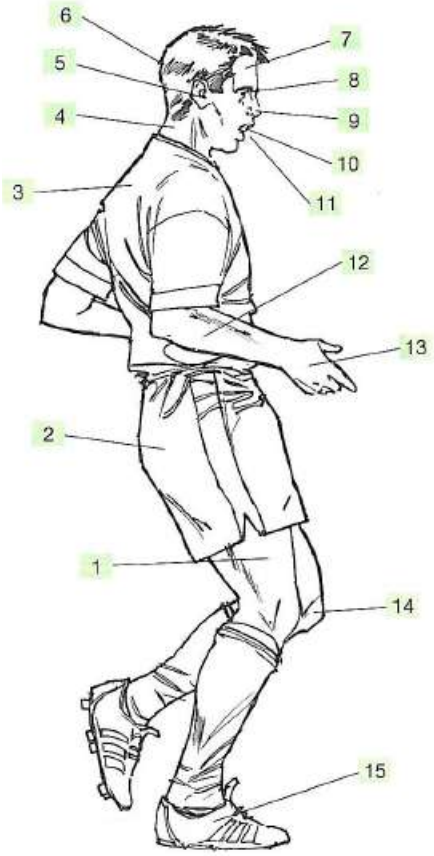


Рисунок 1.

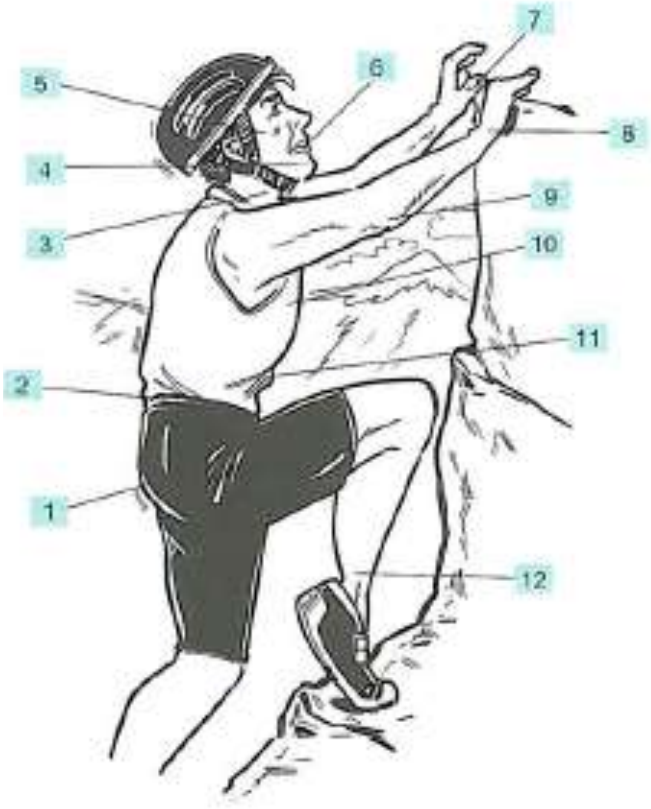
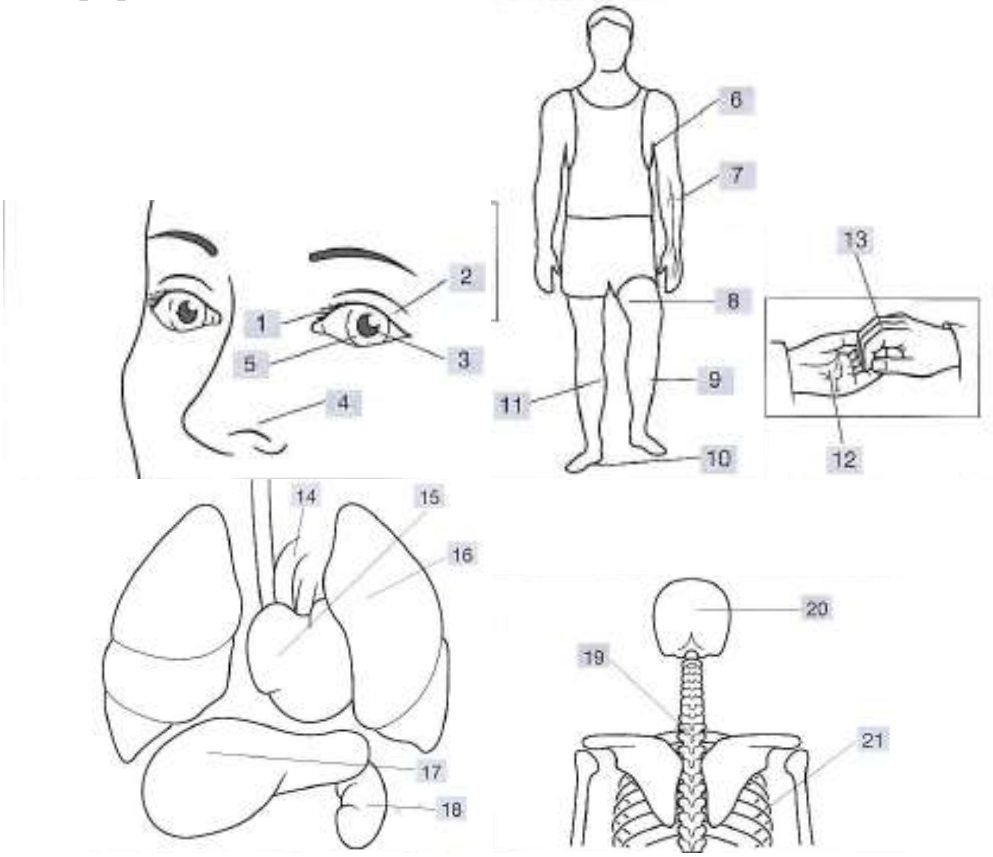


Рисунок 2.

Завдання 3. Впишіть номери відповідних частин тіла людини позначених на рисунку 2.

Ankle ___ Bottom ____ Cheek ____ Chest ____ Chin ____ Elbow ____ Lips ____ Stomach ____ Throat ____ Thumb ____ Waist ____ Wrist _____

Завдання 4. Впишіть назви з запропонованих нижче на відповідні місця: armpit, artery, calf, eyelash, eyelid, heart, iris, kidney, knuckle, liver, lung, nostril, palm, pupil, ribs, shin, skull, sole, spine, thigh, vein.



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11 _____ 12 _____ 13 _____ 14 _____ 15 _____
16 _____ 17 _____ 18 _____ 19 _____ 20 _____
21 _____

Розділ 4. Екологія.

Завдання 1. Прочитайте та перекладіть подані нижче тексти.

UNUSUAL PARTNERSHIPS

There are many types of relationships in the animal world. A very familiar example is when one animal hunts and eats another. This is the predator-prey relationship. Yet nature is not always so cut and dried. On the seashore, as in other habitats, different kinds of animals are regularly seen together. This does not happen by chance - there is a reason. Scientists have different names for these relationships. In the relationship that is called parasitism, one partner, the parasite, benefits, but the other, the host, loses. Some shore crabs are host to *Sacculina*, a strange creature related to the barnacles. *Sacculina* attaches itself to a young crab and then grows "tentacles" that eat into the crab's body. This parasite gets food while disabling the crab. Another type of relationship, in which both partners benefit, is called symbiosis. The hermit crab and the calliactis anemone live in this way. The calliactis is sometimes called the parasitic anemone, but it does not harm its hermit host. It feeds on particles of food that the crab drops, and the crab is protected by the stinging tentacles.

Hermits at home. Hermit crabs do not have shells of their own, so they hide their soft bodies in the shells of dead animals. Sometimes an anemone is attached to the shell. As the crab grows and moves to a larger shell, it often takes the anemone along with it. There are also land hermit crabs in the tropics. Some species live in hollow mangrove roots or bamboo stems.

Three-in-one. Each of the three animals in this "partnership" comes from a different major animal group. The hermit crab is a crustacean. The anemone is a coelenterate (cnidarian). The shell once belonged to a whelk, which is a sea snail and member of the mollusk group.

Sting in the pincer. The boxer crab carries small anemones in its pincers. They act as "stinging clubs" and are waved at any creature posing a threat.

Claw in the door. In its defensive position, the hermit crab pulls itself deep inside the shell. The right front claw (cheliped), which bears the large pincer, is usually bigger than the left one, and the crab holds it across the shell's entrance to make an effective door. (In this example the pincer is missing; it may have been bitten off by a predator or squashed by a boulder.)

Sweeping the floor. The tentacles of anemones reach upward for floating or swimming victims. However, a calliactis anemone on a hermit crab's shell tends to hang down and sweep the rocks for bits of food "spilled" by the hermit crab.

Out of its shell. The hermit crab's soft, curled abdomen is clearly visible when the animal comes out of its shell. When it grows too big for the shell, it looks for another, larger shell. The two back pairs of legs are small and adapted for hanging on to the inside of the shell.

On the move. When the hermit crab is moving around, its head, antennae (feelers), front claws, and first two pairs of legs are exposed. Like its crab cousins, the hermit crab is a scavenger and feeds on plants and bits of dead and dying

animals – in fact on almost anything edible. A dying animal on the shore is soon surrounded by many crabs picking and pulling at its flesh.

Safe among the stings. Clown fish (these are tomato clowns) live among the stinging tentacles of anemones. The fish develop special defenses on their bodies to prevent them from being stung. It is believed that both partners benefit from this arrangement in various ways. The clown fish are safe from predators in the protective tentacles and may eat "leftovers" from the anemone. The anemone may, in turn, be cleaned in the process and eat food dropped by the clown fish. It is also possible that the brightly colored clown fish attract predators, which the anemone then seizes.

Home in a cone. Not all hermit crabs live in whelk shells. This Pacific flat hermit crab is occupying an empty omaria cone shell. Cone shells are tropical mollusks; some species are extremely venomous.

OCEANS IN MOTION

Oceans cover three-fourths of Earth's surface. The amount of water on Earth today is the same as it was 4.5 billion years ago. The water has been recycled from water beneath Earth's crust, to the surface, to the atmosphere, and back billions of times. Water changes state by losing or gaining energy. When more water molecules are escaping than are being captured, evaporation is occurring. When more molecules are being captured than are escaping, condensation is taking place. Ocean water is salty because of the salts dissolved in the water. The salinity of seawater is much greater than that of freshwater sources that empty into it. On average, 34.7 grams of dissolved solids are in each 1000 drams of ocean water. The density of water increases with an increase of salinity. The density of ocean water increases with a decrease of temperature and/or an increase of pressure.

Solar energy and forces within Earth and Earth's rotation are the basis for the circulation of ocean waters and water cycle. The deflection of particles in motion along Earth's surface to the right in the Northern Hemisphere and to the left in the Southern Hemisphere is known as the Coriolis effect.

Earth's rotation also causes patterns in the global climate because of the difference in temperature of air passing over water as opposed to the temperature of air passing over land.

The marine food chain consists of a sequence of organisms that transfer energy from primary producers to primary consumers, to secondary consumers, to tertiary consumers. These kinds of organisms are generally described by their depth in the water and their distance from the shore.

Besides food resources found in oceans, many other resources are found there. The ocean floor contains significant amounts of oil and natural gas.

ACID RAIN

Acid rain occurs after the burning of fossil fuels releases sulphur and nitrogenous compounds into the atmosphere. There, sunlight converts these compounds to nitrogen and sulphur oxides, and they combine with water to

become acid rain (mostly nitric acid and sulphuric acid). Acid rain changes the pH of lakes and streams and kills many organisms in them. It also injures plants upon which it falls. About half of the Black Forest in Germany has succumbed to its effects. Acid rain also affects nonliving materials. For example, the natural weathering of ancient Mayan ruins in southern Mexico, the Parthenon in Greece, and monuments in Washington, D.C. has been accelerated by acid rain during the past decades.

Acid rain is not responsible for all dead or dying trees in the world's foests. Some trees have perished as a result of insufficient rainfall during dry years. Other have succumbed to insect infestations or salt scattered to melt ice and snow on roads, and still others have been weakened by disease.

Завдання 2. Впишіть номери відповідних малюнків назв явищ погоди.

