Flax is an important crop that produces plant fibers. The flax fibers are part of phloem and they are represented as abnormally long sclerenchyma cells that have a thick tertiary cell wall. The main compounds of the tertiary cell wall are cellulose (80-90%) and the important non-cellulosic polymer is the rhamnogalacturonan I (RG-I). We have evaluated RG-I content in the outer fibers collected from divergent selection flax types – fiber flax (cultivars Drakkar, Grant, Laska) and linseed flax (cultivars Orpheus, Lirina). We have analyzed the outer fibers isolated from the flax stems during a rapid growth period, during tertiary cell wall formation. We determined by the chromatographic methods that key buffer-extractable polymers in fibers of all analyzed samples are RG-I and arabinoxylan/arabinogalactan proteins (AGP). The retention time of RG-I polymer during gel filtration chromatography corresponded to pullulans with a molecular weight of 350-950 kDa, and the main AGP fraction was about 70 kDa. The RG-I content was approximately equal to the AGP yield in the fibers collected from fiber flax but lower in linseed outer fibers (especially in Lirina cultivar more than 2 times). The RG-I yield was, on average, 2.8 times higher in fiber flax than in linseed flax. We have also evaluated the expression level of glycosyltransferase of 92 (LusGt92-2) and 47 (LusGt47-1) families, β-galactosidase (LusBGAL) and rhamnogalacturonan lyase (LusRGL6) genes. LusGt92-2 and LusGt47-1 encode enzymes that potentially involved in biosynthesis of RG-I; LUSRGL6 and LUSBGAL modify backbone and side chains, correspondingly, of RG-I. Expression level of LusGt92-2 (Lus10038387) and LusGt47-1 (Lus10013790) was in 5.3-10.7 times higher in fiber flax outer fibers than in linseed flax. The LusBGAL (Lus10028848) and LusRGL6s (Lus10004281/Lus10019231) expression levels were also higher in fiber flax than in linseed flax (4.4-5.1 and 2.5-3.8 times correspondingly). Thus fiber flax and linen seed flax cultivars are differed in RG-I content and have different expression levels of genes that potentially involved in the metabolism of this pectin polysaccharide. This work was partially supported by the grant of the Russian Science Foundation (project 17-76-20049).

Plant proteome. Changes during ageing and under environmental stress conditions

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Proteome is a set of proteins expressed by an organism, tissue or cell at a specified moment of time. Plant proteome represents a labile system and changes with plant age or alterations of the organism’s environment. This phenomenon underlies adaptation of plants to altering environmental conditions.
internal and external conditions. Thereby, not only abundances of individual proteins (so-called protein expression), but also the patterns of post-translational modifications (PTMs) can be affected. For example, protein glycation was proposed as one of the non-enzymatic PTMs, accompanying plant ageing and response to environmental stress. To address this question, experimental models of drought, cadmium and high light stress were established with Arabidopsis thaliana, oilseed rape (Brassica napus) and pea (Pisum sativum). Thereby, physiological state of the plants was characterized with a panel of physiological and biochemical stress markers. Using the methods of bottom-up LC-MS-based in-depth proteomics and state-of-the-art bioinformatic approaches, we describe here the patterns of advanced glycation end products (AGEs) in plants, as well as their changes during plant ageing and under stress conditions. We demonstrate that accumulation of AGEs accompanies both processes, and occurs at specific protein sites – glycation hotspots. Based on structural modeling approach, we assume that site-specific glycation might affect specific protein functions. The work was supported by Russian Science Foundation (project №17-16-01042).

Биохимические изменения, индуцируемые в семенах Brassica napus L. в процессе длительного хранения и под влиянием ускоренного старения

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Семена высокого качества способны долгое время храниться без снижения функциональной активности и питательной ценности. При оптимальных условиях семена могут поддерживать жизнеспособность без потери качества в течение нескольких лет. Однако при длительном хранении (ДХ) в них происходит постепенное накопление структурных и метаболических повреждений. Этот процесс называют «старением» семян. Понимание механизмов старения семян важно для поиска маркеров при сохранении генетических ресурсов. Эффективным приемом, позволяющим в краткие сроки моделировать ДХ, является «ускоренное старение» (УС). Однако, все еще остается открытым вопрос насколько изменения, происходящие в семенах при УС, близки изменениям, происходящим в процессе ДХ. Объектом исследования являлись семена B.napus сорта Оредеж-2 из коллекции ВИР РАН. ДХ осуществлялось 4 и 9 лет при 18°C и 5%-ном влагосодержании. УС проводили путем инкубации семян при 40°C и 10%-ном влагосодержании в течение 1 и 7 суток. Контролем являлись семена со всхожестью 99%. Через 4 года хранения и 1 сутки УС всхожесть семян снижалась до 91%. Через 9 лет хранения и 7 суток УС всхожесть семян снижалась до 46%. Была проведена сравнительная оценка развития окислительного стресса в описанных выше вариантах по нарушению целостности клеточных мембран и содержанию восстановленной (GSH) и окисленной форм глутатиона (GSSG). Установлено, что в условиях УС степень повреждения мембран была в 2 раза выше, чем при ДХ. ДХ также не влияло на содержание GSH и GSSG на