Polar auxin transport provides essential directional and positional information for many developmental processes in plants. At the cellular level, it is realized by both passive diffusion and the active transport through the membrane proteins - AUX1/LAXes, PINs and ABCBs. The aim of this thesis was to characterize the role of ABCB1, ABCB4 and ABCB19 proteins in polar auxin transport using transformed tobacco BY-2 cell lines. It was shown that the plasma membrane (PM) localization of the ABCB1, 4 and 19 is not polar. The ABCB4 was also more stable on PM after the treatment with auxin influx inhibitors; making use of ABCB4-cell line helped to uncover new characteristics of markers of endocytosis – the FM-dyes. The induction of ABCB19 has led to a decrease in ^{3}H-NAA accumulation with characteristic auxin starvation phenotype, similar to PIN7 overexpressing cell line, that could be rescued in case of PIN7 cell line by application of the auxin efflux inhibitor NPA; however, the accumulation of auxin in ABCB19-overexpressing cell line was less sensitive to NPA and the rescue of the auxin starvation phenotype was ineffective. Importantly, unique property of the ABCB4 was demonstrated: It displayed dual, auxin-concentration-dependent auxin transport activity in *Arabidopsis* roots, tobacco BY-2 and yeast cells. The results suggested that the non-competitive inhibition of the ABCB4-mediated auxin efflux contributes to the herbicidal effects of 2,4-D. Besides intercellular transport, there is another process with the potential to modify auxin level, the metabolism. Auxin metabolic profiles together with data from auxin transport assays allowed mathematical modelling of auxin transport on the cellular level. It was shown that NAA is rapidly metabolized in BY-2 cells to one predominant metabolite NAA glucosyl ester that is retained in cells, thus raising intracellular concentration of NAA previously measured during auxin accumulation experiments. This might have led to underestimation of efflux carriers transport capacity for NAA as well as IAA measured in the past. The mathematical modelling using both experimental data on accumulation of auxins together with metabolic profiling is currently in progress.