Hot ___ Rain ___ Frost ____ Freeze ____ Dew ____ Snow ____ Warm _____
Cold ___ Hailstone _____ Sunny ____ Thunder ____ Fog _____ Cloudy _____
Overcast ___ Rain and snow ___ Wind ____ Thunder storm ____ Strong wind ___

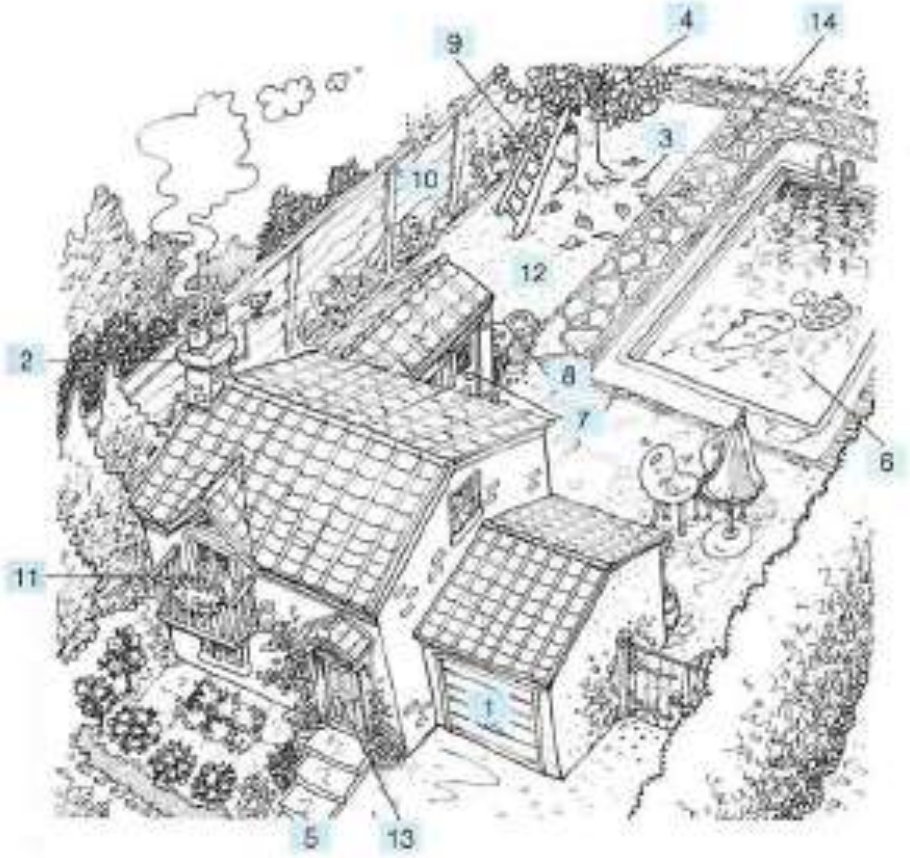
1 2 3 4 5 6

7 8 9 10 11 12

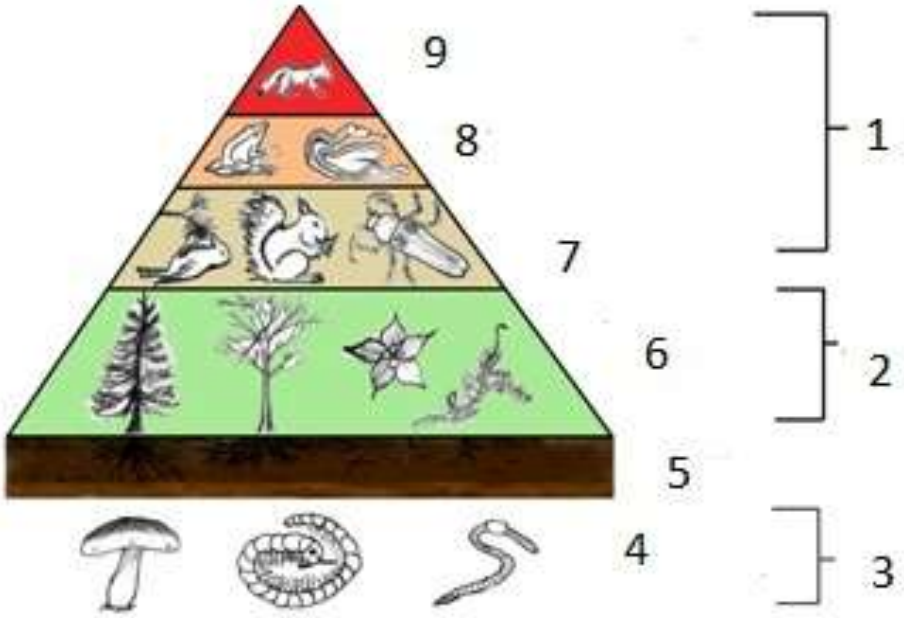
13 14 15 16 17 18

Завдання 3. Впишіть номери назв предметів зображених на рисунку.

Apple tree ____ Back door ___ Balcony ____ Bins ____ Chimney ___ Fence ____
Front door ___ Garage ____ Ladder _____ Lawn _____ Leaves ____ Path ___
Pool _____ Steps _____



Завдання 4. Впишіть номери на відповідні місця: secondary predator, plants, primery predators, soil, herbivores, decay detrivores, heterotrophs (використовується двічі), autotrophs.



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5 _____ 6 _____ 7 _____ 8 _____
9 _____

Розділ 5. Хімія та біохімія.

Завдання 1. Прочитайте та перекладіть подані нижче тексти.

MOLECULAR STRUCTURE

The physical and chemical behavior of molecules is largely determined by their constitution (the type and number of the atoms they contain and their bonding). Structural formulas can therefore be used to predict not only the chemical reactivity of a molecule, but also its size and shape, and to some extent its conformation (the spatial arrangement of the atoms).

Molecule illustrations. In traditional two-dimensional structural formulas, atoms are represented as letter symbols and electron *pairs* are shown as lines. Lines between two atomic symbols symbolize two bonding electrons, and all of the other lines represent free electron pairs, such as those that occur in O and N atoms. Free electrons are usually not represented explicitly (and this is the convention used in this book as well). Dashed or continuous circles or arcs are used to emphasize delocalized electrons. Ball-and-stick models are used to illustrate the spatial structure of molecules. Atoms are represented as colored balls and bonds (including multiple bonds) as gray cylinders. Although the relative bond lengths and angles correspond to actual conditions, the size at which the atoms are represented is too small to make the model more comprehensible. Space-filling van der Waals models are useful for illustrating the actual shape and size of molecules. These models represent atoms as truncated balls. Their effective extent is determined by what is known as the van der Waals radius. This is calculated from the energetically most favorable distance between atoms that are not chemically bonded to one another.

Bond lengths and angles. Atomic radii and distances are now usually expressed in picometers (pm; 1 pm = 10–12 m). The old angstrom unit (E, E = 100 pm) is now obsolete. The length of single bonds approximately corresponds to the sum of what are known as the covalent radii of the atoms involved (see inside front cover). Double bonds are around 10–20% shorter than single bonds. In sp3-hybridized atoms, the angle between the individual bonds is approx. 110°; in sp2-hybridized atoms it is approx. 120°.

Bond polarity. Depending on the position of the element in the periodic table, atoms have different electronegativity – i. e., a different tendency to take up extra electrons. The values given in are on a scale between 2 and 4. The higher the value, the more electronegative the atom. When two atoms with very different electronegativities are bound to one another, the bonding electrons are drawn toward the more electronegative atom, and the bond is polarized. The atoms involved then carry positive or negative partial charges. The van der Waals surface is colored according to the different charge conditions (red = negative, blue = positive). Oxygen is the most strongly electronegative of the biochemically important elements, with C=O double bonds being especially highly polar.

Hydrogen bonds. The hydrogen bond, a special type of noncovalent bond, is extremely important in biochemistry. In this type of bond, hydrogen atoms of

OH, NH, or SH groups (known as hydrogen bond donors) interact with free electrons of acceptor atoms (for example, O, N, or S). The bonding energies of hydrogen bonds (10–40 kJ mol–1) are much lower than those of covalent bonds (approx. 400 kJ mol–1). However, as hydrogen bonds can be very numerous in proteins and DNA, they play a key role in the stabilization of these molecules.

APOPTOSIS

Cell proliferation and apoptosis. The number of cells in any tissue is mainly regulated by two processes – cell proliferation and *physiological cell death*, apoptosis. Both of these processes are regulated by stimulatory and inhibitory factors that act in solute form (growth factors and cytokines) or are presented in bound formon the surface of neighboring cells (see below). Apoptosis is genetically programmed cell death, which leads to "tidy" breakdown and disposal of cells.Morphologically, apoptosis is characterized by changes in the cell membrane (with the formation of small blebs known as "apoptotic bodies"), shrinking of the nucleus, chromatin condensation, and fragmentation of DNA. *Macrophages* and other phagocytic cells recognize apoptotic cells and remove them by phagocytosis without inflammatory phenomena developing. Cell necrosis (not shown) should be distinguished from apoptosis. In cell necrosis, cell death is usually due to physical or chemical damage. Necrosis leads to swelling and bursting of the damaged cells and often triggers an inflammatory response. The growth of tissue (or, more precisely, the number of cells) is actually regulated by apoptosis. In addition, apoptosis allows the elimination of unwanted or superfluous cells – e. g., during embryonic development or in the immune system. The contraction of the uterus after birth is also based on apoptosis. Diseased cells are also eliminated by apoptosis – e. g., tumor cells, virus-infected cells, and cells with irreparably damaged DNA. An everyday example of this is the peeling of the skin after sunburn.

Regulation of apoptosis. Apoptosis can be triggered by a number of different signals that use various transmission pathways. Other signaling pathways prevent apoptosis. At the center of the apoptotic process lies a group of specialized *cysteine-containing aspartate proteinases*, known as caspases. These mutually activate one another, creating an *enzyme cascade* resembling the cascade involved in blood coagulation. Other enzymes in this group, known as effector caspases, cleave cell components after being activated – e. g., laminin in the nuclear membrane and snRP proteins – or activate special DNases which then fragment the nuclear DNA. An important trigger for apoptosis is known as the Fas system. This is used by cytotoxic T cells, for example, which eliminate infected cells in this way. Most of the body's cells have *Fas receptors* (CD 95) on their plasma membrane. If a T cell is activated by contact with an MHC presenting a viral peptide, binding of its *Fas ligands* occurs on the target cell's Fas receptors. Via the mediator protein FADD ("Fasassociated death domain"), this activates *caspase-8* inside the cell, setting in motion the apoptotic process. Another trigger is provided by tumor necrosis factor-α (TNF-α), which acts via a similar protein (TRADD) and

supports the endogenous defense system against tumors by inducing apoptosis. Caspase-8 activates the effector caspases either directly, or indirectly by promoting the cytochrome C from mitochondria. Once in the cytoplasm, cytochrome C binds to and activates the protein Apaf-1 and thus triggers the caspase cascade. Apoptotic signals can also come from the cell nucleus. If irreparable DNA damage is present, the p53 protein – the product of a *tumor suppressor gene* – promotes apoptosis and thus helps eliminate the defective cell. There are also inhibitory factors that oppose the signals that activate apoptosis. These include bcl-2 and related proteins. The genomes of several viruses include genes for this type of protein. The genes are expressed by the host cell and (to the benefit of the virus) prevent the host cell from being prematurely eliminated by apoptosis.

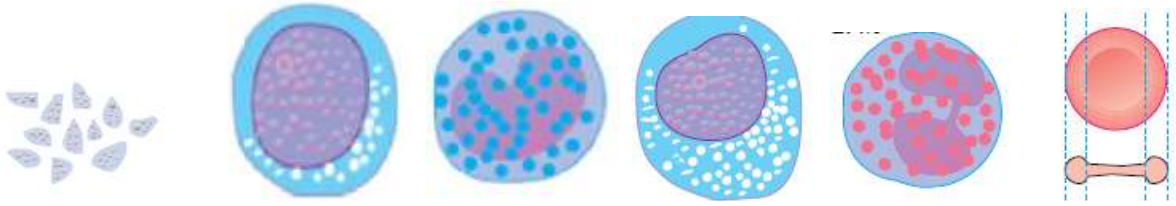
ALKALOIDS

Alkaloids generally include alkaline substances that contain nitrogen as part of a ring structure. The alkaloids, of which more than 6,500 are known, comprise the largest class of secondary metabolites. They occur in several plants families, especially the pea family, the sunflower family, the poppy family, the citrus family, and the potato family. Alkaloids are unknown in mosses, ferns, conifers, and most families of flowering plants.

