

Among these retinoid-dependent genes are included for example genes for fibroblastoid growth factors 8 and 10 (Niederreither et al., 1999; Vermot et al., 2000), for Sonic hedgehog (*Shh*) and *Shh*-pathway genes (Power et al., 1999; Stratford et al., 1999), for bone morphogenetic proteins (Francis et al., 1994; Dupé et al., 1999; Niswander et al., 2000; Pizette and Niswander, 2000), and homeobox genes, namely 5' members of *Hoxd* and *Hoxa* gene clusters, which are downstream mediators of the *Shh* signal and are required for limb skeletal patterning (Small and Potter, 1993; Yokouchi et al., 1995; Carpenter et al., 1997; Goff and Tabin, 1997; Knezevic et al., 1997; Mackem and Knezevic, 1999). Some of the genes coding for bone-specific proteins (osteocalcin) and for enzymes (alkaline phosphatase) are down-regulated by RA (Cohen-Tanugi and Forest, 1998). The gene for tissue transglutaminase, which participates in apoptosis, was induced by RA (Jiang and Kochhar, 1992), and RAREs were found in the promoter of this gene (Nagy et al., 1996).

Some of the genetic factors interacting with RA in our experiments may be included among genes regulated by RA. It follows from the study of apoptosis in limb buds of rat fetuses differing in the *Lx* genotype and in the genetic background that the mutant *Lx* allele manifests itself in the phenotype, among others, by means of apoptosis (Sedmera et al., 1998). While on day 13 of development no differences were found among ND, PD and OD limb buds, on day 14 in OD hind limb buds, an apoptotic zone was found in preaxial mesenchyme, which in ND limb buds was present one day later and in PD limb buds was attenuated. It is in correlation with the present results of RA-*Lx* interaction on day 13 of development, which suggest the possibility that RA interacts with genes participating in apoptosis.

Besides the *Lx* allele, all RA-inducible genes present in the genetic background may play a role in the response to RA teratogenic influence. BN modifying genes may function as normal morphogenes, but excess of RA, the influence of the *Lx* mutant allele, or both these factors can change their expression, and consequently a malformation develops. From this it follows that searching for the polymorphism of the above-mentioned genes between BN and SHR is a promising way for uncovering the major morphogenetic steps involved in realization of the PLS phenotype. In next experiments, we will direct our attention to interstrain polymorphism of modifying genes of the genetic background, which were shown to participate in the expression of mutation or in interaction of the mutant allele with teratogenes. The system of rat congenic, double-congenic and recombinant inbred strains provides genetically defined material for this study.

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