Alkaloids are diverse group of secondary products, ranging from simple compounds like coniine to complex compounds like strychnine and tomatine. They often produce dramatic physiological effects in humans and other animals. For example, coniine, strychnine, and tubocurarine are infamous toxins, while morphine, codeine, atropine, and vincristine are important therapeutic drags. Alkaloids are often bitter; one of the most bitter substances known is the alkaloid quinine.

Завдання 2. Впишіть номери назв типів клітин крову.

Erythrocyte ___ Neutrophilic granulocyte ____ Monocyte ____ Thrombocytes ___ Small lymphocyte ____ Large lymphocyte _____ Eosinophilic granulocyte _____ Basophilic granulocyte _____



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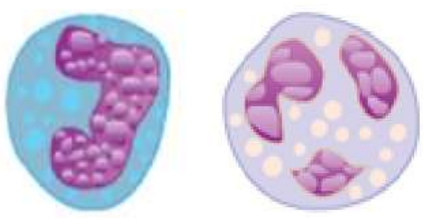

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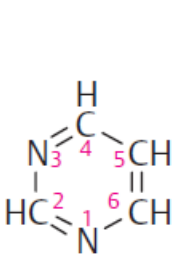
Завдання 3. Впишіть номери назв молекул.

Adenosine _____ Guanine _____ Purimidine _____ Uracil _____
Thymine _____ Purine _____ Cytosine _____ Adenine _____



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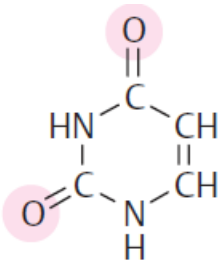

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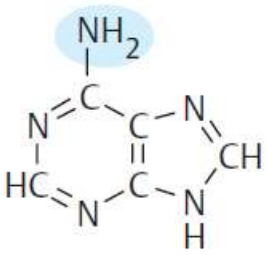

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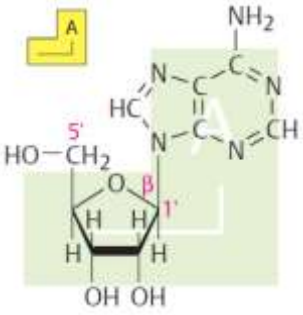

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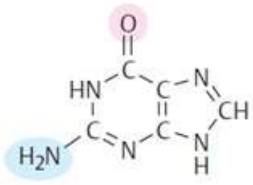

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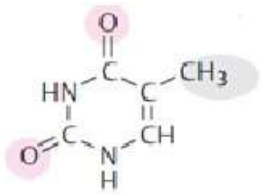

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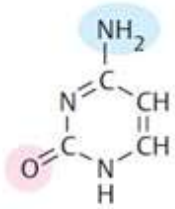

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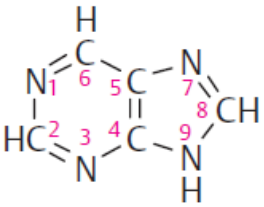

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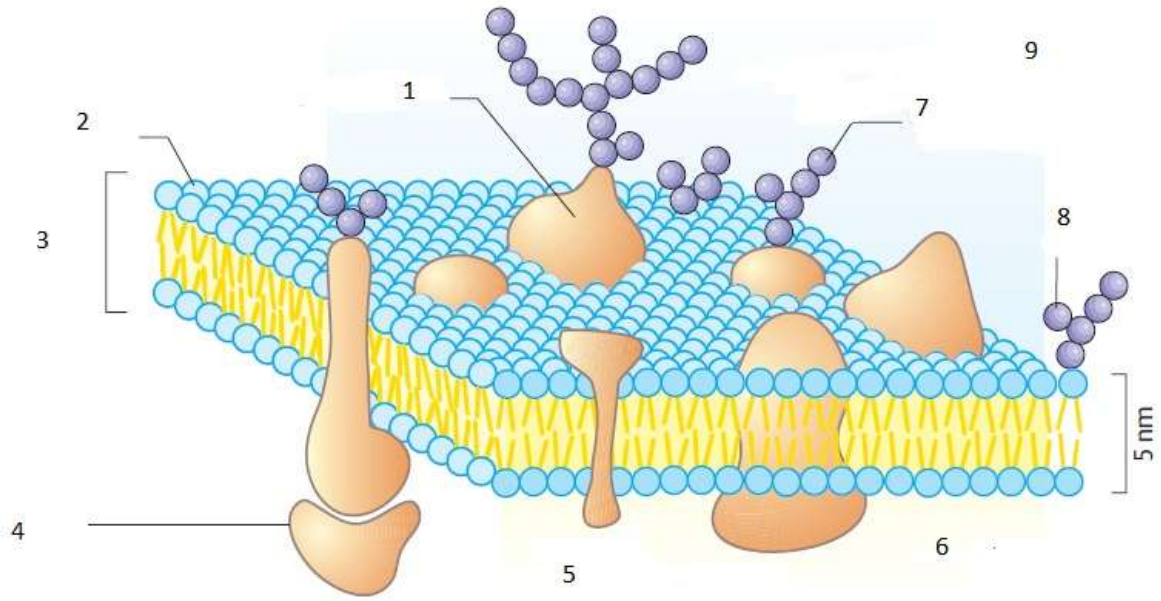
Завдання 4. Впишіть назви з запропонованих нижче на відповідні місця: phospholipid, glycoprotein, extracellular side, oligosaccharide, glycolipid, cytoplasmic side, integral membrane proteins, peripheral membrane protein, lipid bilayer.



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Розділ 6. Генетика.

Завдання 1. Прочитайте та перекладіть подані нижче тексти.

SOURCES OF GENETIC VARIATION

Selection is probably the most important cause of deviation from Hardy-Weinberg equilibrium because it promotes genetic change in the context of the environment and requires genetic variation. Natural selection can change the frequency of phenotypes, but it must have genetic variation as a raw material to effect change. Where does genetic variation originate? Where do new alleles come from? Genetic variation within populations comes from two main sources: gene flow and genetic drift.

Gene flow. Gene flow is the transfer of genetic material from one population to another. The typically occurs through migration of individuals or movement of seeds or pollen to neighboring populations or, in some cases, to distant populations. For example, the grass *Botriochloa intermedia* seems to have incorporated genes from many other grasses, including *B. ischaemum* in Pakistan, *B. insculpta* in eastern Africa, and *Capillipedium parviflorum* in northern Australia.

Gene flow minimizes geographic variation in gene pools; that is, it decreases genetic differences between populations. Gene flow frequently between neighboring populations, and significantly minimize the differences between these populations. Gene flow between distant or isolated populations is rare, which allows their gene pools to diverge over time. Reduction in gene flow partially explains why islands isolated by water are geographically more varied and more likely to produce new species than are vast expanses of grassland, and why lakes and streams contain more geographic variation among populations than oceans. Separated populations of a species are seldom genetically identical, and the differences coincide with the distance between populations.

Gene flow in plant populations is difficult to measure, but it can be experimentally estimated by planting recessive homozygotes at various distances from a strain marked with a dominant allele and then examining the distribution of heterozygous progeny. Using this technique, A. J. Bateman measured pollen dispersal in wind-pollinated (e.g., corn) and insect-pollinated (e.g., radish) crops. The proportion of corn plants receiving the dominant allele by gene flow decreased exponentially with distance and was reduced to 1% at only 13-16 meters from pollen source. Similarly, most pollen of insect-pollinated plants is carried only a short distance; however, the small proportion that is carried farther may contribute importantly to gene flow.

Genetic drift. Genetic drift refers to changes due to chance in the gene pool of a small population. In small populations, chance events such as mutation, mating, or pollination may significantly affect the gene pool and change gene frequencies independently of natural selection. If, for example, one individual in a small population carries the only copy of an allele, then the passage of that allele to the next generation may depend largely on the vagaries of insect pollination or

random, lethal storms rather than natural selection. Favorable alleles in a small population can be eliminated by chance alone. Similarly, catastrophic damage to or death of well-adapted individuals may increase the frequency of the alleles of less fit but surviving individuals. Current research indicates that genetic drift may be a more significant force for changing gene frequencies than previously assumed. This would be especially true for the frequencies of genes that are not subjected to heavy selection pressure.

CYTOPLASMIC INHERITANCE

You learned that chloroplasts and mitochondria contain DNA. Genes in these organelles control certain aspects of photosynthesis and respiration, respectively. Inheritance of these genes is independent of sexual reproduction because they are transmitted to offspring with the cytoplasm, usually that of the maternal parent.

One example of cytoplasmic gene control occurs in certain forms of the cultivated four-o'clock (*Mirabilis jalapa*) that have yellowish0white leaves instead green leaves. This difference in leaf color is caused by defective chloroplast genes. Phenotypic expression depends solely on the seed parent. Thus, when pollen from a white-leaved plant is transferred to a green-leaved plant, all the offspring have green leaves. In contrast, all the offspring of the reciprocal cross have white leaves. This is an example of the cytoplasmic inheritance of non-nuclear genes.

The cooperation of organellar and nuclear genes is often necessary for normal metabolism. For example, the photosynthetic enzyme ribulose-1,5-bisphosphate carboxylase/oxygenase has two subunits, one derived from a nuclear gene and one from a chloroplast gene. Similarly, some ATPases have a dual origin between the nucleus and mitochondria. In each case, the final product – that is, a complete and functional enzyme – depends on genes from two sources in the same cell.

TYPES OF DOMINANCE

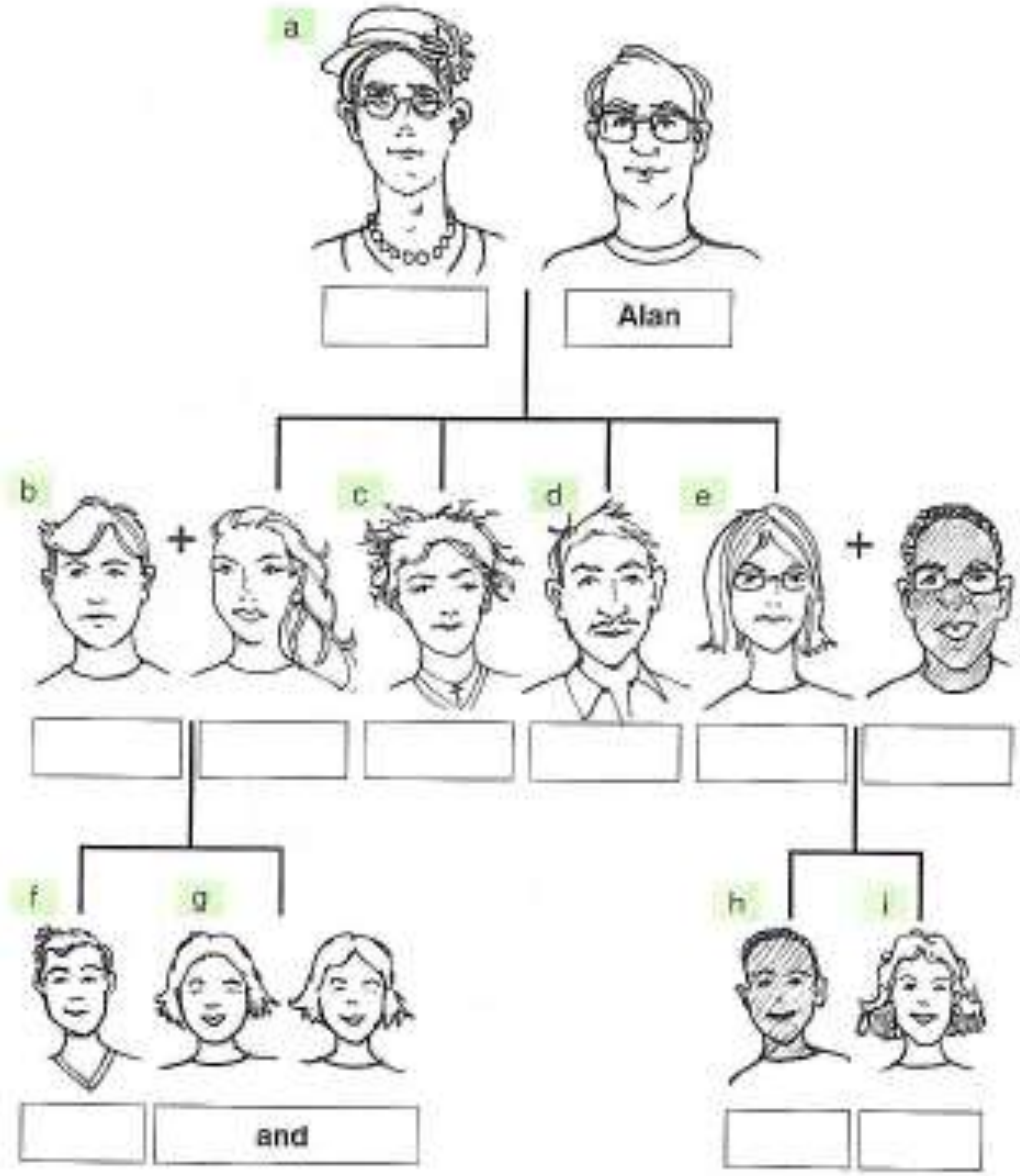
The seven genes by Mendel all exhibit complete dominance, which is a relatively rare type of inheritance. Complete dominance occurs when one trait completely masks its recessive allele. More frequently, the phenotype for one allele is only partly masked by the other, a condition called incomplete dominance. Incomplete dominance occurs when hybrids have a phenotype intermediate between those of the two parents. For example, the allele for red flowers in camellia (*Camellia japonica*) is incompletely dominant over the allele for white flowers. As a result, the F_1 offspring is 1:2:1 (25% red, 50% pink, 25% white). Accordingly, in cases of incomplete dominance, the phenotypic and genotypic ratios are the same.

Codominance occurs when both alleles of heterozygote are expressed equally, so there is really no dominance at all. Codominance is common for heterozygous genes that code for two equally functional enzyme. This means that there is more than one form of the same enzyme. The different forms of enzymes

made by different alleles of the same locus are called allozymes. Although allozymes catalyze the same reaction, they differ from each other by one or a few amino acids, which makes them slightly different from each other in size and overall electric charge. For example, in wild sunflower (Helianthus debilis), there are allozymes of phosphoglucomutase, which catalyzes one of the first reactions in glycolysis. Heterozygotes produce both forms of the enzyme, but homozygotes produce only one or the other.

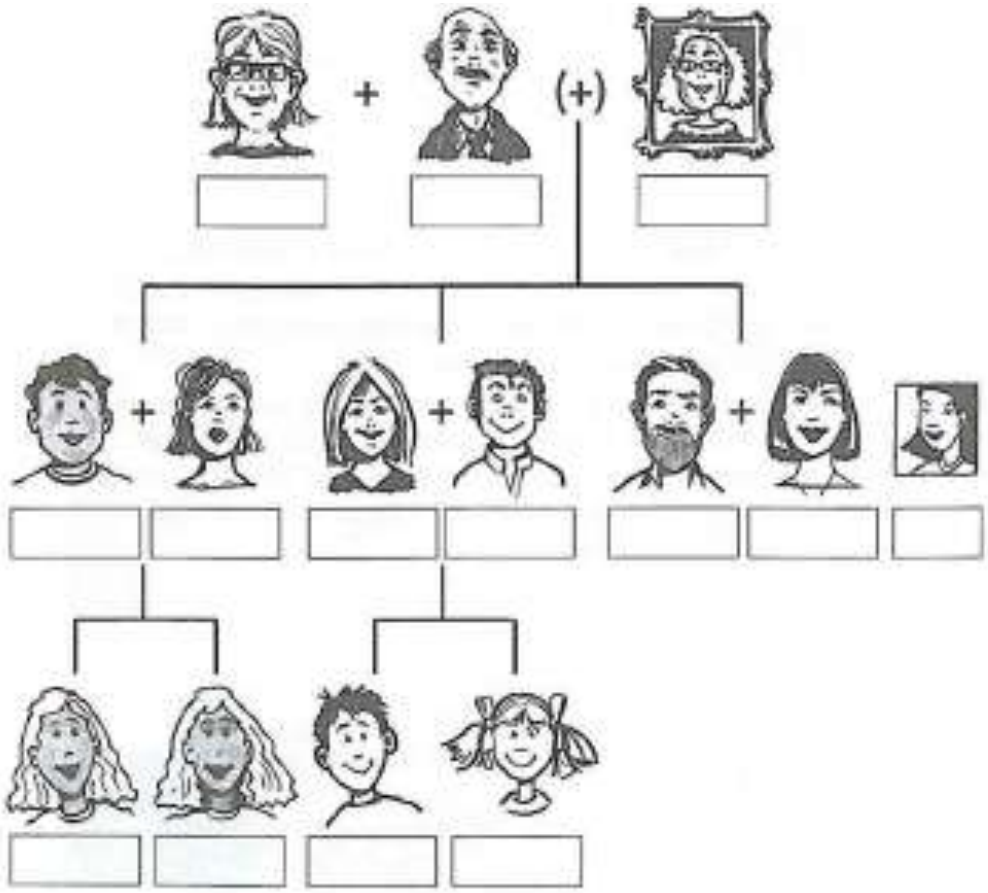
Завдання 2. Впишіть імена відповідних членів родини до родоводу виходячи з поданого нижче опису.

My name's Charlotte. I'm married to John. We have two children, Stephen and Sylvia. My mum's name is Theresa and my father is called Alan. I have two sisters and a brother – Emily, Rebecca and Michael. Emily's married to Craig and they have a son called Freddie and twin daughters, Lizzie and Vicky.



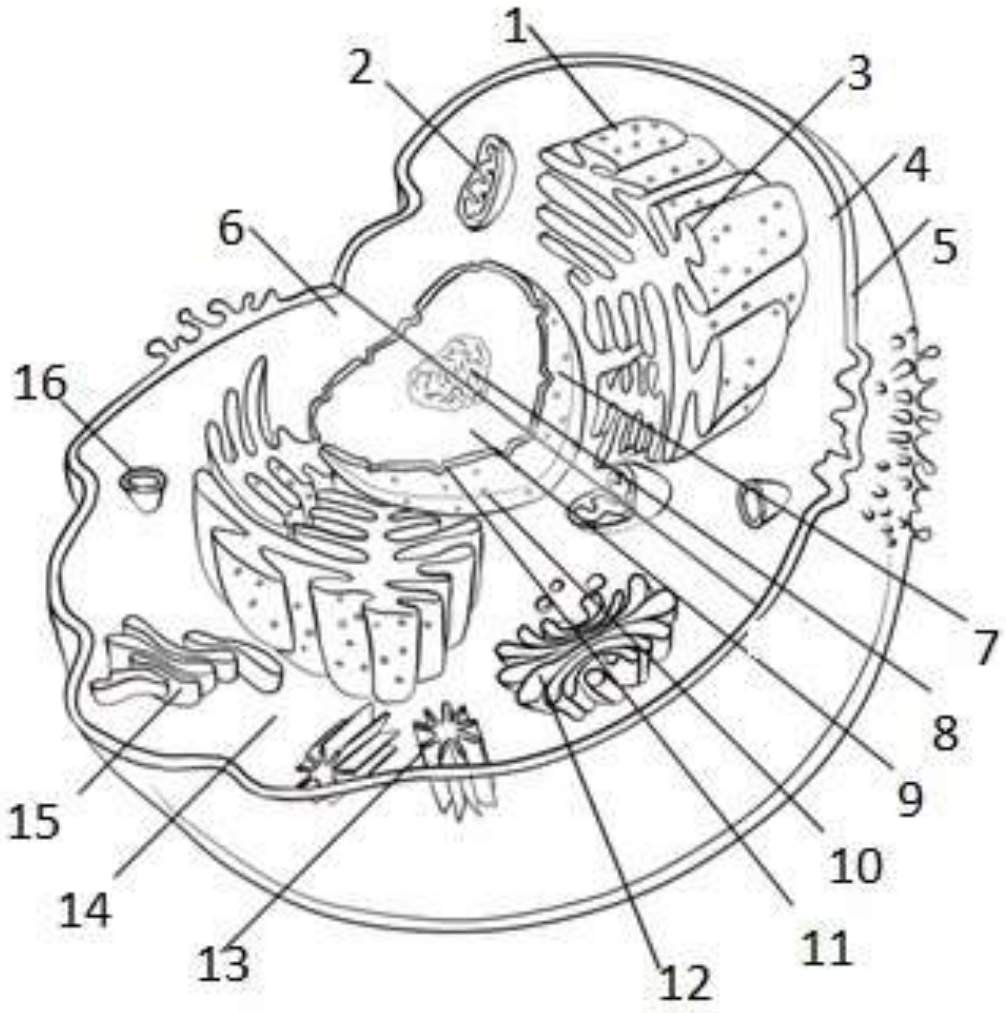
Завдання 3. Впишіть імена відповідних членів родини до родоводу виходячи з поданого нижче опису.

My name's Heidi. I'm married to Kerim. We have two children, Aisha and Leila. My mum, Wendy, died when I was a teenager. My dad, Keith, got married to Katrina fourteen years ago. I've got one sister, Gina, and one brother, Andy. Gina's married to Kean-Claude, who's French. They've got a little girl called Julie and a boy of twelve called Michael. My brother Andy was married to a girl called Caroline but they got divorced. Luckily they didn't have any children. Now he's married to a girl called Susanna.



Завдання 4. Впишіть номери відповідних частин клітини:

Cell coat ____ centriole ____ chromatin ____ cytoplasm ____ free ribosome ____
Goldi body ____ lysosome _____ mitochondrion _____ nuclear envelope _____
nuclear pore _____ nucleolus _____ nucleus _____ plasma membrane _____
ribosome _____ rough endoplasmatic reticulum _____
smooth endoplasmatic reticulum _____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Розділ 7. Наукові статті для самостійного опрацювання.

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Breeding Barley for Multiple Disease Resistance in the Upper Midwest Region of the USA

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Abstract: The Upper Midwest is one of the largest barley production areas in the USA. In this region, diseases can markedly reduce both the yield and quality of the crop. Molecular and classical breeding techniques are being employed to develop cultivars with resistance to five different diseases in the Minnesota barley improvement program. Stem rust and spot blotch have been successfully controlled for many years through the deployment of the major gene *Rpg1* and a major effect QTL, respectively. A sequence characterized amplified region (SCAR) marker developed from the sequence of *Rpg1* has made marker-assisted selection (MAS) for stem rust resistance highly effective. The major QTL controlling durable adult plant spot blotch resistance was first identified in the Steptoe/Morex population. This QTL was completely suppressed in the Harrington/Morex and Dicktoo/Morex populations, highlighting the importance of genetic background for the expression of resistance. The onset of Fusarium head blight (FHB) in 1993 led to dramatic changes in the focus of the breeding program. Significant resources have been expended to develop populations for mapping resistance QTL and identify closely linked markers for MAS. This is a difficult challenge because FHB resistance is controlled by many QTL with small effects. Sources of resistance to net blotch and Septoria speckled leaf blotch (SSLB) have been identified in a number of barley accessions. These resistances are simply inherited and are being introgressed into elite lines via phenotypic and MAS. Continued progress toward multiple disease resistance will require efficient phenotypic screening, MAS, and utilization of discoveries in barley genomics to manage numerous resistance genes and desirable gene complexes assembled over decades of breeding.

Keywords: barley; *Hordeum vulgare* L.; disease resistance; marker-assisted selection

The Upper Midwest region of the USA is one of the most productive cereal-growing regions in the northern Great Plains and the major source of barley for the malting and brewing industries. This region includes the states of Minnesota, North Dakota, and South Dakota and produces over 2000 Mt of barley annually, most of which is intended for malting. In recent years, economic factors and disease pressure have pushed six-rowed malting barley production from an area centred in northwestern Minnesota and eastern North Dakota to north central North Dakota and southern Canada. Diseases that commonly impact barley production in this region include stem rust (caused by *Puccinia graminis* f.sp. *tritici*), spot blotch (caused by *Cochliobolus sativus* [anamorph: *Bipolaris sorokiniana*]), FHB (caused primarily by *Fusarium graminearum* [teleomorph: *Gib-*

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berella zeae]), net blotch (caused by *Pyrenophora teres* f. *teres* [anamorph: *Drechslera teres* f. *teres*]), and Septoria speckled leaf blotch (SSLB) (caused by both *Septoria passerinii* and *Phaeosphaeria avenaria* f.sp. *triticea* [anamorph: *Stagonospora avenae* f.sp. *triticea*]) (Fetch *et al.* 2003; Steffenson 2003). The deployment of host resistance is often the preferred method of control for these diseases because it is an effective, economical, and environmentally sound strategy.

One of the great challenges in breeding malting barley is to incorporate multiple disease resistance while maintaining favourable gene complexes responsible for regional adaptation and acceptable malting and brewing characteristics. Approval of a barley cultivar for use in malting and brewing is based on about 25 different quality traits (Wych & Rasmusson 1983). Additionally, an approved cultivar must also pass taste tests after it is malted and made into beer. These specific requirements have forced breeders to cross closely related parents that already possess superior malting and brewing characteristics. As a result, the Minnesota barley germplasm base has been drastically narrowed to the extent in which 50% of the parentage traces back to only five ancestors (Martin *et al.* 1991). Introgression of genes from exotic sources, such as in the case of disease resistance, requires a process of parent building or cyclical breeding. In this process, the most desirable progenies from crosses in early cycles of breeding are used as parents in subsequent breeding cycles. After several breeding cycles, progenies will be suitable for crosses that will potentially lead to new cultivar candidates. The number of breeding cycles necessary will depend on the ease and reliability of the screening methods and whether the trait exhibits simple or complex inheritance. For more challenging diseases under complex genetic control (e.g. FHB), it is likely that at least 4–5 breeding cycles will be necessary to generate breeding lines that can be used as parents to ultimately produce a new cultivar. Parent building is generally used to improve a single trait. Therefore, breeding for multiple disease resistance can be viewed as a multiple parent building enterprise that will ultimately lead to the combination of desired resistances in a single cultivar. The objective of this paper is to review current and past efforts in breeding six-rowed malting barley cultivars for multiple disease resistance in the Upper Midwest region of the USA. Successes and continuing challenges in this endeavour are discussed as well as prospects for the future.

Stem rust

Stem rust has historically been one of the most devastating diseases of barley in the Upper Midwest region. Since 1942, losses to stem rust in barley have been minimal due to the planting of cultivars with the durable resistance gene *Rpg1* (Steffenson 1992). Pathotypes with virulence for *Rpg1* have been reported periodically in the Upper Midwest region since 1942 (Steffenson 1992). In 1989, a pathotype (QCCJ) with virulence for *Rpg1* became widespread in the Upper Midwest and damaged some barley fields (Roelfs *et al.* 1991). Pathotype QCCJ is still a threat to barley production in the region. To obtain stable stem rust control in the future, breeders may have to combine into cultivars *Rpg1* and gene(s) for resistance to pathotype QCCJ. The retention of *Rpg1* in new cultivars is essential because this gene has proven durable to many pathotypes of *P. g.* f.sp. *tritici* in the region for over 60 years. Resistance to pathotype QCCJ was identified in barley accession Q21861 (PI 584766) and is conferred by a single recessive gene *rpg4* (Jin *et al.* 1994). Prior to the appearance of pathotype QCCJ, breeding for stem rust resistance was easy because it only required the introgression of *Rpg1*. Since all of the elite parents carried *Rpg1*, stem rust resistance was maintained in the program without any phenotypic selection. The transfer of an additional gene (i.e. *rpg4*) for resistance to pathotype QCCJ will complicate the breeding effort. A significant advance for the high-throughput detection of *Rpg1* in the breeding program would be the development of a molecular marker in the gene itself. *Rpg1* was recently isolated by a map-based approach (Brueggeman *et al.* 2002). By exploiting sequence variation in the gene, Eckstein *et al.* (2003) developed a robust, allele specific SCAR marker that can differentiate between lines with the functional resistance gene and those that lack the gene or contain one of several susceptibility alleles. This *Rpg1* marker was 92% accurate in detecting stem rust resistance in a historical set of 100 Minnesota breeding lines and Midwestern cultivars (Condon *et al.* 2004). Development of a molecular marker within the *rpg4* gene is in progress (Kleinhofs

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Table 1. Breeding scheme and timeline for disease screening in the Minnesota barley improvement program

Year	Breeding generation	Time/location	Disease screening[1]
1	parent selection	autumn greenhouse	SB(G), SR(M)
	F_1	winter greenhouse	
	F_2	summer field	FHB(M), SR(M), SSLB(M)
2	F_3	autumn greenhouse	
	F_4	winter nursery (NZ)	SSLB(G), NB(G)
	$F_{4:5}$	summer field	FHB(F), SSLB(F), NB(F)
3	$F_{5:6}$	winter nursery (NZ)	
	$F_{5:7}$ preliminary yield	summer field	FHB(F), SSLB(F), NB(F)
4	$F_{5:8}$ intermediate yield	summer field	FHB(F), SSLB(F), NB(F)
5	$F_{5:8}$ advanced yield	summer field	FHB(F), SSLB(F), NB(F)

[1]SB = spot blotch; SR = stem rust; FHB = Fusarium head blight; SSLB = Septoria speckled leaf blotch; NB = net blotch; (G) = greenhouse disease screen; (M) = DNA marker screen; (F) = field disease screen; (NZ) = New Zealand

et al., unpublished) and when completed it will allow multiplexing molecular markers for the two stem rust resistance genes on parents and in early generation (F_2) segregating populations, thereby increasing the efficiency and throughput of stem rust resistance breeding (Table 1). Still, stem rust phenotyping (Jin *et al.* 1994) must be done to verify the presence of the genes and their expression, since the *Rpg1* marker has not proven infallible.

Spot blotch

Spot blotch was one of the most devastating foliar diseases of barley in the Upper Midwest region. The disease has been successfully controlled for over 40 years through the use of host resistance and is one of the great success stories in breeding barley for resistance. This durable spot blotch resistance was derived from the breeding line NDB112 and has been incorporated into all of the major six-rowed malting cultivars grown in the region (Steffenson *et al.* 1996). To elucidate the genetic basis of durable spot blotch resistance in six-rowed malting cultivars, we studied the Steptoe/Morex (S/M) population. Morex is a resistant six-rowed malting cultivar derived from NDB112, and Steptoe is a susceptible six-rowed feed cultivar. A single gene (designated *Rcs5*) located at the telomeric region of chromosome 1(7H) was found to confer spot blotch resistance at the seedling stage (Steffenson *et al.* 1996). Two quantitative trait loci (QTL) conferred adult plant resistance in the S/M population: one of major effect on chromosome 5(1H) explaining 62% of the variance and the other of minor effect on chromosome 1(7H) explaining 9% of the variance (Table 2). The QTL on chromosome 1(7H)

Table 2. Summary of major QTL (chromosomal location and % phenotypic variance explained) contributing to adult plant spot blotch resistance in three mapping populations derived from resistant parent Morex

Population	Chrom 1(7HS) *iEst5-ABC158*	Chrom 3(3HS) *saflp119-saflp54*	Chrom 3(3HL) *saflp35-saflp53*	Chrom 5(1HL) *ABG500A-ABG452*
S/M	12	–[1]	–	62
D/M	20	36	11	–
H/M	75	–	–	–

[1]No significant QTL detected in this region

mapped to the same region as *Rcs5*. Thus, durable spot blotch resistance in six-rowed malting barley cultivars is conferred mostly by a single QTL of major effect on chromosome 5(1H). To corroborate these findings, the same analysis was conducted on the two- × six-rowed cross of Harrington/Morex (H/M). Harrington is a susceptible two-rowed malting cultivar. As in the S/M population, a single gene (presumably *Rcs5*) on chromosome 1(7H) conferred spot blotch resistance at the seedling stage. However, a different and quite unexpected result was obtained for adult plant resistance in the H/M population: no chromosome 5(1H) effect was detected. Instead, a single gene mapping at or near *Rcs5* on chromosome 1(7H) conferred resistance. When the disease severity data were subjected to quantitative analysis, a single major effect QTL explaining 75% of the variance was identified, again at or near *Rcs5* (Table 2) (Steffenson 2000; Bilgic *et al.* 2006). One additional population involving Morex (Dicktoo/Morex [D/M]) was tested for its reaction to spot blotch. In this case, the susceptible parent was the six-rowed feed cultivar Dicktoo; thus, the D/M population was used to test whether the Morex-derived chromosome 5(1H) adult plant resistance QTL first identified in the S/M population would again be expressed in a different six- × six-rowed cross. Three QTLs were detected at the adult plant stage in the D/M population: one on the short arm of chromosome 3(3H) explaining 36%, the second on the long arm of chromosome 3(3H) explaining 11%, and the third near *Rcs5* on the short arm of chromosome 1(7H) explaining 20% of the phenotypic variation (Bilgic *et al.* 2006). No effect whatsoever was detected in the chromosome 5(1H) region where the adult plant resistance QTL was first discovered in the S/M population (Table 2). Over the past 40 years, breeders have been very successful in retaining the chromosome 5(1H) resistance QTL in their six-rowed malting germplasm, presumably by fixing the resistance allele in elite parents and practicing occasional phenotypic selection. It appears that this resistance is highly expressed in the six-rowed genetic backgrounds of the major malting barley breeding programs in the Midwest. This resistance QTL may, however, be completely suppressed when introgressed into more diverse two- or six-rowed genetic backgrounds (e.g. H/M and D/M populations). Molecular markers for the chromosome 5(1H) spot blotch resistance QTL are being developed. Their utility in MAS for the chromosome 5(1H) QTL may be limited given the suppression that occurs in crosses with both two- and six-rowed susceptible parents. In the future, we will employ MAS to verify that parents used in the breeding program carry the resistance allele at the 5(1H) QTL (Table 1) and continue to screen advanced breeding lines in the field to ensure that the resistance is expressed in the current breeding background.

Septoria speckled leaf blotch

Septoria speckled leaf blotch (SSLB) is a disease complex caused by two different pathogens. In the Upper Midwest region, *S. passerinii* is the most common SSLB pathogen, although *P. a.* f.sp. *triticea* is also frequently isolated from symptomatic barley tissue (Krupinsky & Steffenson 1999). In recent years, SSLB has re-emerged as one of the most important diseases of barley in the Upper Midwest region due to the increased use of minimum tillage and high rainfall during the growing season. Yield losses of 23–38% were reported on barley due to *S. passerinii* infection (Toubia-Rahme & Steffenson 2004). All of the major malting and feed barley cultivars in the Upper Midwest region are highly susceptible to SSLB (Toubia-Rahme *et al.* 2003). Fortunately, many sources of resistance to *S. passerinii* have been identified in both cultivated (Rasmusson & Rogers 1963; Legge *et al.* 1996) and wild barley (*H. vulgare* subsp. *spontaneum* and *H. bulbosum*) (Fetch *et al.* 2003; Toubia-Rahme *et al.* 2003). In the Minnesota barley improvement program, two sources of resistance are being used: CIho 4780 (an accession from northern China) and PC84 (a breeding line from the ICARDA/CIMMYT program in Mexico). Both accessions exhibit high levels of resistance in the field. Resistance in CIho 4780 is conferred by a single dominant gene *Rsp2* (Rasmusson & Rogers 1963), which was recently mapped to the short arm of chromosome 5(1H) (Zhong *et al.* 2006). A SCAR marker cosegregating with *Rsp2* was developed and evaluated for MAS of SSLB resistance. Selection of F_2 plants homozygous for the resistance allele of the SCAR marker in two segregating populations was 96–100% effective in identifying SSLB resistant F_5 lines. Resistance in PC84 is thought to be under the control of a single dominant gene that is different from the one present in CIho 4780 (Steffenson & Smith, unpublished). Our goal is to increase

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the diversity of SSLB resistance by incorporating both genes into new cultivars.

Net blotch

Net blotch is perhaps the most important foliar pathogen of barley in the Upper Midwest on an annual basis given the sporadic nature of SSLB epidemics and the success attained in controlling stem rust and spot blotch by host resistance. The disease is widely distributed and is often found in high severities in commercial fields (STEFFENSON, unpublished). Many sources of net blotch resistance have been described in cultivated and wild barley (SHIPTON *et al.* 1973; FETCH *et al.* 2003). The Canadian cultivar Heartland is currently being used as a source of net blotch resistance in the Minnesota program. Preliminary studies indicate that this resistance is simply inherited. We have initiated work to identify markers that will be useful in MAS for net blotch resistance. Currently, we screen for net blotch resistance in segregating populations during single seed descent using remnant F_4 seed in a greenhouse seedling assay (Table 1). Resistant lines ($F_{4:5}$) are advanced to a field screen on adult plants where selection is based on disease resistance as well as other traits (i.e. lodging, stem strength, height, maturity, etc.).

Fusarium head blight

FHB is one of the most devastating and insidious diseases of barley. In addition to causing yield loss, the primary pathogen, *F. graminearum*, produces various mycotoxins (most notably deoxynivalenol or DON) that are hazardous to humans and animals (STEFFENSON 2003). FHB has been a relatively minor and sporadic disease problem of barley in the United States for many years. Over the past decade, however, it has re-emerged as the most important factor reducing the yield and quality of the crop in the Upper Midwest. The head blight epidemics of the 1990's were particularly devastating and caused severe economic losses, grain processing problems for producers and end-users alike, food/feed safety concerns, and human hardship (STEFFENSON 2003). These epidemics also forced breeders to make drastic changes in their programs. Today, a significant portion of the breeding effort is focused on breeding for resistance to FHB and the accumulation of DON. A number of conventional and molecular mapping studies have been made on the genetics of FHB resistance in barley (reviewed in STEFFENSON 2003). All have reported complex inheritance for the trait. The molecular mapping studies indicate that FHB resistance is a complex quantitative trait controlled, in most cases, by a number of loci with relatively small effects that are scattered across the barley genome. From these genetic studies, it is evident that FHB resistance in barley is under polygenic control and its heritability can vary greatly. Given the great importance of this disease, the numerous challenges in quantifying FHB severity, and the complex genetics of resistance, we have developed a modified FHB breeding strategy in the Minnesota program. The large experimental error and environmental effects on FHB severity have dictated that our early generation screening efforts employ multiple locations and replications. For other diseases such as net blotch, it is possible to do greenhouse screening on seedlings using remnant seed from early generations (F_3, F_4) during single seed descent, followed by a single F_5 head row evaluation in the field for a number of traits. For FHB, we cannot effectively conduct greenhouse screening in early generations. In year two (F_5 generation), we evaluate FHB reaction in misted and inoculated field nurseries (Table 1). Each new breeding line is replicated twice at two locations and evaluated for FHB severity. We harvest grain from resistant lines and checks for quantification of DON. In addition, we grow a fifth row in a non-inoculated nursery and harvest the grain for malting quality evaluation. Because FHB resistance is linked to maturity and plant morphology traits, we have emphasized selection for resistance prior to selection for other traits in the early cycles of breeding.

The need for replication in early generations and the desire to work with more homozygous material (F_4-derived) have forced us to make changes in our single seed descent program. The initial protocols, however, are the same. We make most crosses in the autumn, grow F_1's in the winter greenhouse, and F_2's in a summer field trial (Table 1). We then plant the F_3 generation immediately after harvest in early August to allow for an off-season F_4 generation in New Zealand. The F_4 generation is planted as spaced single plants to allow the harvest of sufficient $F_{4:5}$ seed for growing five 1.8 m rows in the disease and quality nurseries described above. This laborious screening effort has forced us to reduce the number of crosses and

new lines that we can evaluate each year, but has given us much more confidence in our early generation selection. In year three, we evaluate lines selected from year two in five disease nurseries with three replications per nursery. These same lines are evaluated in preliminary yield trials at two locations. Lines that continue on in year four are evaluated in three location trials in Minnesota. The best lines from the advanced yield trials (year five) are evaluated in a collaborative regional FHB nursery with eight locations in Minnesota, North Dakota, and Canada.

Recently, we have begun to evaluate MAS for FHB resistance. We evaluated markers linked to two major QTLs for FHB resistance discovered (De La Pena *et al.* 1999) and validated (Canci *et al.* 2003) from the Chevron source of resistance. The Chevron alleles at the QTL on chromosome 2(2H) reduced FHB by 43% and increased HD by two days as was predicted by the mapping studies (Gustus & Smith 2001). Selection for the Chevron alleles at the chromosome 6(6H) region reduced FHB by 22%, but also increased grain protein by 14 g/kg. We are continuing to evaluate these and other markers to increase the efficiency of FHB selection. MAS is generally used to select lines homozygous for the resistance marker allele in the F_2 generation prior to single seed descent (Table 1).

CONCLUSIONS AND FUTURE DIRECTIONS

The successful development of malting barley cultivars with multiple disease resistance requires the introgression of resistance alleles that function in the target genetic background and are free of linkage to undesirable traits. Past progress has relied on parent building after fixing genes for resistance or by exploiting individual segregating populations using phenotypic selection. For several diseases, markers now allow breeders to track resistance alleles in the broad arrays of breeding lines within the program, thereby reducing the need for expensive and sometimes variable phenotypic screening. In the future, it may be possible to exploit phenotypic variation in the complex pedigree structure of breeding germplasm to identify new QTL through the use of association genetics (Jannink *et al.* 2001). This approach exploits the tremendous amount of phenotypic data generated by breeding programs and the relatively inexpensive DNA genotyping technologies currently available to study important traits. By routinely genotyping breeding lines with a strategic set of DNA markers, it will be possible to validate QTL in the relevant germplasm, identify new QTL for important breeding traits, and determine if alleles introgressed into breeding lines perform as predicted by genetic studies. The rapidly advancing field of genomics is providing information on the location, expression profile, and function of genes that will be important for continued progress in breeding as well as new tools for manipulating them in breeding programs. All of this new technology and information will facilitate the management of multiple disease resistance in barley.

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Intercropping field mustard (*Brassica rapa subsp. oleifera*) with autumn-sown annual legumes and cereals for forage production

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Introduction

Brassica rapa L. is a plant species with a remarkable wide variability of its morphological traits (The Brassica rapa Genome Sequencing Project Consortium 2011). It comprises turnip (*Brassica rapa* L. subsp. *rapa*), a well-known vegetable root crop, several leaf vegetables, such as bok choy (*Brassica rapa* L. subsp. *chinensis* (L.) Hanelt) and napa cabbage (*Brassica rapa* L. subsp. *pekinensis* (Lour.) Hanelt), and field mustard (*Brassica rapa* L. subsp. *oleifera* (DC.) Metzg.), one of the economically important oil crops.

The results of some molecular analyses of field mustard by amplified fragment length polymorphism (AFLP) postulated a possibility that its domestication occurred independently in Europe and East Asia. In both geographic regions, there are the traces of initial breeding attempts, leading to the contemporary genetic diversity of field mustard (Zhao et al. 2005). Today, in the Southeast Europe, field mustard is little known and is often considered a weed and wrongly identified as black mustard (*Brassica nigra* L.).

The main purpose of cultivating field mustard is oil production (Abbasi et al. 2011). Like many other brassica species, it has a numerous additional uses (Hall et al. 2002), such as forage cultivation and green manure. One of the many traits of field mustard desirable in diverse farming systems and crop rotations is prominent earliness, that is, a rather short period from sowing to budding and cutting (Li et al. 2009, Mikić et al. 2014b).

Intercropping is widely regarded as growing at least two plant species at the same place in the same time (Willey 1990). Intercropping brassicas, such as fodder kale (*Brassica oleracea* L. var. *viridis* L.), rapeseed (*Brassica napus* L.) and white mustard (*Sinapis alba* L.), with cereals and legumes for forage production proved rather promising in terms of nutritional, yield and quality aspects (Khan et al. 2005, Jamont et al. 2013, Mihailović et al. 2014, Marjanović-Jeromela et al. 2015a, Mikić et al. 2015).

The goal of this preliminary research was to assess the potential of intercropping field mustard with various autumn-sown annual legumes and cereals for forage production.

Material and methods

A small-plot trial was carried out in 2013 and 2014 at the Experimental Field of the Institute of Field and Vegetable Crops at Rimski Šančevi, in the vicinity of Novi Sad, northern Serbia. An experimental field mustard line TR 04 was chosen for intercropping with four autumn-sown annual legumes and four autumn-sown cereals

on the basis of its performance in the previous testing (Marjanović-Jeromela et al. 2015b). The eight intercrop companions of the field mustard line TR 04 were as follow:

1. Common vetch (*Vicia sativa* L.), cultivar NS Tisa;
2. Hairy vetch (*Vicia villosa* Roth), cultivar NS-Viloza;
3. Hungarian vetch (*Vicia pannonica* Crantz), cultivar Panonka;
4. Pea (*Pisum sativum* L.), cultivar NS Krmni;
5. Barley (*Hordeum vulgare* L.), cultivar Nonius;
6. Common wheat (*Triticum aestivum* L. subsp. *aestivum*), cultivar NS 40S;
7. Oat (*Avena sativa* L.), cultivar NS Jadar;
8. Triticale (×*Triticosecale* spp.), cultivar Odisej.

In both trial growing seasons, all nine intercrop components were sown during the first decade of October, at the usual sowing rates for each in sole crops, such as 200 viable seeds m^{-2} for field mustard (Bilgili et al. 2003) in field mustard, and half-reduced usual sowing rates in the intercrops, with a plot size of 5 m^2 and with three replicates. The sole crops of each species were cut in their own optimum moment: budding in field mustard, full flowering in annual legumes and stage slightly before spikes and racemes appear in cereals.

The intercrops were cut when one of the components was in its optimum moment for cutting, although in most cases they were concurrent in both field mustard and annual legumes or cereals. The fresh forage yield per area unit (t ha^{-1}) in all nine sole crops and all eight intercrops was calculated upon the basis of the fresh forage yield per trial plot (kg 5 m^{-2}), measured immediately after cutting.

The land equivalent ratio (LER), a parameter for economic justification of intercropping (Mead and Willey 1980), for each intercrop was calculated according to the following formula (Kadžiulienė et al. 2011):

$$LER = FM_{IC} / ALC_{SC} + FM_{IC} / ALC_{SC},$$

where FM_{IC} is the fresh forage yield of field mustard in an intercrop with annual legumes or cereals, FM_{SC} is the fresh forage yield of field mustard in its sole crop, ALC_{IC} is the fresh forage yield of an annual legume or cereal component in an intercrop and ALC_{SC} is the fresh forage yield of an annual legume or cereal component in its sole crop.

The results of the trial were processed by means of analysis of variance (ANOVA) and the Least Significant Difference (*LSD*) test.

Results and Discussion

Significant differences were determined among the two-year average values of the fresh forage yield in the fresh forage yield of sole crops, the fresh forage yield of single components, the total fresh forage yield and its LER (Tables 1 and 2).

In the sole crops, field mustard had much significantly higher fresh forage yield (75.1 t ha^{-1}) than the annual legumes and the cereals (Table 1). It had slightly higher fresh forage yield than fodder kale in previous research, with 67.5 t ha^{-1}, as well as than autumn- and spring sown rapeseed and white mustard (Mihailović et al. 2008). The highest values of the fresh forage yield among the annual legumes and the cereals were 50.1 t ha^{-1} in pea and 50.5 t ha^{-1} in triticale, with both achieving better performance than in the trial with intercropping pea with cereals in the same agroecological conditions (Mihailović et al. 2011).

Table 1. Average values of fresh forage yield (t ha^{-1}) in the sole crops of field mustard and autumn-sown annual legumes and cereals in the trial at Rimski Šančevi for 2013 and 2014

Crop	Species	Fresh forage yield
Brassica	Field mustard	75.1
Annual legume	Common vetch	40.4
	Hairy vetch	42.5
	Hungarian vetch	35.7
	Pea	50.1
	Average	42.2
Cereal	Barley	49.2
	Common wheat	40.4
	Oat	40.1
	Triticale	50.5
	Average	45.1
$LSD_{0.05}$		7.7

In the intercrops of field mustard and the autumn-sown annual legumes (Table 2), field mustard had the greatest individual contribution to the total fresh forage yield in the mixture with pea (33.5 t ha^{-1}). On the other hand, hairy vetch proved to be the most aggressive among the annual legumes, at the same time achieving 38.0 t ha^{-1} and leaving field mustard with 16.5 t ha^{-1} of fresh forage. Hairy vetch was also more dominant in a trial with intercropping with fodder kale and rapeseed, with 6.1 t ha^{-1} and 6.6 t ha^{-1} of forage dry matter (Ćupina et al. 2013).

Table 2. Average values of fresh forage yield (t ha^{-1}) its land equivalent ratio (LER) in the intercrops of field mustard with autumn-sown annual legumes and cereals in the trial at Rimski Šančevi for 2013 and 2014

Intercrop	Field mustard fresh forage yield	Annual legume / cereal fresh forage yield	Total fresh forage yield	LER
Field mustard + common vetch	23.1	36.3	59.4	1.21
Field mustard + hairy vetch	16.5	38.0	54.5	1.11
Field mustard + Hungarian vetch	20.1	35.1	55.2	1.25
Field mustard + pea	33.5	36.7	70.2	1.18
Field mustard + legumes average	23.3	36.5	59.8	1.19
Field mustard + barley	24.6	33.5	58.1	0.95
Field mustard + common wheat	28.7	23.8	52.5	1.03
Field mustard + oat	27.6	25.1	52.7	1.02
Field mustard + triticale	25.7	27.5	53.2	0.88
Field mustard + cereals average	26.7	27.5	54.1	0.97
$LSD_{0.05}$	2.3	3.9	2.0	0.05

In average, field mustard had greater contribution to the total fresh forage yield when intercropped with cereals (26.7 t ha^{-1}) than with annual legumes (Table 2). It ranged from 24.6 t ha^{-1} in the intercrop with barley to 28.7 t ha^{-1} in the intercrop with common wheat. Barley demonstrates a similar ability to be highly competitive with other crops, such as annual legumes (Mihailović et al. 2004).

The two-year average fresh forage yield ranged from 52.5 t ha^{-1} in the intercrop of field mustard with common wheat to 70.2 t ha^{-1} in the intercrop of field mustard and pea (Table 2). The intercrops of field mustard with annual legumes had higher two-year average fresh forage yield (59.8 t ha^{-1}) than the intercrops with cereals (54.1 t ha^{-1}), what is congruent with the previously conducted testing (Mikić et al. 2014a).

All four intercrops of field mustard and annual legumes proved economically justified, with the two-year average LER values ranging between 1.11 in the intercrop with hairy vetch and 1.25 in the intercrop with Hungarian vetch. These values were significantly lower in the intercrops with cereals, with those with barley and triticale lower than 1 (Table 2).

Conclusions

There is a solid basis to deem intercropping field mustard with autumn-sown legumes and cereals reliable, in terms of both fresh forage yield and the economic aspect of such production, especially significant in feeding milk cows. The future research efforts should be focused on the quality aspects and stress-related issues.

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Full Length Research Paper

Embryonic diffrentiation of the Jejunum of one Humped Camel (*Camelus dromedarius*): A Histomorphology

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A histomorphological differentiation study was conducted on the jejunum of 35 foetuses (both sex) of the one-humped camel collected from the Sokoto metropolitan abattoir, over a period of five months at different gestational ages. The approximate age of the fetuses was estimated and categorised into first, second and third trimester. Gross observation of the small intestine insitu was recorded. The jejunum was characterised by having an extensive coiling in second and third trimester, with no evidence of segmental differentiation in the first trimesters. Histological observation of the tissues in this study revealed a complete structure of the tubular organ. The jejunum was found to consist of four layers namely: *Tunica mucosa, Tunica sub mucosa, Tunica muscularis and Tunica serosa*. The epithelium of the *Tunica mucosa* was stratified squamous epithelium with varying degree of stratification at first trimester and transformed to low columnar /cuboidal epithelium with prominent villi and crypt of lieberkhum at second trimester. At third trimester, the epithelium was simple columnar epithelium with prominent developed villi, microvilli, and crypt of lieberkhum in the entire tunica mucosa. The lamina propria mucosa was found absent at first trimester but prominent at second and third trimester. The *Lamina muscularis* mucosa was found prominent at third trimester but not identified at first and second trimester. At first trimester of age *tunica submucosa* was prominent while at second trimester, it consisted of connective tissue cells and fibres scattered all over the layers with preliminary blood vessels. The cells and fibres were undifferentiated at this stage. There was evidence of scattered blood vessels within the layer. At third trimester of age, the connective tissues and blood vessels were found prominent throughout the length of the jejunum. The *tunica muscularis* of camel jejunum consist of inner circular and outer longitudinal smooth muscle layers. At first trimester this layer did not differentiate into these two zones but only longitudinal orientation of smooth muscle layer. At second trimester, the layers of two zones with clear demarcation were observed. A thin layer of connective tissue comprising of undifferentiated cells lined the jejunum externally was observed in all the stages of development. Based on the above findings, it showed that development of the camels' jejunum shown an early gross and histologically differentiation compared to other segments of the intestine.

Key words: Camel, Jejunum, Embryonic differenciation, Histomorphology.

INTRODUCTION

Camels are similar to ruminants in several aspects, which include regurgitation of ingesta, and active microbial fermentation in the stomach (Frandson, 1981).The digestive anatomy and physiology of dromedarian camel at embryonic level is least understood when compared to Llama, Guanaco, Cattle, Sheep, Goat and Pig (Yagil and Ezion, 1980, Al-Tarazi, 2001; Bello *et al.*,2012). The description of dromedarian camel is usually made as if it

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Table 1: The CVRL and weight of fetuses at various trimesters (mean±SEM).

Parameters	First Trimester	Second Trimester	Third Trimester
Number of sample (N)	13	11	11
CVRL (cm)	20.06 ± 3.0	60.27 ± 4.0	103.83 ± 6.0
Fetal weight (Kg)	1.40 ± 0. 6	6.10 ± 0.5	17.87 ± 0.6

is identical with Llama specie (Bello *et al.*, 2013). Though, they are pseudo-ruminants that possess a three-chambered stomach, lacking the omasum that is part of the four-chambered stomach of the order Ruminantia (Al-Tarazi, 2001). The true camels (*Camelus dromedarius and Camelus bacterianus*) are closely related anatomically to the South American Camelids (Wilson, *et al.* 1990; Marzook, 1996; Reece, 1997; Ghaji *et al,* 1982; Adogwa, *et al.* 1987; Ghaji, *et al.* 1989; Bello *et al.*, 2013).

Research work dealing with morphology, physiology, pathology, gross and developmental anatomy of various organs and system of dromedarian camel has been carried out in many countries using foetal and adult camel (Wilson, *et al.* 1990; Marzook, 1996; Reece, 1997; Bustinza ,1999; Ghaji *et al,* 1982; Adogwa, *et al.* 1987; Ghaji, *et al.* 1989; Bello *et al.*, 2012; Hena *et al.*, 2012) but little attentions have been paid for the developmental changes of the cranial part of the small intestine of the camel fetus. Thus, paucity of information on the prenatal development of camel jejunum exists; hence the present study was undertaken to bridge the information gap.

MATERIALS AND METHODS

The study was carried out on 35 foetuses of the one-humped camel collected from the metropolitan abattoir, Sokoto using standard animal ethics approved by the government, at different gestational ages. The collected foetuses were then taken to the Veterinary Anatomy laboratory of Usmanu Danfodiyo University; where the weight and age of the foetuses were determined. The foetal body weight was measured using electrical (digital) weighing balance for the smaller foetuses and compression spring balance (AT-1422), size C-1, sensitivity of 20kg X 50g in Kilogram for the bigger foetuses. The approximate age of the foetuses was estimated by using the following formula adopted by El-wishy *et al.* (1981) and Bello *et al.* (2013):

GA = (CVRL + 23.99)/0.366,

Where GA is age in days and CVRL is the Crown Vertebral Rump Length.

Fetuses below 130 days were designated as first trimester, 131- 260 days as second trimester and 261 - 390 days as third trimester (Bello *et al.* 2013). Crown Vertebral Rump Length (CVRL) was measured (cm) as a curved line along the vertebral column from the point of the anterior fontanel or the frontal bone following the vertebral curvature to the base of the tail. Based on this, foetal samples were divided into 3 main groups as described by Bello *et al.* (2013). The digestive tract of each fetus was collected by placing the fetus on dorsal recumbency and a mid-ventral skin incision was made *via* the abdomino-pelvic region down to the thoracic, to the neck up to the inter-mandibular space in order to remove the entire digestive tract.

$1cm^2$ thick of sample from each group was collected and fixed in 10% formalin solution. After fixation was achieved, the tissue sample was processed for paraffin blocks preparation. The sections of 5µm were subjected to haematoxylin and eosin for routine morphology (Luiz and Jose, 2005). The standard sections were examined under light microscope and micrographs taken using motic cam camera with 12.1 mega pixel.

RESULTS AND DISCUSSION

The current study attempted to contribution to the developmental Anatomy of the dromedarian camel at fetal level. Result of the investigation shown that, there was an increase in the body weight, organ weight and individual segments of the small intestine in the fetuses with advancement in gestation period (Table 1). This is in agreement with the observations of Jamdar and Ema (1982), Bello *et al.* (2013), Luciano *et al.* (1979) and Sonfada (2006), who observed obvious body weight increase with advancement of gestation period in different species of animals. Bello *et al.* (2012) suggested that nutritional status and health condition of the dam played a vital role in the development of the fetus hence increase in weight of the fetus.

Grossly, the color of the small intestine was whitish at first trimester and grayish in second and third trimester. The jejunum was characterised by having an extensive coiling in second and third trimester, with no evidence of segmental differentiation in the first trimesters as shown in Plate 1. Similar findings were reported on the gross features of small intestine of various animals at different gestational ages; Llama (Smuts and Benzuidenhout, 1987; Luciano *et al.*, 1979) and nutria (Perez *et al.*, 2008a). On the other hand, the divisions were not reported in sheep (Sisson *et al.*, 1975), cattle (Dyce *et al.*, 2002) and pampas deer (Perez *et al.*, 2008a).

The coil part of the jejunum was not divided at first trimester but differentiated into five parts (descending

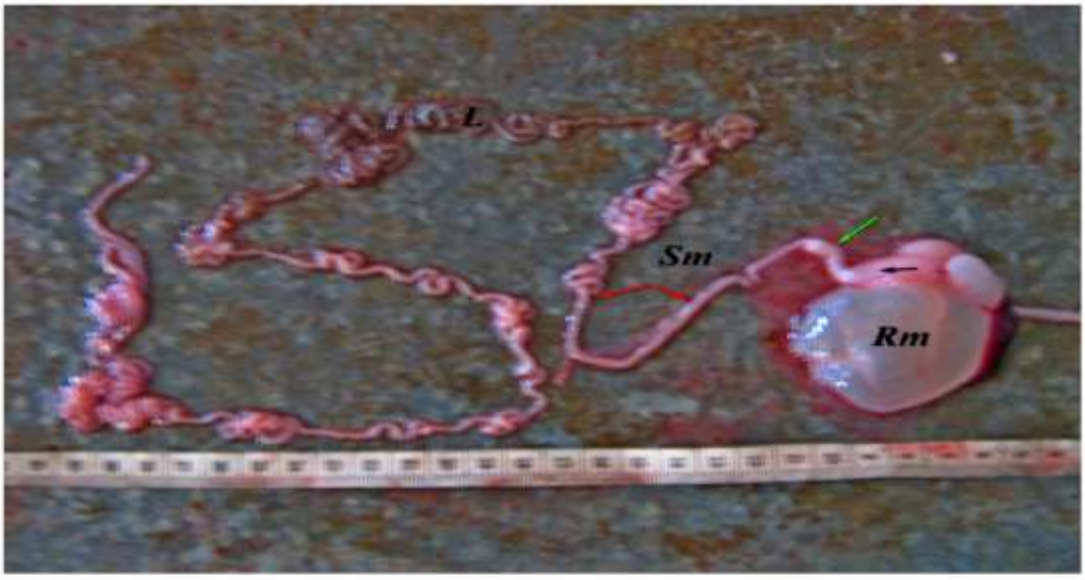

Plate I: Photograph showing the entire digestive tract of camel fetus at first trimester with no clear demarcation in the small intestine (Sm); jejunum (Red arrow), abomasum (Black arrow) and ileum (L), Ampullae (Green arrow), and rumen (Rm) 50x

Plate 2: Photograph showing the entire digestive tract of camel fetus at third trimester with clear demarcation in the small intestine; jejunum (B), jejunum (C) and ileum (D), esophagus (1) caecum (E), colon (2) and rectum (3) 50x

jejunal part, cranial jejunal flexure, transverse jejunal part, caudal jejunal flexure and ascending jejunal part) at second and third trimester as shown in plate 2. This findings agreed with previous work on Llama (Smuts and Benzuidenhout, 1987), canine specie (Perez *et al.*, 2008a), sheep (May, 1977) and feline specie (Dyce *et al.*, 2002).

The internal mucosa of the jejunum of the camel was pinkish at first trimester and grayish in color at second and third trimester, with thin longitudinal folds at the

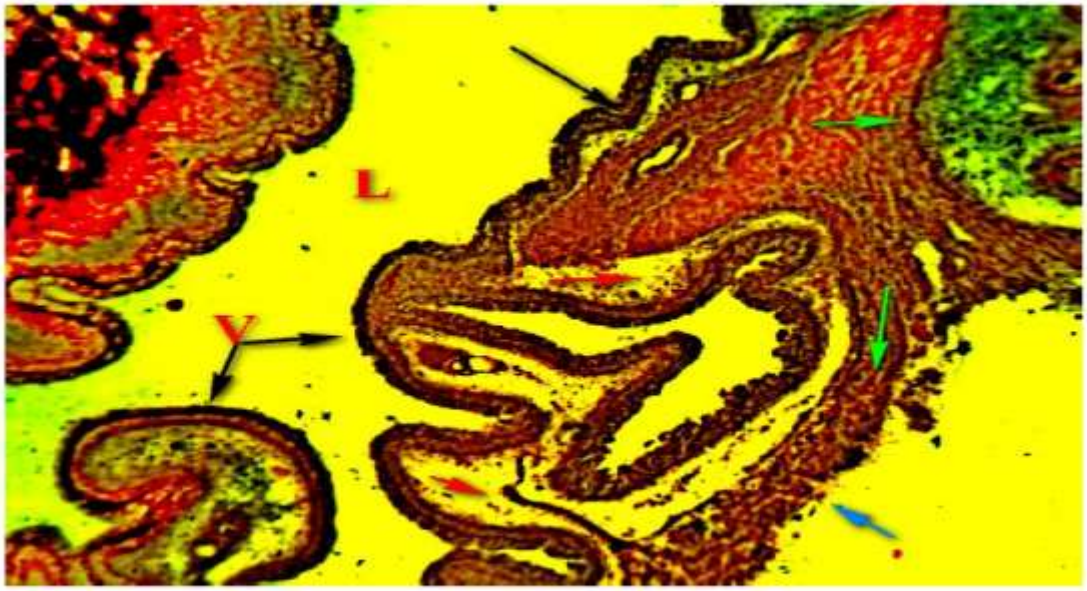

Plate 3: Transverse section of the jejunum at first trimester showing Epithelium (Tmuc), Submucosa (Tsm), tunica muscularis (Tmsc), serosa (White arrow), H & E 250x

visceral surface. This is in line with the findings of some researchers, who reported that the internal mucosa of small intestine of other domestic animals had circular folds "Plicae Circulares" at variable position (Junqueira *et al*., 1995; Dellmann and Eurell, 1998; Wilson, *et al*. 1990; Marzook, 1996; Reece, 1997; Bustinza ,1999; Ghaji *et al*, 1982; Adogwa, *et al*. 1987; Ghaji, *et al*. 1989; Bello *et al*., 2012; Hena *et al*., 2012).

At first trimester, the entire small intestine was small, straight and elliptical in shape. At second and third trimesters, the coiling of the jejunum was prominent, large and rounded in shape followed by slight portion of thin segments. The thin segment was directed craniodorsally forming the cranial and caudal flexure. The study findings agree with those reported in Llama by Smuts and Benzuidenhout, (1987) who concluded that the jejunum begins as a straight and elliptical shape and later coiling appears at variable degree and entirely situated on the entire abdominal cavity below the manubrium of the sternum at second trimester.

Histological observation of the tissues in this study revealed a complete structure of the tubular organ. The jejunum was found to consist of four layers namely: *Tunica mucosa, Tunica sub mucosa, Tunica muscularis and Tunica serosa.* The distinguishing features observed in the developmental stage at tunica mucosa were, *lamina epithalialis, lamina propria mucosa* and *lamina muscularis mucosa.* At *tunica muscularis* the divisions were inner circular muscularis layer and outer longitudinal muscularis layer. From the study, the epithelium of the *Tunica mucosa* was stratified squamous epithelium with varying degree of stratification at first trimester (plate 3) and transformed to low columnar /cuboidal epithelium with prominent villi and crypt of lieberkhum at second trimester (plate 4). At third trimester, the epithelium was simple columnar epithelium with prominent developed villi, microvilli, and crypt of lieberkhum in the entire tunica mucosa (plate 5). The lamina propria mucosa was found absent at first trimester but prominent at second and third trimester. Similar observations were seen on Llama (Heller et al., 1986), cow (Franco *et al*.), sheep (May, 1977), horse (Malie *et al*., 1987), rodent (Asari *et al*. 1985), human (Franco *et al*., 1993c), monkey (Franco *et al*., 1993a), dog (Junqueira *et al*., 1995) and cat (Schummer *et al*., 1979).The *Lamina muscularis* mucosa was found prominent at third trimester (plate 5) but not identified at first and second trimester (plate 3 and 4). The above finding showed that the development of the laminae of the camel's jejunum was in succession.

At first trimester of age *tunica submucosa* was prominent (plate 3) while at second trimester, it consisted of connective tissue cells and fibres scattered all over the layers with preliminary blood vessels (plate 4). The cells and fibres were undifferentiated at this stage. There was evidence of scattered blood vessels within the layer. At third trimester of age, the connective tissues and blood vessels were found prominent throughout the length of the jejunum (plate 5). The above findings were contrary to those of ruminant, horse and cat as reported by Schummer *et al*., (1979), which showed the presence of submucosa lymphatic nodules at the descending part, caudal jejunal flexure and transverse part region only.

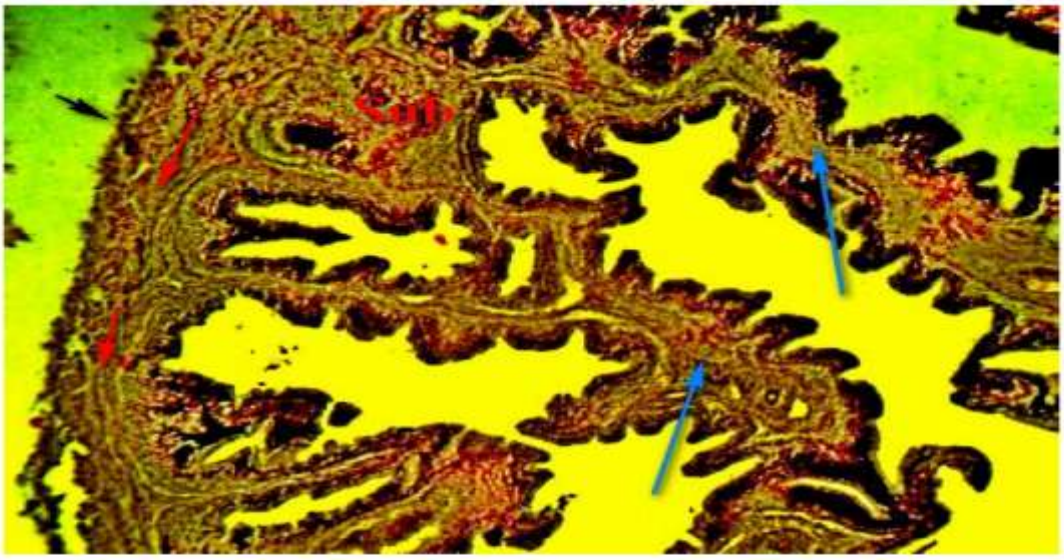

Plate 4: Transverse section of the jejunum at second trimester showing Epithelium (Tmuc), Submucosa (Tsmc), internal (circular) layer of tunica muscularis (Tm2), external (longitudinal) layer of tunica muscularis (Tm1), serosa (Tser), 400x

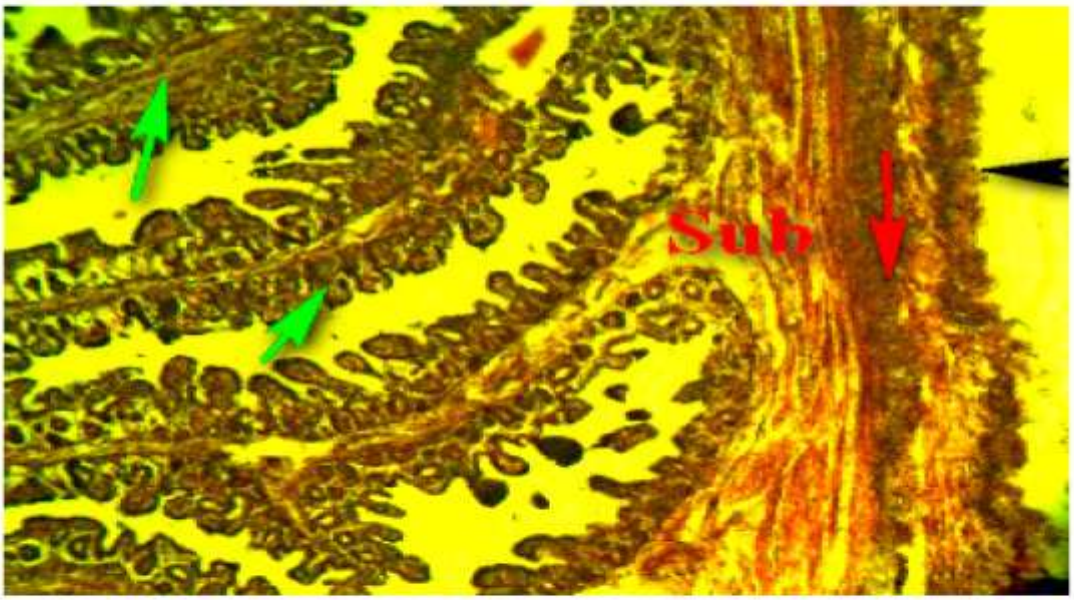

Plate 5: Transverse section of the jejunum at third trimester showing keratinized stratified Epithelium (Tmuc), Submucosa (Tsmc), internal (circular) layer of tunica muscularis (Tm1), external (longitudinal) layer of tunica muscularis (Tm2), serosa (Tser), H & E 250x

The *tunica muscularis* of camel jejunum consist of inner circular and outer longitudinal smooth muscle layers (plate 3, 4 and 5). At first trimester this layer did not differentiate into these two zones but only longitudinal orientation of smooth muscle layer (plate 3). At second and third trimester, the layers of two zones with clear

demarcation were observed (plate 4 and 5). The above finding was in conformity with that of Llama (Watrous *et al.,* 1995) goat (Getty, 1975) and buffalo foetuses (Luciano *et al.*, 1979).

A thin layer of connective tissue comprising of undifferentiated cells lined the jejunum externally was observed in all the stages of development. This was observed at first trimester and became well developed at second and third trimester of age (plate 3, 4 and 5).

CONCLUSION

The development of the camels' jejunum based on embryonic stage was characterised by having an extensive coiling in second and third trimester, with no evidence of segmental differentiation in the first trimesters. The coil part of the jejunum was not divided at first trimester but differentiated into five parts; descending jejunal part, cranial jejunal flexure, transverse jejunal part, caudal jejunal flexure and ascending jejunal part at second and third trimester. Based on the above findings, it showed that development of the camels' jejunum was both gross and histologically in succession and similar to so many domestic animals differentiation.The information obtained in this study will serve as a base-line data for the camel specie in this environment.

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НАВЧАЛЬНО-МЕТОДИЧНЕ ВИДАННЯ
(українською мовою)

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Збірник вправ для самостійної роботи з курсу

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для студентів денного та заочного відділення освітнього рівня магістр спеціальностей «Біологія» та «Генетика»

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